Jahresforschungsbericht
Annual Report
2007

Leibniz-Institut für Pflanzengenetik
und Kulturpflanzenforschung

IPK GATERSLEBEN

Leibniz Gemeinschaft

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Leibniz Gemeinschaft

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Vorwort

Das abgelaufene Jahr war von einer Reihe von Ereignissen geprägt, welche die wissenschaftliche und organisatorische Weiterentwicklung des Instituts widerspiegeln. Im Vordergrund standen hierbei die Sicherung der wissenschaftlichen Leistungs- und Innovationsfähigkeit, die Stärkung bestehender Forschungsschwerpunkte, sowie der weitere Ausbau der Infrastruktur auf dem Campus.

Innovationsfähigkeit erfordert wissenschaftliche Exzellenz. Hier konnte das Institut auch im abgelaufenen Jahr wieder mit sehr guten Ergebnissen aufwarten, was unter anderem durch eine große Zahl wissenschaftlicher Veröffentlichungen und durch die Einwerbung umfangreicher Drittmittel belegt ist.

Innovationsfähigkeit erfordert auch den Aufbau und die Pflege von Kooperationen mit anderen Forschungseinrichtungen im In- und Ausland, um mit vereinter Kompetenz neuen Ideen nachzugehen und gemeinsame Projekte zu realisieren. Hier konnten mit der INRA im September erste, vielversprechende Gespräche zum Aufbau einer zukünftigen Zusammenarbeit geführt werden.

Innovationsfähigkeit bedeutet auch, wissenschaftliche Erkenntnisse in praktische Anwendungen zu überführen. Hierzu wurde im vergangenen Jahr wieder eine große Anzahl von Forschungsprojekten in Zusammenarbeit mit Einrichtungen aus dem privaten Sektor, allen voran der privaten Pflanzenzüchtung, durchgeführt. Die *Public Private Partnerships* im Rahmen des durch das BMBF geförderten Forschungsprogramms GABI-FUTURE liefern hierfür zahlreiche Beispiele.

Die Erhaltung und Nutzung pflanzengenetischer Ressourcen, eine zentrale Aufgabe des IPK, ist längst von einer nationalen zu einer internationalen Aufgabe gewachsen. In der Genbank hängt Innovationsfähigkeit daher, neben der ständigen Verbesserung der Serviceaufgaben und der Vertiefung der Forschung, auch von der effizienteren Gestaltung der internationalen Zusammenarbeit ab. Durch das Mitwirken beim Aufbau eines Europäischen Genbankverbunds für ausgewählte Kulturarten leistet das IPK seinen Beitrag zu der zunehmend wichtigen Aufgabe, den weltweiten Zugang zu pflanzengenetischen Ressourcen und ihrer umfassenden Nutzung zu sichern.

Die Zukunftsfähigkeit einer Gesellschaft beruht in hohem Maße auf dem Vertrauen ihrer Mitglieder in die Forschung. Daher pflegt das Institut den ständigen Dialog mit Vertretern aus Politik und Gesellschaft. Im Zeitalter der Wissensgesellschaft gilt es, Forschungsinhalte über die Grenzen der Fachgemeinde hinaus zu vermitteln, um umgekehrt die Unterstützung der Gesellschaft für die

Foreword

The past year was characterised by a series of events which reflect the scientific and organisational development of the Institute. In the foreground were the securing of scientific performance and innovative ability, the strengthening of existing research foci, as well as the further expansion of campus infrastructure.

Innovative ability demands scientific excellence. In this regard research at the Institute yielded a series of outstanding results in the past year, as exemplified inter alia by the large number of scientific publications and the procurement of substantial external funding.

Innovative ability also demands the expansion and nurturing of cooperation with other research institutions both at home and abroad, in order to pursue new ideas with combined expertise and to realise joint projects. Initial discussions held here with INRA in September regarding the establishment of future cooperation were very promising.

Innovative ability also means translating scientific expertise into practical applications. Once again in the last year a large number of research projects were carried out in cooperation with private sector organisations, in particular with private plant breeding companies. Multiple examples are provided by the *Public Private Partnerships* carried out within the framework of the BMBF sponsored GABI-FUTURE research programme.

The conservation and use of plant genetic resources, one of the IPK's central tasks, has long grown from a national to an international exercise. In addition to continual improvement in service provision and strengthening of research, innovative ability in the Genebank is therefore also dependant on the more efficient organisation of international cooperation. Through participation in the establishment of a European Genebank Network for selected crop species, the IPK is achieving its contribution to the increasingly important task of securing international access to plant genetic resources and their comprehensive use.

The sustainability of a society rests to a great extent on the trust placed by its members in research. Consequently the Institute cultivates continual dialogue with representatives from politics and society. In this age of knowledge-based society, it is necessary to convey research content beyond the borders of the scientific community, in order to obtain society's reciprocal support for research into important issues. In this context the Institute has been particularly actively engaged in the last year in the public debate on green gene technology, in order to con-

Erforschung wichtiger Fragestellungen zu erwerben. In diesem Zusammenhang hat sich das Institut auch im abgelaufenen Jahr besonders in der öffentlichen Diskussion zur Grünen Gentechnik engagiert, um durch Informationen aus erster Hand einen Beitrag zu Versachlichung des Meinungsaustausches zu leisten.

Diese wenigen Beispiele sollen zeigen, dass Innovationsfähigkeit am IPK kein leeres Schlagwort ist, sondern das Bekenntnis darstellt, sich täglich aufs Neue dem internationalen Wettbewerb um die besten Ideen und ihre Umsetzung zu stellen. Wie dies in dem zurückliegenden Jahr im Einzelnen gelungen ist, darüber gibt der nachfolgende Forschungsbericht Auskunft.

Andreas Graner
Geschäftsführender Direktor

tribute to the objectification of this exchange of opinions through first hand information.

These few examples should indicate that innovative ability is no empty buzz word at the IPK, rather a daily renewed commitment to face the challenges of international competition for the best ideas and their realisation. The individual details on how the Institute has succeeded in this in the past year are described in the following research reports.

Andreas Graner
Acting Director

Das Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK)

Aufgabenstellung und Finanzierung

Das IPK wurde auf der Grundlage von Vorgängereinrichtungen 1992 als eine Stiftung des öffentlichen Rechts gegründet. Es ist Mitglied der Leibniz-Gemeinschaft und firmiert seit Januar 2006 als Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung. Sein Zuwendungsbedarf wird nach dem Finanzierungsmodell der „Blauen Liste" zu gleichen Teilen von Bund und Sitzland (plus Länderanteile) erbracht. Zuwendungsgeber ist das Land Sachsen-Anhalt, vertreten durch den Kultusminister.

„Zweck der Stiftung ist die Förderung von Wissenschaft und Forschung. Ihre Aufgabe ist, grundlagen- und anwendungsorientierte Forschung auf den Gebieten der Pflanzengenetik und Kulturpflanzenforschung zu betreiben. Ihre wissenschaftlichen Schwerpunkte liegen insbesondere auf der Erarbeitung neuer Erkenntnisse über Struktur, Funktion und Evolution des Erbmaterials, auf der Erhaltung, Erforschung und Erschließung der erblichen Vielfalt von Kulturpflanzen, ihrer Vorfahren und Verwandten sowie auf Beiträgen zur Züchtungsgenetik im Vorfeld der praktischen Pflanzenzüchtung. Ein wesentliches Anliegen der Stiftung ist die interdisziplinäre Zusammenarbeit der verschiedenen in ihr vertretenen biologischen Fachrichtungen." (zitiert aus der IPK-Satzung)

Stiftungsorgane, Funktionsträger und Organisationsstruktur des IPK

Organe der Stiftung sind der **Stiftungsrat**, das **Direktorium** und der **Wissenschaftliche Beirat** sowie als Unterausschuss des Wissenschaftlichen Beirates der **Genbank-Beirat**. Die personelle Zusammensetzung der Beiräte im Berichtsjahr ist in einer Übersicht auf S. 221 dargestellt. Die Übersicht führt zudem die IPK-Mitarbeiterinnen und Mitarbeiter auf, die mit speziellen Funktionen innerhalb des IPK betraut waren und sind.
Das IPK ist in die vier wissenschaftlichen Abteilungen Genbank, Cytogenetik und Genomanalyse, Molekulare Genetik, Molekulare Zellbiologie und die Abteilung Verwaltung und Zentrale Dienste gegliedert. Innerhalb der Abteilungen bestehen relativ selbstständige Arbeitsgruppen (s. Organigramm, innere Umschlagseite), die durch Einwerbung von Drittmitteln ihre Personal- und Forschungsmittelausstattung wesentlich erweitern (s. Drittmittelübersicht, S. 201 ff.). Die Abteilungen Genbank sowie Cytogenetik und Genomanalyse sind in drei bzw. zwei Bereiche untergliedert, die jeweils mehrere Arbeitsgruppen themengebunden zusammenfassen (s. Organigramm, innere Umschlagseite). Als abteilungsübergreifender Verbund

The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Objectives and Funding

The IPK was formally re-established in 1992 as a Foundation under Public Law, continuing an unbroken tradition reaching back to the Kaiser-Wilhelm-Institute of Crop Plant Research, which was founded in 1943 near Vienna and moved to Gatersleben in 1945. It is administered under the legal and administrative supervision of the State of Saxony-Anhalt, with half of its funding provided by the Saxony-Anhalt Ministry of Education and Cultural Affairs (along with contributions from other German States), and half by the Federal Ministry of Education and Research.

The Institute's statutes state: *"The mission of the Foundation is the advancement of science and research. Its goals are to carry out basic and application-oriented research in the fields of plant genetics and crop plant research. Special emphasis is given to the generation of new knowledge on the structure, function and evolution of genetic material, on the preservation, research and use of the biodiversity of crop plants and their wild relatives, as well as contributions to applied genetics relevant to crop breeding. A major concern of the Foundation is to encourage interdisciplinary cooperation of the various biological disciplines in the Institute."* (translated from the German original)

Boards, Staff with Functional Responsibilities and Organisational Structure of the IPK

The organisational bodies of the Foundation are the **Governing Council**, the **Board of Directors** and the **Scientific Advisory Board** with its subcommittee, the **Genebank Advisory Board**. Members of these bodies are listed on p. 221. In addition, the list includes all IPK staff members with specific functional responsibilities.

The Institute consists of four scientific departments Genebank, Cytogenetics and Genome Analysis, Molecular Genetics and Molecular Cell Biology, as well as the department Administration and Central Services. Each scientific department is organised into a number of relatively independent research groups, whose activities are heavily dependent on attracting additional research funding at the national and international level. The Genebank and Cytogenetics and Genome Analysis departments are further divided into, respectively, three and two Programmes, each of which brings together several research groups

mit spezieller Aufgabenstellung fungiert das **Pflanzengenom-Ressourcen-Centrum (PGRC, S. 142)**. Darüber hinaus werden die Forschungs- und Entwicklungsarbeiten auf dem Gebiet der **Bioinformatik** abteilungsübergreifend koordiniert (s. S. 144).

Forschungskonzept

Die strategische Ausrichtung der Forschungsarbeiten am Institut ist in einer jährlich aktualisierten Programmplanung festgelegt, die folgende Programmthemen umfasst:

1. **Management, Analyse und Evolution pflanzengenetischer Ressourcen** (Abteilung Genbank)
2. **Cyto-molekulare Genomanalyse** (Abteilung Cytogenetik und Genomanalyse)
3. **Molekulare Entwicklungsphysiologie** (Abteilung Molekulare Genetik)
4. **Angewandte Zellbiologie** (Abteilung Molekulare Zellbiologie).

Die Programmthemen spiegeln in wesentlichen Zügen die sich komplementierenden zentralen Arbeitsfelder der Abteilungen wider und werden in den einführenden Abteilungskapiteln näher spezifiziert.

Im Rahmen der genannten, weitgehend disziplinär ausgerichteten Forschungsprogramme werden Beiträge zu drei großen Schwerpunkten erarbeitet:

(a) **Diversitätsforschung**, die zunehmend die an Modellarten wie *Arabidopsis* und Reis gewonnenen Erkenntnisse nutzt, um die genetischen Grundlagen der enormen Vielfalt pflanzlicher Formen und Leistungen zu verstehen, gleichzeitig aber auch das Verständnis evolutiver Vorgänge fördert, um aus beiden Erkenntnissträngen Handlungsanweisungen für eine bessere Nutzung pflanzengenetischer Ressourcen zu gewinnen;
(b) Forschung zur **Dynamik pflanzlicher Genome**, die das Bild von der Starrheit der Genome zunehmend ändert und insbesondere die Rolle epigenetischer (bedingt vererbbarer, nicht auf DNA-Sequenzebene wirkender) Prozesse erhellt, deren Kenntnis mehr und mehr praktische Bedeutung gewinnt und
(c) systembiologisch orientierte Forschung zur **integrativen Biologie pflanzlicher Leistungen**, die aus der Fülle der mit neuen Methoden gewonnenen Daten versucht, systematische Zusammenhänge zu entwickeln, diese längerfristig zu modellieren und daraus ein neues Verständnis des komplexen Systems Pflanze zu gewinnen.

Im Zentrum der Arbeiten stehen Kulturpflanzen, doch arbeiten einige Gruppen auch mit der Modellpflanze *Arabidopsis* und nicht-pflanzlichen Organismen, wie zum Beispiel mit Hefe in der Abteilung Molekulare Zellbiologie und mit Säugerstammzellen in der Abteilung Cytogenetik und Genomanalyse. Als Resultat strategischer Überlegungen und eines koor-

according to their research areas (see the organisational schema on the inside back cover). The **Plant Genome Resources Centre (PGRC, p. 142)** performs tasks relevant to all departments. Regarding bioinformatics, research and service activities in the different departments are coordinated via the **IPK Bioinformatics Platform (p. 144)**.

Research Mission

The strategic development of the research programme is outlined in a budgeted programme that is updated annually. It presently comprises the following fields:

1. **Management, Analysis and Evolution of Plant Genetic Resources** (Genebank)
2. **Cyto-molecular Genome Analysis** (Cytogenetics and Genome Analysis)
3. **Molecular Physiology of Development** (Molecular Genetics)
4. **Applied Cell Biology** (Molecular Cell Biology).

Details are described in the relevant departmental reports.

The research fields contribute to three priority themes of contemporary plant research, which are outlined in the strategic research agenda of the IPK as follows:

(a) **CropPlant Diversity**, which is increasingly drawing on the knowledge gained from model plants such as *Arabidopsis thaliana* and rice, to understand the genetic basis of the diversity of plant form and function and its evolutionary origin. This knowledge can translate into improved approaches to use plant genetic resources;
(b) **Dynamics of Plant Genomes**, which is increasingly challenging the conventional static picture of the genome and is leading to a realisation of the importance of epigenetic processes. This knowledge is becoming of increasing practical significance;
(c) **Integrative Biology of Plant Performance**, which strives to generate a holistic understanding of plants based on multi-disciplinary investigation, incorporating a strong component of bioinformatics with a long-term goal of process modelling, i.e. pursuing a systems biology approach.

Although the major focus is on crop plants, model plants such as *Arabidopsis thaliana* are also being exploited by several research groups, while two groups exploit non-plant organisms: yeast in the Department of Molecular Cell Biology, and mammalian stem cells in the Department of Cytogenetics and Genome Analysis. Flowing from a strategic decision and the major commitment of many IPK researchers, barley is being developed as the direct model for the Triticeae cereals, which include, in addition to barley, both wheat and rye. This has led, in recent years, to a large number of projects in the area of barley

dinierten Engagements vieler Forscher am IPK wird die Gerste als direktes Modell für die Triticeae-Getreide entwickelt. Dies führte in den vergangenen Jahren zu einer beträchtlichen Anzahl an Projekten zur Genetik und Genomstruktur/-funktion der Gerste, die bereits viele wichtige Erkenntnisse erbrachten. Hervorzuheben ist in diesem Zusammenhang die Option, Resultate der Gerste direkt auf den Weizen, als eine der weltweit wichtigsten Kulturpflanzen, übertragen zu können.

Integrative Strukturen

Das 1997 gegründete **Pflanzengenom-Ressourcen-Centrum (PGRC)** bildet weiterhin die integrierte Forschungs- und Dienstleistungsplattform für die Genomforschung, insbesondere an Gerste.

Um nach dem Auslaufen des vom BMBF über einen Zeitraum von fünf Jahren geförderten Bioinformatik Centrums Gatersleben-Halle die Abstimmung der fünf innerhalb der **IPK-Bioinformatik-Plattform** angesiedelten Arbeitsgruppen zu fördern, wurde Ende des Jahres im Rahmen einer gemeinsamen Berufung mit der Martin-Luther-Universität Halle-Wittenberg die Stelle eines Bioinformatik-Koordinators besetzt.

Das 2003 gegründete **Europäische Genomforschungs-Netzwerk Gerste (BarleyGenomeNet – BGN)** ist ein Zusammenschluss von Forschungseinrichtungen, welche sich schwerpunktmäßig mit der Genomforschung bei Gerste befassen. Im Jahr 2007 trat mit dem Parco Tecnologico Padano (PTP) in Lodi (Italien) der achte Partner dem Netzwerk bei. Mitglieder des BarleyGenomeNet kooperieren gegenwärtig im Rahmen von zwei EU-Verbundprojekten, die im Rahmen der ERA-PG (European Research Area-Plant Genomics) gefördert werden. Für 2008 ist ein Antrag für ein Marie-Curie-Netzwerk geplant. Weitere Einzelheiten sind unter www.barleynet.org zu finden.

Das **International Barley Sequencing Consortium** (IBSC, http://barleygenome.org) wurde im Dezember 2006 gegründet. Das Ziel ist die Totalsequenzierung des Gerstengenoms. Basierend auf einer unter den acht Mitgliedsinstitutionen aus sechs Ländern abgestimmten Forschungsagenda werden erste Forschungsprojekte durch das BMBF (GABI-FUTURE) und die DFG (ERA-PG) gefördert.

Das IPK gehört dem Forschungsnetzwerk **PlantMetaNet** an. Hierbei handelt es sich um einen Verbund aus den Leibniz-Instituten IPK und IPB, Halle, sowie den Max-Planck-Instituten in Golm und Jena zur Forschung auf dem Gebiet des pflanzlichen Stoffwechsels.

Ergänzend zu den genannten Plattformen und Verbünden gibt es ein umfangreiches Netzwerk von nationalen und internationalen Verbundprojekten sowie arbeitsgruppen- und abteilungsübergreifenden IPK-internen Projekt-Kooperationen (s. dazu die Abschnitte „Collaboration" in den Berichten der Arbeitsgruppen).

genetics and genomics, and these are seen to be paving the way to important discoveries. The expectation is that many of these will be readily transferable to wheat, one of the most important food crops on the planet.

Integrative Structures and Networks

The **Plant Genome Resources Centre (PGRC)**, established in 1997, continues to provide an integrated research and service platform for genome research, with special emphasis on barley.

Research into bioinformatics is being performed in close collaboration with the experimental groups within the different departments. To coordinate the research and service activities within the **IPK Bioinformatics Platform**, a coordinator was appointed in 2007 in the context of a joint appointment with the Martin Luther University Halle-Wittenberg.

The **European Barley Genomic Research Network** (BarleyGenomeNet, BGN) was founded in 2003, and represents a consortium of presently eight institutions, focussing on genome research of barley. In 2007 the Parco Tecnologico Padano (PTP) in Lodi (Italy) joined the network as eighth member. BGN partners presently collaborate within two EU projects, which are funded through the ERA-PG (European Research Area-Plant Genomics). Further information can be retrieved from the BGN website (www.barleynet.org).

In late fall of 2006, IPK scientists initiated the foundation of the **International Barley Sequencing Consortium** (IBSC, http://barleygenome.org). The consortium presently comprises eight members from six countries and aims at generating a full genome sequence of barley. Based on a commonly agreed research agenda, first proposals have been funded by BMBF (GABI-FUTURE) and the EU (ERA-PG).

IPK is a member of **PlantMetaNet,** which is a research network to foster coordinated research activities into plant metabolism. The network includes two Leibniz Institutes (IPB in Halle and IPK) and the two Max Planck Institutes (Golm MPI-MPP and Jena MPI-CE).

In addition to the platforms and networks mentioned above, there is an extensive network of collaborations within the institute across research groups and departments. In addition, numerous national and international collaborations are being maintained, as detailed in the individual reports of the research groups under the heading "Collaboration".

Das Institut im Jahr 2007

Die nachfolgenden Abschnitte sollen dem Leser einen Überblick zu den wichtigsten Entwicklungen des vergangenen Jahres liefern. Weitere Informationen zu den Forschungsarbeiten sind den Berichten der Abteilungen und der einzelnen Arbeitsgruppen zu entnehmen.

Organisatorische Veränderungen

Seit der Neugründung im Jahre 1992 stand Prof. Ulrich Wobus dem IPK als wissenschaftlicher Direktor vor. Anlässlich seines 65. Geburtstags übergab er die Amtsgeschäfte zum 1. April 2007 an seinen Nachfolger, Prof. Andreas Graner. In den 15 Jahren seiner Tätigkeit als Institutsleiter hat Prof. Wobus die Erfolgsgeschichte des Instituts vielfältig geprägt. Seine Verabschiedung als Geschäftsführender Direktor und die Amtseinführung seines Nachfolgers erfolgten im Rahmen einer feierlichen Festveranstaltung, an der über 200 Gäste aus Forschung, Politik und Wissenschaft teilnahmen. Für seine vielfältigen Verdienste in Wissenschaft, Gesellschaft und Kultur wurde Prof. Wobus vom Kultusminister des Landes Sachsen-Anhalt, Prof. Jan-Hendrik Olbertz, das Bundesverdienstkreuz am Bande überreicht (s. Fig. 1).

The Institute in 2007

The following section should provide the reader with an overview of the most important developments in the last year. Further information on research is provided in the department and individual research group reports.

Organisational changes

Prof. Ulrich Wobus led the IPK as scientific director from the re-establishment of the Institute in 1992. On the occasion of his 65th birthday, he has handed over, as of 1st April 2007, this official function to his successor, Prof. Andreas Graner. In the 15 years of his activity as institute director, Prof. Wobus has shaped the success story of the Institute like no other. His farewell as Acting Director and the inauguration of his successor were carried out in a celebratory event, attended by over 200 guests from research, politics and science. For his diverse services in science, society and culture, Prof. Wobus was awarded the Cross of the Order of Merit of the Federal Republic of Germany, presented to him by the Minister of Education and Cultural Affairs of Saxony-Anhalt, Prof. Jan-Hendrik Olbertz (see Fig. 1).

Fig. 1: Der Kultusminister von Sachsen-Anhalt, Prof. Jan-Hendrik Olbertz (r.), überreichte Prof. Ulrich Wobus das Bundesverdienstkreuz./ The Minister of Education and Cultural Affairs of Saxony-Anhalt, Prof. Jan-Hendrik Olbertz (r.), presents the Cross of the Order of Merit of the Federal Republic of Germany to Prof. Ulrich Wobus. Der Vorsitzende des Stiftungsrates, MinDirig Dr. Joachim Welz (r.), übergab symbolisch die Institutsführung an Prof. Andreas Graner (l.) (Fotos: B. Schäfer)./ The Chairman of the Governing Board, MinDirig Dr. Joachim Welz (r.), handed the direction of the institute symbolically to Prof. Andreas Graner (l.) (Photos: B. Schäfer).

Im abgelaufenen Jahr wurden zwei Mitarbeiter an die Martin-Luther-Universität Halle-Wittenberg berufen: Prof. Ivo Große, der Leiter der Arbeitsgruppe Plant Data Warehouse, nahm einen Ruf auf die W2-Professur „Bioinformatik" an. Prof. Falk Schreiber hat im Rahmen einer gemeinsamen W2-Berufung mit der Martin-Luther-Universität Halle-Wittenberg, neben der Leitung seiner Arbeitsgruppe Pflanzenbioinformatik, die institutsweite Koordination der wissenschaftlichen Bioinformatik am IPK übernommen.
Ende Oktober lief nach über fünf Jahren die BMBF-Förderung des Bioinformatik Centrums Gatersleben-Halle (BIC-GH) aus. Mit dem Projekt wurde ein wesentlicher Beitrag zum Auf- und Ausbau einer leistungsfähigen Bioinformatik am IPK geleistet. Daher wird ein Großteil der mit diesem Projekt angelegten Strukturen und Entwicklungen in Zukunft im Rahmen haushaltsfinanzierter Maßnahmen fortgeführt. Weitere Verstärkung erfuhren die Forschungsarbeiten im Bereich Bioinformatik durch die Einrichtung einer mit Landesmitteln geförderten Nachwuchsgruppe Dateninspektion (Leiter: Dr. Marc Strickert). Im Rahmen des GABI-Programms wurde die Projektgruppe Hybridweizen (Leiter: Dr. Mario Gils) als neue Arbeitsgruppe an der Abteilung Molekulare Genetik etabliert.

Entwicklungen von zentraler Bedeutung

(1) Auch in der 3. Förderrunde des BMBF-Programms zur Genomforschung im biologischen System Pflanze (GABI-FUTURE) konnte sich das IPK erfolgreich platzieren und als erfolgreichste Forschungseinrichtung abschneiden. Wissenschaftler/-innen des Instituts sind mit insgesamt 12 Projekten an dem Programm beteiligt, davon werden 7 Verbundprojekte am IPK koordiniert. Besonders hervorzuheben ist hierbei, stellvertretend für alle, das mit einem Gesamtvolumen von 6 Mio. EUR geförderte Verbundprojekt „Exploring the Barley Genome" (BARLEX). Zusammen mit den Partnern am Leibniz-Institut für Altersforschung – Friedrich-Lipmann-Institut in Jena, dem Munich Information Center for Protein Sequences und dem Julius Kühn Institut in Quedlinburg werden in diesem Projekt wichtige Beiträge zu Genomsequenzierung bei Gerste erarbeitet.
Auch im dritten Jahr in Folge war das Institut mit dem Antrag „Etablierung einer Plattform zur Kartierung und Klonierung für quantitativ vererbte, agronomisch bedeutsame Eigenschaften der Gerste und des Weizens" bei der Einwerbung von Projektmitteln aus dem Pakt für Forschung und Innovation erfolgreich. Auf EU-Ebene wurden jeweils zwei Projekte begonnen, die über das Förderprogramm für Genetische Ressourcen (GEN RES) und das Förderprogramm ERA-PG finanziert werden.
Ein vollständiger Überblick zur Drittmitteleinwerbung kann der Aufstellung auf S. 201 ff. entnommen werden.

(2) Mit der Zertifizierung des Qualitätsmanagements in den Abteilungen Genbank sowie Verwaltung und Zen-

In the past year two employees have been appointed professors at the Martin Luther University Halle-Wittenberg. Prof. Ivo Große, leader of the research group Plant Data Warehouse, accepted a position as W2-Professor of "Bioinformatics". Prof. Falk Schreiber has accepted, in the context of a joint W2-position with the Martin Luther University Halle-Wittenberg and in addition to his research group Plant Bioinformatics, the Institute-wide coordination of scientific bioinformatics at the IPK.

The five-year BMBF funding of the Bioinformatics Centre Gatersleben-Halle (BIC-GH) ended in October. This project achieved a significant contribution to the establishment and expansion of effective bioinformatics at the IPK. Consequently a large part of the structures and developments established by this project will be continued in the future through internal funding. Research in the field of bioinformatics is further strengthened by the establishment of a state-funded junior research group Data Inspection (Head: Dr. Marc Strickert). In the Molecular Genetics Department a new research group Hybrid Wheat (Head: Dr. Mario Gils) has been established within the scope of the GABI-Programme.

Developments of central importance

(1) In the third funding round of the BMBF-Programme for genome research in the plant biological system (GABI-FUTURE), the IPK was once again fruitful and ranked as the most successful research institution. Institute scientists are involved in a total of 12 projects in the programme and coordinate 7 joint projects. Representing all others exemplary, the joint project "Exploring the Barley Genome" (BARLEX), with a total amount of 6 million euro, may be particularly highlighted here. Important contributions towards sequencing the genome of this crop plant will be provided in collaboration with partners from the Leibniz Institute for Age Research – Fritz Lipmann Institute in Jena, the Munich Information Center for Protein Sequences, and the Julius Kühn Institute in Quedlinburg.

The Institute was also successful for the third year running in obtaining project funding through the Joint Initiative for Research and Innovation with the proposal "Establishing a platform for mapping and cloning quantitatively inherited, agronomically important characteristics in barley and wheat".

At the EU level, two projects were started in each of the funding programmes GEN RES (for genetic resources) and ERA-PG. A complete overview of third-party funding achievements can be seen in the table on page 201 ff.

(2) An important step towards further improvement of conservation management in the Genebank, as well as long-term retention of the knowhow of individual employees, was taken in May through the quality manage-

trale Dienste nach DIN EN ISO 9001:2000 konnte im Mai ein wichtiger Schritt zur weiteren Verbesserung des Erhaltungsmanagements an der Genbank sowie zur langfristigen Sicherung des *Know-hows* der einzelnen Mitarbeiter/-innen getätigt werden. Mit der erfolgreichen Zertifizierung des Qualitätsmanagements zählt die Genbank zu den weltweit führenden Einrichtungen ihrer Art.

(3) Die im Jahr 2006 begonnenen Bauarbeiten zum Umbau des ehemaligen Physikgebäudes zur Aufnahme der Bibliothek wurden abgeschlossen. Seit Mai 2007 steht die Bibliothek in den neuen Räumlichkeiten sowohl für die Mitarbeiter des IPK als auch für externe Nutzer zur Verfügung. Ebenfalls Mitte des Jahres wurde mit dem Umbau des zentralen Hörsaalgebäudes in der ehemaligen Bibliothek in ein zentral auf dem Campus angesiedeltes Kommunikationszentrum mit Hörsaal und Kantinenbetrieb begonnen.

(4) Aufgrund des breiten öffentlichen Interesses an dem in der Vegetationsperiode 2006/2007 auf dem IPK-Gelände durchgeführten Freisetzungsversuch an Weizen, zur Erhöhung des Protein- und Stärkegehalts im Korn (s. auch S. 101), wurde die Presse- und Öffentlichkeitsarbeit verstärkt. In der Öffentlichkeit geäußerte Bedenken hinsichtlich einer von dem Freisetzungsversuch ausgehenden Gefährdung der Vermehrungsbestände der Genbank wurden vom Genbank-Beirat in einer schriftlichen Stellungnahme als unbegründet erachtet.

Die Arbeit der Gremien

Der **Wissenschaftliche Beirat** und **der Genbank-Beirat** nahmen am 22. und 23. Oktober 2007 gemeinsam am Institutstag teil. In diesem Jahr wurden die Forschungsarbeiten in den Abteilungen Molekulare Genetik und Molekulare Zellbiologie durch den Wissenschaftlichen Beirat begutachtet. Die Sitzungen der beiden Gremien fanden am 23. (Genbank-Beirat) und 24. Oktober (Wissenschaftlicher Beirat) statt. Der Wissenschaftliche Beirat bescheinigte dem Institut auch in diesem Jahr ein hohes Niveau der wissenschaftlichen Arbeiten, welches sich auch in einer entsprechenden Publikationstätigkeit widerspiegelt.

Die Sitzung des **Stiftungsrates** wurde am 25. Oktober 2007 unter der Leitung des Vorsitzenden, MinDirig Dr. Joachim Welz, einberufen. Im Mittelpunkt der Besprechungen standen die Fortführung des Programmbudgets, Planungen zum weiteren Ausbau der Gewächshaus- und Klimakammerkapazitäten, die Beschaffung von Großgeräten sowie die weiteren Planungen zur Nachbesetzung der Stelle des Administrativen Leiters in 2009 (Nachfolge von Bernd Eise).

ment certification of the Genebank and the Administration and Central Services departments in accordance with the DIN EN ISO 9001:2000 standard. With this successful quality management certification, the Genebank is one of the leading institutions of its kind worldwide.

(3) The construction work begun in 2006, to convert the former Physics building to house the library, was finished. The library has been open for the use of IPK employees and visitors in its new accommodation since May 2007. Likewise in the middle of the year, construction work was started to convert the central auditorium of the former library building into a new communication centre with auditorium and cafeteria.

(4) Press and public relations efforts were strengthened in the light of broad public interest in field trials of transgenic wheat to increase protein and starch content in the grain (see also page 101) carried out in the growing period 2006/2007 on the premises of IPK. Publicly expressed concerns regarding the danger of these open field experiments to the reproductive collections of the Genebank were deemed to be unfounded by the Genebank Advisory Board in a written statement.

The activities of the advisory boards

The **Scientific Advisory Board** and **the Genebank Advisory Board** took part in the Institute Day events on 22 and 23 of October. This year the research activities in the Departments of Molecular Genetics and Molecular Cell Biology were appraised by the Scientific Advisory Board. The sessions of the two boards took place on 23rd October (Genebank Advisory Board) and 24th October (Scientific Advisory Board). The Scientific Advisory Board attested to the high level of scientific achievement, as reflected also in a corresponding number of scientific publications.

The **Governing Board** session was convened on 25th October 2007 by its chairperson, MinDirig Dr. Joachim Welz (of Ministry of Education and Cultural Affairs of the Federal State of Saxony-Anhalt). Discussions focussed on the continuation of the programme budget, plans for further expansion of greenhouse and climatic chamber capacities, the procurement of large equipment, as well as further plans for the filling of the post of administrative director (the successor to Bernd Eise).

Symposia and conferences

The 3rd International Conference on Apomixis, which took place simultaneously with the 9th Gatersleben Research Conference, from 27th June to 2nd July in Wernigerode, was a particular highlight of the year. During a workshop in the run-up to the conference, PhD candidates from various EU member states had the opportunity to present

Symposien und Tagungen

Ein besonderer Höhepunkt des Jahres war die 3rd International Conference on Apomixis, die gleichzeitig als 9th Gatersleben Research Conference vom 27. Juni bis 2. Juli in Wernigerode veranstaltet wurde. Während eines Workshops im Vorfeld der Konferenz nutzten Doktoranden aus verschiedenen EU-Mitgliedsländern die Möglichkeit, ihre Forschungsarbeiten vorzustellen. Die Konferenz stieß mit etwa 130 Teilnehmern aus 20 Ländern auf reges Interesse (s. Fig. 2).

At the conclusion of the funding period for the BMBF-funded Bioinformatics Centre Halle-Gatersleben a final symposium "Plant Bioinformatics – A BIC-GH-Symposium" was held on 24th and 25th September 2007 at the Martin Luther University Halle-Wittenberg. Scientists from the BIC-GH presented their results and discussed these with guests from science and industry.

Fig. 2: Teilnehmer der 3. Apomixis-Konferenz, die vom 27. Juni bis 2. Juli in Wernigerode von IPK-Wissenschaftlern als Gatersleben Research Conference organisiert wurde, beim Besuch des Institutes am 30. Juni 2007 (Foto: H. Ernst)./ Guests of the 3rd Apomixis conference, organised by IPK scientists from 27th June to 2nd July in Wernigerode, in the frame of the Gatersleben Research Conference, visited the Institute on 30th June 2007 (Photo: H. Ernst).

Zum Abschluss der Förderperiode des BMBF-geförderten Bioinformatik Centrum Gatersleben-Halle wurde ein Abschlusssymposium „Plant Bioinformatics – A BIC-GH-Symposium" am 24. und 25. September an der Martin-Luther-Universität Halle-Wittenberg veranstaltet. Wissenschaftler des BIC-GH stellten ihre Ergebnisse vor und diskutierten diese mit Gästen aus Wissenschaft und Wirtschaft.

Im vergangenen Jahr fand die 3. Plant Science Student Conference vom 5. bis 8. Juni erstmals außerhalb des IPK am Leibniz-Institut für Pflanzenbiochemie (IPB) in Halle statt. Mit Doktoranden der Max-Planck-Institute aus Jena und Golm sowie dem IPB bot sich den Doktoranden die Möglichkeit eines intensiven Austausches über die verschiedenen Arbeiten auf dem Gebiet der Pflanzenforschung.

The third Plant Science Student Conference took place on 5th to 8th June last year, for the first time outside of the IPK, at the Leibniz Institute of Plant Biochemistry (IPB) in Halle. Doctoral candidates from the Max Planck Institutes in Jena and Golm as well as from the IPB were also there to make use of the opportunity for intense communication over diverse activities in the field of plant research.

Ausbildung, Zusammenarbeit mit Universitäten und das IPK-Doktorandenprogramm

Wissenschaftler des Instituts führten Lehrveranstaltungen an oder in Zusammenarbeit mit den Universitäten Halle-Wittenberg, Potsdam, Kassel, Jena, Magdeburg und Greifswald sowie der Hochschule Anhalt an den Standorten Bernburg und Köthen fort. Daneben boten

Training, cooperation with universities, and the IPK PhD programme

IPK scientists continued to teach courses at or in cooperation with the Universities of Halle-Wittenberg, Potsdam, Kassel, Jena, Magdeburg, and Greifswald, as well as the Anhalt University of Applied Sciences at its campuses in Bernburg and Köthen. In addition scientists offered courses and internships for university students at the IPK. During the year a total of 20 Masters/Diploma theses and three PhD theses were completed. Details of the research topics can be found in the individual research group reports.

The PhD programme established at the IPK is actively organised by the "Student Board". Activities included events in the PhD seminar series, the invitation of exter-

Wissenschaftler Kurse und Praktika für Studierende am IPK an. Im Laufe des Jahres wurden insgesamt 20 Master-/Diplomarbeiten und drei Doktorarbeiten abgeschlossen. Einzelheiten zu den bearbeiteten Themen sind den Berichten der einzelnen Arbeitsgruppen zu entnehmen.

Das am IPK etablierte Doktorandenprogramm wird durch das „Student Board" aktiv geführt. Zu den Aktivitäten zählten die Veranstaltungen in der Reihe der Doktorandenseminare, Einladungen von externen Wissenschaftlern für Seminarvorträge und die Überarbeitung und Einbettung der Webseiten des Doktorandenprogramms im Rahmen der Neugestaltung der Institutsseiten.

Öffentlichkeitsarbeit und öffentliche Wirkung

Die Ergebnisse der Forschungsarbeiten am IPK wurden in 136 wissenschaftlichen Publikationen, darunter Originalarbeiten, Übersichtsarbeiten, Buchbeiträge und Dissertationen veröffentlicht. Weiterhin präsentierten die Wissenschaftler/-innen ihre Ergebnisse in einer Vielzahl von Vorträgen, auf Postern sowie über das Internet. Neben diesen wissenschaftlichen Veröffentlichungen wurde die breite Öffentlichkeit mit elf Presseinformationen über aktuelle Entwicklungen am Institut und dem Biotechnologie-Campus informiert.

Im Rahmen der Öffentlichkeitsarbeit wurden im Jahr 2007 insgesamt 76 Besucherführungen in Gatersleben bzw. in den beiden Außenstellen der Genbank durchgeführt.

Die öffentliche Diskussion über den Versuchsanbau transgener Weizenpflanzen auf dem Gelände des IPK hat das Institut zu Beginn des Jahres 2007 in das Zentrum der Debatte zur Grünen Gentechnik in Deutschland gerückt. Insbesondere die kontroverse Debatte über die Koexistenz

Fig. 3: Vertreter der CDU/CSU-Bundestagsfraktion und Mitglieder des Ausschusses für Umwelt, Naturschutz und Reaktorsicherheit sowie der CDU-Fraktion des Landtages besuchten am 25. Juni 2007 das IPK, um sich vor Ort über den Freilandversuch zu genetisch neuem Winterweizen zu informieren (Foto: H. Ernst)./ Representatives of the CDU/CSU parliamentary group and members of the Parliamentary Committee for Environment, Ecology and Reactor Safety as well as of the CDU group of the State Parliament seeked first-hand information on the field trial of genetically modified winter wheat on 25th June 2007 (Photo: H. Ernst).

nal scientists for seminars, and the revision and embedding of the doctoral programme website into the framework of the new Institute website.

Public relations and public impact

IPK research results were published in 136 scientific publications, including original work, surveys, book contributions, and theses. Furthermore scientists presented their results in a variety of oral presentations, in poster presentations, as well as via the internet. In addition to these scientific publications, the wider public was informed of recent developments at the Institute and the Biotechnology Campus through eleven press releases.

In the course of public relations activities a total of 76 visitor tours were carried out in Gatersleben and at the external branches in 2007.

At the beginning of 2007 public discussion regarding the field trial of transgenic wheat plants on IPK premises brought the Institute into the spotlight of the debate over green gene technology in Germany. In particular the controversial debate concerning the coexistence of the *ex situ* Genebank and the cultivation of transgenic wheat on Institute grounds required extensive public relations activities, in order to confront with relevant facts the scenarios envisioned by ecological farming and anti-gene-technology interest groups of the destruction of the Genebank as world heritage. The Institute accomplished this actively through intense media activity and the informing of political decision-makers. The highlight of this debate were the demonstrations carried out by gene technology critics outside the Institute gates on the first and 21st May, which were accompanied by intense press activity on the Institute's part. Moreover the Institute reported on the field trials in June to the German Parliamentary Committee on Food, Agriculture and Consumer Protection. On 25th June around 20 representatives of the CDU/CSU parliamentary group as well as the state legislative assembly group visited the IPK in order to acquaint themselves with the field trials and the activities of the Genebank (see Fig. 3). Legal action over the open field trials by the Association for the Conservation and Re-cultivation of Useful Plants in Brandenburg (VERN) through the administrative court in Cologne was withdrawn in December.

The Institute's new internet presence was introduced in March. The website has reappeared with a new layout and a revised structure.

As in past years, the Open Day at the Biotechnology Campus Gatersleben on 9th June was an important opportunity for the local and regional community to learn about research activities at the Institute (Events Section, p. 189). It was co-organised with local companies, the Green

der *ex situ*-Genbank und den Anbau transgenen Weizens auf dem Institutsgelände erforderte eine umfangreiche Öffentlichkeitsarbeit, um dem von Interessengruppen des ökologischen Landbaus und Gentechnikgegnern entworfenen Szenario zur Vernichtung der Genbank als Welterbe mit entsprechenden Fakten entgegen zu treten. Dies hat das Institut durch intensive Medienarbeit und durch Information von politischen Entscheidungsträgern aktiv getan. Höhepunkt dieser Debatte waren Kundgebungen von Gentechnikkritikern vor den Toren des Instituts am 1. und 21. Mai 2007, die seitens des Instituts durch eine intensive Pressearbeit begleitet wurden. Ferner berichtete das IPK im Juni im Bundestag dem Ausschuss für Ernährung, Landwirtschaft und Verbraucherschutz über den Freisetzungsversuch. Am 25. Juni besuchten etwa 20 Vertreter der CDU/CSU-Bundestagsfraktion sowie der Fraktion des Landtages das IPK, um sich vor Ort über den Freisetzungsversuch und die Arbeit der Genbank am IPK zu informieren (s. Fig. 3, S. 15). Eine Klage des Vereins zur Erhaltung und Rekultivierung von Nutzpflanzen in Brandenburg VERN e.V. gegen den Freisetzungsversuch vor dem Verwaltungsgericht in Köln wurde im Dezember zurückgezogen.

Im März des Jahres wurde die neue Internetpräsenz des Instituts eingeführt. Die Seiten erscheinen in neuem Layout und mit überarbeiteter Struktur.

Wie in den vergangenen Jahren war der Tag der offenen Tür am Biotechnologie-Campus Gatersleben am 9. Juni ein wichtiger Anlass, um die lokale und regionale Bevölkerung über die Forschungsarbeiten am Institut zu informieren (Abschnitt Veranstaltungen, S. 189). Er wurde in Zusammenarbeit mit den Firmen des Standortes, dem Grünen Labor, dem Biotech-Gründerzentrum sowie dem InnoPlanta e.V. organisiert und lockte knapp 1.000 Besucher zu den verschiedenen Ausstellungen. Am Standort Malchow konnten zum Tag der offenen Tür am 5. Mai etwa 200 interessierte Besucher begrüßt werden.
Auf der BIOTECHNICA 2007 vom 9. bis 11. Oktober in Hannover präsentierte das Institut mit den zwei Exponaten „Biosensor zum Nachweis östrogenwirksamer Substanzen im Wasser“ und „DNA-Sensor zum Nachweis mykorrhizierter Pflanzen“ ausgewählte Forschungsergebnisse auf dem Gemeinschaftsstand „Forschung für die Zukunft“ der Länder Sachsen, Sachsen-Anhalt und Thüringen. Zur Vorbereitung dieser Messe und anderer Veranstaltungen führte das Institut seine Mitarbeit im Arbeitskreis „Messe“ des Landes Sachsen-Anhalt fort.

Im Rahmen des Institutstages am 22. und 23. Oktober wurde der durch die „Gemeinschaft zur Förderung der Kulturpflanzenforschung e.V.“ gestiftete Rudolf-Mansfeld-Preis an die Diplom-Agrarwissenschaftlerin Vanessa Prigge von der Universität Hohenheim für ihre Diplomarbeit zu dem Thema „Untersuchungen zur Eignung europäischer Maislandrassen als genetische Ressourcen für den Ökologischen Landbau“ verliehen (s. Fig. 4).

Fig. 4: Prof. Andreas Graner (l.) überreicht der Agrarwissenschaftlerin Vanessa Prigge (r.) von der Universität Hohenheim am 23. Oktober im Rahmen des Institutstages 2007 den Rudolf-Mansfeld-Preis (Foto: H. Ernst)./ Prof. Andreas Graner (l.) presents the Rudolf-Mansfeld-Award to Vanessa Prigge (r.), agronomist of the University of Hohenheim, on 23rd October in the frame of the Institute's Day (Photo: H. Ernst).

Laboratory, the Biotech Start-up Centre, as well as InnoPlanta, and attracted almost 1,000 visitors to the diverse exhibitions. At the external branch in Malchow around 200 interested visitors were welcomed to the Open Day on 5th May.

With the two exhibits “Biosensor for the detection of estrogen-like substances in water” and “DNA-sensor for the detection of mycorrhiza-affected plants”, the Institute presented selected research results at the joint Saxony – Saxony-Anhalt – Thuringia information stand “Research for the Future” at the Biotechnica 2007 in Hannover from 9 to 11 of October. The Institute continues its collaboration in the Saxony-Anhalt State Working Committee “Trade Fairs” for the purpose of preparation for this trade fair and other events.

The Rudolf-Mansfeld-Award, endowed by the Society for the Advancement of Crop Plant Research, was awarded in the course of the Institute Day events (22 – 23 October) to Vanessa Prigge (Diploma of Agronomy) of the Hohenheim University for her Diploma thesis on the topic “Analysis of the suitability of European maize landraces as genetic resources for organic farming” (see Fig. 4).

The Green Laboratory held a school action week from 12th to 16th November, in order to give about 300 school pupils from secondary schools in the region the opportunity to acquaint themselves with careers in biotechnology and with the Biotech Campus. The IPK was involved

In der Woche vom 12. bis 16. November 2007 veranstaltete das Grüne Labor eine Schulaktionswoche, um ca. 300 Schülern der Realschulen bzw. der Gymnasien der Region die Möglichkeit zu geben, sich über Berufe in der Biotechnologie sowie den Biotech-Campus zu informieren. Das IPK beteiligte sich mit Führungen und Präsentationen. Besonderes Interesse fand die Möglichkeit, selbst im Labor zu experimentieren (vgl. S. 195).

Neben den wissenschaftlichen Arbeiten unterstützt das IPK aktiv kulturelle Aktivitäten am Institut bzw. in der Region durch die „Gesellschaft zur Förderung der Kultur Gatersleben e.V.".

Der Biotechnologiestandort Gatersleben

Als wissenschaftliches Zentrum ist das Institut auf vielfältige Weise an der Standortinitiative Green Gate Gatersleben beteiligt und unterstützt die Weiterentwicklung des Biotechnologiestandorts. Im März des Jahres wurde mit dem Kommunikationszentrum des Bioparks, neben dem bereits in 2006 eröffneten Gewächshaus- und Laborkomplex, der zweite Gebäudekomplex feierlich eröffnet. Vertreter der Standortinitiative nahmen an verschiedenen Messen (ABIC, BIOTECHNICA) teil, um die Sichtbarkeit von Gatersleben als Standort für Grüne Biotechnologie weiter zu verbessern. Die Arbeit des Grünen Labors fand mit ca. 1.900 Besuchern auch in diesem Jahr wieder starke Resonanz insbesondere bei Lehrer- und Schülergruppen.

with tours and presentations. The opportunity to experiment in the laboratories met with particular interest (see p. 195).

In addition to scientific activities, the IPK actively supports cultural activities at the Institute and in the region through the "Gatersleben Society for the Promotion of Culture".

Gatersleben as a biotechnology centre

As a scientific centre the Institute is involved in various ways in the Green Gate Gatersleben Initiative, and supports the further development of Gatersleben as a biotechnology centre. The Biopark Communications Centre was ceremoniously opened in March, and joins the greenhouse and laboratory complex opened in 2006 as the second building complex in the Biopark. Representatives of the Green Gate Gatersleben Initiative took part in various trade fairs (ABIC, BIOTECHNICA) in order to improve the visibility of Gatersleben as a centre for green biotechnology. With around 1,900 visitors over the year, the activities of the Green Laboratory met with great response, in particular from teacher/pupil groups.

Verwaltung und technische Infrastruktur/ Administration and Technical Infrastructure

Personal und Finanzierung der Stiftung/Human Resources and Foundation Funding

Personal/Staff

Im Berichtsjahr hat sich der Gesamtpersonalbestand gegenüber dem Vorjahr am Stichtag 31. Dezember 2007 von 450 auf 449 Personen verändert. Darunter befinden sich 262 (2006: 265) Mitarbeiter/-innen auf Planstellen. Neben 105 (2006: 108) Drittmittelbeschäftigten waren 57 (2006: 53) Mitarbeiter/-innen auf Annexstellen angestellt. Das gleichbleibend hohe Niveau an Projektpersonal konnte maßgeblich durch die Drittmitteleinwerbung gehalten werden. Besonders erfolgreich schnitt das IPK im BMBF-Pflanzengenomprogramm GABI-FUTURE ab. Des Weiteren wurde auch in diesem Jahr ein Projektantrag im Rahmen des Paktes für Forschung und Innovation bewilligt. Zum anderen wurde IPK-intern erneut ein Ideenwettbewerb initiiert, der zur verstärkten Umsetzung anwendungsorientierter Forschung beitragen soll. Zum Stichtag waren insgesamt 25 Ausbildungsplätze vergeben; darunter zwei Bürokaufleute, 17 Biologielaboranten/-innen, zwei Fachinformatiker Systemintegration, eine Fachangestellte für Medien- und Informationsdienste und drei Gärtner/-innen für Gemüsebau.
Einzelheiten sind in der nachfolgenden Tabelle 1 dargestellt.

Tabelle/Table 1: Personalentwicklung im IPK/Staff Development at IPK

Personen	31.12.1992		31.12.1996		31.12.2002		31.12.2007	
	gesamt	darunter Wissensch.	gesamt	darunter Wissensch.	gesamt	darunter Wissensch.	gesamt	darunter Wissensch.
Stellenplanpersonal	261	51	269	53	256	57	262	57
Verstärkerfondspersonal	57	32	15	7	0	0	0	0
HSP III-Personal	0	0	1	1	0	0	0	0
Drittmittelfinanziertes Personal	71	47	105	74	166	100	105	75
Annexpersonal	12	0	27	6	19	8	57	31
Auszubildende	2	0	11	0	16	0	25	0
Gesamt	**403**	**130**	**428**	**141**	**457**	**165**	**449**	**163**
davon:								
Vollzeitbeschäftigte	267	93	281	92	320	121	270	99
Teilzeitbeschäftigte	136	37	147	49	137	44	179	64

Am 31. Dezember 2007 waren 227 Personen in einem befristeten Arbeitsverhältnis tätig. Auf Zeit angestellt waren von den 163 Wissenschaftler/-innen insgesamt 133. Von den 57 Wissenschaftler/-innen im Planstellenbereich sind 27 befristet beschäftigt.

Die Verteilung der Stellen auf die jeweiligen Programme entsprechend Programmbudget wird in der folgenden Übersicht dargestellt (Tabelle 2, S. 20).

Tabelle/Table 2: Beschäftigte nach Programmen in Personen (Stand 31. Dezember 2007)/
Programme Staff (as of 31st December 2007)

Programm	Planstellen-personal	Drittmittel-personal	Annex-personal	Auszubildende	Summe
Management, Analyse und Evolution pflanzengenetischer Ressourcen	71	17	13	0	101
Cyto-molekulare Genomanalyse	51	33	15	0	99
Molekulare Entwicklungsphysiologie	30	31	9	0	70
Angewandte Zellbiologie	30	24	17	0	71
Administration:					
Wiss. Dienstleistungen	27	0	1	0	28
Zentrale Dienste	24	0	1	0	25
Verwaltung	22	0	1	25	48
Geschäftsführung und Stabsfunktionen (einschl. Sekretariate)	7	0	0	0	7
Gesamt	**262**	**105**	**57**	**25**	**449**

Wirtschaftsplan 2007/Budget in 2007

In 2007 wurden der Stiftung im Rahmen der Grundfinanzierung 22,1 Mio. EUR zugewendet. Die institutionelle Förderung in Höhe von 22,0 Mio. EUR erfolgte durch das Land Sachsen-Anhalt und wurde anteilig vom Bund und der Gemeinschaft der Länder mitfinanziert. In der Gesamtzuwendung sind Mittel aus dem Europäischen Fonds für Regionale Entwicklung (EFRE) als Anteilsfinanzierung für die Baumaßnahme „Errichtung Kommunikationszentrum" enthalten. Es wurden Wettbewerbsmittel im Rahmen des Paktes für Forschung und Innovation in Höhe von 809 TEUR vom Zuwendungsgeber für drei Projekte bereitgestellt. 512 TEUR entfallen auf das Projekt „Entwicklung einer physischen Karte für das Gerstengenom". Für ein Projekt des IGZ Großbeeren, in dem das IPK als Kooperationspartner mitwirkt, wurden 35 TEUR Paktmittel zugewendet. 2007 begannen die Arbeiten an dem Paktprojekt APOMIXIS, für das 262 TEUR zusätzlich im Rahmen der Grundfinanzierung bereitgestellt worden sind. 53 TEUR erhielt das IPK als sonstige Zuwendungen von der Bundesagentur für Arbeit zur Finanzierung von Altersteilzeit sowie von Krankenkassen als Erstattungen im Zusammenhang mit Mutterschaft.

Im Bereich der institutionellen Förderung stellen die Personalausgaben mit 12.177 TEUR (48 %) die größte Position dar, gefolgt von den Sachausgaben einschließlich Zuweisungen mit 7.390 TEUR (29 %), den Bauinvestitionen mit 4.661 TEUR (18 %) und den Geräteinvestitionen mit 1.266 TEUR (5 %).

Drittmittel 2007/Third Party Funding in 2007

Trotz allgemein rückläufiger Projektbewilligungen konnte das IPK das Drittmittelvolumen 2007 im Vergleich zum Vorjahr mit 97 % auf fast gleichem Niveau halten. Erfreulich ist ein weiterer Anstieg der Bewilligungen des Kultus- und des Wirtschaftsministeriums des Landes Sachsen-Anhalt. Über den Sonderforschungsbereich 648 wurden im Berichtsjahr 98 TEUR eingenommen. Die Einnahmen von der DFG sind weiter gestiegen und liegen fast auf dem Niveau von 2004.

Für 119 Projekte (Vorjahr 103) wurden im Berichtsjahr Einnahmen (ohne Partner) in Höhe von 5.392 TEUR (Vorjahr 5.536 TEUR) erzielt. Die Einnahmen BMBF resultierten überwiegend aus der Teilnahme des IPK an Programmen des BMBF „Genom-Analyse im biologischen System Pflanze (GABI 2)" und „GABI-FUTURE" sowie aus der Durchführung des Großprojektes „Bioinformatik-Centrum Gatersleben-Halle", das im Oktober 2007 erfolgreich abgeschlossen werden konnte. Mit 12 Projekten und einer Gesamtzuwendungssumme von über 11 Mio. EUR ist das IPK im Programm „GABI-FUTURE" vertreten, das im Juli 2007 begann und voraussichtlich 2012 enden wird. Hauptzuwendungsgeber sind das Bundesministerium für Bildung und Forschung mit 2.525 TEUR (Vorjahr 2.974 TEUR), die Deutsche Forschungsgemeinschaft mit 1.053 TEUR (Vorjahr 885 TEUR), das Land Sachsen-Anhalt mit 574 TEUR (Vorjahr 498 TEUR) und die Europäische Union mit 303 TEUR (Vorjahr 387 TEUR).

Mit 846 TEUR Einnahmen im Rahmen der Auftragsforschung (Vorjahr 670 TEUR) ist die Forschung allein mit Wirtschaftsunternehmen wieder zunehmend. Daneben sind in einer Vielzahl der Projekte mit dem BMBF oder der EU Betriebe der Wirtschaft als Partner involviert; Tendenz steigend. Außerdem gab es Mittel von sonstigen Zuwendungsgebern in Höhe von 122 TEUR (Vorjahr 26 TEUR). Zusätzlich zu den Einnahmen für das IPK sind im Rahmen von zwei Projekten 50 TEUR (Vorjahr 520 TEUR) für Partner eingenommen und weitergereicht worden. Die Entwicklung der Einnahmen für Projekte von 2005 über 2006 bis 2007 ist in der Fig. 5 dargestellt.

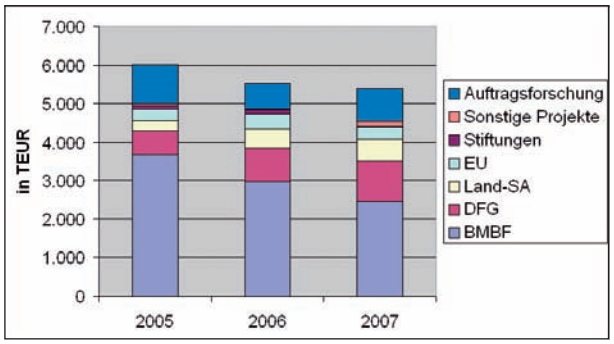

Fig. 5
Entwicklung der Drittmitteleinnahmen nach Mittelherkunft ohne Anteil für Partner/Development of third party funds excl. partner shares (source of funds).

Gesamteinnahmen und -ausgaben 2007/ Total Revenues and Expenditure in 2007

Die gesamten Einnahmen und Ausgaben des IPK von der Grundfinanzierung einschließlich EFRE-Mittel über sonstige Zuwendungen, eigene Einnahmen bis hin zur Drittmittelfinanzierung in 2007 sind in ihrer Zusammensetzung in den Abbildungen 6 und 7 dargestellt. Grundsätzlich wurden die Einnahmen und Ausgaben für Ausbaumaßnahmen wegen ihres einmaligen Charakters aus der Betrachtung ausgeklammert.

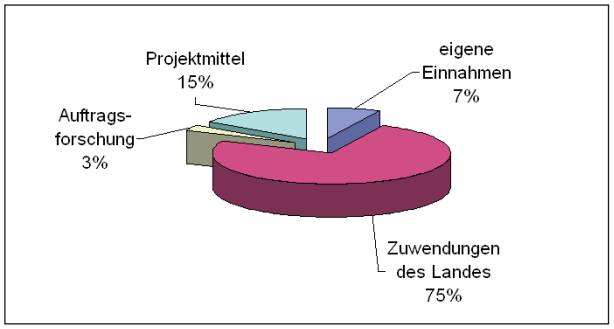

Fig. 6
Gesamteinnahmen des IPK 2007: 29.648 TEUR/Total revenues of IPK 2007: EUR 29,648 k.

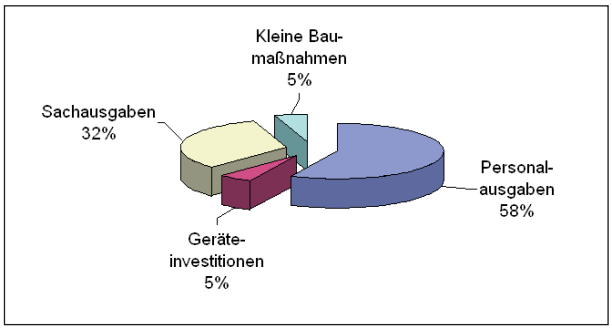

Fig. 7
Gesamtausgaben des IPK 2007: 28.032 TEUR/
Total expenditure of IPK 2007: EUR 28,032 k.

Kostenrechnung/Cost Calculation

Für das Berichtsjahr 2007 wird die Kostenstellenrechnung in Tabelle 3, S. 28 auf Programmebene zusammengefasst dargestellt. Zu den Forschereinzelkosten (FEK) zählen die Personalkosten, die Reisekosten und die Dienstleistungen Dritter in den wissenschaftlichen Arbeitsgruppen, einschließlich Ausgaben für Partner in Projekten. Gemeinkosten sind durch direkte Erfassung auf den Kostenstellen wie Reparaturen, Kosten für Telefon, Veröffentlichungen, Patentaufwendungen, Abschreibungen etc. oder durch Umlagen entstanden. In den Umlagen sind die Kosten für Wasser, Heizung, Energie, Bauunterhaltung, Abteilungsleitung, Querschnitt, Versuchsfeld und Gärtnerei, zentrale Datenverarbeitung usw. enthalten. Sie werden über spezifische Verteilerschlüssel den Kostenstellen zugeordnet. Die Gemeinkosten im Verhältnis zur Summe der Einzelkosten ergeben den Gemeinkostensatz. Gegenüber den Vorjahren ist ein Ansteigen der Gemeinkosten, speziell bei den Abschreibungen, zu verzeichnen. Die umfangreichen Sanierungsmaßnahmen in den Gebäuden und der technischen Infrastruktur wirken sich jetzt kostenseitig aus.

Tabelle/Table 3: Komprimierte Kostenstellenrechnung nach Programmen (Angaben in TEUR)/
Consolidated Cost Calculation for Programmes (in k EUR)

	Wissenschaftliche Programme gesamt	Management, Analyse und Evolution pflanzengenetischer Ressourcen	Cytomolekulare Genomanalyse	Molekulare Entwicklungsphysiologie	Angewandte Zellbiologie
Summe FEK [1]	12.480,8	3.951,3	3.692,9	2.550,3	2.286,3
Verbrauchsmaterial	1.937,9	621,6	601,2	333,3	381,8
Summe Einzelkosten	**14.418,7**	**4.572,9**	**4.294,1**	**2.883,6**	**2.668,1**
Gemeinkosten dir. gebucht	1.025,2	262,8	297,1	141,0	324,3
Abschreibungen	4.452,0	1.261,5	1.014,4	666,7	1.509,4
Zwischensumme	**5.477,2**	**1.524,3**	**1.311,5**	**807,7**	**1.833,7**
Summe Umlagen	5.037,2	2.119,2	1.277,6	712,7	927,7
Summe Forschergemeinkosten	**10.514,4**	**3.643,5**	**2.589,1**	**1.520,4**	**2.761,4**
Materialgemeinkosten	773,9	190,7	224,7	168,7	189,8
Verwaltungsgemeinkosten	2.432,1	795,4	672,5	432,6	531,6
Gemeinkosten gesamt	**13.720,4**	**4.629,6**	**3.486,3**	**2.121,7**	**3.482,8**
Selbstkosten	**28.139,1**	**9.202,5**	**7.780,4**	**5.005,3**	**6.150,9**
Gemeinkostensatz	**95 %**	**101 %**	**81 %**	**74 %**	**131 %**

[1] FEK = Forschereinzelkosten

Technologietransfer/Technology Transfer

Das IPK verfügte zum Jahresende 2007 über 16 Betriebsgeheimnisse und war als alleiniger oder Mitanmelder an 24 Patentfamilien mit Anmeldungen in Deutschland und im Ausland beteiligt. Daneben sind IPK-Erfinder an 29 Patentfamilien beteiligt, die durch Industriepartner im Rahmen von FuE-Verträgen angemeldet wurden.
Das Institut ging im Jahr 2007 insgesamt sechs Kooperationsverträge im Rahmen der 2007 gestarteten BMBF-Förderung GABI-FUTURE ein. Daneben wurden zwölf weitere Kooperations- bzw. Konsortialverträge sowie sieben neue Forschungs- und Entwicklungsverträge (einschließlich einer Vertragsverlängerung und eines Rahmenvertrags) abgeschlossen. Für zwei Technologien des IPK konnten Lizenzverträge abgeschlossen werden. Für ein Vorhaben aus dem Ideenwettbewerb 2006 konnte ein Kooperationsvertrag mit zwei Pflanzenzüchtern vereinbart werden. Darüber hinaus wurden im Jahr 2007 insgesamt 66 Materialtransfer- und Geheimhaltungsvereinbarungen mit in- und ausländischen Forschungseinrichtungen sowie Wirtschaftsunternehmen abgeschlossen.

Die seit 2004 bestehende Zusammenarbeit mit der Ascenion GmbH zur Bewertung und Verwertung von Erfindungen wurde im Rahmen eines vom BMBF geförderten Projektes fortgesetzt. Die vor diesem Hintergrund am IPK etablierte Möglichkeit, in einer monatlichen „Erfindersprechstunde" Fragen und Probleme rund um die Verwertungschancen von vor Ort entwickelten Technologien mit einem erfahrenen Experten zu diskutieren, wurde von den Wissenschaftlern des Instituts weiterhin rege in Anspruch genommen.

Im Jahre 2007 wurde schließlich zum dritten Mal ein „Ideenwettbewerb" zur Förderung anwendungsorientierter Forschungsprojekte durchgeführt. Von den insgesamt elf eingereichten Projektanträgen konnten sechs mit einem Volumen von 227 TEUR bewilligt werden, darunter z. B. ein Vorhaben zur Erprobung und Optimierung von IPK-eigenen Plasmidvektoren und *Bacillus*-Wirtsstämmen zur stabilen und extrachromosomalen Amplifikation von Expressionskassetten für extrazelluläre Enzyme in *Bacillus*, welches anschließend erfolgreich auslizenziert werden konnte.

Gemeinsam mit LeibnizX, der Gründungs- bzw. Entrepreneurship-Beratungsstelle der *WGL*, setzte das IPK die nachhaltige Unterstützung der Ausgründungspläne einer ehemaligen Wissenschaftlerin des Instituts und ihrer Geschäftspartnerin in 2007 fort. Für beide Geschäftspartnerinnen konnten erfolgreich EXIST-Gründerstipendien im Rahmen des BMBF-Programms „Existenzgründungen aus der Wissenschaft" eingeworben werden.

Mit insgesamt drei eingereichten Projektskizzen nahm das IPK auch an dem im Sommer 2007 erstmals ausgelobten Wettbewerb um eine Projektförderung im Rahmen des BMBF-Programms „ForMaT" (Forschung für den Markt im Team), einem Bestandteil der BMBF-Innovationsinitiative Neue Länder „Unternehmen Region", teil. Eine dieser Projektskizzen, welche die Etablierung eines

„Hormon-Biosensorsystems“ zum Gegenstand hat, wurde vom Zuwendungsgeber auch für förderungswürdig befunden, so dass in 2008 ausreichend Mittel für die Einrichtung eines sogenannten Konzeptteams am IPK zur Verfügung stehen werden. Alle Anstrengungen in der aktuellen Projektphase werden dann darauf gerichtet sein, ein schlüssiges Innovations-Portfolio aufzubauen, auf dessen Grundlage eine Förderung der geplanten Forschungs- und Entwicklungsarbeiten und Verwertungsaktivitäten im Rahmen von interdisziplinären Innovationslabors für die Jahre 2009–2011 erfolgreich beantragt werden kann.

Raum- und Geräteangebot, sonstige Infrastruktur/ Facilities, Equipment and Infrastructure

Baumaßnahmen/Construction Projects

Im Berichtsjahr wurden für die Verbesserung des Raumangebotes Bauleistungen in Höhe von ca. 5,2 Mio. EUR aufgewandt. Die neue Bibliothek im ehemaligen Gebäude „Physik" unter Einbeziehung eines Teils des Laborcontainers ist seit Mai 2007 in Benutzung (s. Fig. 8). Die Sanierung der technischen Infrastruktur wird abhängig vom Baufortschritt bei den Gebäudesanierungen fortgesetzt. Mit der Errichtung des Kommunikationszentrums ist im Juli 2007 begonnen worden. Bereits zum „Tag der offenen Tür" im Juni 2008 soll es feierlich in Betrieb genommen werden. Im Rahmen der Kleinen Neu-, Um- und Erweiterungsbauten ist für den Umbau der Genbank „Nord" am Standort Groß Lüsewitz die Entscheidung zu Gunsten eines Laborcontainers gefallen. Er wird ab 2008 errichtet. Außerdem wurden durch die Sanierung der „Genetik G" und die Errichtung eines automatischen Gewächshauses die Bedingungen für den Versuchsanbau sowie die Auswertung der wissenschaftlichen Parameter wesentlich verbessert.

Fig 8: Nach den Umbaumaßnahmen nahm die Wissenschaftliche Bibliothek im Mai ihren Betrieb in den neuen Räumlichkeiten, dem ehemaligen Physikgebäude, auf (Foto: H. Ernst)./ The scientific library shifted operation to its new premises in the former Physics building in May (Photo: H. Ernst).

Tabelle/Table 4: Baumaßnahmen/Construction Projects

In 2007 fertiggestellte Baumaßnahmen:

Lfd. Nr.	Maßnahme	Gesamtkosten (Ist) in TEUR	Ausgaben 2007 in TEUR
1	Errichtung Bibliothek	2.935	1.205
2	Sanierung „Genetik G"	1.559	640
3	Automatisches Gewächshaus	725	725
4	Installation Regeltechnik Trafo 3	189	31
5	Sanierung Säulengang	60	60
6	Wegebau	60	60
7	Kleingewächshäuser	90	90
8	ca. 200 Kleinaufträge Bauunterhaltung	202	202

Weiterlaufende Baumaßnahmen:

Lfd. Nr.	Maßnahme	Geplante Gesamtkosten in TEUR	Ausgaben 2007 in TEUR
9	Sanierung technische Infrastruktur	7.095	68
10	Errichtung Kommunikationszentrum	3.664	2.050
11	Errichtung Laborcontainer in Groß Lüsewitz	700	21
12	Sanierung „Genetik 0507“	200	20
	Insgesamt		**5.172**

Informationstechnologie/Information Technology

Das Jahr 2007 war geprägt durch organisatorische Umstrukturierungen. Es wurde ein Konzept mit dem Ziel entwickelt, die sich immer stärker manifestierenden fachlichen Zusammenhänge zwischen Wissenschaft und Informationstechnologie zusammenzuführen. Der Vorschlag war die Integration des IT-Teils der Arbeitsgruppe Informationstechnologie und Wissenschaftliche Bibliothek in die wissenschaftliche Arbeitsgruppe Bioinformatik. Als Ergebnis wurde am 1. Juli 2007 die Arbeitsgruppe Bioinformatik und Informationstechnologie (Ag BIT) gegründet. Neben der wissenschaftlichen Arbeit dieser Arbeitsgruppe soll der IT-Service gleicher Qualität aber in engerer Kopplung an die wissenschaftlichen Arbeitsgruppen angeboten werden.
Ziel des IT-Teils der Ag BIT ist die Konsolidierung und Weiterentwicklung der Informationstechnologieressourcen des IPK, um den steigenden Anforderungen an die Leistungsfähigkeit und die Verfügbarkeit des operativen IT-Systembetriebs gerecht zu werden. Zu den zentralen Aufgaben gehören der Betrieb von zentralen IT-Diensten, wie Netzwerk, zentrale Dateisysteme, Archivierung und Backup. Schwerpunkt im Berichtsjahr war die Migration von weiteren Arbeitsgruppen in die zentrale Windowsdomäne und der damit verbesserten Möglichkeiten für Softwareinstallation und -verteilung sowie die homogene, zentrale und somit ressourcensparende Verwaltung von Nutzerdaten, Dateien und Druckern.
Zwei weitere IT-Projekte wurden im Berichtzeitraum erfolgreich umgesetzt. So ist im März 2007 die neue Internetpräsenz aktiviert worden. Weiterhin wurde das neue Intranet-Portal in Betrieb genommen. Dies dient vor allem der Verbesserung der IPK-internen Kommunikation, Arbeitsorganisation und des Informationsaustausches. Gleichzeitig konnte mit der Einführung des Intranet eine Umorganisation von Abläufen angestoßen werden, um so Synergieeffekte nutzen zu können.
Für alle IPK-Mitarbeiter konnte im Berichtszeitraum der neue Mailserver-Cluster in Betrieb genommen werden. Diese neue Infrastruktur unterstützt den komfortableren Umgang mit der DV-Technik in allen Bereichen.
Neben diesen geschaffenen zentralen Lösungen stellt weiterhin die individuelle Betreuung von wissenschaftlichen und nicht-wissenschaftlichen IT-Nutzern und Computerarbeitsplätzen eine wichtige Aufgabe dar. So wurden im Berichtsjahr 1.405 DV-Aufträge (Vorjahr 1.462) bearbeitet. Für alle Aktivitäten auf dem Gebiet der Informationstechnologie wurden im Berichtszeitraum 325 TEUR für Sachausgaben (Vorjahr 290 TEUR) und 197 TEUR für Investitionen (Vorjahr 169 TEUR) zur Verbesserung der IT-Infrastruktur bereitgestellt.

Neue Geräte im Jahr 2007/New Equipment in 2007

In 2007 wurden wissenschaftliche Geräte mit einem Gesamtwert (brutto) von 1,0 Mio. EUR beschafft. Darunter waren acht Geräte mit einem Bruttoanschaffungswert von je über 25 TEUR für insgesamt 547 TEUR. Herausragend ist ein Gaschromatograf GS/MS-MS im Wert von 249 TEUR, der in der Arbeitsgruppe Angewandte Biochemie zum Einsatz kommt.

Der relativ geringe Investitionsumfang im Vergleich zu den Vorjahren ist den zwei unbesetzten Abteilungsleiterstellen geschuldet. Die nicht in Anspruch genommenen Mittel können dank der ab 2007 flexibleren Bewirtschaftungsgrundsätze nach 2008 übertragen werden.

Versuchsfeld und Gärtnerei/Experimental Fields and Nurseries

Am IPK werden folgende Versuchsflächen bewirtschaftet:

Art	Nutzfläche
Gewächshäuser mit z. T. hochwertiger, multivalenter Ausstattung	3.054 m²
Kleingewächshäuser (170 Stück)	2.595 m²
Foliengewächshäuser	344 m²
Phytokammern	143 m²
Frühbeetkästen und Lagenquartiere als Doppel- und Einfachkästen	1.460 m²
Freilandversuchs- und Reproduktionsflächen	ca. 18 ha

Daneben werden zur Zeit weitere 42 ha Ackerfläche auf dem Institutsgelände in eigener Regie landwirtschaftlich bearbeitet. Neben dem eigenen Freisetzungsversuch mit transgenem Winterweizen wurden ein Versuch der Firma Novoplant GmbH mit transgenen Erbsen sowie ein umfangreicher Versuch für die BASF Plant Science GmbH mit transgenen Kartoffellinien betreut. Die multivalente Ausstattung der Gewächshäuser wurde durch die Installation einer „Phenotyping-Plattform" für Getreide ergänzt. Die Anlage soll zukünftig eine weitgehend automatische Durchführung von Exaktversuchen und die Erfassung phänotypischer Daten an Ganzpflanzen ermöglichen.
Für den Anbau transgener Pflanzen wurden zwölf zusätzliche Kleingewächshäuser mit einer Nutzfläche von ca. 250 m² ergänzt. Die Häuser dienen insbesondere zum Anbau transgener Gersten-, Weizen- und Erbsenpflanzen.

Wissenschaftliche Bibliothek/Scientific Library

Der Bestand präsentiert sich mit 76.301 Medieneinheiten seit Mai 2007 im neuen, nutzerfreundlichen Bibliotheksgebäude über zwei Etagen auf 928 m² oder 3.800 laufenden Metern in Freihandaufstellung. Mit der Bereitstellung von zwölf Arbeitsplätzen, darunter sechs mit PC, und zwei Studienkabinen wird die neue Bibliothek modernsten Ansprüchen gerecht. Durch die räumliche Integration von zwei Außenmagazinen wurde der Zugang zu den vorhandenen Ressourcen deutlich verbessert.
Schwerpunkte des Bestandsaufbaus sind die Gebiete: Molekularbiologie, Genetik, Zytologie, Taxonomie und Kulturpflanzenforschung. 2007 durchliefen 989 Monographien, Serien, Periodika etc. als Neuzugang die Geschäftsgänge der Bibliothek. Von den 250 laufend gehaltenen Periodika in Printversion ist auf 92 Ausgaben der Online-Zugriff möglich.
Die interne Ausleihe umfasst für den Berichtszeitraum 4.597 Bände (ohne Dauerausleihen). 1.712 Anfragen aus anderen Bibliotheken wurden im Leihverkehr bearbeitet; davon wurden 220 Bände im Original und 1.195 Bestellungen als Kopie versandt. Im nehmenden Leihverkehr wurden aus anderen Bibliotheken 1.897 Bestellungen angefordert. Die Informationsdienste der Bibliothek umfassen außerdem Fachauskünfte sowie die Recherche in diversen Online-Datenbanken und Fachdiensten wie „ISI Web of Science" und überregionalen Bibliothekskatalogen und Fachdatenbanken. Neben der mittels „Biblio" laufend gepflegten Inhouse-Datenbank dokumentiert eine weitere die Publikationen, Vorträge und Poster der Wissenschaftler des IPK.
Seit Anfang der 90er Jahre ist die Spezialbibliothek in ein von der Deutschen Forschungsgemeinschaft gefördertes Programm zum „Ausbau von Spezialbeständen an wissenschaftlichen Bibliotheken" integriert, in welchem acht namentlich genannte Einrichtungen mit überregional bedeutenden Beständen gefördert werden. Die jährlichen Zuwendungen belaufen sich auf 8 TEUR. Durch die Teilnahme am DFG-Projekt „Nutzung von Nationallizenzen" konnte das Angebot an elektronischen Zeitschriften, z. B. der Verlage Springer und Elsevier, wesentlich erweitert werden. Die Bibliothek beteiligt sich auch weiterhin am *WGL*-Konsortium, welches allen Wissenschaftlern die Recherche in der Fachdatenbank „ISI Web of Knowledge" und dem „Journal Citation Reports" vom Arbeitsplatz aus ermöglicht.

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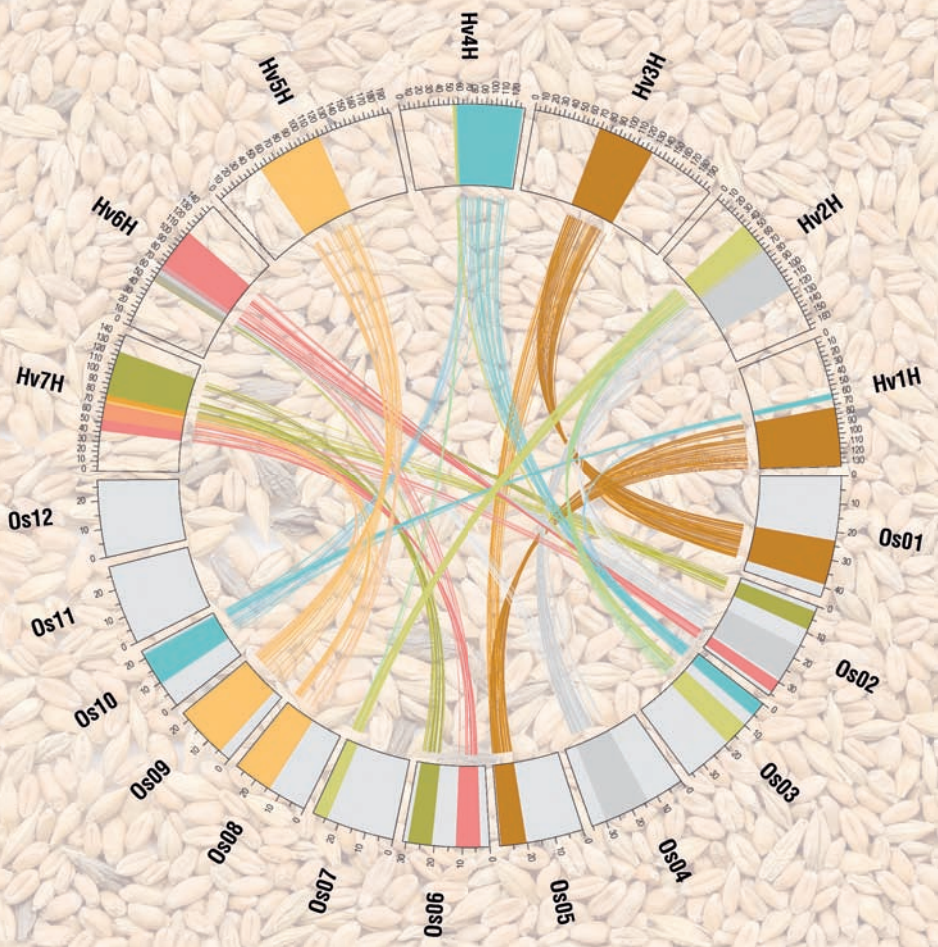

Fig. 9: Das Gerstengenom – ein Flickwerk duplizierter Chromosomenfragmente.
Durch den Vergleich der DNA-Sequenzen genetisch kartierter Gersten-ESTs mit der des Reisgenoms können konservierte Chromosomenbereiche identifiziert werden. Die chromosomale Verteilung der Gersten-ESTs im Vergleich zu putativ orthologen (dunklere Linien) und paralogen (hellere Linien) Reisgenen erlaubt den Nachweis von sieben segmentellen Duplikationen im Gerstengenom. Duplizierte Bereiche sind in den kreisförmig angeordneten Chromosomen mit der gleichen Farbe gekennzeichnet. Insgesamt wurden in Gerste auf diese Weise 7 der 10 in Reis vorhandenen duplizierten Chromosomenbereiche (> 10 Mb) wiedergefunden. Deren Duplikation erfolgte dementsprechend bereits vor über 45 Millionen Jahren im Vorläufergenom beider Arten. Reischromosomen (Os01 - Os12) sind im unteren und Gerstenchromosomen (Hv1H - Hv7H) im oberen Teil des Kreises dargestellt (T. Thiel et al.).

The barley genome – a patchwork of segmental duplications.
Sequence comparison between genetically mapped barley ESTs and the rice genome sequence allows for the visualisation of conserved duplications between both genomes. Seven segmental duplications were identified in barley by comparing the distribution of putative orthologous (darker colour) and paralogous rice genes (brighter colour) to the corresponding barley ESTs. Chromosomes of barley (Hv1H - Hv7H) and rice (Os01 - Os12) are represented in a circle. Duplicated segments are marked by the same colour. The presence of 7 out of 10 segmental rice duplications (> 10 Mb) can be deduced for the barley genome due to their syntenic organisation in the two species. The conservation of segmentally duplicated regions in the barley and rice genomes implies their presence in the ancestral progenitor genome before the species diverged some 45 million years ago (T. Thiel et al.).

Abteilung Genbank

Leiter: Prof. Dr. Andreas Graner

Allgemeine Forschungsziele

Im Mittelpunkt der in der Abteilung durchgeführten Forschungs- und Servicearbeiten steht die Betreuung und Weiterentwicklung der bundeszentralen *ex situ*-Genbank. Die Forschungsthemen umfassen die weitere Optimierung des Erhaltungsmanagements, die molekulargenetische Analyse agronomischer Merkmale sowie die Untersuchung von Artbildungs- und Anpassungsprozessen bei Nutzpflanzen und damit verwandten Wildarten und deren taxonomische Einordnung. Neben den Forschungsarbeiten bietet die Genbank Serviceleistungen für ein breites Spektrum wissenschaftlicher, züchterischer und kulturhistorischer Fragestellungen an. Auf diese Weise leistet die Abteilung einen wichtigen Beitrag zu den globalen Aktivitäten zur Erhaltung der Kulturpflanzenvielfalt sowie zur verbesserten Nutzung pflanzengenetischer Ressourcen.

Entwicklung im Berichtsjahr

Im Zentrum des Sammlungsmanagements stand die Fortführung und Weiterentwicklung der bundeszentralen *ex situ*-Genbank für landwirtschaftliche und gärtnerische Kulturpflanzen. Sie umfasst zum gegenwärtigen Zeitpunkt 148.113 Akzessionen aus 3.049 Arten und 801 Gattungen. Die Erhaltungsarbeiten erfolgen in Gatersleben (128.083 Akzessionen) und an der Außenstelle mit den beiden Standorten Groß Lüsewitz (Kartoffelsortiment, 5.945 Akzessionen) und Malchow (Öl- und Futterpflanzen, 14.085 Akzessionen). Der Feld- und Gewächshausanbau bewegte sich mit 12.591 Mustern auf ähnlichem Niveau wie im vergangenen Jahr (13.644). Eine detaillierte Aufstellung des Sortimentsbestands und des Feldanbaus ist in Tabelle 5, S. 29 aufgeführt. Die Anzahl der in Gatersleben und Groß Lüsewitz gehaltenen *in vitro*-Muster beläuft sich auf 3.351 (darunter 2.762 Kartoffeln). Die in flüssigem Stickstoff gelagerte Cryo-Sammlung bei Kartoffeln umfasst gegenwärtig 1.046 Akzessionen. Im Berichtszeitraum wurden im Rahmen von 611 Bestellungen 12.253 Muster abgegeben. Im Dezember 2006 wurde das Online-Bestellsystem des Genbank-Informationssystems (GBIS) frei geschaltet. Es ermöglicht die Auswahl von Saatgutmustern und ihre Bestellung mit einem Warenkorbsystem. Entsprechend den Empfehlungen des Internationalen Vertrags zu Pflanzengenetischen Ressourcen wurde im Oktober 2007 das „standardised Material Transfer Agreement“ (sMTA) eingeführt. Die durchschnittliche Bearbeitungsdauer für Bereitstellung und Versand des

Department of Genebank

Head: Prof. Andreas Graner

Research Goals

The central activity within the department consists of the management of the Federal *ex situ* Genebank for agricultural and horticultural plant species. Major research themes comprise the optimisation of the collection management, molecular genetic analysis of agronomic traits, investigation of speciation and adaptation in crop plants and their wild relatives as well as taxonomic studies. Service activities of the Genebank range from the distribution of seed samples and the provision of herbarium vouchers to the retrieval of information on a broad spectrum of topics related to plant genetic resources. In this way the department contributes to the global efforts towards both conservation of biological diversity and an enhanced utilisation of plant genetic resources.

Developments during 2007

The Federal *ex situ* Genebank presently holds 148,113 accessions representing 3,049 botanical species and 801 genera. Collections are located at Gatersleben (128.083 accessions), Groß Lüsewitz (potato, 5,945 accessions) and Malchow (oil and forage crops, 14,085 accessions). During the past year, 13,644 accessions were grown for seed multiplication or for botanical characterisation. Details on the size of individual collections and their regeneration are given in Table 5, see p. 29. The number of *in vitro* samples kept at Gatersleben and Groß Lüsewitz amounts to 3,351 (including 2,762 potatoes). The cryo-collection of potato consisting of virus-free tissue explants kept under liquid nitrogen amounts to 1,046 samples. In the past twelve months 611 requests were processed and 12,253 accessions were shipped. To further ease the ordering process, a new online ordering system, which forms part of the Genebank Information System, was launched in December 2006. It allows querying of the database and the selection of accessions into a shopping cart system. Following the recommendations of the International Treaty on Plant Genetic Resources for Food and Agriculture, a “standardised Material Transfer Agreement” (sMTA) was introduced in October 2007. In comparison to the previous year, the average processing time for distribution of seeds/tubers could be further improved and now amounts to 12.6 days upon receipt of the signed sMTA. Like in previous years, research institutes formed the largest user group receiving 52 % of the shipped samples.

Materials betrug 12,6 Tage ab dem Eingang des MTAs und konnte gegenüber dem Vorjahr nochmals verbessert werden. Forschungsinstitute stellen mit 52 % der Abgaben nach wie vor die weitaus größte Nachfragergruppe dar. 4.351 Muster (36 %) wurden in das Ausland abgegeben. Eine Aufschlüsselung der abgegebenen Muster nach Sortimenten und Nutzergruppen ist der Abbildung 10, S. 30 zu entnehmen.

Tabelle/Table 5: Sortimentsbestand der Genbank 2007 exkl. Cryo-Sammlung (1.046 Muster)/Inventory of the *ex situ* collection 2007 excl. the cryo-collection (1,046 specimen)

Gatersleben

	Bestand/ Total number of accessions	Anbau/ Cultivation (accessions)
Getreide und Gräser/ Cereals and Grasses	**64.318**	**1.510**
Weizen/Wheat	28.190	578
Gerste/Barley	21.457	422
Hafer/Oats	4.829	99
Roggen/Rye	2.455	32
Triticale	1.755	31
Aegilops	1.536	34
Hirsen/Millets	834	33
Mais/Maize	1.661	41
Gräser/Grasses	1.601	240
Leguminosen/ Legumes	**27.986**	**1.469**
Phaseolus	8.638	236
Ackerbohnen/ Field beans	3.325	137
Sojabohnen/Soybeans	1.507	61
Bohnen-Sonder-kulturen/Other beans	844	91
Erbsen/Pea	5.510	74
Kichererbsen/ Chickpea	492	92
Lathyrus	528	117
Wicken/Vetches	1.885	285
Lupinen/Lupines	2.777	70
Linsen/Lentils	463	67
Kleearten/Clover	2.017	239
Cucurbitaceae	**2.716**	**96**
Kürbisse/Pumpkins	904	26
Melonen/Melons	452	21
Gurken/Cucumbers	702	27
Sonstige/Others	658	22
Gemüse (+Rüben)/ Vegetables	**15.654**	**2.308**
Tomaten/Tomatoes	3.317	89
Paprika/Red pepper	1.524	17
Eierfrüchte/Eggplant	84	9
Beta	2.317	154
Raphanus	735	44
Möhren/Carrots	488	57
Zichorie/Chicory	682	52
Zwiebeln/Onions	1.446	1.250
Brassica	2.198	255
Salat/Lettuce	1.151	235
Spinat/Spinach	216	7
Sellerie/Celery	247	23
Sonstiges/Others	1.249	116
Öl-, Faser- und Farbpflanzen/Oil, Fibre and Dye Plants	**8.324**	**925**
Lein/Flax	2.322	86
Sonnenblumen/ Sunflower	695	128
Farbpflanzen/Dye plants	481	86
Faserpflanzen/Fibre plants	133	14
Sonstige/Others	3.554	252
Arznei- und Gewürz-pflanzen/Medicinal and Spice Plants	**6.364**	**1.439**
Mutanten/Mutants	**2.721**	**458**
Tomaten/Tomatoes	736	16
Soja/Soybean	1.450	420
Antirrhinum	535	22
Gesamt/Total	**128.083**	**8.205**
Außenstelle „Nord"/External Branch "North"		
Kartoffeln/Potatoes[2]	**5.945**	**3.056**
Öl- und Futterpflanzen/ Oil and Forage Crops	**14.085**	**1.330**
Raps und Futterkohl/ Rapeseed and feeding kale	2.454	64
Futtergräser/Forage grasses	10.408	1.246
Rotklee und Luzerne/ Red clover and alfalfa	1.223	20
Gesamt/Total	**148.113**	**12.591**

[2] ausschließlich Cryo-Sammlung (1.046 Muster)/excluding the cryo-collection (1,046 specimen)

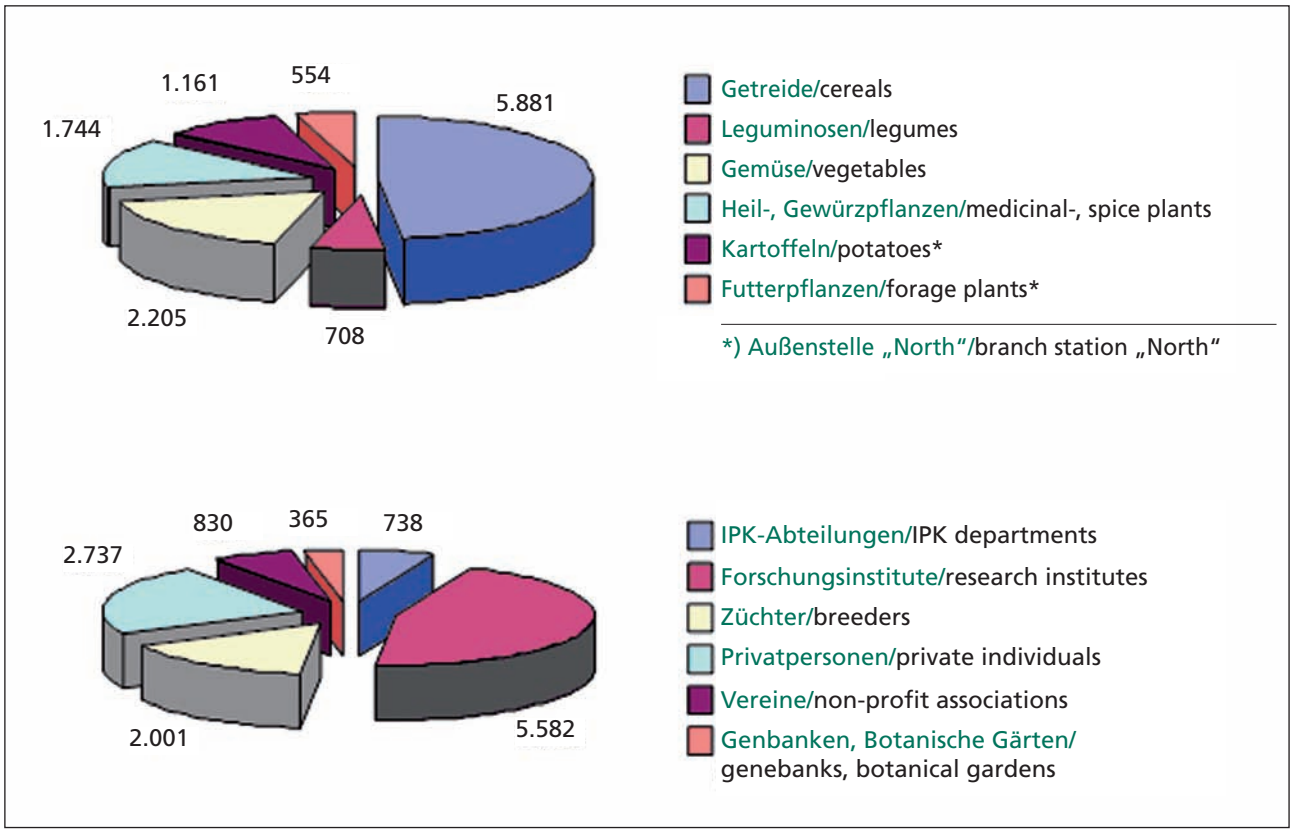

Fig. 10 Materialabgabe im Jahr 2007, aufgeschlüsselt nach Fruchtarten und Nutzergruppen (insgesamt 12.253 Muster)./
Material transfer in 2007, according to crop assortments and user groups (total of 12,253 accessions).

Qualitätsmanagement

Einen wichtigen Meilenstein in der Entwicklung der Genbank stellte die im März erfolgte Zertifizierung des Qualitätsmanagements (QM) nach DIN EN ISO 9001:2000 dar. Sämtliche Kernprozesse in der Genbank sind nun dokumentiert und durch Verfahrensregelungen und Arbeitsanweisungen unterlegt. Die Dauerhaftigkeit der Qualitätssicherung in Service und Forschung wird durch die Überprüfung ausgewählter Leistungskennziffern, wie Drittmitteleinwerbung, Publikationstätigkeit oder Kundenzufriedenheit sowie durch regelmäßige Audits gesichert. Mit der erfolgreichen Etablierung eines QM-Systems wurde eine wichtige Voraussetzung für die Schaffung zukünftiger Management-Standards zur internationalen Zusammenarbeit sowie für die nachhaltige Sicherung des bei den Sortimentsleiter/-innen vorhandenen Know-hows geschaffen. Die im Rahmen der Einführung des QM festgelegte, strikte Trennung des Genbankmaterials von gentechnisch veränderten Pflanzen bei Anbau, Ernte und Lagerung stellen eine wichtige Grundlage zur Absicherung der „Gentechnikfreiheit“ der Vermehrungsbestände der Genbank dar.

Forschung

Die Forschungs- und Erhaltungsarbeiten der Genbank sind in drei Bereiche gegliedert: Management und Evaluierung, Charakterisierung und Dokumentation sowie Taxonomie und Evolution. Der weit überwiegende Teil

4,351 samples (36 %) were sent abroad. More details on the distribution of genebank accessions are given in Fig. 10.

Quality management

Back in 2005 the establishment of a quality management system (QM) was initiated. Its successful certification according to DIN EN ISO 9001:2000 represents an important milestone in the strategic development. In the QM system all core processes of the collection management are described in a handbook and are documented by procedure instructions. These also include measures to avoid any admixture with genetically modified seed or pollen. This is achieved by means of a strict separation between plant genetic resources of the Genebank and transgenic plants regarding cultivation, harvest and seed storage. The quality of the service and research activities will be secured by monitoring key indicators such as extramural funding, publications or satisfaction of users and by performing regular audits. The QM also represents a guardrail for the development of management standards for international collaboration and to secure the knowledge and know-how of individual curators.

Research

Along with the collection management the scientific activities within the department are organised in three programmes: Management and Evaluation, Characterisa-

der F&E-Arbeiten wird über Drittmittel finanziert. Im Berichtszeitraum konnten neue Drittmittelprojekte bei der EU (EURALLIVEG, ERA-Net), dem BMBF (mehrere GABI-Projekte) sowie bei der DFG eingeworben werden. Im Folgenden sollen die wichtigsten Entwicklungen und Ergebnisse zusammengefasst werden. Für weitere Einzelheiten wird auf die Berichte aus den einzelnen Arbeitsgruppen verwiesen.

Im Zentrum des **Forschungsbereichs Taxonomie und Evolution** steht die Bearbeitung von Fragestellungen der Kulturpflanzenevolution, wobei Artbildungsprozesse sowie die Beziehung von Artbildung und Ausbreitung untersucht werden. Von besonderem Interesse ist hierbei die Aufklärung des Zusammenhangs zwischen Anpassung und Artbildung sowie die Untersuchung der populationsgenetischen Effekte von Domestikationsprozessen. Über weite Strecken werden die genannten Fragestellungen bei Gerste studiert.
Besonders hervorzuheben ist der Abschluss der Arbeiten zur phylogeographischen Analyse der europäischen Strandgerste in der Arbeitsgruppe Experimentelle Taxonomie. Die Ergebnisse zeigen, dass es sich bei den beiden bisher als Unterarten aufgefassten Taxa um zwei klar getrennte Arten handelt, die während des Pleistozäns in einem westlichen (Iberische Halbinsel) und einem östlichen (östlicher Mittelmeerraum) Glazialrefugium entstanden sind.

Im **Bereich Management und Evaluierung** sind alle Arbeitsgruppen zusammengefasst, die in das Erhaltungsmanagement der Genbank eingebunden sind. Am 1. April wurde zusammen mit sieben Partnern das GEN RES-Projekt „EURALLIVEG" gestartet, dessen Koordination in der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung angesiedelt ist. Ziel ist die Ermittlung von Duplikaten (*Allium sativum*) in unterschiedlichen Sammlungen sowie der Aufbau einer Cryo-Sammlung bei dieser Kulturart. In der Arbeitsgruppe Ressourcengenetik und Reproduktion wurden im Januar die Arbeiten an einem weiteren EU GEN RES-Projekt begonnen („Leafy Vegetables Germplasm, Stimulating Use"). Das IPK ist hierbei für die Koordination des Arbeitspakets „Regeneration und Charakterisierung" zuständig. Die Verlängerung der maximalen Lagerdauer von Saatgut ist ein wichtiges Thema im Bereich der sammlungsbezogenen Forschung. Untersuchungen an Weizensaatgut, welches über 30 Jahre gelagert wurde, zeigten, dass die Keimfähigkeit des Saatguts signifikant durch genetische Effekte beeinflusst wird. Die Unterschiede zwischen Akzessionen mit hoher und niedriger Keimkraft konnten auch im Rahmen eines Schnelltests bestätigt werden. Damit steht in Zukunft ein geeignetes Testsystem für genetische Kartierungsexperimente zur Verfügung.

Der **Bereich Charakterisierung und Dokumentation** befasst sich mit der Beschreibung von Genbankmaterial auf DNA-Ebene sowie mit der Entwicklung und Pflege

tion and Documentation and Taxonomy and Evolution. The majority of the research projects are extramurally funded. During the reporting period several new grants were acquired from the EU (EURALLIVEG, ERA-Net), the Federal Ministry of Education and Research (BMBF) as well as from the German Research Council (DFG). In the following, the most significant developments are summarised. Further details can be retrieved from the reports of the individual research groups.

The major focus of the **research programme Taxonomy and Evolution** is the investigation of processes leading to speciation and the interplay between speciation and radiation. Of particular interest are the relation between adaptation and speciation and the effects of domestication processes, as they are investigated using population genetic approaches. In the research group Experimental Taxonomy, a study on phylogeographic analysis of the wild barley *Hordeum marinum* complex has been completed. The results demonstrate that two taxa, which were hitherto regarded as subspecies, are clearly distinct species, which originated during the last Pleistocene in a western (Iberian peninsula) and an eastern (Eastern Mediterranean) glacial refuge.

The programme Management and Evaluation comprises all groups that are involved in the management of the collections. On April 1st the EU GEN RES project "EURALLIVEG", which is coordinated by the research group *In vitro* Storage and Cryopreservation was started together with seven partners. The principal objective of this project is the identification of duplicate samples in garlic (*Allium sativum*) collections and the establishment of a cryo-collection for this species. Another GEN RES project ("Leafy Vegetables Germplasm, Stimulating Use") has been started in the research group Resources Genetics and Reproduction. Prolongation of the maximum storage time of seeds is an important prerequisite for the optimisation of the collection management. After more than 30 years of storage the analysis of wheat seeds revealed that the germination rate is significantly influenced by genetic factors. Differences between accessions with high and low germination vigour could be confirmed using an alternative assay, inducing rapid senescence. These findings now open the opportunity to perform genetic analysis using appropriate mapping populations.

The third **programme, Characterisation and Documentation**, deals with the description of genetic resources at the DNA level as well as the development and curation of databases related to genetic resources. After completion of the 5-years funding by BMBF, the research group Plant Data Warehouse was closed in October 2007. In addition to the development and integration of databases, the research group provided a significant contribution to the comparative analysis of the genomes of barley and rice thus providing novel insight into the evolution of the barley genome (see Fig. 9, p. 27).

von Datenbanken zur Speicherung und Bereitstellung von genbankbezogenen Daten. Die Förderung der ausschließlich über Projektmittel des BMBF finanzierten Arbeitsgruppe Plant Data Warehouse lief zum 31. Oktober 2007 aus. Neben der Entwicklung verschiedener Datenbanken leistete die Arbeitsgruppe einen wichtigen Beitrag zur vergleichenden Kartierung der Genome von Reis und Gerste und den sich daraus ableitenden Erkenntnissen zur Genomevolution der Gerste (s. Fig. 9, S. 27).

In der Arbeitsgruppe Genomdiversität wurde die Entwicklung einer Gerstenpopulation für ein systematisches Mutantenscreening (TILLING) fortgesetzt. Diese stellt eine wichtige Ressource für die funktionelle Überprüfung von Kandidatengenen dar. Eine wichtige Grundlage für die systematische Identifizierung und Isolation von Genen bei Gerste ist die Verfügbarkeit einer physischen BAC-Kontig-Karte, bzw. darauf aufbauend, die Sequenzierung des Genoms. Als Grundlage hierfür wurde im August 2006 durch das IPK die Gründung des International Barley Sequencing Consortiums (IBSC) initiiert, in welchem sich führende Forschungsgruppen aus sechs Ländern und vier Kontinenten zusammengeschlossen haben und aufbauend auf einem gemeinsamen Forschungsplan an der Sequenzierung des Gerstengenoms arbeiten (http://barleygenome.org). Zur Fortführung der Arbeiten zur Entwicklung einer BAC-Kontig-Karte und zur Sequenzierung definierter Chromsomenbereiche konnten zusätzlich zu den Projektgeldern aus dem *WGL* „Pakt für Forschung und Innovation" weitere Projektmittel von der EU (ERA-Net) und dem BMBF (GABI-FUTURE) eingeworben werden.

Andreas Graner, Januar 2007

In the research group Genome Diversity the development of a TILLING population in barley was continued. It represents an important resource for the functional analysis of candidate genes in barley. Another resource for the systematic identification and isolation of genes is the availability of a physical BAC-contig map and building on this resource the subsequent sequence analysis of the barley genome. To spur the latter, the International Barley Sequencing Consortium (IBSC) bringing together leading research groups from four continents became effective in 2007 by adopting and implementing a common research agenda (http://barleygenome.org). To continue the development of a physical map and to start sequencing of selected chromosome segments, additional funding was obtained from EU (ERA-Net) and BMBF (GABI-FUTURE).

Andreas Graner, January 2007

Programme: Characterisation und Documentation

Research Group: Genome Diversity

Head: Prof. Andreas Graner, Dr. Nils Stein

Scientists

IPK financed
Ariyadasa, Ruvini Tharanga, Dr. (Pakt für Forschung und Innovation, since 15.08.2007)
Haseneyer, Grit (0,5 P, since 01.08.2007)
Rizvi, Reshma (0,5 P, since 01.09.2007)
Schulte, Daniela, Dr. (Pakt für Forschung und Innovation, till 31.12.2007)
Sretenovic-Rajicic, Tatjana, Dr. (Pakt für Forschung und Innovation, till 30.06.2007)
Stracke, Silke, Dr. (P, till 31.03.2007)
Giang, Vu Thi Ha (0,5 Annex, since 01.06.2007)

Grant Positions
Athmer, Benedikt (0,5 Saxony-Anhalt)
Gottwald, Sven, Dr. (BMBF)
Haseneyer, Grit (0,5 BMBF, till 31.07.2007)
Rizvi, Syed Massod, Dr. (BMBF, since 01.08.2007)
Shahinnia, Fahimeh, Dr. (DFG, since 01.09.2007)

Visiting Scientists
Barabaschi, Delfina, Dr. (self-financed, since 15.06.2007)
Große, Ivo, Prof. (Martin Luther University Halle-Wittenberg, since 01.10.2007)
Perovic, Dragan, Dr. (BAZ, since 07.06.2007)
Sabetta, Wilma (PhD scholarship, since 09.03.2007)

Scholars
Xianghua, Li (InWEnt, 02.05.-14.09.2007)

Goals

Development of genome-based strategies for the characterisation and utilisation of plant genetic resources.

Research Report

Research activities of the group aim at refining the knowledge on the structure and function of plant genomes. In addition to deepening the insight into genetic and biological processes, this will support the efficient management of genetic resources and the identification of novel alleles to promote their genetic improvement. Barley (*Hordeum vulgare*) is being used as model system, due to its salient agricultural importance and because its seven chromosomes represent the base genome of all species within the Triticeae tribe. To attain these goals, the research group follows a two-tiered approach: the **development and the enhancement of resources** for structural and functional genome analysis and **hypothesis-driven research on biological and genetic problems**. Genetic issues are investigated on the level of structural genetics (meiotic mapping, physical mapping) and on the functional level. Regarding the latter, transcript profiling is being applied to associate the differential abundance of RNA levels with seed traits in barley and abiotic stress in barley and rye (M. Rizvi, B. Athmer). In the following, recent developments in the field of structural genetics will be reported, though.

The availability of a whole genome sequence represents an essential resource for the systematic investigation of a genome to uncover basic principles of evolution and adaptation, the map-based isolation of genes, and the exploitation of its genetic and allelic diversity. Hence, the generation of the complete genomic sequence of barley represents a paramount goal in the strategic research activities of the group. As an important step to reach this objective the **International Barley Sequencing Consortium** (IBSC) has been founded in December 2006 and is presently chaired by the PIs of this research group. Additional funding for physical map construction and targeted sequencing could be acquired in the reporting period from the EU (ERA-Net) and the BMBF (GABI-FUTURE). To facilitate a clone-by-clone sequencing approach along a minimum tilling path, the **construction of a physical map** using a BAC fingerprinting approach was continued. To this end, DNA of individual BACs, selected from three different libraries of the cultivar "Morex", are restricted with five restriction enzymes. Sticky ends are labelled with different fluorescent dyes by a SNaPshot reaction (Applied Biosystems) and the resulting fragments are analysed on an ABI 3730xl sequencing machine. The experimental conditions for high information content fingerprinting of BAC clones were adjusted and a data analysis pipeline was established to allow for high throughput analysis. Based on theoretical considerations, 15-fold coverage should yield between 7,000 and 8,000 contigs. As of December 2007, high-quality fingerprints were obtained from 176,096 BAC clones corresponding to about 4-fold genome coverage. 140,707 BACs fall into 25,408 contigs, while 35,389 BACs are still unlinked singletons. The average number of BAC clones per contig amounts to 5.3 (D. Schulte, T. Sretenovic Rajicic, R. Ariyadasa).

In the context of the map-based isolation of the **GA-insensitive semi-dwarfing gene *sdw3***, the target interval, comprising 0.04 cM on a high resolution genetic map of barley, has been further analysed by comparative mapping in rice and *Brachypodium sylvaticum*. As to the latter, a contiguous sequence of 365 kb was obtained from screening a BAC library and sequence analysis of an overlapping set of four BACs. The target interval in rice encompasses 180 kb and comprises 24 genes of which 15 are not present in *Brachypodium*. The corresponding region in *Brachypodium sylvaticum* measures about 220 kb with 16 annotated genes of which seven are not present in rice. The remaining nine genes are conserved between both species and show perfect collinearity. Screening of a barley BAC library by using eight genes from the target interval led to the identification of seven BAC contigs. Of these, only two contigs identified by two genes spaced by 800 bp in *Brachypodium* showed overlaps. Based on survey sequencing of one representative BAC per barley contig, 11 complete and two fragmented genes were identified. Seven genes were found in a colinear position in rice while four genes are unique to barley. The results confirm previous observations on varying gene repertoires of orthologous regions in rice, *Brachypodium* and Triticeae and provide further proof of the necessity to rely on several genomes when exploiting synteny with model genomes for map-based cloning. Based on the sequence information, three candidate genes for GA-signalling are further investigated by re-sequencing *sdw3* mutant and wild type genotypes in barley and by analysing induced mutants identified from a TILLING population (V.T.H. Giang).

To assist the functional verification of candidate genes a **TILLING** (targeted induced local lesions in genomes) population is being developed. The establishment of an M_2 mutant population consisting of 10,492 independent plants was completed. For systematic screening of this population, DNA of 8,500 M_2 mutants has been arranged in 8-fold 2D pools. During the reference period, screening of a subset comprising 7,348 lines was completed for five genes. The averaged mutation frequency amounts to 1/500kb. 35 % of the mutations revealed missense alleles and 4 % resulted in truncations. 35 % of the silent mutations were present in noncoding regions (S. Gottwald).

As a step towards the development of genome-based strategies for the utilisation of genetic diversity a study on **linkage disequilibrium (LD) mapping** in barley has been completed. To this end, a world-wide collection of 225 spring barley cultivars was phenotyped in multi-location trials for five agronomic traits (heading date, plant height, thousand grain weight, starch content, protein content). Single Nucleotide Polymorphisms (SNPs) in nine candidate genes were correlated with trait data in order to identify associations. Using a mixed model that includes information on population structure, row-type and origin of the accessions, significant marker trait associations were identified for five of the candidate genes explaining up to 25 % of the phenotypic variation, respectively (see Fig. 11). Interestingly, heading date in the present population was influenced only by allelic variation in the gene *PpdH1*, while allelic variation in other candidate genes of the flowering time signalling pathway (*Hv-CO1, Hv-FT1*) did not yield significant effects. While the results are very encouraging regarding the potential of LD-based association mapping approaches in barley, they also demonstrate that population structure is a major limitation for the statistic and genetic power of the approach. Hence,

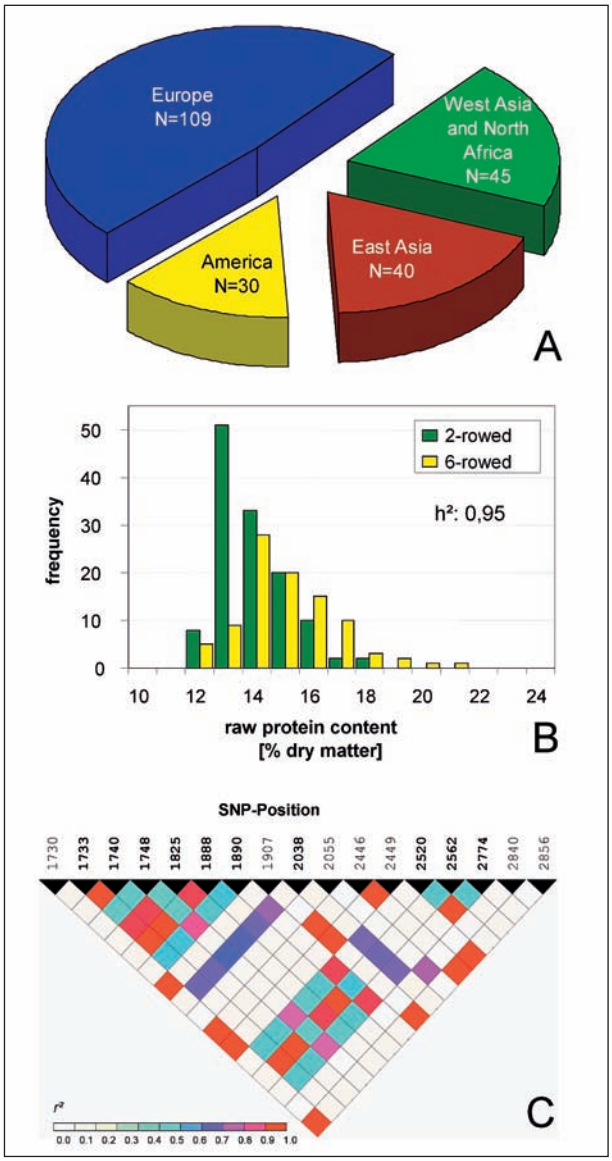

Fig. 11 Association mapping in spring barley. A) Geographic origin of 224 accessions used for LD mapping of candidate genes. B) Frequency distribution and broad sense heritability (h^2) for Raw Protein Content (RPC) for the subpopulations of 2-rowed (n=96) and 6-rowed barleys (n=128). C) Association analysis of SNPs detected in the candidate gene *Blz1*, a bZIP transcription factor expressed in early endosperm development. SNPs with minor allele frequencies > 5 % are indicated on top by their respective position in the annotated gene. SNPs printed in bold are associated ($p< 0.05$) with RPC. Haplotypes of that gene explain 10.5 % of the phenotypic variation. Pairwise LD values were calculated as r^2. The r^2 scale is binned by a colour code. Complete LD (1.0) is indicated by red whereas white refers to alleles at Hardy Weinberg equilibrium ($r^2=0$) (G. Haseneyer et al.).

further work is needed to statistically handle this issue, to monitor the decay of LD on a genome-wide level and to develop non-structured populations for further analysis (S. Stracke, G. Haseneyer).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, T. Thiel, Ch. Künne, J. Keilwagen;
Dept. of Genebank, External Branch "North"; Dr. K.J. Dehmer, E. Willner;
Dept. of Genebank, Research Group Quantitative Evolutionary Genetics; Dr. K. Schmid;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder, Dr. I. Matthies;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke, Dr. N. Sreenivasulu;
Dept. of Molecular Genetics, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Plant Genome Resources Centre (PGRC); Dr. P. Schweizer.

Outside the Institute:

Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute for Resistance Research and Stress Tolerance, Quedlinburg; Prof. F. Ordon, Dr. A. Habekuss;
University of Hohenheim, Institute for Plant Breeding, Seed Science and Population Genetics, Hohenheim; Prof. H. Geiger;
University of Hohenheim, Bioinformatics Section, Hohenheim; Prof. H.-P. Piepho;
University of Potsdam, Institute of Biochemistry and Biology, Potsdam; Prof. T. Altmann;
KWS Saat AG, Einbeck; Dr. A. Zacharias;
Lochow-Petkus GmbH, Bergen; Dr. V. Korzun;
Dr. J. Ackermann & Co., Irlbach; Dr. C.H.P. Einfeldt;
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CIRAD-Biotrop, Montpellier, France; Dr. B. Courtois, Dr. C. Dupuits;
INRA, Clermont-Ferrand, France; Dr. C. Ravel, Dr. G. Charmet, Dr. C. Feuillet;
INRA, Evry, France; Dr. D. Brunel;
INRA, Gif sur Yvette, France; Prof. A. Charcosset, Dr. D. Manicacci;
Australian Centre for Plant Functional Genomics (ACPFG), Glen Osmond, Australia; Prof. P. Langridge;
International Crops Research Institute for Semi Arid Tropics (ICRISAT), Patancheru, India; Dr. R. Varshney;
National Institute of Agrobiological Sciences, Tsukuba, Japan; Dr. T. Komatsuda, Dr. T. Matsumoto;
Parco Tecnologico Padano, Department of Plant Genomics, Lodi, Italy; Dr. C. Pozzi;
University of Udine, Udine, Italy; Prof. M. Morgante;
Scottish Crop Research Institute (SCRI), Dundee, UK; Prof. R. Waugh, Dr. D. Marshall;
University of California, Dept. Botany & Plant Sciences, Riverside, USA; Prof. T. Close;
University of Olomouc, Olomouc, Czech Republic; Prof. J. Doležel;
University of Zurich, Institute of Plant Biology, Zurich, Switzerland; Dr. T. Wicker.

Publications

Peer Reviewed Papers

Komatsuda, T., M. Pourkheirandish, C.F. He, P. Azhaguvel, H. Kanamori, D. Perovic, N. Stein, A. Graner, T. Wicker, A. Tagiri, U. Lundqvist, T. Fujimura, M. Matsuoka, T. Matsumoto & M. Yano: Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. Proc. Natl. Acad. Sci. U. S. A. 104 (2007) 1424-1429.

Marcel, T.C., R.K. Varshney, M. Barbieri, H. Jafary, M.J.D. de Kock, A. Graner & R.E. Niks: A high-density consensus map of barley to compare the distribution of QTLs for partial resistance to *Puccinia hordei* and of defence gene homologues. Theor. Appl. Genet. 114 (2007) 487-500.

Perovic, D., P. Tiffin, D. Douchkov, H. Bäumlein & A. Graner: An integrated approach for the comparative analysis of a multigene family: The nicotianamine synthase genes of barley. Funct. Integr. Genomics 7 (2007) 169-179.

Pourkheirandish, M., T. Wicker, N. Stein, T. Fujimura & T. Komatsuda: Analysis of the barley chromosome 2 region containing the six-rowed spike gene *vrs1* reveals a breakdown of rice-barley micro collinearity by a transposition. Theor. Appl. Genet. 114 (2007) 1357-1365.

Stein, N.: Triticeae genomics: advances in sequence analysis of large genome cereal crops. Chromosome Res. 15 (2007) 21-31.

Stein, N., M. Prasad, U. Scholz, T. Thiel, H.N. Zhang, M. Wolf, R. Kota, R.K. Varshney, D. Perovic, I. Grosse & A. Graner: A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. Theor. Appl. Genet. 114 (2007) 823-839.

Stracke, S., T. Presterl, N. Stein, D. Perovic, F. Ordon & A. Graner: Effects of introgression and recombination on haplotype structure and linkage disequilibrium surrounding a locus encoding *Bymovirus* resistance in barley. Genetics 175 (2007) 805-817.

Varshney, R.K., U. Beier, E.K. Khlestkina, R. Kota, V. Korzun, A. Graner & A. Börner: Single nucleotide polymorphisms

in rye (*Secale cereale* L.): discovery, frequency, and applications for genome mapping and diversity studies. Theor. Appl. Genet. 114 (2007) 1105-1116.

Varshney, R.K., K. Chabane, P.S. Hendre, R.K. Aggarwal & A. Graner: Comparative assessment of EST-SSR, EST-SNP and AFLP markers for evaluation of genetic diversity and conservation of genetic resources using wild, cultivated and elite barleys. Plant Sci. 173 (2007) 638-649.

Varshney, R.K., P. Langridge & A. Graner: Application of genomics to molecular breeding of wheat and barley. Adv. Genet. 58 (2007) 121-155.

Varshney, R.K., T.C. Marcel, L. Ramsay, J. Russell, M.S. Röder, N. Stein, R. Waugh, P. Langridge, R.E. Niks & A. Graner: A high density barley microsatellite consensus map with 775 SSR loci. Theor. Appl. Genet. 114 (2007) 1091-1103.

Other Publications

Altmann, T., G. Strompen, S. Gottwald, N. Stein, U. Hohmann, C. Jung, D. Holtgräwe, B. Weisshaar, J. Lunn & M. Stitt: GABI-TILL: Zentrale Plattform zur funktionalen Untersuchung von Leitgenen in Feldfrüchten mit Hilfe der TILLING-Technologie. GenomXPress Sonderausgabe März (2007) 15.

Stein, N.: Cereal genome collinearity revisited – advances through cereal genomics. Vortr. Pflanzenzücht. 71 (2007) 282-288.

Stein, N.: Der Countdown läuft – Wissenschaftler am IPK übernehmen führende Rolle in der Gersten-Genomforschung. GenomXPress 4 (2007) 4-6.

Stracke, S., G. Haseneyer, A. Graner, S. Sauer, H.H. Geiger, H.-P. Piepho, C. Paul, A. Charcosset, L. Camus-Kulandaivelu, J.-B. Veyrieras, M. Rousset, D. Manicacci, I. Bonnin, J. Cornoullier, D. Brunel, C. Dupuits, G. Charmet, C. Ravel, B. Courtois, M. Deu, P. Dubreuil & A. Murigneux: GABI-RYE-BARLEY-DIVERSITY: Von der Genomik zur genetischen Diversität: Zusammenhang zwischen genetischer Vielfalt und Merkmalsvariationen bei Getreide. GenomXPress Sonderausgabe März (2007) 20.

PhD and Diploma Theses

Giang, V.T.H.: Towards map based cloning of the Gibberellin-insensitive dwarfing gene *sdw3* of barley. (PhD Thesis) Ernst-Moritz-Arndt-Universität, Greifswald (2007) 88 pp.

Lectures, Posters and Abstracts

V2, V3, V14, V58, V59, V60, V61, V62, V63, V64, V65, V66, V67, V68, V82, V219, V247, V248, V249, V250, V251, V252, V253, V254, P9, P61, P62, P65, P66, P81, P82, P109, P110, P111, P112, P113, P127, P128, P150, P194, P207, P208, P214.

Additional Funding

For further information see the survey page 201–202

Research Group: Genebank Documentation

Head: Dr. Helmut Knüpffer

Scientists

IPK financed
Narang, Ram, Dr. (P)
Oppermann, Markus (P)

Scholars
Chol, Kim Yun (InWEnt, 02.05.-14.09.2007)

Goals

Development, maintenance and utilisation of information systems for plant genetic resources with the aim to collate, consolidate, and provide information on plant genetic resources (PGR) on internet-based platforms to researchers, breeders and other users, and to support the management of genebank accessions.

Research Report

The group's activities were focussed on the continuous extension and improvement of the Genebank Information System (GBIS). GBIS is being implemented in an Oracle environment.

(1) GBIS/M, the internal genebank management software, offers numerous functions supporting the day-to-day genebank activities. The development environment was changed to a new version of the IDE JDeveloper, and the GBIS/M deployment process was renewed fundamentally. The GBIS/M seed ordering module was further developed and improved. The taxonomy module was newly developed. The compilation of the developer's documentation and of the user manual for GBIS/M was started. Bug fixing, the implementation of change requests, and improving the user-friendliness of GBIS were continuously carried out. The data were further consolidated, and their quality was improved. Adaptation to new user requirements and the development of additional features are ongoing. The daily operation of the genebank was supported by GBIS/M in numerous ways, including seed stock data management and germination tests, management of passport data, handling of samples, support of the "seed cycle", processing of seed requests (submitted via GBIS/I; see below), the preparation of sowing lists based on seed stock data, printing labels for fields, greenhouses and distribution bags (M. Oppermann, W. Schölch, H. Knüpffer). Geographical data were consolidated and georeferenced (S. Schiebold).
(2) GBIS/I, the internet portal (http://gbis.ipk-gatersleben.de/gbis_i/), which includes search possibilities for passport data and an online seed ordering component, was extended by implementing the standardised Material Transfer Agreement (sMTA), to comply with the requirements of the Multilateral System. It allows to query information on more than 147,000 accessions of the IPK Genebank collections at Gatersleben, Malchow and Groß Lüsewitz (M. Oppermann, H. Knüpffer).
Passport data of genebank accessions were exported and submitted to the German National Inventory of PGR (PGRDEU), the European Central PGR Search Catalogous

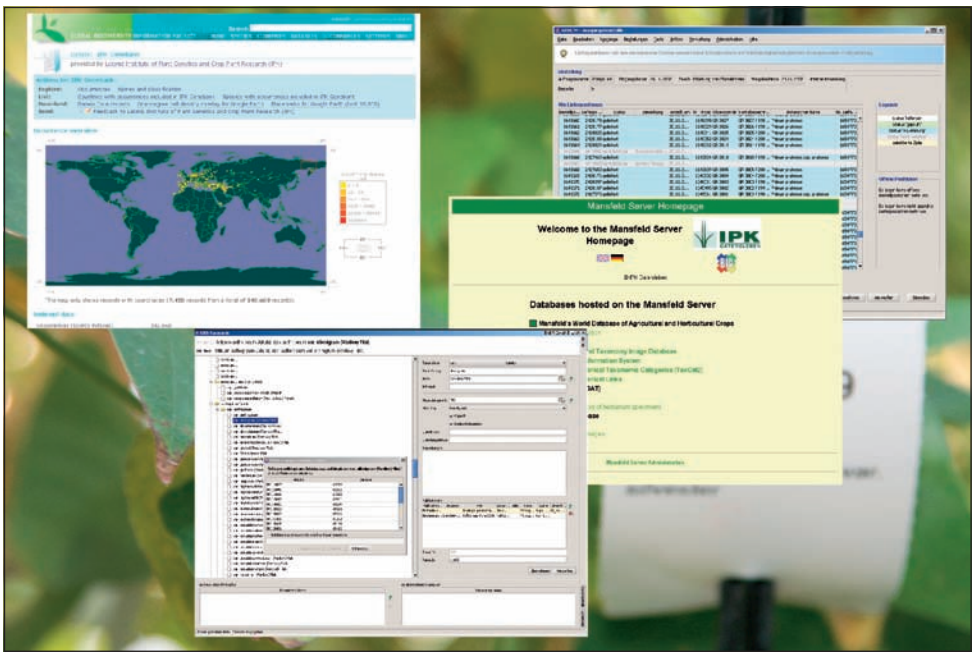

Fig. 12: Top left: Georeferenced Genebank accessions of IPK Gatersleben shown on an interactive map via the new portal of the Global Biodiversity Information Facility (GBIF) – http://www.gbif.org. Top right: Tracking of seed requests in GBIS/M, the internal management component of the Genebank Information System. Centre right: Entry screen of the Mansfeld Server, with the possibility to search Manfeld's World Database of Agricultural and Horticultural Crops. Bottom: Taxonomy client of GBIS/M, supporting the management of scientific names in GBIS (M. Oppermann).

(EURISCO), and numerous European Central Crop Databases. A webservice was configured to provide passport data to GBIF (Global Biodiversity Information Facility). Numerous information requests from users have been answered.

Other databases. The remaining MS Access and MS FoxPro databases on the Mansfeld Server – TaxCat2 (Database of Taxonomic Categories) and Links (Database of Botanical Links) – were migrated to the Oracle 10g database system. This included a comparative analysis of source and target databases with respect to data types, variable declarations, assignment statements, queries, functions, cursors, etc., and the transfer of the data into the target schemas. The corresponding web applications of TaxCat2, links and the Herbarium database were migrated to Oracle Application Express (APEX) pages, retaining the full functionality. All images related to the migrated databases are now stored in an operating system file outside the database, and a PL/SQL-based APEX web application was written to read these images and deliver them to the browser through the DBMS_LOB package.
The functionality of the migrated web applications was tested. To increase performance, summary tables and indexes were created. The application was deployed online in July.
In a second step, **Mansfeld's World Database of Agricultural and Horticultural Crops** (http://mansfeld.ipk-gatersleben.de), which had been migrated to an Oracle 10g database by the end of 2006, is being transferred to the "Berlin Model" for taxonomic databases, after migrating the model from MS SQL Server to Oracle 10g. User-defined procedures and functions as well as database triggers controlling data integrity and taxonomic logic in the "Berlin Model" were translated into their PL/SQL equivalents. Taxonomic authors and bibliographic references from the Mansfeld Database were parsed and atomised using special scripts, and inserted into the corresponding sections of the "Berlin Model" (R. Narang).

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner, Dr. U. Lohwasser;
Dept. of Genebank, Research Group External Branch "North"; Dr. K.J. Dehmer, E. Willner;
Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, T. Funke;
Dept. of Cytogenetics, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, S. Weise.

Outside the Institute:
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Quedlinburg; Dr. L. Frese, Dr. C. Germeier;
Federal Agency for Agriculture and Food (BLE), Information Centre for Biological Diversity (IBV), Bonn; Dr. F. Begemann, S. Harrer;
University of Kassel, Faculty of Agriculture, Institute of Crop Science, Department of Agricultural Biodiversity, Witzenhausen; Prof. K. Hammer;
Botanical Garden and Botanical Museum, Berlin-Dahlem; Prof. W. Berendsohn;
International Plant Genetic Resources Institute (IPGRI), Rome, Italy; Dr. J. Engels, L. Maggioni, S. Gaiji;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Dr. Th. van Hintum;
Nordic Gene Bank, Alnarp, Sweden; D.T.F. Endresen;
Research Institute of Bioresources, Kurashiki, Japan; Prof. K. Sato.

Publications

Peer Reviewed Papers
Kell, S.P., S.L. Jury, H. Knüpffer, B.V. Ford-Lloyd & N. Maxted: PGR Forum: serving the crop wild relative user community. Bocconea 21 (2007) 413-421.
Logozzo, G., R. Donnoli, L. Macaluso, R. Papa, H. Knüpffer & P.S. Zeuli: Analysis of the contribution of Mesoamerican and Andean gene pools to European common bean (*Phaseolus vulgaris* L.) germplasm and strategies to establish a core collection. Genet. Resour. Crop Evol. 54 (2007) 1763-1779.
Weise, S., S. Harrer, I. Grosse, H. Knüpffer & E. Willner: The European *Poa* Database (EPDB). Plant Genet. Resour. Newsl. 150 (2007) 64-70.

Electronic Publications
Kleijer, G., R. Häner & H. Knüpffer: Triticale and Rye Genetic Resources in Europe: *Ad hoc* Meeting, 28 September 2006, Nyon, Switzerland. http://www.ecpgr.cgiar.org/Networks/Cereals/Triticale_Rye_Sept06.pdf (2007).
Knüpffer, H.: Anbindung des Genbankinformationssystems (GBIS) als Data Provider für die Global Biodiversity Information Facility (GBIF), mit Hilfe der BioCASE-Provider-Software. www.gbif.org (2007).

Lectures, Posters and Abstracts

V111, V112, V113, V114, V115, V116, V117, V118, P160.

Additional Funding

For further information see the survey page 202.

Research Group: Plant Data Warehouse (BIC-GH Group)

(till 31.10.2007)

Head: Prof. Ivo Große

Scientists

Grant Positions
Funke, Thomas (0,5 BMBF, till 30.04.2007; BMBF, 01.05.2007–15.07.2007)
Keilwagen, Jens (BMBF, till 30.09.2007)
Künne, Christian (BMBF, till 31.10.2007)
Mielordt, Sven (BMBF, till 30.04.2007)
Mohr, Michaela (BMBF, till 31.10.2007)
Seifert, Michael (BMBF, till 30.09.2007)
Thiel, Thomas (0,66 BMBF, till 31.10.2007)

Visiting Scientists
Mielordt, Sven (self-financed, 01.05.-30.06.2007)

Goals

Development of a plant data warehouse as a flexible software platform for the integration and analysis of molecular, phenotypic, and taxonomic data as well as data on plant genetic resources from IPK-internal and worldwide distributed sources.

Research Report

Two major projects, the **trilateral project ARABIDO-SEED** funded by the BMBF for three years and the **Plant Data Warehouse project** funded by the BMBF for five years, were completed in 2007. The software developed and the data analysed within the project ARABIDO-SEED were integrated into the Plant Data Warehouse. The software developed within the Plant Data Warehouse project, including all databases, integrated data, and integrated analysis software, was successfully transferred to the research group Bioinformatics and Information Technology. The following six paragraphs exemplify the work conducted by the group in its last ten months.

Pyrosequencing data from the *Lolium* collection of the IPK Genebank comprising 2,906 accessions were integrated from the pyrosequencing database PSQDB into the Marker Mart of the Plant Data Warehouse in collaboration with the research groups Bioinformatics and Information Technology, External Branch "North", Genebank Documentation, and Genome Diversity. In addition, the associated **passport data** as well as **characterisation and evaluation data** were integrated from the Genebank Information System (GBIS) into the Passport Mart and Phenome Mart of the Plant Data Warehouse. The **Diversity Mart** was developed und filled with a structured subset of the integrated data to allow domain-spanning analyses of these data. A web-based software application, the **Diversity Studies Toolkit (DiSTo)**, was developed that allows biologists and breeders to perform these analyses in an intuitive manner. DiSTo offers generic query forms for clustering and classifying Genebank objects, such as accessions, parties, or growths. For example, it provides (i) descriptive statistics of user-specifiable subsets of genetic, phenotypic, and passport attributes, (ii) the calculation of population genetic parameters by AMOVA, (iii) the calculation of different genetic and phenotypic dissimilarity matrices and their visualisation, (iv) several algorithms for clustering and the reconstruction of phylogenetic trees, and (v) principle component and principle coordinate analyses and the visualisation of the results in two and three dimensions. The Diversity Mart was designed such that it allows the storage and analysis of genetic, phenotypic, and passport data from different germplasm collections and different species, and DiSTo was designed such that it allows analyses, including analyses across multiple collections or multiple species, of any data integrated into the Diversity Mart (C. Künne).

A web-application of the **Garlic Core Collection** was developed and integrated into the Plant Data Warehouse in collaboration with the research groups External Branch "North", Genebank Documentation, Genome Diversity, *In vitro* Storage and Cryopreservation, and Taxonomy of Plant Genetic Resources. It provides information about **passport data** as well as **characterisation and evaluation data** together with **images about morphologic characteristics** of currently 124 accessions. In addition, it provides a collection of ontogenetic images presenting developmental stages of different parts of the growing plant (T. Funke).

Resistance against the Barley Yellow Mosaic Virus (BaYMV) and the Barley Mild Mosaic Virus (BaMMV) is associated with sequence polymorphisms in the barley gene eIF-4E. 672 accessions were sequenced by the research group Genome Diversity, yielding **30 polymorphic sites** within coding exons and **44 haplotypes**. Software for **allele mining** was developed in collaboration with the research groups Genome Diversity and Quantitative Evolutionary Genetics addressing the following specific tasks: (i) estimate the number of haplotypes in the coding region of the eIF-4E gene in the entire barley collection of the IPK Genebank, and (ii) predict subsets of the entire collection with a high probability of containing novel haplotypes. Population genetic models are not well-suited for these tasks and provide estimates with surprisingly large error bars. Hence, models from statistics and sequence analysis were employed, yielding substantially lower error bars

when applied to experimentally verified sequences using a 10,000-fold stratified holdout sampling procedure. The most promising model turned out to be a **Bayesian tree**, yielding an estimate of 275 ± 15 haplotypes for a population with 13,799 accessions. Using **passport data** as well as **characterisation and evaluation data**, the error bars of the estimates could be further reduced and lead to the conclusion that stratification by **resistance** and **origin** provided the subsets with the highest predicted fraction of novel haplotypes per 1,000 accessions (J. Keilwagen).

Genome and segmental duplications are common in the plant kingdom, and the detection and evolutionary analysis of duplications in the barley genome can advance our understanding of genome evolution in the grass family with implications for molecular breeding in barley. The **barley-rice synteny model** was extended by integrating 1,026 Illumina markers based on the HarvEST #32 assembly into the existing IPK barley transcript map of barley comprising approximately 1,000 EST markers. It was found that 90 % of the markers show **sequence homology** to rice, and 50 % of them are located in **syntenic regions** of barley and rice, covering 80 % of the barley genetic map and 60 % of the rice genome, respectively. Using the extended barley-rice synteny model together with evidence from (i) measurements of synonymous and non-synonymous **substitution rates** as well as (ii) the location of **second-best homologs** of barley genes, it could be inferred that 40 % of the barley genome covered by the barley genetic map shows traces of genome duplications originating from the common ancestor of barley and rice (see Fig. 9, p. 27) (T. Thiel).

Several transcription factors responsible for the regulation of seed development in *Arabidopsis thaliana* were studied by ChIP/chip experiments within the trilateral project ARABIDO-SEED. A **software pipeline** for the efficient analysis of the **ChIP/chip data** and **gene expression data** generated by all of the participating partners from Spain, France, and Germany was developed in collaboration with the research groups Expression Mapping, Gene Regulation, and Phytoantibodies as well as with the other external partners of the project. This pipeline allows a **normalisation of the ChIP/chip data** and a **prediction of putative target genes** as well as subsequent analyses of gene expression data and conserved DNA motifs. The pipeline was designed such that it can handle ChIP/chip, expression, and sequence data from different projects and different species (M. Seifert).

The prediction of novel binding sites in the promoters bound by the studied transcription factors was one of the main goals of the trilateral project ARABIDO-SEED. The previously developed **EMMA algorithm**, which extends the widely used MEME algorithm, was extended in multiple directions. Motivated by the fact that ChIP/chip data as well as expression data are intrinsically noisy, the algorithm now allows that promoters may or may not contain binding sites. The user may specify either the expected percentage of promoters containing a binding site or, for each of the studied promoters individually, the **probability of containing a binding site**. Such probabilities can be obtained, for example, from the analysis pipeline described above. A second extension improves the recognition of binding sites with correlated nucleotides by recruiting **Variable-Order Markov models**, **Bayesian networks**, and **Variable-Order Bayesian networks**. A third extension allows the prediction of **cis-regulatory modules**, consisting of multiple binding sites with variable composition, spacing, and orientation (M. Mohr).

Today, the Plant Data Warehouse is a useful software platform for the integration and analysis of molecular, phenotypic, and taxonomic data as well as data on plant genetic resources. Currently, it is used more than 1,000 times per month, and its future maintenance is secured by the research group Bioinformatics and Information Technology. T. Funke, C. Künne, and S. Mielordt continue their careers in industry, J. Keilwagen, M. Mohr, M. Seifert, and T. Thiel continue their PhD studies at IPK, and I. Große continues his work at the Martin Luther University Halle-Wittenberg.

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Genebank, External Branch "North"; Dr. K.J. Dehmer;
Dept. of Genebank, Research Goup Quantitative Evolutionary Genetics; Dr. K. Schmid;
Dept. of Genebank, Research Group Taxonomy of Plant Genetic Resources; Dr. R. Fritsch;
Dept. of Cytogenetics and Genome Analysis, Research Group Expression Mapping; Dr. L. Altschmied;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert.

Outside the Institute:
B.I.M.-Consulting mbH, Magdeburg; Dr. R. Paul;
Biobase GmbH, Wolfenbüttel; Dr. A. Kel, Dr. O. Kel, Prof. E. Wingender;

Free University, Berlin; Prof. K. Reinert;
Friedrich Miescher Laboratory, Tübingen; Dr. G. Rätsch;
Humboldt University, Berlin; Prof. S. Hougardy, Dr. A. Schmitt;
Leibniz Institute of Plant Biochemistry, Halle/S.; Dr. S. Neumann, Dr. S. Rosahl;
Martin Luther University Halle-Wittenberg, Halle/S.; Prof. P. Molitor, Prof. S. Posch;
Max Planck Institute for Molecular Genetics, Berlin; Dr. A. Schliep;
Max Planck Institute for Molecular Plant Physiology, Golm; Dr. B. Kersten;
Max Planck Institute for Plant Breeding Research, Cologne; Dr. H. Schoof;
University of Bielefeld, Bielefeld; J. Baumbach, T. Kohl, Prof. B. Weisshaar;
Berlex Bioscience, San Francisco, USA; Dr. J. Fickett;
Ciudad Universitaria, Madrid, Spain; Prof. J. Vicente Carbajosa;
Cold Spring Harbor Lab, Cold Spring Harbor, USA; Dr. A. Smith, Dr. D. Ware, Prof. M. Zhang;
European Bioinformatics Institute, Hinxton, UK; M. Hoffman;
Institut Curie, Paris, France; P. Neuvial;
Max Perutz Labs, Vienna, Austria; Prof. A. v. Haeseler, Dr. D. Holste;
St. Petersburg Polytechnical University, St. Petersburg, Russia; Prof. M. Samsonova;
Tel Aviv University, Tel Aviv, Israel; Prof. I. Ben-Gal;
University Evry Val d'Essonne, Evry, France; Dr. P.-Y. Bourguignon;
University of Barcelona, Barcelona, Spain; Prof. J. Cerquides;
University of Pennsylvania, Philadelphia, USA; Prof. A. Hatzigeorgiou;
University of Rijeka, Rijeka, Croatia; Prof. B. Podobnik;
University Pompeu Fabra, Barcelona, Spain; Dr. R. Castelo;
URGV, Evry, France; Prof. M. Caboche, Dr. A. Lecharny.

Publications

Peer Reviewed Papers

Laurent, V., P. Devaux, T. Thiel, F. Viard, S. Mielordt, P. Touzet & M.C. Quillet: Comparative effectiveness of sugar beet microsatellite markers isolated from genomic libraries and GenBank ESTs to map the sugar beet genome. Theor. Appl. Genet. 115 (2007) 793-805.

Podobnik, B., J. Shao, N.V. Dokholyan, V. Zlatic, H.E. Stanley & I. Grosse: Similarity and dissimilarity in correlations of genomic DNA. Physica A 373 (2007) 497-502.

Stein, N., M. Prasad, U. Scholz, T. Thiel, H.N. Zhang, M. Wolf, R. Kota, R.K. Varshney, D. Perovic, I. Grosse & A. Graner: A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. Theor. Appl. Genet. 114 (2007) 823-839.

Weise, S., S. Harrer, I. Grosse, H. Knüpffer & E. Willner: The European *Poa* Database (EPDB). Plant Genet. Resour. Newsl. 150 (2007) 64-70.

Other Publications

Grau, J., J. Keilwagen, I. Grosse & S. Posch: On the relevance of model orders to discriminative learning of Markov models. Proceedings of the Workshop "Lernen – Wissen – Adaption", 24.-26.09.07, Halle/S. (2007) 61-66.

Grau, J., J. Keilwagen, A. Kel, I. Grosse & S. Posch: Supervised posteriors for DNA-motif classification. Proceedings of the German Conference on Bioinformatics (GCB) 2007, 26.-28.09.2007, Potsdam (2007) 123-134.

Keilwagen, J., J. Grau, S. Posch & I. Grosse: Recognition of splice sites using maximum conditional likelihood. Proceedings of the Workshop "Lernen – Wissen – Adaption", 24.-26.09.07, Halle/S. (2007) 67-72.

Mönke, G., T.M. Linh, U. Conrad, U. Hähnel, L. Altschmied, M. Mohr, I. Grosse, A. Vorwieger, H. Bäumlein, B. Weisshaar & P. Viehöver: GABI-ARABIDO-SEED: Wie steuern Transkriptionsfaktoren die Samenentwicklung bei Pflanzen? GenomXPress Sonderausgabe März (2007) 16.

Electronic Publications

Keller, E.R.J. & T. Funke: Die Knoblauch-Kernkollektion des IPK – IPK's Core Collection of Garlic. http://pgrc-35.ipk-gatersleben.de/apps/gcc/index.htm (2007).

Scholz, U., C. Künne, M. Lange, H. Miehe & T. Funke: IPK Crop EST Database: CR-EST (Version 1.5). http://pgrc.ipk-gatersleben.de/cr-est/ (2007).

PhD and Diploma Theses

Mauritz, J.: Erkennung von DNA-Bindungsstellen mittels Maximum Conditional Likelihood. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Informatik, Halle/S. (2007) 111 pp.

Lectures, Posters and Abstracts

V25, V69, V70, V71, V72, V73, V96, V97, V125, V157, V158, V159, V227, V264, V265, P11, P12, P53, P54, P55, P56, P57, P58, P67, P69, P77, P109, P110, P111, P112, P113, P127, P128, P153, P154, P155, P156, P157, P158, P159, P169, P196, P197, P198, P199, P214, P227, P228.

Additional Funding

For further information see the survey page 202.

Programme: Management and Evaluation

Research Group: Resources Genetics and Reproduction

Head: Dr. Andreas Börner

Scientists

IPK financed
Dittbrenner, Anke (0,5 P)
Lohwasser, Ulrike, Dr. (P)
Navakode Gangadharan, Sheeba (0,5 P)
Tikhenko, Natalya, Dr. (0,75 Annex, 03.09.-30.11.2007)
Weidner, Annette, Dr. (0,75 Annex)

Grant Positions
Neumann, Kerstin (0,5 Saxony-Anhalt)

Visiting Scientists
Daniel, Isaac, Dr. (Humboldt Foundation)
Dobrovolskaya, Oxana (DFG, 15.07.-12.10.2007)
Landjeva, Svetlana (DFG, 22.09.-22.12.2007)
Schloenvoigt, Michael, Dr. (InWEnt, 25.04.-30.09.2007)
Zaynali Nezhad, Khalil (Iranian government)

Scholars
Liu, Ligong (InWEnt, 02.05.-14.09.2007)
Liu, Dongyon (InWEnt, 02.05.-14.09.2007)

Goals

Long-term seed storage; reproduction, evaluation and genetic characterisation of genebank collections.

Research Report

The total number of accessions maintained at the Gatersleben site comprises 128,083 samples, of which 122,468 are preserved in the cold store. Safety duplicates are available for 9,605 accessions. 8,867 samples were used for performing germination tests. 10,538 accessions (excluding the External Branch "North") were distributed to users, two thirds of which were provided to research institutes including IPK (S. Pistrick, A. Börner). During the growing season 2006/2007 a total of 8,205 accessions were cultivated, including 1,205 samples grown for evaluation only. A taxonomic classification was performed for 2,716 accessions. Descriptor lists were created or revised for the genera/species *Spinacia, Cichorium, Eruca, Valerianella* and *Vicia faba* as well as the forage grasses (U. Lohwasser, E. Willner, M. Grau).

In March 2007, a **Quality Management System** according to the international standard DIN EN ISO 9001:2000 was implemented successfully. After passing an external audit the Genebank was certified for the scope "Research and Service on Plant Genetic Resources". The Genebank activities are divided into four main processes. Herein individual tasks and processes are described by procedure and working instructions in order to ensure an efficient and well-documented work. Five procedure instructions define the operations performed within the Resources Genetics and Reproduction group: handling of new seed material, seed reproduction, pollination, maintenance of vegetative plant material, and taxonomical determination of the genebank material. Reproducible and traceable processes ensure the high quality of the genebank material (U. Lohwasser, A. Graner, A. Börner).

The collection-related research focussing on **seed longevity studies** was continued. Analysing wheat accessions stored up to 33 years in the cold store, it was demonstrated that beside the duration of storage the germination rate is significantly influenced by the genotype. Furthermore, it was found that germinability of identical accessions after accelerated (ISTA) and natural aging was highly comparable (see Fig. 13). It was clearly demonstrated that by applying the accelerated aging test, it is possible to differentiate between high-vigour and lower-vigour accessions (S. Landjeva, M. Nagel, S. Pistrick, A. Börner).

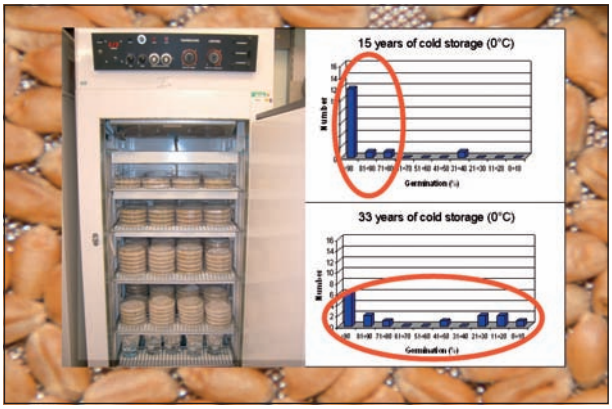

Fig. 13: Longevity of wheat accessions stored at 0 °C. Whereas after 15 years high germination rates were maintained for nearly all accessions analysed an increased variation ranging between > 90 and < 10 % germinability was obtained after more than 30 years of storage, determined by genotype (S. Landjeva, M. Nagel, S. Pistrick, A. Börner).

Activities on **characterisation and evaluation** were directed to *Papaver*, *Petroselinum* and a range of leafy vegetables. Morphological field evaluations of 300 *Papaver* and 220 *Petroselinum* accessions representing the Gatersleben collections but also material from the BAZ Quedlinburg (parsley) were performed and were/will be followed by biochemical (alkaloids, oils), aromatic (taste, flavour), disease resistance and molecular (AFLPs, RAPDs, SRAPs) analyses. The investigation of *Petroselinum* is a joint activity between IPK and BAZ (A. Dittbrenner, R. Kurch, U. Lohwasser, H.-P. Mock, F. Blattner).

With the aim to establish a network of partners active in the conservation and utilisation of plant genetic resources of leafy vegetables (*Lactuca, Spinacia, Cichorium, Valerianella, Eruca, Diplotaxis*) a **European Project** was initiated. IPK is coordinating the European activities on regeneration and characterisation (F. Kellner, M.-L. Graichen, A. Börner).

Research aimed to improve the utilisation of the cereal collection was continued with the focus on **abiotic stress tolerance**. Mapping populations of wheat and barley were phenotyped for tolerance against drought, salt, aluminium and pre-harvest sprouting. Major QTLs were detected at different growth stages in repeated experiments. Beside the classical QTL mapping approach, the phenotyping of an association mapping population consisting of 227 different barley genotypes including wild barley (*Hordeum spontaneum* Koch) and cultivated barley (*Hordeum vulgare* L.) was started (K. Neumann, K. Zaynali Nezhad, A. Weidner, S.G. Navakode, U. Lohwasser).

In close collaboration with the research group Gene and Genome Mapping the **molecular tagging of genes/QTLs** in the Triticeae was continued. The main focus was on genes determining spike morphology in wheat and rye. Loci determining multifloral spikelets were detected in homoeologous regions on the short arms of chromosomes 2D and 2R, close to the centromeres (O. Dobrovolskaya, M.S. Röder, A. Börner). In another study earlier developed *Triticum aestivum/Aegilops tauschii* introgression lines were employed for the detection of a gene (*Stb5*) determining resistance to *Septoria tritici* blotch. It was demonstrated that the analysis of introgression lines allows the detection and location of genes/QTLs originating from the progenitor of the D genome of hexaploid wheat (M.S. Röder, A. Börner).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Genebank, Research Group External Branch "North"; Dr. K.J. Dehmer, E. Willner;
Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry, Dr. H.-P. Mock.

Outside the Institute:

Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute of Plant Analysis, Quedlinburg; Prof. H. Schulz, Dr. W. Schütze;
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute of Horticultural Crops, Quedlinburg; Dr. F. Marthe, Dr. H. Budahn;
Martin Luther University Halle-Wittenberg, Institute for Plant Breeding and Plant Protection, Halle/S.; Prof. W.E. Weber, Dr. E. Schumann;
Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/S.; Prof. M. Röser;
University of Hohenheim, Seed Science and Technology, Hohenheim; Prof. M. Kruse;
Fa. Lochow-Petkus GmbH, Bergen; Dr. V. Korzun;
RAGT 2n, Silstedt; A. Fürste, H. Cöster;
Fa. Nordsaat, Böhnshausen; Dr. R. Schachschneider;
Fa. Plant Breeding GmbH, Gülzow; Dr. G. Melz;
University of Veterinary Medicine, Institute for Applied Botany and Pharmacognosy, Vienna, Austria; Prof. J. Novak;
John Innes Centre, Cereals Research Department, Norwich, UK; Prof. J.W. Snape;
St. Petersburg State University, St. Petersburg, Russia; Dr. A. Voylokov, Dr. N. Tikhenko;
Institute of Cytology and Genetics, Novosibirsk, Russia; Dr. E. Salina, Dr. T. Pshenishnikova, Dr. E. Khlestkina, Dr. O. Dobrovolskaya;
Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvasar, Hungary; Dr. G. Galiba, Dr. A.F. Bálint;
South Plant Biotechnology Centre, Odessa, Ukraine; Dr. S. Chebotar;
Universidad Nacional de La Plata, Facultad de Ciencias Agrarias y Forestales, La Plata, Argentina; Dr. A.M. Castro, Dr. M.R. Simón;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Dr. C. Kik, I. Boukema;
Institute of Field and Vegetable Crops, University of Novi Sad, Novi Sad, Yugoslavia; Dr. B. Kobiljski;
Leopold Franzens University Innsbruck, Institute of Pharmacy, Dept. of Pharmacognosy, Innsbruck, Austria; Prof. C. Zidorn.

Publications

Peer Reviewed Papers

Bálint, A.F., M.S. Röder, R. Hell, G. Galiba & A. Börner: Mapping of QTLs affecting copper tolerance and the Cu, Fe, Mn and Zn contents in the shoots of wheat seedlings. Biol. Plant. 51 (2007) 129-134.

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Dobrovolskaya, O., T.A. Pshenichnikova, V.S. Arbuzova, U. Lohwasser, M.S. Röder & A. Börner: Molecular mapping of genes determining hairy leaf character in common wheat with respect to other species of the Triticeae. Euphytica 155 (2007) 285-293.

Iqbal, N., F. Eticha, E.K. Khlestkina, A. Weidner, M.S. Röder & A. Börner: The use of SSR markers to identify and map alien segments carrying genes for effective resistance to leaf rust in bread wheat. Plant Genet. Resour. 5 (2007) 100-103.

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Varshney, R.K., U. Beier, E.K. Khlestkina, R. Kota, V. Korzun, A. Graner & A. Börner: Single nucleotide polymorphisms in rye (*Secale cereale* L.): discovery, frequency, and applications for genome mapping and diversity studies. Theor. Appl. Genet. 114 (2007) 1105-1116.

Book Chapters

Varshney, R.K., T. Mahendar, R.K. Aggarwal & A. Börner: Genetic molecular markers in plants: Development and applications. In: Varshney, R.K. & R. Tuberosa (Eds.): Genomics-Assisted Crop Improvement: Vol. 1: Genomics Approaches and Platforms. Springer, Dordrecht/The Netherlands (2007) 13-29.

Other publications

Börner, A., N. Iqbal, E.K. Khlestkina, S. Landjeva, U. Lohwasser, S. Navakode, K. Neumann, E.G. Pestsova, M.S. Röder, M.R. Simon, A. Weidner & K. Zaynali Nezhad: *Rht* dwarfing genes specific markers – Stripe rust adult plant resistance – Leaf rust resistance originated form *Ae. markgrafii* – Detection of *Septoria tritici* blotch resistance genes employing wheat – *Ae. tauschii* introgressions – Osmotic stress response in wheat seedlings – Salt tolerance – Aluminium tolerance – Pre-harvest sprouting/Dormancy. Ann. Wheat Newsl. 53 (2007) 21-26.

Börner, A. & V. Korzun: Rye as a candidate for gene tagging in the Triticeae – a review. Vortr. Pflanzenzücht. 71 (2007) 194-204.

Chesnokov, Y.V., N.V. Pochepnya, V.G. Verzhuk, L.V. Kozlenko, E.A. Goncharova, A.M. Kapeshinskiy, L.G. Tyryshkin & A. Börner: Identification of adaptively important quantitative trait loci in hexaploid wheat *Triticum aestivum* L. at different ecological zones. Proc. VI Congress of Russian Society of Plant Physiologists, 18.-24.06.2007, Syktyvkar (2007) 420-422.

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PhD and Diploma Theses

Nagel, M.: Langlebigkeit von Saatgut unter ambienten Lagerungsbedingungen in der *ex situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen in Gatersleben. (Master) Georg-August-Universität, Göttingen (2007) 131 pp.

Lectures, Posters and Abstracts

V36, V37, V38, V39, V40, V42, V46, V49, V50, V106, V133, V138, V139, V140, V141, V142, V162, V163, V164, V165, V166, V167, V272, V273, V274, V301, P30, P35, P36, P37, P62, P117, P142, P143, P144, P145, P164, P182, P223, P239, P240, P241.

Additional Funding

For further information see the survey page 203.

Research Group: In vitro Storage and Cryopreservation

Head: Dr. Joachim Keller

Scientists

IPK financed
Kaczmarczyk, Anja (0,5 P)

Grant Positions
Kästner, Ute, Dr. (0,5 BMBF)
Zanke, Christine, Dr. (EU, since 01.04.2007)

Visiting Scientists
Altieri, Luciana (EU, 20.05.-01.06.2007)
Khairullina, Alfia (self-financed, 07.-12.10.2007)
Ohlsson, Pia (self-financed, 07.-12.10.2007)
Olas, Marta (EU, 11.-27.04.2007)

Scholar
Mercado Zubieta, Gisell (InWEnt, 02.05.-14.09.2007)

Goals

In vitro maintenance of vegetatively propagated genebank accessions, cryopreservation of potato, garlic, and mint. Research on tissue water conditions and cold adaptation connected with influence of ultra-low temperatures on plant organs.

Research Report

Accessions of the genera ***Allium, Antirrhinum, Artemisia, Brassica, Dioscorea, Mentha, Orthosiphon,*** **and** ***Sechium*** are kept *in vitro* comprising **592 clones of 504 genebank accessions**. Amongst them, **71 clones of garlic and 26 of shallot** are maintained virus-free. For distribution to the users **17 samples of mint were provided** (D. Büchner, M. Grübe, A. Senula).

The **potato cryopreservation** research programme was continued. The focus was again on cold preculture with constant or alternating temperatures. Two **wild, frost-resistant species *Solanum acaule* and *S. demissum* were compared with *S. tuberosum* "Désirée" and "King Edward".** Biochemical analyses on soluble sugars, starch, and amino acid concentrations were performed. **Soluble sugar concentrations** increased for all accessions after alternating temperature preculture, whereas starch concentration decreased for three accessions. The improvement of potato cryopreservation might be tightly **regulated by the carbohydrate metabolism**, which plays a crucial role at low temperatures. **Comparisons between DMSO droplet method and droplet vitrification method** were conducted with *S. demissum* and *S. tuberosum* "Désirée". Both methods confirmed the improvement of cryopreservation results using alternating temperature preculture. **Measurements with a Differential Scanning Calorimeter (DSC)** were performed to compare cryoprotectant solutions, different incubation times of shoot tips in cryoprotectants and to analyse the water state during cooling and rewarming of shoot tips (see Fig. 14). **Glass transition** could be found after incubation in PVS2, but **ice crystallisation** was found after incubation in DMSO solution. The **cryo-collection of potato** was increased to **1,028 clones.** Furthermore, the quality of **11 accessions** was improved by **replacing virus-infected** or weakly reacting material **by virus-free** and more vigorous **material. 12 samples** were provided to the External Branch "North" **for distribution to the users** (A. Kaczmarczyk, M. Grübe, G. Mercado Zubieta).

The recently established collection of **garlic** in **cryopreservation** amounts to **35 accessions** with a higher safety standard as compared to 2006. The transfer of **virus-free garlic** material into protected greenhouse and field conditions was continued. Virus-free material was provided to the cryopreservation routine (J. Keller, D. Büchner, A. Senula).

The droplet vitrification method was further used routinely for cold-hardened plants of mint. A total of **22 accessions from 11 species** are in cryopreservation with 200 explants each**.** Regeneration rates varied between 30 and 98 %. Screening for **endophytic bacteria in the *in vitro* donor plants** on different media was performed to assess the quality of the explants for cryopreservation. Endophytes were only safely detectable if infection was strong. In case of weak infections and unclear situation, **antibiotics were added to the regeneration media** after cryopreservation. Five antibiotics were successfully tested on their effect of repressing bacteria while not influencing plant growth. Investigations on **cryopreservation of *Orthosiphon*** were continued. As a result of DSC measurements, the duration of cryoprotection in solution PVS2 was increased to achieve optimal glass transition. As of now, the regeneration after cryopreservation is still low (A. Senula).

The **EU-funded GEN RES project on garlic and shallot EURALLIVEG (**AGRI GEN RES 050) started in April. Initially, two training courses were held for the partner laboratories and the project website was implemented. The group organised the acquisition of the leaf material for **molecular marker analyses** from the partners amounting

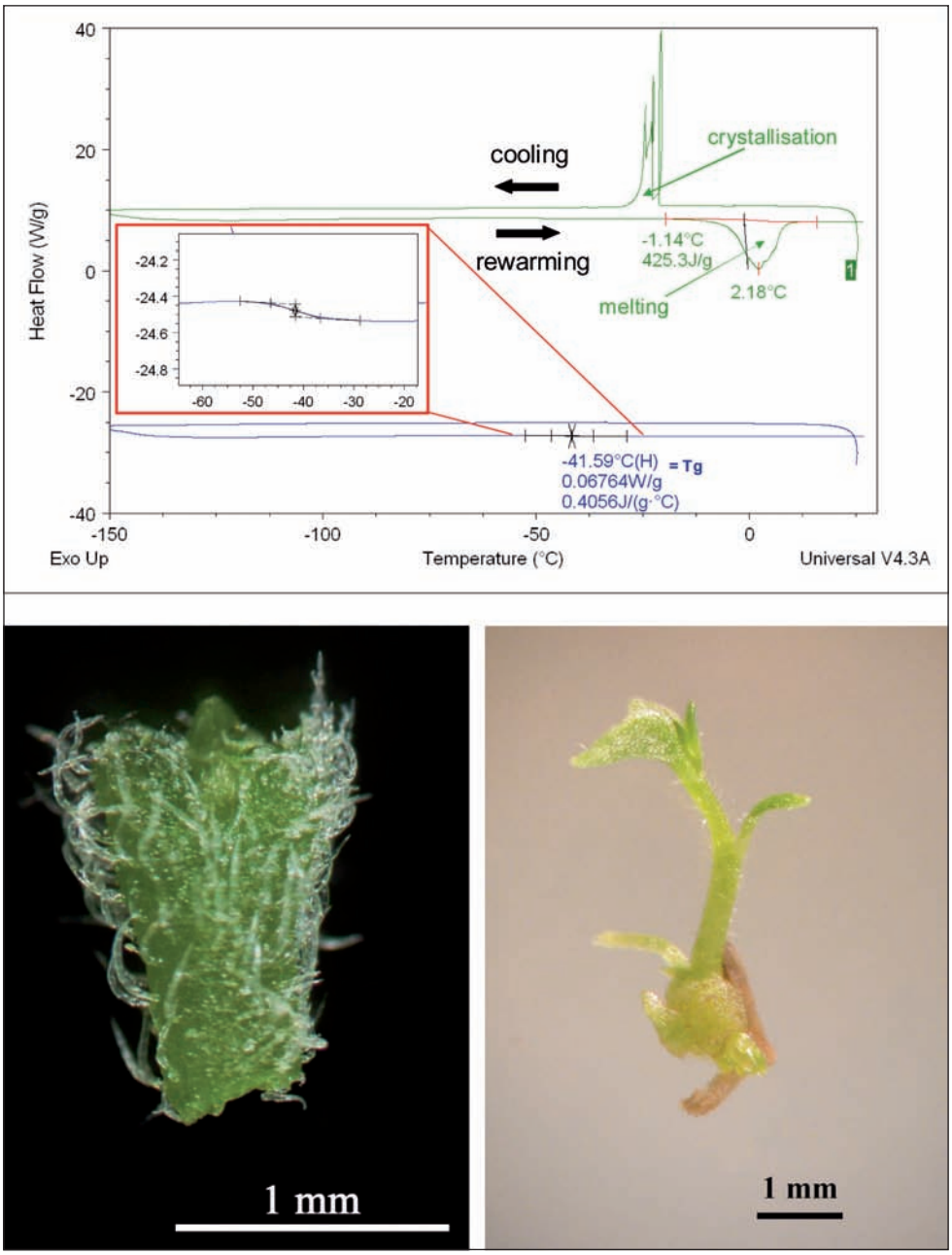

Fig. 14: Example of two records of Differential Scanning Calorimeter measuring heat flow in shoot tips of *Solanum tuberosum* L. "Désirée". Samples were cooled from 20 to -150 °C and afterwards rewarmed from -150 to 20 °C, both with a speed of 10 °C/min. **Green line**: control without cryoprotection. High water contents are documented by the crystallisation and melting peaks. **Blue line**: sample after cryoprotection with PVS2 (0.4 M sucrose + 30 % glycerol + 15 % ethylene glycol + 15 % DMSO) for 30 min. The cryoprotected tips exhibited glass transition (Tg) at -41.59 °C (magnified part of the record in the inlay marked by red lines). Transfer of the cell solution from freezable water to highly viscous solution being able to form stable glasses is one of the main principles of cryopreservation. **Pictures below the diagram**: Shoot tip isolated from an *in vitro* plantlet of *S. tuberosum* "Désirée" prior to cryopreservation (left); regenerated shoot eight weeks after rewarming (right) (Photo: A. Kaczmarczyk).

to **1,433 accessions of garlic and 460 of shallot**. The DNA isolation was performed in **collaboration with the research group Experimental Taxonomy**. The project-based **cryopreservation** activity comprises **40 accessions in preparatory *in vitro* propagation and three accessions in final cryopreservation**. For virus elimination five accessions were sent to the partners. The garlic **image database was transferred** into the group **from the research group Plant Data Warehouse** (C. Zanke, G. Matzig, J. Keller, F. Blattner, T. Funke, U. Scholz, M. Lange).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;

Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann;

Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, T. Funke, S. Weise;

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;

Dept. of Genebank, Research Group External Branch "North"; Dr. K.J. Dehmer;
Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, Dr. M. Lange;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M.-R. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer, Dr. T. Rutten.

Outside the Institute:
Array-On GmbH, Gatersleben; Dr. D. Fischer;
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute of Plant Analysis, Quedlinburg; Prof. H. Schulz;
Max Planck Institute for Molecular Plant Physiology, Central Infrastructure Group Transcript Profiling, Golm; Dr. D.K. Hincha;
German Collection of Microorganisms and Cell Cultures (DSMZ), Brunswick, Dr. H.-M. Schumacher;
Crop Research Institute (CRI), Prague and Olomouc, Czech Republic; Dr. J. Zameník, Dr. H. Staveliková;
Research Institute of Vegetable Crops (RIVC), Skierniewice, Poland; Dr. T. Kotlinska;
Nordic Gene Bank (NGB), Alnarp, Sweden; Dr. A. Kolodinska Brantestam;
University of Warwick, Genetic Resources Unit, Wellesbourne, UK; Dr. D. Astley;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Dr. C. Kik;
National Institute for Agricultural Research (INRA), Domaine de Keraïber, Ploudaniel, France; F. Esnault;
Dipartimento di Scienze dei Sistemi Colturali, Forestali e dell´Ambiente, Università degli Studi della Basilicata (UNIBAS); Prof. V. Miccolis;
International Plant Genetic Resources Institute (IPGRI), Bioversity International, Rome, Italy; L. Maggioni;
Institute of Plant Production Research (VIR), St. Petersburg, Russia; Prof. T. Gawrilenko;
ARC-Roodeplaat Vegetable and Ornamental Plant Institute (VOPI), Pretoria, South Africa; Dr. P. Adebola.

Publications

Peer Reviewed Papers

Keller, E.R.J.: Cryopreservation for maintenance of plant germplasm in Germany. Adv. Hort Sci. 21 (2007) 228-231.

Murín, G., K. Micieta, A. Ligasova, J. Chrenova, J. Keller, M. Savova & D. Slade: Manifestation of aging via tests of the different *Vicia faba* L. cultivars in the seed bank as marker of time of storage. Acta Botanica Universitatis Comenianae 43 (2007) 33-36.

Senula, A., E.R.J. Keller, T. Sanduijav & T. Yohannes: Cryopreservation of cold-acclimated mint (*Mentha* spp.) shoot tips using a simple vitrification protocol. Cryo Lett. 28 (2007) 1-12.

Other Publications

Fritsch, R.M., M.-L. Graichen, C. Zanke & E.R.J. Keller: *Allium* genetic resources in Germany: crop and wild species, maintenance and research projects. In: Astley, D. et al. (Eds.) Report of a Vegetative Network, 2nd Meeting, 26.-28.06.2007, Olomouc (2007) 8-13.

Kaczmarczyk, A., M. Grübe & E.R.J. Keller: Cryopreservation of potato: New results from the IPK Gatersleben, Germany. Mem. Int. Congr. Plant Biotechnol. & Agricult. (BioVeg2007). 07.-08.05.2007, Ciego de Avila, Cuba, CD ROM (2007) 8 pp.

Kaczmarczyk, A., E.R.J. Keller, N.A. Shvachko & Y.V. Lupysheva: Optimization of cryopreservation conditions for two potato accessions (*Solanum tuberosum* 'Desiree' and *S. acaule*). Proc. 2nd Vavilov International Conference, 26.-30.11.2007, St. Petersburg/Russia (2007) 195-197.

Keller, E.R.J. & C. Zanke: EURALLIVEG Project: "Vegetative *Allium*, Europe's Core Collection, safe & sound". Biodiversity Newsl. Europe 34 (2007) 17.

Lynch, P., G. Souch, S. Trigwell, E.R.J. Keller & K. Harding: Plant cryopreservation: from laboratory to genebank. Book of Abstracts of the Asia Pacific Conference on Plant Tissue Cultures and Agrobiotechnology, 17.-21.06.2007, Kuala Lumpur/Malaysia (2007).

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Keller, E.R.J. & T. Funke: Die Knoblauch-Kernkollektion des IPK – IPK's Core Collection of Garlic. http://pgrc-35.ipk-gatersleben.de/apps/gcc/index.htm (2007).

Keller, E.R.J., C. Zanke & U. Scholz: EURALLIVEG – Vegetative Allium, Europe's Core Collection, Safe and Sound http://euralliveg.ipk-gatersleben.de/ (2007).

Lectures, Posters and Abstracts

V6, V91, V92, V93, V94, V95, V98, V99, V100, V101, V102, V103, V104, V220, V235, V236, V237, P55, P99.

Additional Funding

For further information see the survey page 204.

Research Group: External Branch "North"

Head: Dr. Klaus J. Dehmer

Scientists

IPK financed
Willner, Evelin (P)

Goals

Collection, conservation, characterisation, evaluation, service, documentation and research activities of/on potato, oil and forage crop plant genetic resources.

Research Report

Within three collections – clonally propagated genotypes of Andean or equatorial origin (AKS; 490 entries, mainly seven cultivated species), 2,590 cultivars and breeding lines of *Solanum tuberosum* ssp. *tuberosum* (KKS, vegetatively propagated) and 2,859 accessions of 139 wild and cultivated species from Central and South America (WKS, propagated as populations via seeds); the **Groß Lüsewitz Potato Collections** (GLKS; K.J. Dehmer) contain a total of **5,945 accessions** and **140 species**. **1,161 genebank accessions** were distributed to **177 requestors**, 15 coming from foreign countries (71 accessions shipped).
In 2007, 63 AKS and 609 KKS accessions were cultivated and characterised in the field with ten plants each, and 226 WKS accessions (194 from seedlings, 32 from tubers) were sexually propagated in the greenhouse. Via *in vitro* cultivation, 2,272 KKS and 490 AKS accessions are maintained, while more than 1,000 KKS entries are cryopreserved at Gatersleben (research group *In vitro* Storage and Cryopreservation).
According to the respective ELISA tests, **2,508 *in vitro* samples** are **free of** the six most common **potato viruses**. The Plant Protection Offices at Hannover and Rostock tested GLKS potato material for quarantine viruses (330 accs.), quarantine bacteria (349), and PSTVd (586).
Evaluations were carried out for resistance to ***Globodera pallida*** (43 WKS accessions/203 genotypes, State Plant Protection Office Rostock) and ***Phytophthora infestans*** on tubers (91 WKS accessions/449 genotypes; BAZ/ILK). Tubers of 39 KKS entries were cultivated for the evaluation of their **taste**, while tuber material of 24 selected accessions was propagated for a stability research project. In the greenhouse, 40 WKS accessions with ten genotypes each were grown for the production of tubers to be used in potato wart resistance tests and as base material for protoplast fusions within the KOSY project (BBA, Phytowelt).
Regarding research on duplicate identification within the KKS, **efforts to homologise SSR marker sets for germplasm characterisations on an international level** were continued.

The **Oil Plants and Forage Crops Collections** at Malchow (E. Willner) maintain **14,089 accessions** (2,455 samples of oil plants, 10,407 forage grasses, 1,227 forage legumes). A further increase in the number of accessions resulted from the transfer of varieties no longer listed on the official variety list from the Federal Seed Board (Bundessortenamt) to Malchow (48 cultivars). In 2007, a total of 1,330 accessions were cultivated, either for multiplication (738) and/or characterisation (488) or evaluation (104).
Germination tests were conducted for 1,744 accessions. According to FAO genebank standards, **54** % of the whole Malchow collection is **stored as an active and base collection with safety duplicates** at IPK Gatersleben (7,673 accessions), while 81 % of the whole collection is available for seed requests. A total of **554 samples were provided to 36 users,** whereof 19 seed deliveries with 408 samples were for foreign countries.
Characterisations were performed on 1,142 grass accessions, 64 samples of rape, mustard or forage kale accessions for an initial description of their morphological and phenological traits as well as for the confirmation of their botanical classification. **Field evaluations** were carried out for *Lolium perenne* (81 accessions)*;* 50 accessions collected from different European countries and 31 breeding lines were analysed for trait variability and/or green matter yield.
For the Genebank management processes that are supported by the Genebank Information System (GBIS/M), data were further consolidated (collaboration with M. Oppermann, H. Knüpffer, U. Lohwasser, research group Genebank Documentation, research group Resources Genetics and Reproduction).
The **European Central *Poa* Database** (http://poa.ipk-gatersleben.de) was further advanced, containing passport data of 5,216 accessions from 38 *Poa* species (in collaboration with S. Weise, research group Bioinformatics and Information Technology). These originate from 56 different countries and are maintained at 21 institutes in 18 European countries. Progress was made in the identification of "Originality" and "Primary Holder" matters, which will allow to avoid unnecessary regenerations and to improve the sharing of responsibilities.
As a result of a former and joint *Lolium* project with the research group Genome Diversity, both E. Willner and K.J. Dehmer contributed essentially to the development of a **Di**versity **S**tudy **To**olkit (DiSTo) for a combined and web-based analysis of passport, characterisation, evaluation and molecular data by the Plant Data Warehouse group.

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner, Dr. T. Sretenovic Rajicic, R. Rizvi;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann;
Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, C. Künne;
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner, Dr. U. Lohwasser;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, S. Weise.

Outside the Institute:
Agricultural Research Institute Mecklenburg-Vorpommern, Institute for Animal Production, Dummerstorf; Dr. H. Jänicke;
Chamber of Agriculture, Plant Protection Office, Hannover; Dr. V. Zahn;
Euro Grass Breeding, Hof Steimke; Dr. U. Feuerstein;
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute of Abiotic Stress Tolerance (IST), Groß Lüsewitz; Dr. A.G. Badani-Dehmer;
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Institute of Agricultural Crops (ILK), Groß Lüsewitz; Dr. T. Hammann, Dr. H. Lellbach;
Martin Luther University Halle-Wittenberg, Institute of Plant Breeding and Plant Protection Halle/S.; Prof. W.E. Weber;
NORIKA Kartoffelzucht- und Vermehrungs GmbH, Groß Lüsewitz; Dr. H. Junghans;
Federal Biological Research Centre for Agriculture and Forestry (BBA), Institute for Plant Protection in Field Crops and Grassland, Kleinmachnow; Dr. K. Flath;
State Plant Protection Office of Mecklenburg-Vorpommern, Rostock; Dr. I. Wulfert, Dr. J. Kruse;
Information and Coordination Centre for Biological Diversity (IBV), Bonn; Dr. F. Begemann, S. Harrer;
Bavarian State Research Center for Agriculture, Institute of Plant Production and Plant Breeding, Freising-Weihenstephan; Dr. S. Hartmann;
Max Planck Institute for Plant Breeding Research, Cologne; Dr. C. Gebhardt;
Phytowelt Green Technologies GmbH, Cologne; Dr. A. Müller, Dr. R. Lührs;
Bioplant Biotechnologisches Forschungslabor GmbH, Ebstorf; Dr. E. Tacke;
Saatzucht Steinach GmbH, Steinach and Bornhof; Dr. F. Eickmeyer;
SaKa-Pflanzenzucht GbR, Windeby; Dr. J. Lübeck;
APIC potato genebanks, e.g. CGN, VIR, CIP, Sturgeon Bay;
ECP/GR Working Group on Forages; ECP/GR Working Group on Potatoes;
Agroscope Changins-Wädenswil ACW, Nyon, Switzerland; Dr. C.-L. Lê, E. Droz;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Ir. R. Hoekstra;
Swiss Federal Research Station for Agroecology and Agriculture, FAL Reckenholz, Zurich, Switzerland; Dr. B. Boller.

Publications

Peer Reviewed Papers

Lebeda, A., I. Doležalová, E. Křístková, K.J. Dehmer, D. Astley, C.C.M. van de Wiel & T. van Treuren: Acquisition and ecological characterization of *Lactuca serriola* L. germplasm collected in the Czech Republic, Germany, The Netherlands and United Kingdom. Genet. Resour. Crop Evol. 54 (2007) 555-562.

Weise, S., S. Harrer, I. Grosse, H. Knüpffer & E. Willner: The European *Poa* Database (EPDB). Plant Genet. Resour. Newsl. 150 (2007) 64-70.

Lectures, Posters and Abstracts

V47, V282, V283, V284, P31, P76, P127, P128, P234.

Additional Funding

For further information see the survey page 204.

Programme: Taxonomy and Evolution

Research Group: Experimental Taxonomy

Head: Dr. Frank Blattner

Scientists

IPK financed
Baier, Christina (0,5 P)
Ekhvaia, Jana (0,5 Annex, 01.09.-30.11.2007)
Jakob, Sabine, Dr. (P, till 18.06.2007)
Köhnen, Ines (0,5 P, since 01.07.2007)

Grant Positions
Köhnen, Ines (0,25 DFG, till 30.06.2007)
Nürk, Nicolay (0,5 DFG, since 01.09.2007)
Pleines, Thekla (0,5 DFG)

Visiting Scientists
Achigan-Dako, Enoch (DAAD)
Bachmann, Konrad, Prof. (self-financed)
Esfeld, Korinna (SMNC, 16.04.-11.05.2007;
University of Heidelberg, 28.08.-28.09.2007)
Kotseruba, Violetta (DAAD, 20.09.-19.11.2007;
self-financed, 20.11.-26.12.2007)

Goals

Development and application of molecular marker methods and the identification, characterisation and phylogenetic classification of crops and their wild relatives. Experimental studies to link **molecular markers** and **phylogenetic data** with taxonomically and agronomically significant characters, and to analyse **plant–environment interdependency** on the species level.

Research Report

The major aim of the group is to understand mechanisms resulting in **speciation** processes in specific plant groups. This involves the study of the **distribution** of species, populations and genotypes **in time and space** together with the analysis of character state changes involved in **environmental adaptation** and reproductive isolation. These characters (e.g., abiotic stress tolerance) influence the ecological niches of organisms and are often also **important agronomic traits**. Thus, the study of naturally occurring genetic diversity in wild species could show ways to breed improved crops for changing environmental conditions.

On the basis of a large data set of chloroplast haplotypes and their relationships, we analyse monophyletic species groups of ***Hordeum*** in a phylogeographic context. We include climate models to infer past and present distribution areas of species together with genetic data to analyse the history of species and species groups. In the Mediterranean *Hordeum marinum* group these analyses revealed the existence of two good species instead of a single species with two subspecies, and proved clear ecological differences between the diploid and tetraploid cytotypes of *H. gussoneanum* (Jakob et al. 2007). Up to now, no convincing phylogeny could be obtained for the closely related New World species of *Hordeum*, as these species evolved only during the last two million years, resulting in minute genetic differences among the taxa. To solve this problem, we initiated an AFLP study of all diploid species from the Americas, which should result in better phylogenetic hypotheses for this species group (T. Pleines, F. Blattner).

In a greenhouse experiment, where we grow three closely related **sympatric species** of *Hordeum*, we simulate **niche differences** along **salt and drought gradients**. This experiment combines a competition approach with different soil parameters with a common garden experiment. First results demonstrate that some species-specific differences in their ecological niche use (salt vs. drought stress) are inheritable and are maintained in the greenhouse (T. Pleines, S. Jakob, F. Blattner). For these species, gene expression experiments under different stress conditions were also conducted to analyse the genetic response to salt, drought and cold stress. These analyses complement the greenhouse experiments. Thus, we get information on niche use and the genes involved in niche adaptation (T. Pleines, F. Blattner).

Cucurbitaceae provide an important group of **crop species** in **Western African countries**. They are used as oil seeds, fruits, and vegetable. In several expeditions E. Achigan-Dako was able to collect the species diversity in the phylogeographic regions of West Africa, ranging from the tropical rainforest of the southern part to the Sahel zone in the north. For this group, we are now analysing the biodiversity present in West Africa. Morphometric analyses and genome size measurements with flow cytometry, in conjunction with phylogenetic and phylogeographic analyses are currently undertaken to identify new species and subspecies and get insights in domestication of native crops of this region (E. Achigan-Dako, F. Blattner).

Species of the Euphorbiaceae genus ***Macaranga*** are important Southeast Asian pioneer shrubs and trees of areas where the rainforest was freshly logged. Many of

Fig. 15: Hollow stem of *Macaranga winkleri* inhabited by mutualistic *Crematogaster* ants (C. Baier).

these species co-occur with **mutualistic ants**. Here we study speciation processes, probably driven by **co-evolution** between plants and their ant partners. Nuclear microsatellites are used together with chloroplast variation in comparative population genetic and phylogeographic studies of two widespread Bornean *Macaranga* species, one a myrmecophye (ant-plant, see Fig. 15), the other without ant symbionts. In the last year we could increase the number of available microsatellite loci and start population genetic analyses of both taxa (C. Baier, F. Blattner).

The orchid taxon ***Vanilla planifolia*** is an important species for the extraction of flavours. Originally this species occurs in Central America but is cultivated worldwide in the tropics. It is assumed that the genetic diversity within cultivated varieties of vanilla might be low, although no explicit population genetic studies were conducted. For this purpose and to support breeders in finding genetically diverse lineages of the species, we currently develop microsatellite markers for this species and analyse the genetic diversity present in commercially available vanilla capsules (I. Köhnen).

Funded by the DFG, we started a new project on ***Hypericum*** systematics. Initially we conduct an analysis of morphological characters of all ~ 400 species of the genus to obtain a subdivision into manageable groups. These will be analysed in more detail with molecular markers. The project is part of a collaboration with the Natural History Museum of London, and connected to projects on *Hypericum* in the Apomixis group of T. Sharbel at the IPK and M. Koch's group at the University of Heidelberg (N. Nürk, F. Blattner).

Collaboration

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. J. Fuchs;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert, A. Ihlow.

Outside the Institute:

Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/S.; Prof. I. Hensen, Dr. M.H. Hoffmann, Prof. M. Röser, Dr. B. von Hagen;

University of Kassel, Systematics and Morphology of Plants, Kassel; Dr. D. Guicking, Prof. K. Weising;

University of Osnabrück, Botanical Institute and Botanical Garden, Osnabrück; Dr. N. Friesen;

University of Heidelberg, Institute of Plant Sciences, Heidelberg; Prof. M. Koch;

Ludwig Maximilians University, Systematic Botany, Munich; Prof. S.S. Renner;

Natural History Museum, London, UK; Dr. J. Vogel, Dr. N. Robson;

University of Abomey-Calvi, Faculty of Agronomic Sciences, Cotonou, Benin; Prof. A. Ahanchede;

Natural History Museum "Bernado Rivadavia", Buenos Aires, Argentina; Dr. M. Arriaga.

Publications

Peer Reviewed Papers

Fehrer, J., B. Gemeinholzer, J. Chrtek & S. Bräutigam: Incongruent plastid and nuclear DNA phylogenies reveal ancient intergeneric hybridization in *Pilosella* hawkweeds (*Hieracium*, Cichorieae, Asteraceae). Mol. Phylogenet. Evol. 42 (2007) 347-361.

Gurushidze, M., S. Mashayekhi, F.R. Blattner, N. Friesen & R.M. Fritsch: Phylogenetic relationships of wild and cultivated species of *Allium* section *Cepa* inferred by nuclear rDNA ITS sequence analysis. Plant Syst. Evol. 269 (2007) 259-269.

Jakob, S.S., A. Ihlow & F.R. Blattner: Combined ecological niche modelling and molecular phylogeography revealed the evolutionary history of *Hordeum marinum* (Poaceae) – niche differentiation, loss of genetic diversity, and speciation in Mediterranean Quaternary refugia. Mol. Ecol. 16 (2007) 1713-1727.

Marschner, S., A. Meister, F.R. Blattner & A. Houben: Evolution and function of B chromosomal 45S rDNA sequences in *Brachycome dichromosomatica*. Genome 50 (2007) 638-644.

Book Chapters

Blattner, F.R. & N. Friesen: Relationship between Chinese chive (*Allium tuberosum*) and its putative progenitor *A. ramosum* as assessed by random amplified polymorphic DNA (RAPD). In: Zeder, M.A., D.G. Bradley, E. Emshwiller & B.D. Smith (Eds.): Documenting domestication. New genetic and archeological paradigms. University of California Press., Ltd., Berkeley – Los Angeles – London, California – England (2007) 134-142.

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Vegetabile 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Lectures, Posters and Abstracts

V1, V18, V20, V27, V28, V74, V75, V173, P1, P13, P35, P36, P75, P168, P183, P184.

Additional Funding

For further information see the survey page 204.

Research Group: Quantitative Evolutionary Genetics

Head: Dr. Karl Schmid

Scientists

IPK financed
Höffken, Matthias (0,5 Annex)

Visiting Scientists
Puglia, Guiseppe (FIDAF scholarship, since 29.11.2007)

Goals

Characterisation of **genome-wide patterns of genetic variation** in *Arabidopsis thaliana* and in wild barley *Hordeum spontaneum* in its native habitat. Identification of genes, which are targets of positive Darwinian selection. Development of bioinformatics and population genetic methods for **natural selection mapping** (i.e., the detection of genes with a footprint of natural selection) as complementary methods to association studies and QTL mapping.

Research Report

The research group aims at analysing genome-wide patterns of variation in *A. thaliana* and in wild barley *Hordeum spontaneum*. Genome-wide SNP data are analysed from the *A. thaliana* populations that were collected in putative refugia in the Mediterranean region to describe the **population structure** and to test hypotheses about the role of ice ages in the **geographic history** of the species (M. Höffken, K. Schmid).

A multiannual reciprocal transplantation experiment on **ecological adaptation** to the contrasting climates in Central Europe and Central Asia was set up at research locations in Shortandy, Kazakhstan and in Halle, Germany. This experiment will reveal whether the extensive population structure in *A. thaliana* is a result of local adaptation (K. Schmid, together with M. Hoffmann, University of Halle). The first year of the experiment was used to adjust the methodology and measure plant survival to obtain samples that are large enough for subsequent statistical analysis of fitness measurements.

We have used our results on the **demographic history of *A. thaliana*** to investigate fitness effects in the epistatic interaction of two flowering time genes, *FRIGIDA* (*FRI*) and *FLOWERING LOCUS C* (*FLC*) (K. Schmid, together with J. Schmitt, Brown University, USA). By comparing patterns of linkage disequilibrium of different alleles at *FRI* and *FLC* with genome-wide levels of LD, we showed that the high level of LD at the two loci is non-random. Because the different combinations of *FRI* and *FLC* alleles have a strong fitness effect on flowering time and survival, proposed that the non-random LD results from epistatic selection.

We have characterised the **molecular evolution in an imprinted gene**, *MEDEA*, which controls endosperm and embryo development (K. Schmid, together with C. Spillane, University of Cork, Ireland and U. Grossniklaus, University of Zurich, Switzerland). Particularly, we tested whether *MEDEA* is involved in a parental genomic conflict on resource allocation to the embryo. Our results show that *MEDEA* evolves much more rapidly than its paralog, *SWINGER*, and that its evolution is driven by positive Darwinian selection. Therefore, our results are consistent with the hypothesis that a conflict on resource allocation to embryo exists in plants.

The **geographic population structure of wild barley across** micro- and macroecological gradients in Israel was determined by the analysis of 36 short genomic regions. Population genetic analysis showed that along those gradients there is a high level of genetic population structure that may result from local adaptation and reproductive isolation of different populations (K. Schmid, together with A. Korol, Haifa University, Israel). To further test this hypothesis, we are currently characterising genetic variation in 50 populations of wild barley with 20 individuals each across Israel using microsatellites (M. Höffken, K. Schmid, together with E. Fridman, Agricultural University of Rehovot, Israel).

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity;
Dr. S. Stracke, Dr. N. Stein.

Outside the Institute:
Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/S.;
Dr. M.H. Hoffmann;
Haifa University, Institute of Evolution, Haifa, Israel;
Prof. A. Korol;
Agricultural University of Israel, Rehovot, Israel;
Dr. E. Fridman;
University College, Department of Biochemistry, Cork, Ireland; Dr. C. Spillane;
University of Zurich, Institute of Plant Biology, Zurich, Switzerland; Prof. U. Grossniklaus.

Publications

(All publications marked with "*" are based on work that has been carried out when Karl Schmid was at the Max Planck Institute for Chemical Ecology in Jena, Germany)

Peer Reviewed Papers

*Korves, T.M., K.J. Schmid, A.L. Caicedo, C. Mays, J.R. Stinchcombe, M.D. Purugganan & J. Schmitt: Fitness effects associated with the major flowering time gene *FRIGIDA* in *Arabidopsis thaliana* in the field. Am. Nat. 169 (2007) e141-157.

Spillane, C., K.J. Schmid, S. Laoueille-Duprat, S. Pien, J.M. Escobar-Restrepo, C. Baroux, V. Gagliardini, D.R. Page, K.H. Wolfe & U. Grossniklaus: Positive Darwinian selection at the imprinted MEDEA locus in plants. Nature 448 (2007) 349-352.

Other Publications

Spillane, C., K.J. Schmid, S. Laoueille-Duprat, S. Pien, J.M. Escobar-Restrepo, C. Baroux, V. Gagliardini, D.R. Page, K.H. Wolfe & U. Grossniklaus: Geschlechterkonflikt bei Pflanzen – Wettstreit um das Gen MEDEA. GenomXPress 3 (2007) 10-11.

PhD and Diploma Theses

*Navarro-Quezada, A.: Molecular evolution of tropinone-reductase-like and tau GST genes duplicated in tandem in *Brassicaceae*. (PhD Thesis) Ludwig-Maximilian-Universität München, München (2007), 146 pp.

Lectures, Posters and Abstracts

V9, V84, V183, V184, V185, V186, V187, V188, V189, V190, P90, P91.

Research Group: Taxonomy of Plant Genetic Resources

Head: Dr. Frank Blattner (temp.)

Scientists

IPK financed
Fritsch, Reinhard, Dr. (0,5 P, till 31.01.2007)
Gurushidze, Maia (0,5 P, since 01.11.2007)
Pistrick, Klaus, Dr. (P)

Visiting Scientists
Gurushidze, Maia (Industry scholarship, till 31.10.2007)

Goals

Curatorial management of living and archived taxonomic collections, investigations of morphological, karyological and anatomical characters to perform taxonomic determinations. The studies target general questions of the taxonomy of crop plants jointly with the other research groups of the programme Taxonomy and Evolution.

Research Report

The **custodial management of the taxonomic reference collections** is a continuous activity of the research group. During 2007, about 6,800 herbarium sheets (half of them documenting genebank accessions), 2,400 fruit and seed samples, and more than 200 cereal spikes were added to the collection. The collections were also used by many visitors of the IPK facilities or vouchers were sent abroad in the frame of international herbarium exchange. This part of the work involves also taxonomical determination of genebank material from a wide variety of plant families (K. Pistrick).

Taxonomic supervision of the living ***Allium*** **reference collection** was continued, including new material from West and Central Asia, which was collected during several research missions within the "PharmAll" project funded by the VolkswagenStiftung. About 300 accessions could be determined, resulting in 1,827 out of 2,126 accessions with clarified taxonomic status growing currently in the field and greenhouses of the IPK (R. Fritsch, K. Pistrick).

Members of the research group were co-organisers or participants of the **"First Kazbegi workshop on botany, taxonomy and phytochemistry of wild *Allium* species of the Caucasus and Central Asia"** (R. Fritsch, M. Gurushidze, K. Pistrick).

A large molecular phylogeny of the members of ***Allium*** **subgenus *Melanocrommyum*** was used to infer the relationships of newly collected material of the group. The

Fig. 16: *Lupinus pilosus*, clearly differing by its larger seeds, has been determined as "Altreier Kaffee", cultivated as an endemic coffee substitute in Northern Italy (Alto Adige/Südtirol) since the middle of the nineteenth century (Heistinger & Pistrick 2007). Seeds of *L. pilosus* (upper row) from Altrei, Italy and *L. cosentinii* (lower row) from the Gatersleben Genebank reference collection (K. Pistrick).

analyses resulted in the detection of more than ten species and probably several subspecies, which are new to science, and allowed to estimate that the Iranian region is a centre of diversity of this group. The *Allium* biodiversity in this region seems only marginally explored up to now (R. Fritsch, M. Gurushidze). Also, a phylogenetic analysis of *Allium* section *Cepa* was published (Gurushidze et al. 2007), which for the first time included a certain number of individuals per species in a phylogeny of this group. This analysis clearly showed that *A. vavilovii* is the progenitor of common onion (*A. cepa*) and clarified species relationships among the wild taxa of this group, which all are collected locally for consumption.

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. U. Lohwasser;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. V. Schubert, Dr. G. Jovtchev;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

Outside the Institute:
International Seeds Processing, Quedlinburg; A. Boteff;
Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/S.; Prof. E. Jäger, Dr. M.H. Hoffmann;
Landeskriminalamt Saxony-Anhalt; Dr. U. Pich;
University of Kassel, Department of Agrobiodiversity, Witzenhausen; Prof. K. Hammer;
Bundessortenamt; Prüfstelle Dachwig; H. Eger;
University of Osnabrück, Botanical Institute and Botanical Garden, Osnabrück; Dr. N. Friesen;
Philipps University Marburg, Institute of Pharmaceutical Chemistry, Marburg; Prof. M. Keusgen;
Scientific-Productive Centre "Botanika" of the Uzbek Academy of Sciences, Tashkent, Uzbekistan; Dr. F. Khassanov;
Botanical Institute of the Tajik Academy of Sciences, Dushanbe, Tajikistan; Prof. H. Hisoriev, P. Kurbonova;
Niko Ketskhoveli Institute of Botany, Georgian Academy of Sciences, Tbilisi, Georgia; Prof. G. Nakhutsrishvili, Prof. Dr. M. Akhalkatsi;
Plant Pests and Diseases Research Institute, Teheran, Iran; Dr. M. Abbasi;
Botanical Institute "V. L. Komarov" of the Russian Academy of Sciences, St. Petersburg, Russia; Dr. V. Kotseruba.

Publications

Peer Reviewed Papers

Adoukonou-Sagbadja, H., V. Schubert, A. Dansi, G. Jovtchev, A. Meister, K. Pistrick, K. Akpagana & W. Friedt: Flow cytometric analysis reveals different nuclear DNA contents in cultivated fonio (*Digitaria* spp.) and some wild relatives from West-Africa. Plant Syst. Evol. 267 (2007) 163-176.

Filatenko, A.A. & K. Hammer: A new gross morphological variation in the genus *Triticum* L. Genet. Resour. Crop Evol. 54 (2007) 231-232.

Gurushidze, M., S. Mashayekhi, F.R. Blattner, N. Friesen & R.M. Fritsch: Phylogenetic relationships of wild and cultivated species of *Allium* section *Cepa* inferred by nuclear rDNA ITS sequence analysis. Plant Syst. Evol. 269 (2007) 259-269.

Heistinger, A. & K. Pistrick: 'Altreier Kaffee': *Lupinus pilosus* L. cultivated as coffee substitute in Northern Italy (Alto Adige/Südtirol). Genet. Resour. Crop Evol. 54 (2007) 1623-1630.

Khoshbakht, K., K. Hammer & K. Pistrick: *Eryngium caucasicum* Trautv. cultivated as a vegetable in the Elburz Mountains (Northern Iran). Genet. Resour. Crop Evol. 54 (2007) 445-448.

Other Publications

Fritsch, R.M., M.-L. Graichen, C. Zanke & E.R.J. Keller: *Allium* genetic resources in Germany: crop and wild species, maintenance and research projects. In: Astley, D. et al. (Eds.) Report of a Vegetative Network, 2nd Meeting, 26.-28.06.2007, Olomouc (2007) 8-13.

Pistrick, K. & K. Hammer: Richard N. Lester (1937-2006). Genet. Resour. Crop Evol. 54 (2007) 449.

Pistrick, K. & K. Hammer: John G. Hawkes (1915-2007) – Obituary. Genet. Resour. Crop Evol. 54 (2007) 1635.

Additional Publications of 2006

Fritsch, R.M., A.R. Abbasi & M. Keusgen: Useful wild *Allium* species in northern Iran. Rostaniha 7 (2006) 189-206.

Fritsch, R.M., Y. Salmaki, S. Zarre & M. Joharchi: The genus *Allium* (*Alliaceae*) in Iran: Current state, new taxa and new records. Rostaniha 7 (2006) 255-282.

Lectures, Posters and Abstracts

V54, V55, V74, V75, V171, V172, P49, P75, P93, P114, P115, P116, P218.

Additional Funding

For further information see the survey page 205.

Abteilung Cytogenetik und Genomanalyse/ Department of Cytogenetics and Genome Analysis

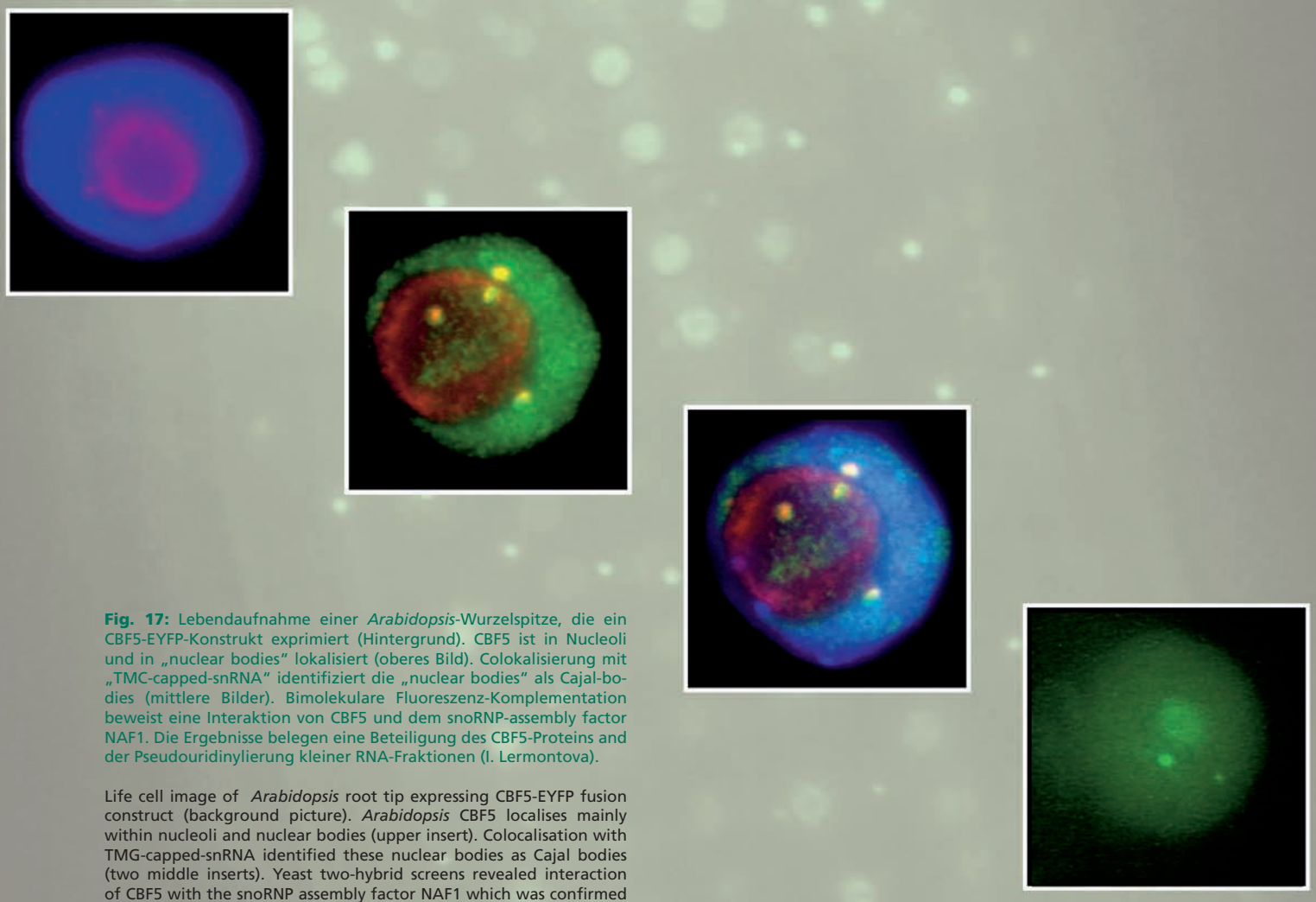

Fig. 17: Lebendaufnahme einer *Arabidopsis*-Wurzelspitze, die ein CBF5-EYFP-Konstrukt exprimiert (Hintergrund). CBF5 ist in Nucleoli und in „nuclear bodies" lokalisiert (oberes Bild). Colokalisierung mit „TMC-capped-snRNA" identifiziert die „nuclear bodies" als Cajal-bodies (mittlere Bilder). Bimolekulare Fluoreszenz-Komplementation beweist eine Interaktion von CBF5 und dem snoRNP-assembly factor NAF1. Die Ergebnisse belegen eine Beteiligung des CBF5-Proteins and der Pseudouridinylierung kleiner RNA-Fraktionen (I. Lermontova).

Life cell image of *Arabidopsis* root tip expressing CBF5-EYFP fusion construct (background picture). *Arabidopsis* CBF5 localises mainly within nucleoli and nuclear bodies (upper insert). Colocalisation with TMG-capped-snRNA identified these nuclear bodies as Cajal bodies (two middle inserts). Yeast two-hybrid screens revealed interaction of CBF5 with the snoRNP assembly factor NAF1 which was confirmed *in vivo* by "bimolecular fluorescence complementation" (lower insert). These data indicate the involvement of the CBF5 protein in RNA pseudouridinylation. (I. Lermontova).

Abteilung Cytogenetik und Genomanalyse

Leiter: Prof. Dr. Ingo Schubert

Allgemeine Forschungsziele

Die Forschungsschwerpunkte der Abteilung sind die Genomdynamik auf molekularer und mikroskopischer Ebene unter evolutionären, ontogenetischen und experimentellen Gesichtspunkten (vor allem Bereich Cytogenetik) sowie die Genetik pflanzlicher Leistungen unter Einbeziehung genomweiter, vorwärts- und revers-genetischer sowie bioinformatischer Ansätze (vor allem Bereich Genomanalyse).
Eine Arbeitsgruppe (*In vitro*-Differenzierung) arbeitet mit embryonalen und adulten Stammzellen vornehmlich der Maus.

Folgende Themenkomplexe stehen im Vordergrund:

Bereich Cytogenetik (Leiter: Prof. Dr. Ingo Schubert)
- Analyse der Anordnung und Dynamik von Chromosomenterritorien und Chromatindomänen unter evolutionären, ontogenetischen und experimentellen Gesichtspunkten (Arbeitsgruppe Karyotypevolution).
- Aufklärung von Mechanismen der artspezifischen Genomeliminierung in Embryonen aus weiten Kreuzungen sowie der Entstehung und Funktion von B-Chromosomen (Arbeitsgruppe Chromosomenstruktur und -funktion).
- Molekularcytogenetische Analyse der DNA- und Proteinzusammensetzung und deren funktionsbezogene epigenetische Modifikation in spezifischen Domänen pflanzlicher Chromosomen (v. a. Zentromer, Eu- und Heterochromatin) während des Zellzyklus und der Ontogenese (Arbeitsgruppen Karyotypevolution, Chromosomenstruktur/-funktion).
- Aufklärung von Evolution und genetischen Mechanismen der apomiktischen Samenbildung bei ausgewählten Angiospermen-Gruppen (Arbeitsgruppe Apomixis).
- Aufklärung von Polyploidie-Effekten auf Genomstruktur und Genexpression (Arbeitsgruppe Genomplastizität).
- Molekulargenetische Analyse epigenetischer Mechanismen, die der RNA-abhängigen Inaktivierung von Transgenen und der Kontrolle endogener pararetroviraler Sequenzen in Pflanzen zu Grunde liegen (Arbeitsgruppe Epigenetik).
- Aufklärung des Differenzierungspotenzials und der genetischen und epigenetischen Regulation von Differenzierungsprozessen pluripotenter embryonaler und adulter Säugerstammzellen *in vitro* für künftige Entwicklungsstrategien zur Zell- und Geweberegeneration (Arbeitsgruppe *In vitro*-Differenzierung).

Department of Cytogenetics and Genome Analysis

Head: Prof. Ingo Schubert

Research Goals

The research topics of the Department are focussed on genome dynamics at the molecular and the microscopic level under evolutionary, developmental and experimental aspects (in particular Programme Cytogenetics) as well as on the genetic dissection of crop plant's performances using forward and reverse genetic as well as bioinformatic approaches (predominantly Programme Genome Analysis).
One research group (*In vitro* Differentiation) is working with embryonic and adult murine stem cells.

The Department's research groups are working on the following topics:

Programme Cytogenetics (Head: Prof. Ingo Schubert)
- Analysis of interphase arrangement and dynamics of chromosome territories and specific chromatin domains under evolutionary, developmental and experimental aspects (research group Karyotype Evolution).
- Investigation of mechanisms responsible for parent-specific genome elimination within nuclei of embryos resulting from wide crosses; and of the origin and potential function of B chromosomes (research group Chromosome Structure and Function).
- Molecular-cytogenetic analysis of DNA and protein composition and of epigenetic modification related to the functions of specific chromatin domains (in particular centromeres, eu- and heterochromatin fractions) during cell cycle and plant development (research groups Karyotype Evolution, Chromosome Structure and Function).
- Elucidation of the evolution and genetic mechanisms of apomictic seed formation within selected angiosperm species (research group Apomixis).
- Investigation of the impact of polyploidy on genome structure and gene expression (research group Genome Plasticity).
- Molecular-genetic analysis of epigenetic mechanisms underlying RNA-dependent transcriptional silencing of transgenes and control of endogenous pararetroviral sequences in plants (research group Epigenetics).
- Modelling, classification, and reduction of dimensions of high dimensional data (3D microscopic images, NMR, micro- and macroarray data) and implementa-

– Modellierung, Klassifizierung und Dimensionsreduktion hochdimensionaler Daten (3-D mikroskopische Bilder, NMR, Mikro- und Makroarray-Daten) und Implementierung von Bild- und Datenverarbeitungsalgorithmen auf parallele Hardware (Arbeitsgruppe Mustererkennung).

Bereich Genomanalyse (Leiter: Dr. habil. Patrick Schweizer)
– Erfassung und Nutzung der natürlichen genetischen Diversität von Getreide- und nahe verwandten Wildarten zur Identifizierung, Kartierung, Isolierung und gezielten Übertragung von Genen und Genkomplexen für landwirtschaftlich bedeutsame Merkmale (Arbeitsgruppe Gen- und Genomkartierung).
– Analyse des Transkriptoms resistenter *versus* suszeptibler Pflanzenzellen nach Inokulation mit Pathogenen zur Aufklärung von Pathogen-Pflanze-Wechselwirkungen und zum Nachweis pathogenregulierter Gene und deren Bedeutung für Wirts- bzw. Nichtwirtsresistenzen (Arbeitsgruppe Transkriptomanalyse).
– Vergleichende Transkriptanalyse von pflanzlichen Entwicklungsprogrammen (z. B. sexuelle *versus* parthenogenetische Samenentwicklung) einschließlich der Konstruktion von Gewebe- und Promoter-Arrays (Arbeitsgruppe Expressionskartierung).
– Etablierung von Ontologien bzw. kontrollierten Vokabularien zur Strukturierung, Integration und Vernetzung diverser Datenbanken (Arbeitsgruppe Bioinformatik und Informationstechnologie).

Im Mittelpunkt der Arbeiten stehen neben Erkenntnisgewinn die Schaffung von Voraussetzungen für eine gezielte Modifikation pflanzlicher Genome sowie die Etablierung und Verbreiterung biotechnologisch und züchterisch nutzbarer Techniken und Ressourcen. Diese Arbeiten finden zu einem wesentlichen Teil im Rahmen des **Pflanzengenom-Ressourcen-Centrums (PGRC**) statt, einer abteilungsübergreifenden Forschungs- und Dienstleistungsplattform. In PGRC-Dienstleistungsmodulen, die in den Arbeitsgruppen Transkriptomanalyse, Expressionskartierung und Bioinformatik und Informationstechnologie verankert sind, werden DNA-Sequenzierung, -Arraying, EST Shipping, und bioinformatischer Service angeboten.

Im Rahmen der gruppenspezifischen Forschungsarbeiten wird die Erhaltung und Weiterentwicklung von Spezialsortimenten v. a. der Gerste und der Ackerbohne und weiterer Gramineen mit modifizierten Gen- und Chromosomenbeständen betrieben (Arbeitsgruppen Chromosomenstruktur und -funktion, Gen- und Genomkartierung, Karyotypevolution).

Entwicklung im Berichtsjahr

Nachdem die Abteilung 2006 durch Bildung der Bereiche Cytogenetik und Genomanalyse sowie durch die Etablierung der Gruppe Genomplastizität im Bereich Cytogenetik, und Aufnahme der Gruppen Bioinformatik und Expressionskartierung in den Bereich Genomanalyse umstruktion of algorithms for image and data processing on parallel hardware (research group Pattern Recognition).
– Elucidation of potential and regulation of differentiation of pluripotent embryonic and adult mammalian stem cells in culture for future tissue regeneration (research group *In vitro* Differentiation).

Programme Genome Analysis
(Head: Dr. Patrick Schweizer)
– Exploration and use of the natural genetic diversity of cultivated and closely related wild cereals for identification, mapping, isolation and transfer of genes and complex traits of agronomic interest into commercial cultivars (research group Gene and Genome Mapping).
– Analysis of gene expression profiles of resistant *versus* susceptible target cells after pathogen attack to elucidate plant-pathogen-interactions, to identify pathogen-regulated genes and their impact on host/non-host resistances (research group Transcriptome Analysis).
– Comparative transcriptome analysis during developmental stages (e. g. sexual *versus* parthenogenetic seed formation) and construction of tissue and promoter arrays (research group Expression Mapping).
– Establishing of ontologies and controlled vocabularies for structuring, integration and linking of diverse databases (research group Bioinformatics and Information Technology).

In addition to obtaining basic knowledge, it is intended to establish the prerequisites for directed modification of plant genomes and to provide technological platforms and resources for biotechnology and breeding purposes. These efforts are largely integrated within the frame of the **Plant Genome Resources Centre (PGRC**) involving all departments of the IPK. PGRC services such as DNA sequencing, arraying, clone shipping and bioinformatics services are provided by the research groups Transcriptome Analysis, Expression Mapping, and Bioinformatics and Information Technology.

Special germplasm collections (barley, field bean, and other crops) with gene and chromosome mutations are developed, characterised and maintained within the framework of the research programmes of the research groups Chromosome Structure and Function, Gene and Genome Mapping, and Karyotype Evolution.

Developments during the year 2007

After reorganisation of the Department in 2006 by subdividing into the Programmes Cytogenetics and Genome Analysis, establishing of the research group Genome Plasticity and including the Bioinformatics and Expression Analysis groups into the Programme Genome Analysis, in 2007 the Bioinformatics group became merged with the

turiert wurde, ist 2007 die ursprünglich in der Abteilung Verwaltung und Zentrale Dienste (VZD) angesiedelte Servicegruppe Informationstechnologie zwecks effizienter und ressourcensparender Koordinierung mit der Arbeitsgruppe Bioinformatik unter der Leitung von Dr. U. Scholz zur Gruppe Bioinformatik und Informationstechnologie (BIT) zusammengeführt worden.
Aus der Gruppe Mustererkennung ist die vom Land Sachsen-Anhalt geförderte Nachwuchsgruppe Dateninspektion unter Leitung von Dr. Marc Strickert hervorgegangen, die der Abteilung Molekulargenetik angegliedert wurde.

Im Jahr 2007 wurden zwei Dissertationen und sieben Diplomarbeiten erfolgreich abgeschlossen.

Für die abteilungsinterne, die institutsweite und die institutsübergreifende Zusammenarbeit spielten auch im Jahr 2007 molekulare Markersysteme, Macroarray-basierte Transkriptprofilierung, lasergestützte Durchflusszytometrie, Fluoreszenzmikroskopie und Bioinformatik eine wesentliche Rolle. Alle Gruppen der Abteilung kooperieren innerhalb und außerhalb des IPK, z. B. im Rahmen von GABI und anderen institutionsübergreifenden Verbünden. Für die vielfältig verflochtene Zusammenarbeit zwischen den Gruppen der Abteilung, innerhalb des IPK und darüber hinaus siehe die Berichte der jeweiligen Arbeitsgruppen und deren Publikationsverzeichnisse.

Unter den in 2007 erbrachten Forschungsleistungen seien die Folgenden besonders hervorgehoben:

– Nachdem (erstmals für einen eukaryotischen Organismus) am Beispiel von *Arabidopsis* die Zellzyklusphase bestimmt worden war, in der die Histonvariante CENH3 in das Chromatin eingebaut wird, um aktive Zentromeren zu etablieren bzw. aufrecht zu erhalten (Lermontova et al., Plant Cell 2006), konnte nun gezeigt werden, dass Pflanzen in dieser Hinsicht von Tieren verschieden sind. Wie *Arabidopsis* inkorporieren auch Gerste, *Luzula* und Rotalgen CENH3 während der (späten) G2-Phase, während bei *Drosophila* und Mensch dieser Prozess zwischen Telophase und G1 erfolgt, d. h., erst nach der Trennung der Schwesterchromatiden während der Kernteilung (Lermontova et al., Chromosoma 2007).
  Weiterhin wurde gezeigt, dass in allen getesteten Pflanzen Schwesterchromatiden (außer an Zentromeren und hochrepetitiven Sequenzdomänen) entlang der Chromosomenarme nicht durchgängig gepaart sind (V. Schubert et al., MGG 2007), dass in *Arabidopsis* weder „hot spots“ noch „cold spots“ für Schwesterchromatidenkohäsion nachweisbar sind, und dass Schwesterchromatiden über Mb-Bereiche hinweg separiert sein können (s. Fig. 18, S. 64, V. Schubert et al., Chromosoma 2008) (Arbeitsgruppe Karyotypevolution).

– Im Rahmen des vom Land Sachsen-Anhalt geförderten Exzellenz-Netzwerkes mit der Martin-Luther-Universität Halle-Wittenberg „Biowissenschaften – Strukturen und

Information Technology group (formerly belonging to the Department of Administration and Central Services) into the research group Bioinformatics and Information Technology headed by Dr. Uwe Scholz with the aim to improve coordination efficiency.
A junior research group Data Inspection headed by Dr. Marc Strickert has been derived from the Pattern Recognition group and integrated into the Department of Molecular Genetics.

Two dissertations (PhD) and seven Diploma theses have been finished successfully.

Besides PGRC services, molecular marker systems, microarray-based transcript profiling, and flow-cytometry were important issues for collaboration within the Department and with other groups inside and outside the IPK last year. All groups of the Department collaborate with internal and external partners within the frame of large national and international research networks such as GABI projects and others. For the multiple cooperative links of the individual groups see their detailed reports and publication records.

The following scientific achievements are considered as highlights of the Department in 2007:

– After determining the cell cycle stage for deposition of the centromere-defining histone variant CENH3 in *Arabidopsis thaliana* (the first time for a eukaryotic organism), it could be shown that plants (barley, *Luzula*, red algae) in general differ from metazoa in this respect. While plants load CENH3 during (late) G2, when sister kinetochores become microscopically distinguishable; CENH3 deposition in *Drosophila* and human cells occurs between telophase and early G1, i.e., after separation of sister chromatids (Lermontova et al., Chromosoma 2007).
  Except for centromeres and highly repetitive domains, sister chromatids are not consistently aligned along chromosome arms in higher plants (V. Schubert et al., MGG 2007); cohesion “hot spots” or “cold spots” are not detectable, and non-alignment can extend over Mb-ranges in *A. thaliana* (see Fig. 18, p. 64 and V. Schubert et al., Chromosoma 2008) (research group Karyotype Evolution).

– Within the frame of the Excellence Network "Biowissenschaften – Strukturen und Mechanismen der Biologischen Informationsverarbeitung", in collaboration with the Martin Luther University Halle-Wittenberg and supported by the Federal State of Saxony-Anhalt, the Karyotype Evolution, Chromosome Structure and Function, and Epigenetics groups investigated the impact of epigenetic modifications on interphase arrangement of tandem repeats and the cell cycle-dependent cross-talk of histone modifications. Large transgenic repeat arrays

Mechanismen der Biologischen Informationsverarbeitung" untersuchen die Arbeitsgruppen Karyotypevolution, Chromosomenstruktur und -funktion und Epigenetik den Einfluss epigenetischer Veränderungen auf die Interphaseanordnung tandem-repetitiver Sequenzen sowie Zellzyklus-abhängige Histonmodifikationen. Transgene Tandem-Repeats von ca. ≥10 kb verändern die lokale Chromatinanordnung. Sie sind häufiger mit Heterochromatin assoziiert und paaren häufiger homolog miteinander als die entsprechenden Loci im Wildtyp, besonders wenn die Repeatsequenzen stark methyliert sind und/oder mehr als einmal per Chromosomenarm vorkommen (Jovtchev et al., Chromosoma 2008). Die Phosphorylierung von Histon H3 am Serinrest10 durch AtAurora1-Kinase wird durch Lysin9-Acetylierung verstärkt und durch Lysin14-Acetylierung als auch durch Threonin11-Phosphorylierung vermindert.

– Umfangreiche quantitative Segregationsanalysen hinsichtlich der beiden Apomixiskomponenten Apomeiose und Parthenogenese in *Hypericum perforatum* führten zu einem Modell, das die Regulation der apomiktischen Samenbildung über allele und nicht-allele, dosis-abhängige Wechselwirkungen zwischen sechs Genen erklärt. Damit wurde eine testbare Hypothese aufgestellt und hinsichtlich ihres Vermehrungsmodus definierte Pflanzenpopulationen generiert.
Von zwei diploid sexuellen und zwei diploid apomiktischen *Boechera*-Pflanzen wurden je zehn lebende Eiapparate mikrodissektiert und daraus 450.000 mRNA-tags sequenziert. Dies ergab 6.000 Kandidaten-mRNAs, die in sexuellen bzw. apomiktischen Ovulen differenziell exprimiert werden. Von diesen Kandidaten-mRNAs wurden Mikroarrays erzeugt, um zu testen, welche dieser Gene konsistent in sexuellen *versus* apomiktischen Ovulen aus unterschiedlichen Herkünften exprimiert werden (s. Fig. 21, S. 71, Arbeitsgruppe Apomixis).

– RT-PCR Experimente mit Gen-spezifischen Amplicons wurden zur Untersuchung der transkriptionellen Aktivität homeologer *Brassica napus*-Gene genutzt. Unter homeologen *B. napus*-Genen wurden oft Paare hochähnlicher Gene gefunden, in denen sich jeweils eine der Kopien von dem *B. oleracea*- bzw. *B. rapa*-Vorläufergenom ableitete. Gene, die solche Paare darstellten, zeigten in der Regel sehr ähnliche Expressionsmuster und auch die Höhe der Expression war für beide Kopien vergleichbar. Ausnahmen konnten jedoch auch beobachtet werden (s. Fig. 22, S. 74, Arbeitsgruppe Genomplastizität).

– *AtERI1* aus *A. thaliana* ist ein Kandidat für eine siRNA-spezifische RNase. Pflanzen, die für ein nicht mehr funktionelles *ateri1* T-DNA-Insertionsallel homozygot sind, zeigen häufiger „post-transcriptional gene silencing" eines *GUS*-Reportergens als der Wildtyp (s. Fig. 23, S. 77, Arbeitsgruppen Epigenetik und Genomplastizität).

(≥10 kb) frequently modify local chromatin arrangement by increased frequency of homologous pairing and association with endogenous heterochromatin, in particular when the arrays are strongly methylated and/or more than two arrays occur on one chromosome arm (Jovtchev et al., Chromosoma 2008). Phosphorylation of histone H3 at serine10 via AtAurora1-kinase turned out to be increased by lysine9 acetylation and decreased by lysine14 acetylation as well as by threonine11 phosphorylation.

– Comprehensive quantitative segregation analyses for the two components (apomeiosis and parthenogenesis) of apomictic seed formation in *Hypericum perforatum* led to a model, explaining the regulation of apomixis expression by allelic and non-allelic, dosage-dependent interactions between six genes, and resulted in populations defined as to their mode of reproduction.
From two diploid sexual and two diploid apomictic *Boechera* plants, ten live ovules were microdissected and 450,000 mRNA tags were sequenced to yield 6,000 candidate mRNAs that were differentially expressed between the two reproductive forms. From these candidate mRNAs, microarrays are being generated to test for consistent expression in sexual *versus* apomictic ovules from different genetic backgrounds (see Fig. 21, p. 71, research group Apomixis).

– Gene-specific amplicons were used in RT-PCR experiments to assess the transcriptional activity of homeologous genes in *Brassica napus*. Pairs of highly similar genes in which one of the gene copies each was derived from the *B. oleracea* and *B. rapa* progenitor genomes, respectively, were often detected among homeologous *B. napus* genes. Genes composing such pairs, generally showed very similar expression patterns and the expression level of both copies was comparable, however exceptions were also found (see Fig. 22, p. 74, research group Genome Plasticity).

– *AtERI1* is a candidate for a siRNA-specific RNase in *A. thaliana*. Plants homozygous for a non-functional *ateri1* T-DNA-insertion allele show post-transcriptional gene silencing of a *GUS* reporter gene more often than wild-type plants (see Fig. 23, p. 77, research groups Epigenetics and Genome Plasticity).

– Five hundred barley genes, that were found to be induced after pathogen attack, were tested by means of the "transient induced gene silencing" with an automated microscopic recognition system. Thirtyseven genes affected host resistance against powdery mildew. Surprisingly, most of these genes support the pathogen, because their silencing enhanced resistance (see Fig. 25, p. 84, research groups Transcriptome Analysis and Pattern Recognition).

– Fünfhundert Gerstengene, die nach Pathogenattacke induziert waren, wurden im RNAi-basierten „Transient Induced Gene Silencing"-Assay unter Verwendung eines automatisierten mikroskopischen Pilzerkennungssystems getestet. Davon zeigten 37 Gene einen Effekt auf die Basalresistenz gegen den Gerstemehltau. Unerwarteter Weise scheint die Mehrzahl dieser induzierten Pflanzengene das Pathogen zu unterstützen, da TIGS zu einer Erhöhung der pflanzlichen Resistenz führte (s. Fig. 25, S. 84, Arbeitsgruppen Transkriptomanalyse und Mustererkennung).

– Für eine einfache Selektion von Gerste-Genotypen mit Resistenz gegen *Rhynchosporium secalis* sind PCR-basierte Marker entwickelt worden (s. Fig. 27, S. 89, Arbeitsgruppe Gen- und Genomkartierung).

Ingo Schubert, Januar 2008

– PCR-based markers have been developed, which allow an easy selection of barley genotypes resistant to scald (*Rhynchosporium secalis*) (see Fig. 27, p. 89, research group Gene and Genome Mapping).

Ingo Schubert, January 2008

Programme: Cytogenetics

Research Group: Karyotype Evolution

Head: Prof. Ingo Schubert

Scientists

IPK financed
Berr, Alexandre, Dr. (0,5 P, till 31.01.2007)
Fuchs, Jörg, Dr. (P)
Kim, Young-Min (Annex, till 31.03.2007)
Malysheva-Otto, Ludmilla, Dr. (Annex, 15.02.-14.06.2007)
Schubert, Veit, Dr. (P)
Weißleder, Andrea, (0,5 P)

Grant Positions
Jovtchev, Gabriele, Dr. (0,5 Saxony-Anhalt, till 19.09.2007)
Lermontova, Inna, Dr. (DFG)
Watanabe, Koichi, Dr. (DFG, till 30.09.2007; BMBF, 01.10.-31.12.2007)

Visiting Scientists
Endo, Takashi R., Prof. (IPK, 30.08.-04.09.2007)
Kim, Young-Min (01.04.-30.04.2007)
Malysheva-Otto, Ludmilla, Dr. (self-financed, 01.01.-14.02.2007; 15.06.-31.12.2007)
Matzk, Fritz, Dr. (self-financed, 01.07.-31.12.2007)
Mohammed Ali, Hoda Badry, Dr. (IPK, till 27.04.2007)
Rudnik, Radek (University of Kassel, 05.11.-14.12.2007)

Goals

Elucidation of structure, plasticity, evolution and epigenetic modifications of plant genomes and functional chromosome domains.

Research Report

Centromere research. After defining the late G2 phase as the cell cycle stage for deposition of the centromeric histone variant CENH3 in *Arabidopsis*, the same could be shown for the monocot barley. Thus, **plants load CENH3 before sister chromatid separation**, in contrast to the situation in **metazoa**, where CENH3 deposition occurs **after mitotic sister chromatid segregation** (I. Lermontova, J. Fuchs, V. Schubert, I. Schubert, Chromosoma 2007). CENH3-RNAi plants display a short stature, slow growth, reduced amounts of CENH3 transcripts and proteins, but no obvious alteration in nuclear division, cell size and fertility. The impact of suppression and over-expression of endogenous and alien CENH3 genes on kinetochore assembly and centromere function will be tested further (DFG; I. Lermontova).
A conserved putative kinetochore protein, CBF5, was shown to be located in nucleoli and Cajal bodies and to be involved in RNA pseudouridinylation, rather than displaying a centromere function in *A. thaliana* (DFG; I. Lermontova, V. Schubert, F. Börnke, J. Macas, I. Schubert, Plant Mol. Biol. 2007).

Chromatin modifications. Studies of the subchromosomal distribution of histone modifications (in particular, mono-, di- and tri-methylation of lysine residues) between eu- and heterochromatin in angiosperms and gymnosperms led to the conclusions that (i) methylation of H3K4 is restricted to euchromatin in plants; (ii) H3K9me1, H3K9me2 and H3K27me1 mark heterochromatin in angiosperms, although spreading into euchromatin is possible within species with a genome size larger than 500 Mb/1C; (iii) H3K27me2 and H3K27me3 show species-specific chromosomal distribution and (iv) the heterochromatin in gymnosperms is characterised by H3K9me2,3 and H3K27me1,2,3. Comparative studies on mosses and ferns are ongoing (Saxony-Anhalt Excellence Cluster, J. Fuchs, G. Jovtchev).

Interphase chromatin arrangement. Together with C. Baroux, University of Zurich, a peculiar chromatin organisation could be shown for triploid endosperm nuclei of *A. thaliana*, deviating from that of sporophytic and gametophytic nuclei. Endosperm nuclei revealed a lower chromatin density and the appearance of mainly maternally derived "endosperm-specific interspersed heterochromatin foci" (C. Baroux, A. Pecinka, J. Fuchs, I. Schubert, U. Grossniklaus, Plant Cell 2007).
For transgenic lacO and tetO operator repeat arrays, it could be shown that: i) The frequency of somatic homologous pairing is increased at insertion sites of large (≥9.3 kb) repeat arrays, in particular if these are strongly methylated and two arrays occur on one chromosome arm. ii) The association frequency of repeat arrays with CCs apparently depends on size and number of repeat units per locus, but not on their methylation status.
iii) **Low-copy inserts** do (independent of their transcriptional activity) not significantly alter interphase chromatin arrangement, even if strongly methylated and **are** thus **more suitable for chromatin tagging than multiple copy arrays** (Saxony-Anhalt Excellence Cluster; G. Jovtchev, K. Watanabe, A. Pecinka, F. Rosin, M.F. Mette, E. Lam, I. Schubert, Chromosoma 2008).
Sister chromatid alignment at various chromosome positions in 4C nuclei of two monocot and two dicot species was shown to be similar as in *A. thaliana*. The highest alignment frequency (in >90 % of homologues) occurred

at centromeres and other high-copy loci and a significantly lower frequency at single or low-copy loci along chromosome arms (V. Schubert, Y.-M. Kim, A. Berr, J. Fuchs, A. Meister, S. Marschner, I. Schubert, Mol. Genet. Genomics 2007). In ***A. thaliana,* sister chromatids** were found to be **aligned or separated in a Megabase range** along chromosome arms; **"hot spots" or "cold spots" of alignment were not detectable** (see Fig. 18) and therefore, the average distances of cohesion sites must be much larger than in yeast, the only eukaryote well studied in this respect (V. Schubert Y-M. Kim, I. Schubert; Chromosoma 2008). The effects of cohesin mutants on sister chromatid alignment and nuclear divisions is under study now (V. Schubert, A. Weißleder).

The average positional **sister chromatid alignment frequency** in *A. thaliana* 4C leaf nuclei **increases** immediately **after X-irradiation** and returns to the basic level after 1 hour of recovery, when most of the double-strand breaks are repaired. This phenomenon is clearly less pronounced in T-DNA insertion mutants of genes encoding a cohesin (SMC6), known to be recruited to double-strand breaks. These observations indicate an **active movement of homologous positions towards each other after DNA breakage** (GABI-PRECISE expected; K. Watanabe et al., in preparation).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner, E. Achigan-Dako, S. Jakob;

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben, Dr. D. Demidov;

Dept. of Cytogenetics and Genome Analysis, Research Group *In vitro* Differentiation; Prof. A.M. Wobus, Dr. S. Sulzbacher, Dr. I. Schröder, A. Daniel-Wojcik;

Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke, Dr. A. Tewes;

Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

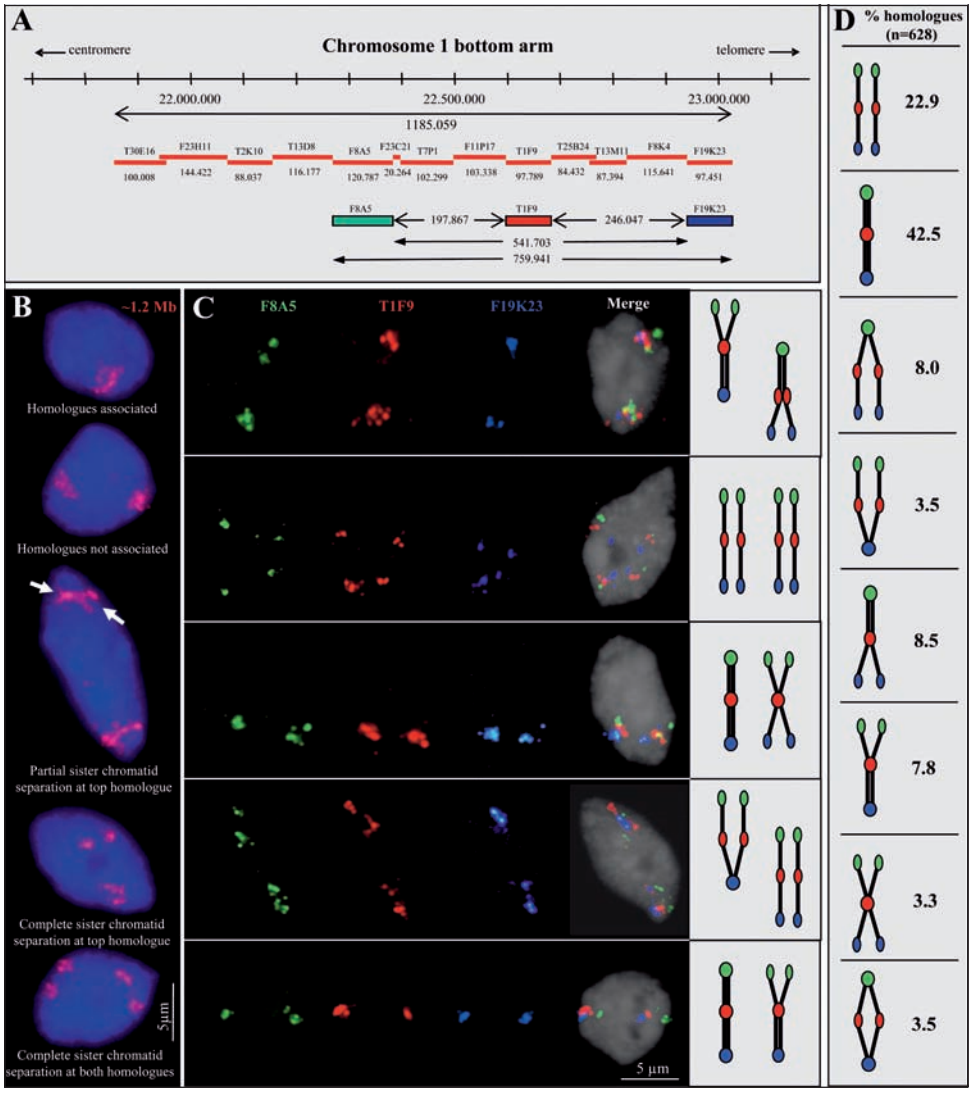

Fig. 18: FISH with BACs of a ~1.2 Mb contig from bottom arm of *Arabidopsis* chromosome 1 to 4C leaf nuclei shows that Mb-sized regions are mostly either completely aligned or completely separated, and cohesion "hot spots" do not occur. (A) The 13 BACs labeled in red and three BACs labeled in different colours used for FISH in (B) and (C), respectively. (B) Configurations of associated or non-associated homologues as well as of different states of sister chromatid alignment of the ~1.2 Mb segment. (C) Examples of aligned or separated sister chromatids at positions of three BACs within a ~760 kb segment and (D) summary of the frequencies of the individual configurations analysed in 314 nuclei (V. Schubert, Y.-M. Kim and I. Schubert).

Outside the Institute:
University of Karlsruhe, Institute of Botany II, Karlsruhe; Prof. H. Puchta, Dr. F. Hartung;
Max Planck Institute for Plant Breeding Research, Cologne; Dr. B. Reiss;
University of Hannover, Institute of Botany, Hannover; A. Islam;
Friedrich Alexander University Erlangen-Nuremberg; Dr. F. Börnke;
Georg-August-University Göttingen, Albrecht von Haller Institute of Plant Sciences, Göttingen; Dr. M. Kessler;
Justus v. Liebig University, Institute of Plant Production & Plant Breeding, Gießen; H.A. Sagbedja;
Martin Luther University Halle-Wittenberg, Institute of Genetics, Halle/S.; Prof. G. Reuter;
Martin Luther University Halle-Wittenberg, Institute of Biology/Geobotany and Botanical Garden, Halle/S.; Dr. A. Schmidt-Lebuhn;
Institute of Vegetable and Ornamental Crops, Erfurt; Dr. A. Hohe, T. Borchert;
University of Kyoto, Kyoto, Japan; Prof. T.R. Endo;
Rutgers State University, New Brunswick, USA; Prof. E. Lam;
Institute for Crop and Food Research, Christchurch, New Zealand; Dr. R. Pickering;
University of Zurich, Zurich, Switzerland; Prof. U. Grossniklaus, Dr. C. Baroux;
Institute of Plant Molecular Biology, Academy of Sciences, Ceské Budejovice, Czech Republic; Dr. J. Macas;
Masaryk University, Brnó, Czech Republic; Dr. M. Lysak;
University of Clermont-Ferrand, Clermont-Ferrand, France; Dr. I. Vaillant, Dr. S. Tourmente;
University of Wageningen, Lab of Molecular Biology, Wageningen, The Netherlands; S. de Nooijer, Dr. T. Bisseling.

Publications

Peer Reviewed Papers

Adoukonou-Sagbadja, H., V. Schubert, A. Dansi, G. Jovtchev, A. Meister, K. Pistrick, K. Akpagana & W. Friedt: Flow cytometric analysis reveals different nuclear DNA contents in cultivated fonio (*Digitaria* spp.) and some wild relatives from West-Africa. Plant Syst. Evol. 267 (2007) 163-176.

Baroux, C., A. Pecinka, J. Fuchs, I. Schubert & U. Grossniklaus: The triploid endosperm genome of *Arabidopsis* adopts a peculiar, parental-dosage-dependent chromatin organization. Plant Cell 19 (2007) 1782-1794.

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Borchert, T., J. Fuchs, T. Winkelmann & A. Hohe: Variable DNA content of *Cyclamen persicum* regenerated via somatic embryogenesis: rethinking the concept of long-term callus and suspension cultures. Plant Cell Tiss. Organ. Cult. 90 (2007) 255-263.

Hartung, F., R. Wurz-Wildersinn, J. Fuchs, I. Schubert, S. Suer & H. Puchta: The catalytically active tyrosine residues of both SPO11-1 and SPO11-2 are required for meiotic double-strand break induction in *Arabidopsis*. Plant Cell 19 (2007) 3090-3099.

Houben, A. & I. Schubert: Engineered plant minichromosomes: A resurrection of B chromosomes? Plant Cell 19 (2007) 2323-2327.

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Jovtchev, G., M. Barow, A. Meister & I. Schubert: Impact of environmental and endogenous factors on endopolyploidization in angiosperms. Environ. Exp. Bot. 60 (2007) 404-411.

Lermontova, I., J. Fuchs, V. Schubert & I. Schubert: Loading time of the centromeric histone H3 variant differs between plants and animals. Chromosoma 116 (2007) 507-510.

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Marschner, S., A. Meister, F.R. Blattner & A. Houben: Evolution and function of B chromosomal 45S rDNA sequences in *Brachycome dichromosomatica*. Genome 50 (2007) 638-644.

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Schubert, I.: Chromosome evolution. Curr. Opin. Plant Biol. 10 (2007) 109-115.

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Vaillant, I., S. Tutois, C. Cuvillier, I. Schubert & S. Tourmente: Regulation of *Arabidopsis thaliana* 5S rRNA genes. Plant Cell Physiol. 48 (2007) 745-752.

Books and Book Chapters

Barow, M. & G. Jovtchev: Endopolyploidy in plants and its analysis by flow cytometry. In: Doležel, J., J. Greilhuber & J. Suda (Eds.): Flow cytometry with plant cells. Analysis of genes, chromosomes and genomes. WILEY-VCH Verlag, Weinheim (2007) 349-372.

Houben, A. & I. Schubert (Eds.): Special Issue: The cytogenetics and genomics of crop plants. Chromosome Res. 1 (2007) 121 pp.

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Vegetabile 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Meister, A. & M. Barow: DNA base composition of plant genomes In: Doležel, J., J. Greilhuber & J. Suda (Eds.): Flow cytometry with plant cells. Analysis of genes, chromosomes and genomes. WILEY-VCH Verlag, Weinheim (2007) 177-215.

Pfündel, E. & A. Meister: Flow cytometry of chloroplasts. In: Doležel, J., J. Greilhuber & J. Suda (Eds.): Flow cytometry with plant cells. Analysis of genes, chromosomes and genomes. WILEY-VCH Verlag, Weinheim (2007) 251-266.

Other Publications

Houben, A. & I. Schubert: The cytogenetics and genomics of crop plants - Foreword. Chromosome Res. 15 (2007) 1-2.

PhD and Diploma Theses

Kim, Y.-M.: Untersuchungen zur Schwesterchromatidenkohäsion mittels Fluoreszens *in situ* Hybridisierung bei Angiospermen unter besonderer Berücksichtigung von *Arabidopsis thaliana*. (Diploma Thesis) Universität Kassel, Fachbereich 18 – Naturwissenschaften, Kassel (2007) 45 pp.

Lectures, Posters and Abstracts

V11, V137, V214, V215, V216, V217, V218, V268, V269, P1, P32, P35, P36, P40, P41, P50, P51, P52, P96, P97, P138, P139, P140, P191, P192, P193, P206, P229, P230.

Additional Funding

For further information see the survey page 205.

Research Group: Chromosome Structure and Function

Head: Dr. Andreas Houben

Scientists

IPK financed
Carchilan, Mariana (0,5 Annex)

Grant Positions
Agueci, Francesco (0,5 Saxony-Anhalt)
Banaei Moghadam, Ali Mohammad (0,5 DFG)
Demidov, Dmitri, Dr. (DFG)
Karimi Ashtiyani, Raheleh (0,5 Saxony-Anhalt)
Sanei, Maryam (0,5 DFG, since 01.10.2007)
Vlasenko, Liudmila (0,5 DFG)

Visiting Scientists
Pickering, Richard, Dr. (New Zealand, 16.05.-16.07.2007)

Goals

Analysis and manipulation of structure and regulation of plant chromosomes.

Research Report

Chromosome condensation and segregation has been linked to dynamic histone H3 phosphorylation and AtAurora1 activity. *In vitro* kinase assays demonstrate that the recombinant AtAurora1 phosphorylates not only histone H3S10 *in vitro* but also histone H4, the spindle checkpoint proteins MAD2, Bub1 and Mob1, and most likely the centromeric histone CENH3, too. As demonstrated by immunoprecipitation using AtAurora1-TAP (tandem affinity purification) transformants MAD2 and Bub1 form a complex with AtAurora1 *in vivo*. To find interacting partners of the kinetochore protein CENH3, interaction assays were performed with recombinant CENH3 and *Arabidopsis* protein extracts. Treatment of an *Arabidopsis* suspension culture and an *in vitro* kinase assay with the Aurora-inhibitors Hesperadin and inhibitor II significantly reduced the level of histone H3S10 phosphorylation. Inactive AtAurora results in lagging chromatids, while the cell cycle progressed. Overexpression of AtAurora1, fused with a TAP-tag, results in an increased level of endopolyploidisation, mainly in older leaves. To test whether a cross-talk exists between phosphorylation of histone H3 Ser10 and other post-translational modifications, an *in vitro* kinase assay was performed using N-terminal peptides of H3 with different post-translation modifications as AtAurora1 substrates. We found that phosphorylation of H3S10 is weakly influenced by K9-methylation but significantly increased by K9-acetylation and decreased by K14-acetylation and Thr11-phosphorylation (D. Demidov, L. Vlasenko and O. Weiß in collaboration with A. Tewes, A. Matros, H.-P. Mock).

An orthologue of the putative threonine 3 histone H3-specific **Haspin kinase** of mammals has been **analysed in *Arabidopsis***. Down-regulation (via RNAi) or overexpression of AtHaspin results in phenotypes with defects in floral organs and vascular tissue, loss of apical dominance and multiple rosettes with a weak primary stem. 35S: AtHaspin-YFP and AtHaspin promoter: GUS-signals are mainly localised in the vascular system (see Fig. 19, p. 68). A novel function, namely a role in the vascular formation and in the auxin signal transduction pathway has been proposed for Haspin in plants (R. Karimi in collaboration with T. Rutten and A. Tewes).

The kinase NIMA of *A. nidulans* is involved in the phosphorylation of histone H3 at serine 10. To study the function of this highly conserved kinase in plants, the transcriptional behaviour of **AtNIMA2, a member of the *Arabidopsis* NIMA-like kinase family** was analysed using T-DNA insertion and a RNAi construct. Complete inactivation of AtNIMA2 (via T-DNA insertion) is lethal. Partial inactivation of AtNIMA2 results in smaller plants with a delayed development and leaves with structural defects. No obvious difference in the level of histone H3S10 phosphorylation was detected in plants with a down-regulated AtNIMA2 activity (F. Agueci in collaboration with T. Rutten).

The origin and activity of B chromosomes (Bs) of *Brachycome dichromosomatica* and of rye were analysed. Phylogenetic analysis of ITS2 sequences identified no *Brachycome* species that contained a sequence more similar to either large B or micro B-chromosome-located 45S rDNA than that of the *B. dichromosomatica* A chromosomes. Thus, an origin of the Bs from A chromosomes is most likely. Frequent lack of nucleolar association of micro Bs suggests inactivity of micro B-45S rDNA. The global transcription activity of rye Bs was investigated by comparing the cDNA-AFLP profiles of 0B/+B plants. Among more than 2,000 transcripts, 16 putative rye B-specific transcripts were identified. The B-specific transcripts B1334, B8149 and B2465 are members of a high-copy mobile element family. High sequence similarity to the A chromosome located members of these families confirms the A chromosome origin of rye Bs (M. Carchilan, S. Marschner, K. Kumke, A. Houben).

Extrachromosomal circular DNA (eccDNA) indicates plasticity of non-plant eukaryotic genomes. We have found

eccDNA in small as well as in large plant genomes. The size of plant eccDNA ranges from >2 kb to <20 kb, which is similar to the sizes found in other organisms. These DNA molecules correspond to 5S rDNA, telomeric DNA and other tandem repeats. Such circular multimers, also found in animals, suggest a common mechanism for eccDNA formation among eukaryotes via intra-chromosomal homologous recombination (A. Houben in collaboration with S. Cohen, Tel Aviv University, Israel).

Analysis of the **relationship between intra-specific hybridisation/heterosis and epigenetic modifications** has been conducted using *Arabidopsis* (lines Col-0, C24 and their F1 hybrids) as a model. No microscopically detectable alterations of DNA/histone methylation were found in the hybrids. However, ChIP/chip experiments revealed a few genomic regions with novel histone H3K4 dimethylation patterns in the hybrid progeny. Comparative genomic hybridisation uncovered copy number differences of mobile and satellite repeat elements between both parental genomes (A. Banaei in collaboration with F.M. Mette, research group Epigenetics; V. Colot, Epigenomics and Epigenetics of *Arabidopsis* group, France).

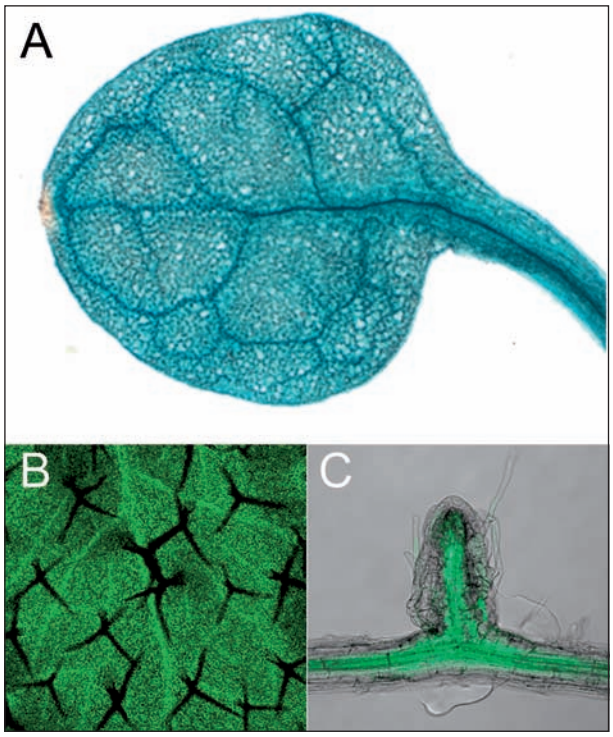

Fig. 19: Cellular distribution of AtHaspin kinase from *Arabidopsis thaliana*. (A) GUS expression driven by the AtHaspin promoter. Localisation of 35S: AtHaspin-YFP fusion protein in leaf (B) and root (C) by confocal laser scanning microscopy (R. Karimi, T. Rutten). Note that AtHaspin-signals are mainly localised in the vascular system.

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;
Dept. of Genebank, Research Group Taxonomy of Plant Genetic Resources; Dr. K. Pistrick;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. I. Lermontova, Dr. J. Fuchs, Prof. I. Schubert;
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. F.M. Mette;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. A. Tewes;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. A. Matros, Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

Outside the Institute:

Martin Luther University Halle-Wittenberg, Institute of Genetics, Halle/S.; Prof. G. Reuter;
Free University Berlin, Institute for Biology, Berlin; U. Dubiella, Prof. T. Romeis;
Max Planck Institute for Molecular Plant Physiology, Golm; Prof. T. Altmann, Dr. R. Meyer;
Ludwig Maximilians University, Munich; Prof. G. Wanner, Dr. E. Schroeder-Reiter;
Friedrich Alexander University Erlangen-Nuremberg, Erlangen; Dr. R. Börnke;
Adelaide University, Adelaide, Australia; Prof. J. Timmis, Dr. C. Leach;
Universidad Complutense, Madrid, Spain; Prof. M. Puertas;
Instituto Superior de Agronomia, Centro de Botânica Aplicada à Agricultura, Lisboa, Portugal; Dr. A. Caperta, Prof. W. Viegas;
University of Wales, Aberystwyth, UK; Prof. J.N. Jones;
Okayama University, Okayama, Japan; Prof. M. Murata, Dr. K. Nagaki;
Kyoto University, Kyoto, Japan; Prof. T.R. Endo, Dr. S. Nasuda, Dr. T. Nomura;
University Aalborg, Aalborg, Denmark; Prof. K.D. Grasser;
Institute for Crop and Food Research, Christchurch, New Zealand; Dr. R. Pickering;
Epigenomics and Epigenetics of *Arabidopsis* group, Ecole Normale Supérieure, Paris, France; Prof. V. Colot;
Institute of Experimental Botany, Olomouc, Czech Republic; Dr. J. Doležel;
Tel-Aviv University, Tel-Aviv, Israel; Dr. S. Cohen, Prof. D. Segal;
University of St. Petersburg, St. Petersburg, Russia; Dr. N.D. Tikhenko.

Publications

Peer Reviewed Papers

Carchilan, M., M. Delgado, T. Ribeiro, P. Costa-Nunes, A. Caperta, L. Morais-Cecílio, R.N. Jones, W. Viegas & A. Houben: Transcriptionally active heterochromatin in rye B chromosomes. Plant Cell 19 (2007) 1738-1749.

Gernand, D., H. Golczyk, T. Rutten, T. Ilnicki, A. Houben & A.J. Joachimiak: Tissue culture triggers chromosome alterations, amplification, and transposition of repeat sequences in *Allium fistulosum*. Genome 50 (2007) 435-442.

Houben, A., D. Demidov, A.D. Caperta, R. Karimi, F. Agueci & L. Vlasenko: Phosphorylation of histone H3 in plants-A dynamic affair. Biochim. Biophys. Acta 1769 (2007) 308-315.

Houben, A., E. Schroeder-Reiter, K. Nagaki, S. Nasuda, G. Wanner, M. Murata & T.R. Endo: CENH3 interacts with the centromeric retrotransposon *cereba* and GC-rich satellites and locates to centromeric substructures in barley. Chromosoma 116 (2007) 275-283.

Houben, A. & I. Schubert: Engineered plant minichromosomes: A resurrection of B chromosomes? Plant Cell 19 (2007) 2323-2327.

Marschner, S., K. Kumke & A. Houben: B chromosomes of *B. dichromosomatica* show a reduced level of euchromatic histone H3 methylation marks. Chromosome Res. 15 (2007) 215-222.

Marschner, S., A. Meister, F.R. Blattner & A. Houben: Evolution and function of B chromosomal 45S rDNA sequences in *Brachycome dichromosomatica*. Genome 50 (2007) 638-644.

Schubert, V., Y.M. Kim, A. Berr, J. Fuchs, A. Meister, S. Marschner & I. Schubert: Random homologous pairing and incomplete sister chromatid alignment are common in angiosperm interphase nuclei. Mol. Genet. Genomics 278 (2007) 167-176.

Books (Edited Journal)

Houben, A. & I. Schubert (Eds.): Special Issue: The cytogenetics and genomics of crop plants. Chromosome Res. 1 (2007) 121 pp.

Other Publications

Houben, A. & I. Schubert: The cytogenetics and genomics of crop plants – Foreword. Chromosome Res. 15 (2007) 1-2.

PhD and Diploma Theses

Marschner, S.: Ursprung, Zusammensetzung und Transkriptionsaktivität der B-Chromosomen von *Brachycome dichromosomatica*. (PhD Thesis) Humboldt-Universität zu Berlin, Berlin (2007) 91 pp.

Lectures, Posters and Abstracts

V4, V5, V41, V48, V85, V86, V87, P4, P5, P14, P15, P32, P33, P50, P51, P216, P217.

Additional Funding

For further information see the survey page 206.

Research Group: Apomixis

Head: Dr. Timothy F. Sharbel

Scientists

IPK financed
Aliyu, Olawale Mashood, Dr. (Annex, since 01.09.2006)
Corall García, José María, Dr. (Pakt für Forschung und Innovation, since 24.04.2007)
Matzk, Fritz, Dr. (0,5 P, till 30.06.2007)
Puente Molins, Marta, Dr. (Pakt für Forschung und Innovation, 01.02.-23.04.2007)
Voigt, Marie-Luise (0,5 P, since 15.03.2005)

Grant Positions
Puente Molins, Marta, Dr. (DFG, since 01.06.2007)
Thiel, Thomas (International Max Planck Research School grant, since 01.12.2007)

Visiting Scientists
Bringezu, Thomas, Dr. (Martin Luther University Halle-Wittenberg)
Galla, Giulio (University of Padua, since 05.03.2007)
Hamilton, Navina (Max Planck Institute Jena, 01.01.-31.07.2007)
Poyato, Manrique Inmaculada (University of Granada, 05.09.-22.12.2007)
Puente Molins, Marta, Dr. (self-financed, 24.04.-31.05.2007)

Scholars
Corall García, José María, Dr. (*WGL*/DAAD, 01.01.-23.04.2007)

Goals

Genomic and transcriptomic analyses to identify candidate apomixis factors in wild accessions of *Hypericum perforatum* and in the *Boechera holboellii* complex.

Research Report

***Hypericum perforatum*:** We have chosen 650 accessions, representing different ploidies and worldwide geographic origins, from which an analysis of 30 microsatellite markers is underway. The results demonstrate very high levels of polymorphism and heterozygosity, which support hypotheses of the allopolyploid origin of *H. perforatum*. A flow cytometric analysis of 96 seeds per one individual of each of the 650 accessions is also being performed in order to measure quantitative variation in sexual and apomictic seed production. The ploidy, microsatellite, and seed screen data will be combined in a cluster analysis in order to identify genetically-divergent clonal lineages from which crosses will be made in 2008. The idea is to test whether genetic distance between parents used in a cross has a quantitative effect on sexual versus different modes of apomictic seed production in their offspring. We are furthermore performing embryological analyses of different sexual and apomictic accessions in order to compare the origin of aposporous initial cells in different genetic lineages (see Fig. 20) (J.M. Corral, M. Molins, O.M. Aliyu in collaboration with H. Bäumlein, research group Gene Regulation; G. Galla, G. Barcaccia, Padua; J. Maron, Montana).

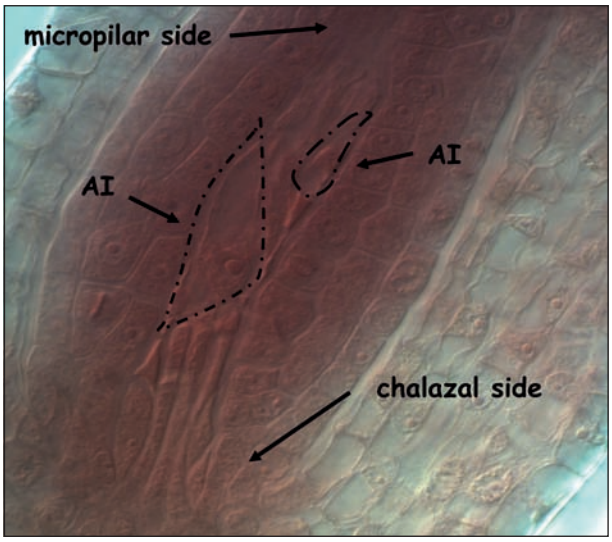

Fig. 20: Cleared and stained ovule from an apomictic *H. perforatum* accession, demonstrating a degenerated megaspore mother cell and 2 different aposporous initial (AI) cells, one of which appears to be degenerating (G. Galla, T. Sharbel).

The *Boechera holboellii* complex: We have chosen two diploid sexual and two unrelated diploid apomictic accessions, from which ten live ovules from a single developmental stage were isolated. **Using** a **SuperSAGE** (serial analysis of gene expression) approach, over **450,000 mRNA tags were DNA sequenced from** the **four microdissected ovule samples**. A comparison of the four gene expression profiles demonstrates over **6,000 candidate mRNAs**, including (1) mRNA tags **only found in sexual or apomictic ovules, and** (2) mRNA tags **up- or down regulated** when **comparing** the two **sexual and** two **apomictic ovules** (see Fig. 21, p. 71). Over **30 tags**, from which significant BLAST results **were** obtained, are homologous to **previously-identified candidate apomixis genes** in other species.

The mRNA sequences generated in the SuperSAGE analysis are derived from the 3'-untranslated region of each mRNA, a highly variable region which

is under little to no selection pressure, and hence sequence homology (BLAST) searches to the *Arabidopsis* genome yield very little information. To obtain whole gene sequence information from the candidate mRNA tags identified in the SuperSAGE analysis, flowers of different developmental stages were pooled for a single apomictic and sexual accession separately, a normalised cDNA amplification was performed and this material was sequenced using 454 technology (with Agencourt Bioscience Corporation, USA). Considering high-quality sequences only, **12.4 and 14.6 Mbp of DNA were sequenced for the sexual and apomictic flower-specific libraries respectively**. In order to test the SuperSAGE analysis, 50 candidate mRNA's were chosen and BLASTED to the 454 sequence data to obtain the full-length gene sequences. Using this data, gene-specific primers were developed and the gene expression profiles of these candidates have been confirmed using our newly-purchased GeXP system on the microdissected tissues of sexual and apomictic *Boechera* accessions. We are presently designing microarrays with the 6,000 candidate loci for an analysis of different microdissected tissues from multiple developmental stages and different apomictic *Boechera* accessions in order to identify consistently-expressed candidates (M.-L. Voigt, J.M. Corral, O.M. Aliyu, T. Thiel in collaboration with J. Kumlehn, research group Plant Reproductive Biology; H. Vogel, MPI Jena; B. Rotter, GenXPro Frankfurt).

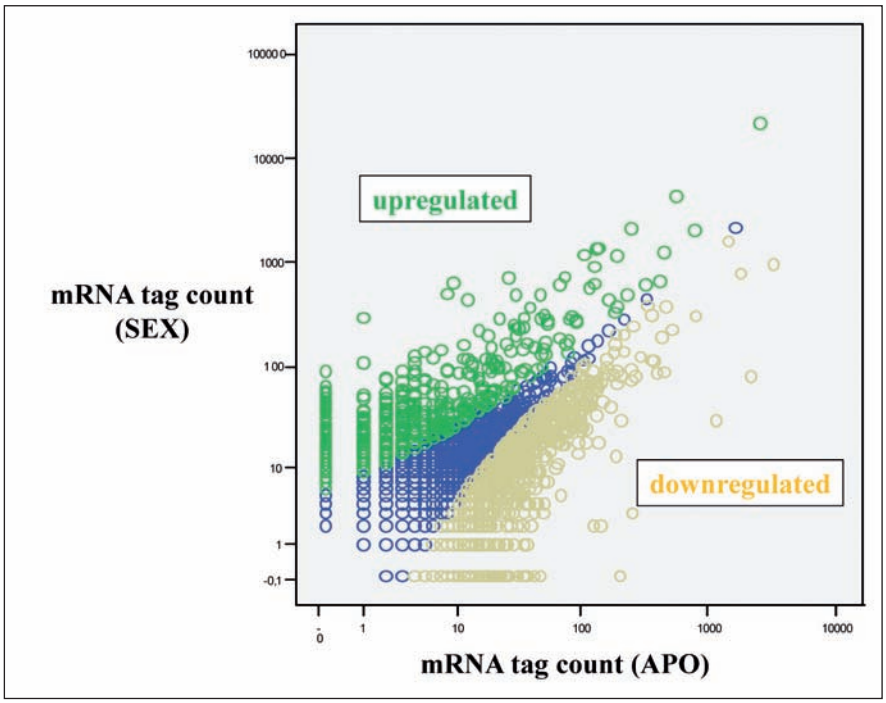

Fig. 21: Comparison of mRNA tag count between microdissected ovules taken from 2 sexual and 2 apomictic *Boechera* accessions, as measured in a SuperSAGE analysis (T. Sharbel, M.-L. Voigt, J.M. Corral, A. Varshney, J. Kumlehn, H. Vogel, B. Rotter).

Collaboration

Within the Institute:

Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

University of Heidelberg, Institute of Plant Sciences, Department of Biodiversity and Plant Systematics, Heidelberg; Prof. M. Koch, Dr. C. Dobeš;
Max Planck Institute for Chemical Ecology, Jena; Dr. H. Vogel;
GenXPro GmbH, Frankfurt am Main; Dr. B. Rotter;
Saaten-Union Resistenzlabor GmbH, Leopoldshöhe; Dr. J. Weyen;
Euro Grass Breeding GmbH & Co. KG, Asendorf; Dr. C. Schumann;
Duke University, Durham, North Carolina, USA; Prof. T. Mitchell-Olds;
Wageningen Agricultural University, Laboratory of Genetics, The Netherlands; Dr. H. de Jong;
University of Granada, Department of Genetics, Granada, Spain; Prof. J.M. Camacho;
University of Perugia, Department of Plant Biology and Agroenvironmental and Animal Biotechnology, Perugia, Italy; Dr. E. Albertini;
University of Padova, Department of Environmental Agronomy and Crop Science, Padova, Italy; Dr. G. Barcaccia;
University of Montana, Missoula, Montana, USA; Prof. J. Maron.

Publications

Peer Reviewed Papers

Dobeš, C., T.F. Sharbel & M. Koch: Towards understanding the dynamics of hybridization and apomixis in the evolution of genus *Boechera* (Brassicaceae). Syst. Biodivers. 5 (2007) 321-331.

Kantama, L., T.F. Sharbel, M.E. Schranz, T. Mitchell-Olds, S. de Vries & H. de Jong: Diploid apomicts of the *Boechera holboellii* complex display large-scale chromosome substitutions and aberrant chromosomes. Proc. Natl. Acad. Sci. USA 104 (2007) 14026-14031.

Books and Book Chapters

Barcaccia, G., H. Bäumlein & T.F. Sharbel: Apomixis in St. John's wort (*Hypericum perforatum* L.): an overview and glimpse towards the future. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 259-280.

Hörandl, E., U. Grossniklaus & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 424 pp.

Matzk, F.: Reproduction mode screening. In: Doležel, J., J. Greilhuber & J. Suda (Eds.): Flow cytometry with plant cells. Analysis of genes, chromosomes and genomes. WILEY-VCH Verlag, Weinheim (2007) 131-152.

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Vegetabile 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Voigt, M.-L., M. Melzer, T. Rutten, T. Mitchell-Olds & T.F. Sharbel: Gametogenesis in the apomictic *Boechera holboellii* complex: the male perspective. In: Hörandl, E., U. Grossniklaus & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 235-257.

Patents

Sharbel, T., Blumenthal, P.: Filterplatte, Prioritätsdatum: 24.04.2007, Anmelder: IPK/Blumenthal, Gebrauchsmuster 20 2007 005 989.2, Tag der Eintragung 02.08.2007, IPK-Nr.: 2006/08.

Lectures, Posters and Abstracts

V13, V19, V56, V80, V175, V240, V241, V242, V243, V244, V245, V267, P8, P26, P60, P78, P125, P170, P171, P174, P183, P184, P201, P202, P219.

Additional Funding

For further information see the survey page 206.

Research Group: Genome Plasticity

Head: Dr. Renate Schmidt

Scientists

IPK financed
Bach, Katrin, Dr. (Annex, since 01.05.2007)

Goals

A **comparative genomics approach** to reveal patterns of **genome evolution** in members of the Brassicaceae.

Research Report

Comparative genome analysis in cruciferous plants
Studies on genome organisation in *Brassica napus* were initiated at the Max Planck Institute for Molecular Plant Physiology. Since October 2006, this work, that was initially funded by the BMBF within the GABI Bridge project, is being continued at the Leibniz Institute of Plant Genetics and Crop Plant Research. Nine *Arabidopsis thaliana* single-copy genes that probably play a major role in oil biosynthesis were chosen as candidates and used to identify the corresponding segments from a *B. napus* BAC library. An in-depth sequence analysis of these segments revealed insights into the structure of the *B. napus* genome, in particular about the fate of duplicated oilseed rape gene sequences. The *A. thaliana* candidate genes were represented several times in the *B. napus* genome – on average five times. Interestingly, **a considerable proportion of the homeologous copies represented gene fragments rather than genes with a conserved exon/intron structure**. All *B. napus* homeologues that showed a conserved exon/intron structure, when compared to the *A. thaliana* counterpart, were found to be expressed whereas this was only the case for some of the gene fragments. **Collinearity studies revealed many deviations from genome colinearity** not only between *A. thaliana* and *B. napus* segments but also between homeologous *B. napus* regions. Differential gene loss was frequently observed. Gene fragments were particularly often found in non-colinear positions (K. Bach, R. Schmidt).
Gene-specific amplicons suitable for RT-PCR experiments were developed for the different *B. napus* genes corresponding to the *A. thaliana* candidate genes to assess their transcriptional activity in oilseed rape. RNA was isolated from leaf, stem, root, and flower tissues. In addition, siliques, and/or seeds were harvested at different time points after flowering and used for RNA isolation. Sequence comparisons of homeologous *B. napus* genes revealed the presence of highly similar gene pairs in which one of the gene copies each was derived from the *B. oleracea* and *B. rapa* progenitor genomes, respectively. **Genes constituting such gene pairs generally showed very similar expression patterns and the expression level of both copies was comparable**, but exceptions were noted (see Fig. 22, p. 74). The gene-specific amplicons were used to study the influence of allelic diversity on gene expression. Therefore, eleven genetically diverse rapeseed genotypes were chosen. RT-PCR experiments were performed with cDNAs derived from seeds 30 days after flowering. Genomic DNAs of the different genotypes were also used as PCR templates in order to establish whether the gene-specific oligonucleotide pairs are suitable for amplification in the different genotypes. For a considerable proportion of the genes tested, reduced expression was noted in one or several of the genotypes (K. Bach).

Future work will encompass allelic diversity studies in *B. napus* as well as comparative quantitative genetics in *A. thaliana* and *B. napus*. These studies will focus on the trait oil content. Novel candidate genes for this trait shall also be identified in *A. thaliana* using an eQTL analysis. This work is supported by the BMBF as part of the GABI OIL consortium (R. Schmidt).

Collaboration

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. M.F. Mette.

Outside the Institute:
Georg-August University Göttingen, Göttingen; Prof. H. Becker, Dr. W. Ecke;
Deutsche Saatveredelung AG, Lippstadt; Dr. D. Stelling;
KWS SAAT AG, Einbeck; Dr. M. Ouzunova, Dr. F. Breuer;
Leibniz Institute of Plant Biochemistry, Halle/S.; Dr. S. Rosahl;
Max Planck Institute for Molecular Plant Physiology, Golm; Dr. P. Dörmann;
Norddeutsche Pflanzenzucht Hans-Georg Lembke KG, Holtsee; Dr. G. Leckband, Dr. A. Abbadi;
RAPS GbR Grundhof, Grundhof; Dr. P. Duscherer;
SW Seed Hadmersleben GmbH, Hadmersleben; Dr. W. Horn;
Syngenta Seeds GmbH, Bad Salzuflen; Dr. M. Coque;
Cornell University, Ithaca, New York, USA; Prof. J. Nasrallah.

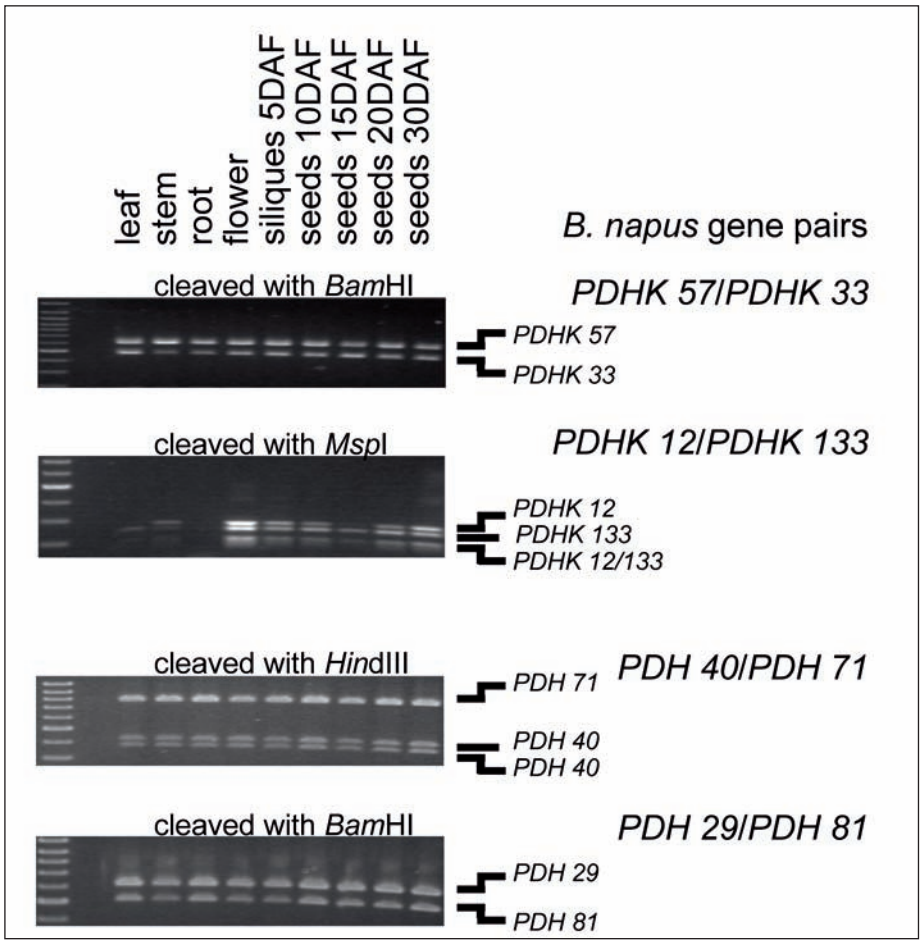

Fig. 22: Expression analysis of homeologous *Brassica napus* genes. Oligonucleotide combinations that amplify pairs of homeologous *B. napus* genes were used for RT-PCR analysis of different tissues and seeds of different developmental stages. Products obtained after 36 PCR cycles were digested with restriction enzymes in order to reveal gene-specific fragments. The analysis of homeologous *B. napus* genes coding for pyruvate dehydrogenase kinase (PDHK) and pyruvate dehydrogenase E1 alpha (PDH) is shown. Among the homeologous *PDHK* genes two highly similar pairs of genes were identified, *PDHK 33/PDHK 57 and PDHK 12/PDHK 133*. *PDHK* genes *33* and *57* showed expression in all tissues analysed, whereas for genes *PDHK 12* and *133* expression in roots was not detectable. Expression was observed for *PDHK* gene *133* in leaves and seeds 15 days after flowering (DAF), but not for the highly similar gene *PDHK 12*. In contrast, the homeologous *PDH* genes showed very similar expression patterns (K. Bach).

Publications

(All publications are based on work that has been carried out when Renate Schmidt was at the Max Planck Institute for Molecular Plant Physiology in Golm, Germany)

Peer Reviewed Papers

Nasrallah, J.B., P. Liu, S. Sherman-Broyles, R. Schmidt & M.E. Nasrallah: Epigenetic mechanisms for breakdown of self-incompatibility in interspecific hybrids. Genetics 175 (2007) 1965-1973.

Other Publications

Ecke, W., M. Lange, R. Schmidt, K. Bach, E. Dietrich, R. Snowdon, K. Link, M. Ouzunova, F. Breuer, D. Stelling, D. Hauska, G. Leckband, F. Dreyer, J. Detering, P. Duscherer, W. Horn & S. Tuvesson: GABI-Bridge: Die Brücke von Sequenz zu Ölgehalt und Resistenz: DNA-Unterschiede kontrollieren agronomisch wichtige Merkmale bei Raps. GenomXPress Sonderausgabe März (2007) 32.

Electronic Publications

Schmidt, R.: Plant Genome Projects. Encyclopedia of Life Sciences. John Wiley & Sons, Ltd., Chichester. http://www.els.net/ [doi: 10.1002/9780470015902.a0002018.pub2] (2007).

PhD and Diploma Theses

Arlt, M.: Studien zur Initiation, Ausbreitung und Übertragbarkeit verschiedener Varianten von posttranskriptionellem Transgensilencing anhand molekularer Charakteristika in *Arabidopsis thaliana*. (Dissertation), Universität Potsdam, Potsdam (2007) 159 pp.

Bach, K.: Duplizierte Gene in *Brassica napus* – genetische Vielfalt in Kandidatengenen für Ölgehalt. (Dissertation), Universität Potsdam, Potsdam (2007) 181 pp.

Lectures, Posters and Abstracts

P10, P22, P42, P129, P130, P131, P132, P133, P134, P175, P188.

Additional Funding

For further information see the survey page 207.

Research Group: Epigenetics

Head: Dr. Michael Florian Mette

Scientists

IPK financed
Bruchmüller, Astrid (Annex)
Weißleder, Andrea (0,5 P)

Grant Positions
Jovtchev, Gabriele, Dr. (0,5 Saxony-Anhalt, till 19.09.2007)
Kuhlmann, Markus, Dr. (Excellence Cluster, DFG SFB 648)
Richert-Pöggeler, Katja, Dr. (Saxony-Anhalt, till 15.07.2007)

Goals

Analysis and utilisation of epigenetic control mechanisms acting at the chromatin level to warrant regulation and structural maintenance of plant genomes.

Research Report

Gene silencing involving double-stranded RNA that is processed into short interfering (si) RNA as a nucleotide sequence-specific signal (RNA silencing) can regulate gene expression at both, the transcriptional and the post-transcriptional level.

RNA-directed transcriptional gene silencing (RdTGS) of transgenes in *Arabidopsis thaliana* provides a versatile experimental system for the genetic study of silencing acting at the chromatin level. So far, factors involved in siRNA binding, siRNA-DNA interaction, *de novo* and maintenance DNA methylation and chromatin remodeling have been demonstrated to be required. A reverse-genetic approach testing T-DNA insertion mutations in putative histone methyltransferases identified SET-domain protein SUVH2 as a candidate for a factor essential for RNA-directed *de novo* DNA methylation of transgenic and plant endogenous DNA sequences. Studies to determine the histone modification(s) performed by SUVH2 in detail are underway. To identify additional mutations releasing RdTGS, EMS mutagenesis of a line showing strong silencing has been performed. Presently, M_2 seeds are screened for reactivation of kanamycin resistance conferred by the pNOS-*NPTII* reporter in the target transgene (DFG/SFB; M. Kuhlmann, M.F. Mette; Fischer et al., Plant J. 2008).
The possible involvement of DNA glycosylase/lyase ROS1, a protein with the potential to antagonise gene silencing by removal of DNA methylation, was tested combining a *ros1* mutant with a silencing-resistant target transgene. As no enhancement of silencing was observed, a role of ROS1 in counteracting RdTGS seems unlikely.
To screen for mutations enhancing RdTGS, a new transgene system based on D-amino acid oxidase (DAAO), a yeast enzyme that converts non-toxic D-amino acid D-Val into metabolites toxic to plants, has been established. Plants containing an only partially silenced DAAO gene are sensitive to D-Val. After EMS mutagenesis, progeny affected in factors counteracting RdTGS is expected to show enhanced DAAO silencing and will become resistant to the selective agent (Saxony-Anhalt, K. Richert-Pöggeler, M.F. Mette).

A transgene system showing dosage-dependent **post-transcriptional gene silencing** (PTGS) is being used to analyse the role of the putative siRNA-specific RNase *At-ERI1* that counteracts RNA silencing by degradation of siRNA (see Fig. 23, p. 77) in *A. thaliana* (M. Kuhlmann, M. F. Mette in collaboration with R. Schmidt, research group Genome Plasticity).

Additionally, in a more applied context, strategies for optimisation of recombinant protein expression in plant seeds by modulation of PTGS pathways are tested in *A. thaliana* and barley (IPK-Ideenwettbewerb, A. Bruchmüller, M. F. Mette in collaboration with J. Kumlehn, research group Plant Reproductive Biology).

The presence of transgenic lacO tandem repeats can alter the architecture of interphase nuclei in *A. thaliana*. In a systematic study employing transgenes containing tetO and lacO tandem repeats of varying size integrated at different chromosomal positions, it was demonstrated that presence of two lacO loci of a minimal size on the same chromosome arm induces enhanced transgene pairing and association with heterochromatin. A possible involvement of histone methylation in these effects is being tested by introduction of mutations in members of the SUVH histone methyltransferase family (Saxony-Anhalt Excellence Cluster, G. Jovtchev, M. F. Mette in collaboration with I. Schubert, research group Karyotype Evolution).

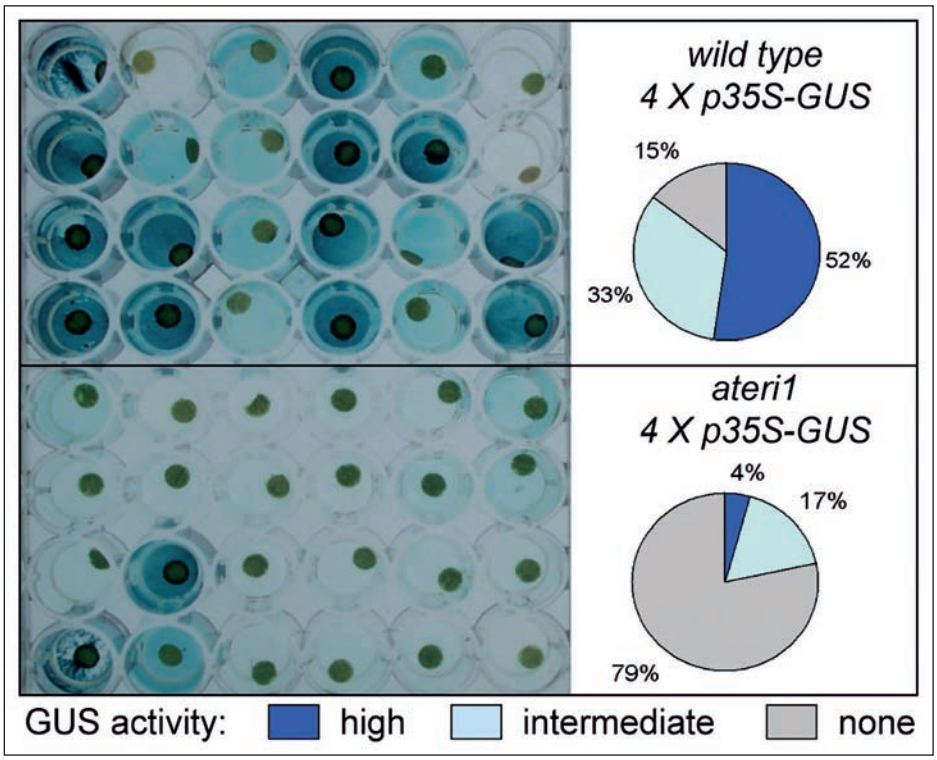

Fig. 23: The T-DNA insertion mutation *ateri1* leads to enhanced dosage-dependent post-transcriptional gene silencing (PTGS) in *A. thaliana*. Semi-quantitative histochemical GUS-staining of leave discs was performed to determine frequencies of PTGS onset in 9 week old wild type (n=48) and *ateri1* mutant (n=46) *A. thaliana* plants containing 4 copies of a p35S-*GUS* reporter gene. Percentages of individuals showing high (dark blue), intermediate (light blue) or no (grey) GUS activity among the evaluated plants are depicted as sectors in pie charts. Leaf discs from different leaves of the same individual plant always gave consistent results (M. Kuhlmann).

Collaboration

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Genome Plasticity; Dr. R. Schmidt;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

Martin Luther University Halle-Wittenberg, Institute of Genetics, Halle/S.; Prof. G. Reuter, Prof. K. Breuning;
Université de Genève, Laboratoire de Génétique Végétale, Genève, Switzerland; Prof. J. Paszkowski;
Chinese Academy of Sciences, Institute of Genetics and Developmental Biology, Beijing, China; Prof. X. Cao.

Lectures, Posters and Abstracts

V126, V127, V128, V152, V153, V179, V180, V246, P14, P15, P22, P40, P96, P97, P129, P130, P131, P132, P133, P134, P175.

Additional Funding

For further information see the survey page 207.

Research Group: Pattern Recognition

Head: Dr. Udo Seiffert

Scientists

IPK financed
Czauderna, Tobias (Annex)

Grant Positions
Bollenbeck, Felix (BMBF)
Brüß, Cornelia (BMBF, till 17.09.2007)
Ihlow, Alexander, Dr. (BMBF, till 30.04.2007)
Pielot, Rainer, Dr. (BMBF, till 30.04.2007, DFG, since 01.05.2007)
Strickert, Marc, Dr. (BMBF, till 31.05.2007)

Visiting Scientists
Ihlow, Alexander, Dr. (self-financed, 01.05.-31.05.2007)

Goals

Recognition of spatio-temporal developmental patterns at cell and organ level utilising computer science and engineering methods.

Research Report

The report period was affected by the end of the initial funding of the group within the framework of the Bioinformatics Centre Gatersleben-Halle (BIC-GH). All work packages could be successfully fulfilled. Moreover, a number of follow-up projects could be acquired to ensure the continuation of the work and to keep the expertise that has been gained by this BMBF funding. A part (gene expression analysis) of the Bioinformatics fields of pattern recognition and spatio-temporal modelling covered by the group will be pursued within the junior research group Data Inspection.

The two major parts of the BIC-GH project could be successfully finished. One subproject, accomplished in collaboration with the Transcriptome Analysis group, has its focus on developing a **high-throughput screening system for automated analyses of plant-pathogen interactions** on the basis of a motorised microscope. Since the core development of the necessary image analysis and pattern recognition algorithms as well as the microscope control software were finshed in 2006, all components were integrated and the system has been linked to a dedicated image and experiment database. A parallel installation of this system has been established at the University of Zurich (B. Keller) and is about to be established at the Technical University Munich (R. Hückelhoven). A further commercial exploitation is feasible (A. Ihlow, U. Seiffert).

In the context of **highly resolved 3-D modelling of barley grains** (collaboration with the Gene Expression group) a significant progress could be gained. Now we are able

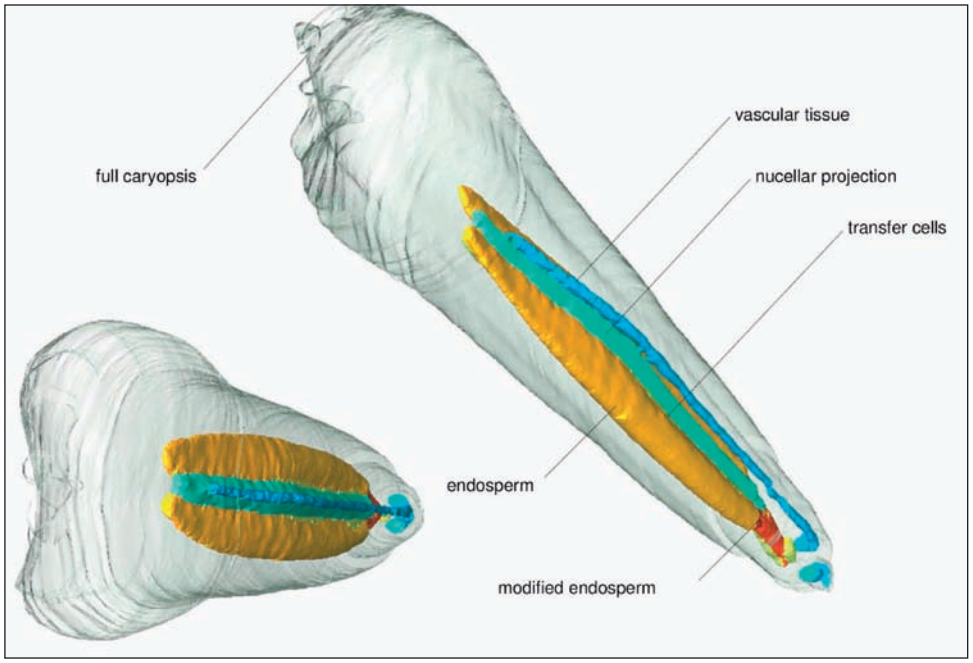

Fig. 24: Automatically obtained three-dimensional model of a barley caryopsis based on about 2,000 two-dimensional cross sections utilising a Machine Learning approach that was trained with a limited number of manually segmented slices to transfer the appropriate expert knowledge into machine readable form (F. Bollenbeck).

to automatically reconstruct correctly aligned and properly segmented three-dimensional models (see Fig. 24, p. 78), based on histological cross-sections as basic image material as well as on appropriate a-priori expert knowledge of the grain histology in form of a limited number of manually segmented slices. These slices are used to implicitly train a Machine Learning-based system. The developed algorithms are also essential for a model-based three-dimensional microdissection of quick-frozen material without the need of embedding or sectioning the original plant material (F. Bollenbeck, C. Brüß, U. Seiffert).

This work is closely related to **NMR imaging of barley grains** that allows to obtain three-dimensional images by non-invasive treatment of the biological material. However, the level of detail cannot compete with histological cross-sections, obtained by classical microscopy. Since NMR images are in a native three-dimensional form, the modelling process is much easier. This enables us, based on sophisticated 4-D warping techniques, to work towards quasi-time-continuous spatio-temporal models containing morphological changes during the development of barley grains. Furthermore, these models are used in an atlas-like manner to visualise spatio-temporal expression gradients in the barley grain during seed development. This interdisciplinary work aims at an integrative approach and systems biological analysis for understanding developmental processes in the barley grain (R. Pielot, U. Seiffert).

In collaboration with the research group Applied Biochemistry our tool for **interactive visualisation and inspection of complex HPLC and UPLC data** has been further advanced. This tool extends the functionality of standard analysis software and is applicable for complex HPLC and UPLC datasets with interactive navigation through the datasets to get a customised zoom-like view of a particular experiment. The tool has now been extended by a special data manager to assemble an arbitrary subset of large-scale raw chromatographic data. Furthermore, guided by potential users, the usability has been improved in order to provide a high efficiency tool for routine interactive work (T. Czauderna, U. Seiffert).

Extensive work has been done on the **analysis of gene expression data** (M. Strickert, U. Seiffert). This work will be continued in the newly founded junior research group Data Inspection. For details see report of this group.

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Experimental Taxonomy; Dr. S. Jakob;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock.

Outside the Institute:
Otto-von-Guericke University Magdeburg, Institute of Electronics, Signal Processing and Communications, Magdeburg; Prof. B. Michaelis;
Martin Luther University Halle-Wittenberg, Institute of Computer Science, Halle/S.; Prof. S. Posch;
Fraunhofer Institute for Factory Operation and Automation, Magdeburg; Dr. R. Mecke;
University of Leipzig, Clinic for Psychotherapy, Leipzig; Dr. T. Villmann;
Konrad Zuse Institute, Dept. of Scientific Visualisation, Berlin; Prof. H.-C. Hege;
Technical University of Clausthal, Theoretical Computer Science and Computational Intelligence, Clausthal-Zellerfeld; Prof. B. Hammer;
Fraunhofer Institute for Biomedical Engineering (IBMT), St. Ingbert; Dr. F. Volke;
University of South Australia, Adelaide, Knowledge-based Engineering Group, Adelaide, Australia; Prof. L.C. Jain.

Publications

Peer Reviewed Papers
Jakob, S.S., A. Ihlow & F.R. Blattner: Combined ecological niche modelling and molecular phylogeography revealed the evolutionary history of *Hordeum marinum* (Poaceae) – niche differentiation, loss of genetic diversity, and speciation in Mediterranean Quaternary refugia. Mol. Ecol. 16 (2007) 1713-1727.
Strickert, M., N. Sreenivasulu, B. Usadel & U. Seiffert: Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. BMC Bioinformatics 8 (2007) 165.

Book Chapters
Villmann, T., M. Strickert, C. Brüss, F.-M. Schleif & U. Seiffert: Visualization of fuzzy information in fuzzy-classification for image segmentation using MDS. In: Verleysen, M. (Eds.): Proc. 15th European Symposium on Artificial Neural Networks ESANN 2007, Bruges/Belgium. D-Side Publications, Evere/Belgium (2007) 103-108.

Other Publications
Strickert, M., F.-M. Schleif & U. Seiffert: Gradients of Pearson correlation for analysis of biomedical data Pro-

ceedings of the Argentine Symposium on Artificial Intelligence (ASAI 2007), August 2007 (2007) 139-150.
Strickert, M. & U. Seiffert: Correlation-based data representation Online Proceedings of the Dagstuhl Seminar 07131, Similarity-based Clustering and its Application to Medicine and Biology, Dagstuhl (2007) http://drops.dagstuhl.de/opus/volltexte/2007/1134/.
Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: „Genetical Genomics" der Gerstenkornentwicklung - von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomX-Press 1 (2007) 12-16.
Wobus, U., H.-P. Mock, C. Pietsch, V. Radchuk, M. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, W. Weschke & K. Witzel: GABI-SEED: Genetische Grundlagen komplexer agronomischer Merkmale im Getreidekorn entschlüsseln. GenomXPress Sonderausgabe März (2007) 19.

Electronic Publications
Brüss, C. & U. Seiffert: Automatic generation of 3-D and 4-D models. http://pgrc-16.ipk-gatersleben.de/wgrp/mue/mue_projects3.php (2007).
Seiffert, U., P. Schweizer, A. Ihlow & C. Schulze: Quantitative assessment of fungal structures on the leaf surface. http://pgrc-16.ipk-gatersleben.de/wgrp/mue/mue_projects6.php (2007).
Strickert, M. & U. Seiffert: Nonlinear gene expression analysis. http://pgrc-16.ipk-gatersleben.de/wgrp/mue/mue_projects7.php (2007).

Lectures, Posters and Abstracts

V29, V30, V169, V170, V228, V229, V230, V231, V232, V233, V234, P17, P24, P27, P34, P92, P195, P210, P215, P231, P237, P238.

Additional Funding

For further information see the survey page 207–208.

Research Group: *In vitro* Differentiation

Head: Prof. Anna M. Wobus

Scientists

IPK financed
Truong, Thuy Thu (0,5 Annex, since 17.02.2007)

Grant Positions
Daniel-Wojcik, Anna (0,5 EU)
Schröder, Insa, Dr. (DFG)
Sulzbacher, Sabine, Dr. (BMBF)

Scholars
Truong, Thuy Thu (MOET-Vietnam, till 15.02.2007)

Goals

Analysis of regulatory mechanisms of *in vitro* differentiation of mouse embryonic stem (ES) cells into endoderm (pancreatic and hepatic) and cardiogenic lineages. In parallel, reprogramming properties and the *in vitro* differentiation capacity of human cord blood-derived cells are analysed.

Research Report

Analysis of pancreatic differentiation by transcriptome analysis: We have shown as "proof-of-principle" the generation of functional insulin-producing islet-like cells (Schröder et al. 2006), however, the efficiency of pancreatic differentiation and the level of insulin production have to be significantly improved. To analyse the differentiation pathway into the pancreatic lineage in more detail, and to identify potential pancreatic regulatory molecules, a comparative microchip (Affymetrix) analysis was performed using wild type (wt) ES cells and ES cells constitutively expressing the pancreatic developmental control gene *Pax4* (Pax4+ cells). Undifferentiated ES cells, committed progenitor and differentiated cells representing islet-like clusters were comparatively investigated and data were verified by real-time RT-PCR. After passing the quality control, transcripts showing a five- or two-fold up-regulation, were identified. At the committed stage, 237 (wt) and 263 (Pax4+), but at the terminal stage, only 28 (wt) and 8 (Pax4+) transcripts, were five- or two-fold up-regulated. The data demonstrated three important findings: (i) Pax4+ cells showed no higher transcript complexity in comparison to wt cells, but up-regulation of apoptotic candidate genes at the terminal stage, (ii) neural-specific candidate genes were up-regulated at the committed progenitor stage supporting the view of a common progenitor type able to differentiate into the neural and pancreatic lineage, and (iii) the comparison of transcript values with those of the embryonic pancreas *in vivo* demonstrated that ES-derived cells resemble an embryonic/fetal stage (Rolletschek et al., manuscript submitted).

Analysis of endoderm differentiation by Activin A induction: To selectively increase the level of endoderm cells and to suppress neuronal cell differentiation, the influence of the signalling molecule Activin A on pancreatic differentiation has been analysed. A chemically defined medium (CDM) and conditions for Activin A application have been established. Activin A at high concentrations (50-100 ng/ml) induced endoderm-specific Sox17, down-regulated extra-embryonic Sox7 and up-regulated pancreas-specific Pdx1 transcript levels (T. Truong, I. Schröder, S. Sulzbacher, studies ongoing).

Lineage selection for endoderm-specific Sox17+ positive cells: By using ES cells expressing pSox17-DsRed-purowe performed experiments to selectively enrich the amount of endoderm and potential pancreatic progenitor cells by lineage selection. The number of Sox17-DsRed-positive cells increased during differentiation and in response to Activin A induction, up to maximum levels around day 8-9 of differentiation. By puromycin selection and FACS sorting we are currently establishing the most efficient strategies to enrich Sox17+ endoderm progenitor cells followed by induction of pancreatic differentiation (I. Schröder, S. Sulzbacher, studies ongoing).

Differentiation of ES cells into hepatocyte-like cells: The three-step differentiation system of ES cells into the hepatic lineage resulted in the formation of hepatocyte-, bile duct epithelial- and oval-like cells. However, the amount of hepatic cells and the maturation status are insufficient. Chromatin-modifying substances (TSA, 5-Aza-C) have been used to activate hepatic differentiation. Although differentiated albumin/AAT-positive clusters could be induced, the overall differentiation efficiency was not significantly enhanced. Present strategies are aimed to selectively enrich Sox17+ cells followed by BMP and FGF4 induction (A. Daniel-Wojcik, S. Sulzbacher, studies ongoing).

Differentiation and reprogramming analysis of cord blood (CB)-derived CD133+ cells: Our previous studies showed that WNT3a-conditioned medium (CM) increased the formation of nestin-expressing cells (suggesting higher plasticity), whereas WNT5a- and WNT11-CM induced endothelial differentiation of CB cells (Nikolova et al. 2007). Reprogramming of CD14+ CB-derived cells by a cocktail of growth factors showed only slight effects on mainte-

nance of Oct4 transcript level (as a marker of undifferentiated cells). Based on the recent data on reprogramming of adult mouse and human cells to "induced pluripotent stem (iPS) cells", we are currently following the reprogramming strategy using ES/EC cell extracts (shown to be efficient in reprogramming adult cells to an ES-like state) to enhance the developmental potential of CB cells (A. Daniel-Wojcik, A.M. Wobus, studies ongoing).

Induction of pacemaker-like cells by Suramin: The generation of pacemaker cells of the cardiac system is a great challenge for stem cell research. Suramin, a naphthylamine derivative of urea, was found to specifically induce the formation of pacemaker-like cells (when applied at a short window of mesodermal specification during ES cell differentiation). Sequential activation and/or downregulation of mesoderm- and cardiac-specific genes (i.e. Brachyury, FGF10, Wnt8, Wnt3a, Nkx2.5, GATA 4/5) were necessary for activation of sinoatrial-specific genes (Tbx2/3, HCN4) and proteins (HCN4). Patch-clamp analysis confirmed the increase in the number of sinoatrial-like cells at the expense of atrial- and ventricular cardiomyocytes (Wiese et al., manuscript submitted).

Collaboration

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. J. Fuchs;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer.

Outside the Institute:

Martin Luther University Halle-Wittenberg, Institute of Anatomy and Cell Biology, Halle/S.; Dr. A. Navarrete-Santos;
University of Leipzig, Laboratory of Molecular Medicine, IZKF, Leipzig; Dr. M. Cross;
Max Delbrück Center of Molecular Biology, Berlin-Buch; Dr. N. Hübner, Dr. H. Schulz;
Max Planck Institute (MPI) for Molecular Genetics, Berlin; Dr. H. Himmelbauer, Dr. T. Nolden;
University of Dresden, Dept. of Pharmacology and Toxicology, Dresden; Prof. U. Ravens;
National Institute on Aging (NIA), NIH, Laboratory of Cardiovascular Science, Baltimore, USA; Prof. K. Boheler;
University of Toronto, Samuel Lunenfeld Research Institute, Toronto, Canada; Dr. A. Nagy, P. Mohseni.

Publications

Peer Reviewed Papers

Gottwald, E., S. Giselbrecht, C. Augspurger, B. Lahni, N. Dambrowsky, R. Truckenmüller, V. Piotter, T. Gietzelt, O. Wendt, W. Pfleging, A. Welle, A. Rolletschek, A.M. Wobus & K.F. Weibezahn: A chip-based platform for the *in vitro* generation of tissues in three-dimensional organization. Lab Chip 7 (2007) 777-785.

Kleger, A., T. Busch, S. Liebau, K. Prelle, S. Paschke, M. Beil, A. Rolletschek, A. Wobus, E. Wolf, G. Adler & T. Seufferlein: The bioactive lipid sphingosylphosphorylcholine induces differentiation of mouse embryonic stem cells and human promyelocytic leukaemia cells. Cell. Signalling 19 (2007) 367-377.

Löser, P. & A.M. Wobus: Aktuelle Entwicklungen in der Forschung mit humanen embryonalen Stammzellen. Naturwiss. Rundschau 60 (2007) 229-237.

Nikolova, T., M. Wu, K. Brumbarov, R. Alt, H. Opitz, K.R. Boheler, M. Cross & A.M. Wobus: WNT-conditioned media differentially affect the proliferation and differentiation of cord blood-derived CD133+ cells *in vitro*. Differentiation 75 (2007) 100-111.

Books and Book Chapters

Müller-Röber, B., F. Hucho, W. van den Daele, K. Köchy, J. Reich, H.-J. Rheinberger, K. Sperling, A.M. Wobus, M. Boysen & M. Kölsch (Eds.): Grüne Gentechnologie. Aktuelle Entwicklungen in Wissenschaft und Wirtschaft. Supplement zum Gentechnologiebericht. Forschungsberichte der interdisziplinären Arbeitsgruppen der Berlin-Brandenburgischen Akademie der Wissenschaften. Bd. 16. Elsevier, Spektrum, Akademischer Verlag, München (2007) 180 pp.

Schmidtke, J., B. Müller-Röber, W. van den Daele, F. Hucho, K. Köchy, K. Sperling, J. Reich, H.-J. Rheinberger, A.M. Wobus, M. Boysen & S. Domasch (Eds.): Gendiagnostik in Deutschland. Status Quo und Problemerkennung. Forschungsberichte der interdisziplinären Arbeitsgruppen der Berlin-Brandenburgischen Akademie der Wissenschaften. Bd.18. Forum W. Wissenschaftlicher Verlag, Limburg a.d. Lahn (2007) 208 pp.

Other Publications

Wobus, A.M.: "Embryonic and somatic stem cells – regenerative systems for cell and tissue repair" – Tagungsbericht und Ausblick (Leopoldina-Jahreskonferenz, Dresden, 24.-27.09.2006). Jahrb. Dtsch. Akad. Naturforsch. Leopoldina 52 (2007) 281-285.

Lectures, Posters and Abstracts

V16, V17, V209, V210, V211, V212, V213, V287, V288, V289, V290, V291, V292, V293, V294, V295, V296, V297, V298, P118, P189, P190, P232, P233.

Additional Funding

For further information see the survey page 208.

Programme: Genome Analysis

Research Group: Transcriptome Analysis

Head: Dr. Patrick Schweizer

Scientists

IPK financed
Gay, Alexandra, Dr. (Annex)
Himmelbach, Axel, Dr. (Annex, since 01.07.2007)
Ihlow, Alexander, Dr. (0,5 Annex, since 01.10.2007)

Grant Positions
Chen, Wanxin, Dr. (BMBF GABI)
Douchkov, Dimitre, Dr. (BASF Plant Science GmbH)
Himmelbach, Axel, Dr. (BMBF GABI, till 30.06.2007)
Johrde, Annika (0,5 EU Bioexploit)
Liu, Luo (BMBF GABI)
Marschner, Silvia (BMBF GABI, 01.09.-31.12.2007)
Marzin, Stephan (Saxony-Anhalt)
Nowara, Daniela (0,5 EU, since 15.12.2007)

Visiting Scientists
Buck-Sorlin, Gerhard, Dr. (DFG and Technical University Cottbus, till 14.12.2007)
Horbach, Ralph (SFB and Martin Luther University Halle-Wittenberg, 24.09.-19.10.2007)
Krijger, Dorrit-Jan, Dr. (Excellence Cluster and Martin Luther University Halle-Wittenberg, 24.09.-19.10.2007)
Metzner, Ernst (Martin Luther University Halle-Wittenberg)
Zellerhoff, Nina (RWTH Aachen, 15.07.-03.08.2007)

Scholars
Urso, Simona (Centre for Genomic Research (CRA), Fiorenzuole d'Arda, Italy, 24.10.-14.11.2007)

Goals

Gene regulation and function analysis (phenomics) in stressed barley and wheat.

Research Report

Phenomics of pathogen-attacked barley: The main objective of the first project is **detailed functional analysis and testing of the application potential of barley genes required for nonhost resistance**. The genes of interest were derived from a single-cell RNAi high-throughput screening called TIGS (Transient Induced Gene Silencing, see Annual Report of 2005) in barley epidermal cells attacked by the wheat powdery mildew. Five out of 11 candidate *RNR* (for *Required for Nonhost Resistance*) genes whose knock-down caused not only a reproducible weakening of nonhost resistance but also affected host basal resistance were analysed further. These genes encode an Armadillo-repeat-containing protein (*RNR5*), a cellulose-synthase-like protein (*RNR6*), a receptor kinase-like protein (*RNR8*), a subtilisin-like protein (*RNR9*), and a stomatin-like protein (*RNR10*). Transgenic barley and wheat plants that carry overexpression or RNAi constructs of these five genes have been produced in collaboration with the Plant Reproductive Biology group (J. Kumlehn, G. Hensel). Approximately ten T_1 transgenic lines per construct are currently being analysed for transgene expression, target gene silencing, resistance and susceptibility to inappropriate and appropriate powdery mildew fungi, respectively. (D. Douchkov, S. Marschner). The preliminary data obtained in these segregating lines will inform further experiments using homozygous T_2 lines. First results indicate enhanced susceptibility of barley *RNR5* RNAi lines to the wheat powdery mildew suggesting a quantitative role of the encoded Armadillo-repeat protein in nonhost resistance. T-DNA insertion lines of *Arabidopsis* carrying mutant alleles of two putative *HvRNR8* orthologuous genes were found to be more susceptible to the wheat powdery mildew, in agreement with the TIGS data in barley. Double mutant lines have been produced and will be tested soon.
The second project is aimed at **identifying genes** from barley that are required **for basal host resistance** or **for host susceptibility** in a compatible interaction with barley powdery mildew. A set of approx. 500 differentially expressed host genes that have been identified in the epidermis of pathogen-attacked leaves were tested for modulation of basal resistance or susceptibility in the TIGS system. For this screening, a fully-automated microscopic system for image production and analysis was used (Fig. 25, p. 84). This novel robot system had been developed in the Pattern Recognition group (U. Seiffert, A. Ihlow). Together with a previously performed, manual screening, a total of 90 host genes whose knock-down strongly affected basal resistance were re-tested in four additional biological replications. This resulted in a list of 37 candidate genes exhibiting a significant effect on basal host resistance upon silencing. Interestingly, about 70 % of these candidates appeared to be involved in support of the successful fungus because silencing enhanced basal resistance without enhancing cell death (D. Douchkov, D. Nowara).

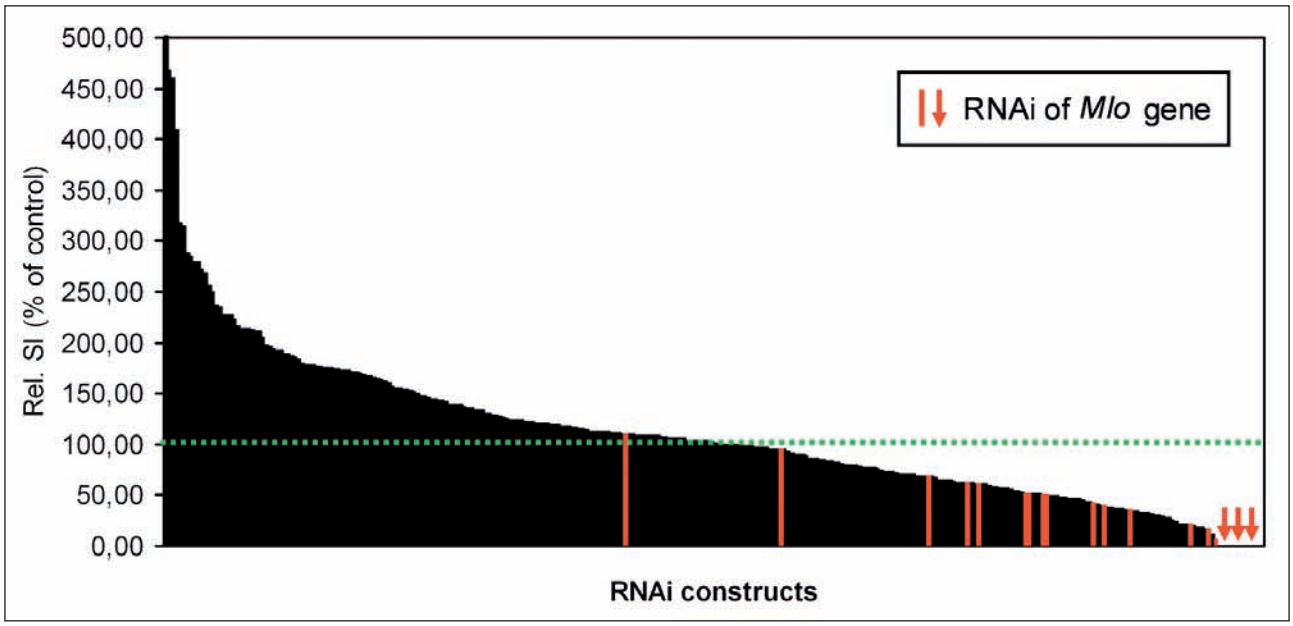

Fig. 25: Screening by Transient-Induced Gene Silencing (TIGS) of ~300 pathogen-induced barley genes (black bars, ordered by effect) to identify genes that affect basal host resistance against the barley powdery mildew fungus. Genes with an effect are expected to shift cell susceptibility index (SI) up or down, relative to the empty vector control that is set to 100 % (dotted green line). An automated microscope, equipped with pattern recognition software for detection of cell susceptibility, has been developed in the group "Pattern Recognition" for this screening. As positive control for RNAi efficiency and reliability of pattern recognition, we included in all experiments an RNAi construct targeting the *Mlo* gene, which is expected to phenocopy recessive *mlo*-mediated resistance. Bombardment with this specific RNAi construct (red bars or arrows) resulted in a low SI, relative to the empty-vector, in most of the experiments and demonstrates the accuracy of the automated TIGS screening system. RNAi-target genes from both ends of the SI spectrum were selected for independent confirmation experiments (D. Douchkov, A. Ihlow).

The novel phenomenon of attenuation of fungal development on barley epidermal cells expressing **RNAi constructs directed against the pathogen-derived transcripts** (named "Host-Induced Gene Silencing", HIGS) is being further analysed by using "Virus-Induced Gene Silencing (VIGS)" and transgenic T_1 lines of barley carrying RNAi constructs directed against beta-1,3-glucosyltransferases of powdery mildew. In both experimental systems, a significant reduction of fungal development was found thus providing proof of concept for the approach. In two TIGS screenings, a total of 86 fungal genes were targeted. RNAi constructs targeting 22 genes caused a significant reduction in fungal haustorium formation. However, no reduction of target RNA was found in epiphytic structures of powdery mildew by RT-qPCR indicating that the silencing was either rather subtle or did not spread beyond the haustorial cell, which is formed inside the host epidermis (D. Nowara, A. Gay).

Promoter development: Besides HvGER4, promoters of two pathogen-induced barley genes were cloned at BASF Plant Science based on expression data of our lab. One of the promoters drives transient GUS-expression in mesophyll cells, as predicted from the localisation of the corresponding endogenous transcript. The HvGER4c promoter was further tested in transgenic barley T_1 lines by using the quantitative MUG assay for GUS activity, which revealed some activity also in non-inoculated roots and coleoptiles. In collaboration with the Plant Reproductive Biology group, a versatile set of binary vectors for transgene expression or RNAi has been established (GABI; A. Himmelbach, F. Beier; Himmelbach et al., Plant Physiol. 2007).

Phenomics of drought tolerance: The aim of this project is to identify new candidate genes for osmotic-stress (drought) tolerance in barley by high-throughput RNAi. Therefore, a new transient assay (TIGS2) that is based on (un)impaired accumulation of the homotetrameric DsRed reporter protein was developed. Four out of approximately 20 drought-related candidate genes with reported drought tolerance phenotypes in transgenic plants or mutants caused significant reduction of DsRed fluorescence in dehydration-stressed leaf segments, thus providing proof of concept. A list of 96 additional candidate genes has been created for a first screening (S. Marzin).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Genome Diversity; Dr. N. Stein, Prof. A. Graner;
Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert;
Dept. of Cytogenetics and Genome Analysis, Research Group Expression Mapping; Dr. L. Altschmied;

Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein.

Outside the Institute:
BASF Plant Science, Ludwigshafen; Dr. T. Wetjen, Dr. S. Bieri;
Leibniz Institute of Plant Biochemistry, Halle/S.; Dr. W. Knogge;
Martin Luther University Halle-Wittenberg, Halle/S.; Prof. K. Humbeck;
Rheinisch-Westfälische Technische Universität, Aachen, Dr. U. Schaffrath;
Agricultural Research Institute, Martonvasar, Hungary; Dr. G. Galiba;
Biological Research Institute, HAS, Szeged, Hungary; Dr. J. Gyorgyey;
Risø National Laboratory, Dept. Plant Research, Roskilde, Denmark; Dr. M. Lyngkjaer;
Scottish Crop Research Institute, Dundee, UK; Dr. Ch. Lacomme;
University of Iowa, Ames, USA; Prof. R. Wise.

Publications

Peer Reviewed Papers

Fischer, A., A. Lenhard, H. Tronecker, Y. Lorat, M. Kraenzle, O. Sorgenfrei, T. Zeppenfeld, M. Haushalter, G. Vogt, U. Gruene, A. Meyer, U. Handlbichler, P. Schweizer & L. Gaelweiler: iGentifier: indexing and large-scale profiling of unknown transcriptomes. Nucleic Acids Res. 35 (2007) 4640-4648.

Gjetting, T., P.H. Hagedorn, P. Schweizer, H. Thordal-Christensen, T.L.W. Carver & M.F. Lyngkjaer: Single-cell transcript profiling of barley attacked by the powdery mildew fungus. Mol. Plant-Microbe Interact. 20 (2007) 235-246.

Himmelbach, A., U. Zierold, G. Hensel, J. Riechen, D. Douchkov, P. Schweizer & J. Kumlehn: A set of modular binary vectors for transformation of cereals. Plant Physiol. 145 (2007) 1192-1200.

Lange, M., A. Himmelbach, P. Schweizer & U. Scholz: Data Linkage Graph: computation, querying and knowledge discovery of life science database networks. J. Integr. Bioinformatics 4 (2007) 68 Online Journal: http://journal.imbio.de/index.php?paper_id=68.

Perovic, D., P. Tiffin, D. Douchkov, H. Bäumlein & A. Graner: An integrated approach for the comparative analysis of a multigene family: The nicotianamine synthase genes of barley. Funct. Integr. Genomics 7 (2007) 169-179.

Schweizer, P.: Nonhost resistance of plants to powdery mildew – New opportunities to unravel the mystery. Physiol. Mol. Plant Pathol. 70 (2007) 3-7.

Vorwieger, A., C. Gryczka, A. Czihal, D. Douchkov, J. Tiedemann, H.-P. Mock, M. Jakoby, B. Weisshaar, I. Saalbach & H. Bäumlein: Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. Planta 226 (2007) 147-158.

Other Publications

Kumlehn, J., P. Schweizer, G. Langen, S. Bieri & T. Wetjen: PRO-GABI: Pflanzliche Abwehrmechanismen gegen Pilzbefall gezielt einschalten. GenomXPress Sonderausgabe März (2007) 24.

Electronic Publications

Seiffert, U., P. Schweizer, A. Ihlow & C. Schulze: Quantitative assessment of fungal structures on the leaf surface. http://pgrc-16.ipk-gatersleben.de/wgrp/mue/mue_projects6.php (2007).

PhD and Diploma Theses

Müller, D.: Funktionelle Charakterisierung des pathogeninduzierbaren *HvGER4c* Promotors der Gerste (*Hordeum vulgare* L.). (Diploma Thesis) Hochschule Anhalt (FH), Köthen (2007) 29 pp.

Lectures, Posters and Abstracts

V12, V221, V222, V223, V224, V225, V226, P38, P39, P88, P89, P92, P94, P95, P105, P163, P177, P195, P242, P244.

Additional Funding

For further information see the survey page 209.

Research Group: Expression Mapping

Head: Dr. Lothar Altschmied

Scientists

IPK financed
Hähnel, Urs, Dr. (P)
Zierold, Annchristin (0,5 Annex)

Goals

Analysis of reproductive development in barley and *Arabidopsis* using EST sequencing, array technology and bioinformatics as well as various approaches for functional characterisation of genes.

Research Report

In collaboration with A. Czihal, D. Koszegi, and H. Bäumlein (Gene Regulation group) we had identified a novel, plant-specific transcription factor from wheat, which is specifically expressed in the egg apparatus. A homologous gene in *Chlamydomonas* is responsible for gamete differentiation of vegetative mt-cells. To clarify the relationship of the wheat gene with four homologous *Arabidopsis* genes and to locate promoter elements responsible for egg apparatus-specific transcription of these genes, we identified genomic sequences from dicots, monocots, lower land plants, and algae encoding members of this family (L. Altschmied). We annotated the exon/intron structure for the second half of these genes containing two highly conserved sequence motifs. Preliminary results from phylogenetic trees indicate, that the wheat gene is closest related to another family member in *Arabidopsis* than previously assumed (L. Altschmied). The identification of start codons and promoter regions remains a challenge, because sequence homology in the first half of these genes is very low (see Fig. 26) and mRNA or EST data are not available for any of these genes.

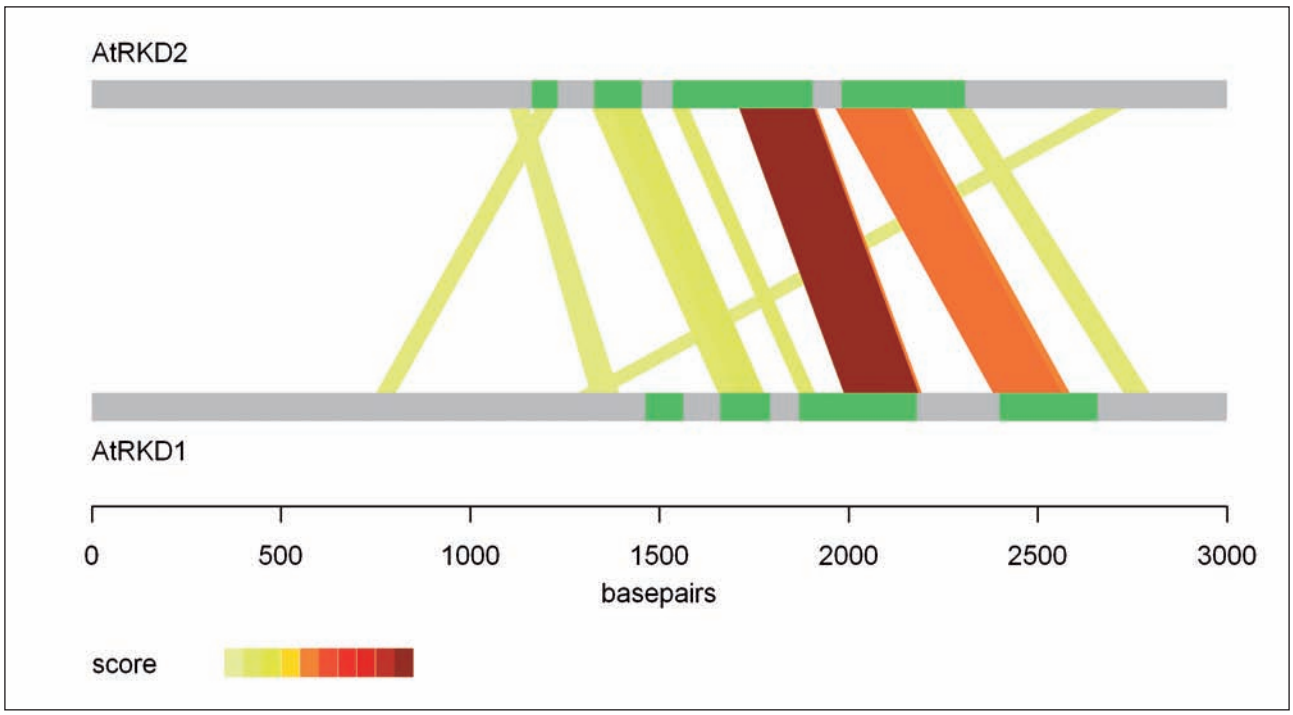

Fig. 26: Comparison of the genomic *Arabidopsis thaliana* sequences encoding the genes AtRKD1 and AtRKD2. Both genes belong to the RKD subfamily of RWP-RK transcription factors and are specifically expressed in the egg apparatus. Grey bars represent genomic sequences, while green bars indicate coding regions. The exon/intron structures have been confirmed by the sequencing of RT-PCR fragments (D. Koszegi - Gene Regulation group). The scores of aligned segments are shown by colored parallelograms. AtRKD1 and AtRKD2 comprise the most highly related gene pair identified in the RKD subfamily of RWP-RK transcription factors. The RWP-RK domains at the end of the third exon and sequence motifs in exon 4 show high sequence conservation. Exons 2 and the 5'-terminal parts of exons 3 do not show more sequence similarity than some other non-coding sequences in these genomic regions. Exons 1 seem to be unrelated. (L. Altschmied)

4,710 ESTs from parthenogenetic egg cells of *kotschyi* Salmon (*kS*) wheat (L. Altschmied/A. Czihal – Gene Regulation group), which represent 1,914 unique genes, had only 125 genes in common with 820 genes defined by 2,391 ESTs from sexual egg cells of *aestivum* Salmon wheat. Furthermore, 272 genes of *kS* wheat represent novel cDNA sequences not present in more than 850,000 wheat ESTs. 59 of these genes show significant nucleotide homologies with rice genes, while 22 genes show amino acid similarities with *Arabidopsis* proteins. The potential functions of these proteins include chromatin binding, transcriptional regulation, RNA binding, intracellular and membrane transport, as well as cell wall formation, but almost none of these functions have been verified experimentally. Currently, in collaboration with P. Rizzo and J. Kumlehn (Plant Reproductive Biology group), we try to identify BAC clones of barley containing those genes (U. Hähnel), to feed them into the BAC sequencing project (A. Graner, N. Stein – Genome Diversity group) at the IPK.

In collaboration with the research groups Phytoantibodies, Plant Data Warehouse, Gene Expression, and Gene Regulation an array of 11,000 intergenic regions of *Arabidopsis* was hybridised with PCR-amplified chromatin (U. Hähnel) from chromatin immunoprecipitation with ABI3, LEC1 and MYB77 antibodies (G. Mönke – Phytoantibodies group). Despite limited reproducibility due to low signal-to-noise ratios, we obtained a list of 40-70 target regions for the transcription factor ABI3 in developing seeds (U. Hähnel/M. Seifert – Plant Data Warehouse group), which are highly enriched for RY- and G-box motifs (U. Hähnel/M. Mohr – Plant Data Warehouse group). More than 20 promoters regions have been cloned and almost exclusively tested positive for their response to ABI3 in transiently transformed *Arabidopsis* protoplasts (U. Hähnel/G. Mönke – Phytoantibodies group, A. Tewes – Gene Expression group). Presently, we are designing Agilent microarrays (L. Altschmied) to transfer the hybridisation step to a platform, which will allow the analysis of all promoter regions in the *Arabidopsis* genome.

A tissue panel for barley is currently constructed by amplifying the mRNA from more than 100 tissue samples (A. Zierold). The latter have been collected in collaboration with the research groups Gene Expression (W. Weschke), Transcriptome Analysis (A. Himmelbach), and Plant Reproductive Biology (J. Kumlehn). The main technical problems, except the selection of housekeeping genes for data normalisation, have been solved using a small test panel (A. Zierold). Spotting the final tissue panel and applying it for the expression analysis of several transcription factors is planned for the first half of 2008.

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, M. Mohr, M. Seifert;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer, Dr. A. Himmelbach, S. König;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein, A. Czihal, D. Koszegi;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, Dr. G. Mönke;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, R. Paride.

Outside the Institute:

University of Bielefeld, Institute for Genome Research, Bielefeld; Prof. B. Weisshaar, Dr. P. Viehöver;
Martin Luther University Halle-Wittenberg, Institute of Computer Science, Halle/S.; Prof. S. Posch;
INRA, Laboratoire de Biologie des Semences, Versailles, France; Dr. B. Dubreucq, Dr. C. Rochat, Dr. M. Miquel, Dr. L. Lepiniec, Prof. M. Caboche;
ETSI Agronomos, Dept. of Biotechnology, Madrid, Spain; Dr. I. Diaz, Dr. V. Carbajosa;
University of Zurich, Institute of Plant Biology, Zurich, Switzerland; Prof. U. Grossniklaus, A.J. Johnston.

Publications

Book Chapters

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Vegetabile 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Other Publications

Mönke, G., T.M. Linh, U. Conrad, U. Hähnel, L. Altschmied, M. Mohr, I. Grosse, A. Vorwieger, H. Bäumlein, B. Weisshaar & P. Viehöver: GABI-ARABIDO-SEED: Wie steuern Transkriptionsfaktoren die Samenentwicklung bei Pflanzen? GenomXPress Sonderausgabe März (2007) 16.

Lectures, Posters and Abstracts

V160, P28, P29, P65, P66, P77, P125, P126, P153, P154, P155, P156, P157, P158, P159, P183, P184, P197, P199.

Additional Funding

For further information see the survey page 210.

Research Group: Gene and Genome Mapping

Head: Dr. Marion Röder

Scientists

IPK financed
Hanemann, Anja (P, Annex)
Pietsch, Christof, Dr. (Annex, since 15.01.2007)

Grant Positions
Matthies, Inge, Dr. (BMBF)
Pietsch, Christof, Dr. (BMBF, till 14.01.2007)

Visiting Scientists
Dawit Bedane, Woubit (DAAD, 05.03.-30.03.2007, 02.07.-30.08.2007)
De Leon Alvarez, José Luis, Dr. (PROMEP-SEP, 03.08.-28.08.2007)
Khlestkina, Elena, Dr. (DFG, 02.06.-28.08.2007)
Kumar, Uttam, Dr. (DAAD, 01.01.-05.12.2007)
Salina, Elena, Dr. (BLE, 05.11.-17.11.2007)
Sharma, Shailendra, Dr. (Humboldt Foundation, 26.07.-31.12.2007)
Woldemariam Teklu, Yifru, Dr. (Humboldt Foundation, 06.09.-31.12.2007)

Scholars
Kalb, Ortrun (self-financed, 17.09.-28.09.2007)

Goals

Exploitation of the natural genetic diversity in plants for identification, genetic mapping and cloning of genes for agronomically important traits in cereals.

Research Report

The structural genetic diversity present in the barley germplasm was harnessed by associating haplotypes of **candidate genes to malting quality parameters** with the goal of marker development for those traits. A total of 48 highthroughput markers from 19 candidate genes (e.g. α-amylase 1, endo-1,4-β-xylanase 1, serine carboxypeptidase I, flavone 3-hydroxylase, proteindisulfide-isomerase) were developed and tested on a set of 500 barley accessions. Association studies could be performed with 29 malting and kernel quality parameters of 140 cultivars. Phenotypic data were obtained from the database "Metabrew", which was developed in collaboration with the Bioinformatics and Information Technology group at IPK (S. Weise, U. Scholz) to get a broader range of malting and brewing quality data and to avoid effects of sample sizes. Population structure analysis with 24 SSR-markers showed that a subset of 342 genotypes was divided into 2 groups (winter and spring barley). Several of the tested markers and resulting haplotypes showed significant associations to the corresponding phenotypes assuming the "General Linear Model" even when population structure was considered. The obtained results and developed markers are of potential interest for future breeding purposes for good malting quality (I. Matthies).

The **regulatory networks in the developing barley seed** were investigated in a set of introgression lines of the cultivar "Brenda" and the *Hordeum vulgare* ssp. *spontaneum* accession "H213". In collaboration with the Gene Expression group (U. Wobus and W. Weschke) more than 40,000 gene expression profiles derived from 12,000 unigenes sampled at four developmental stages of the barley grain were analysed. The QTL analysis was performed with two independently grown sets of introgression lines. We detected 7,059 QTL in the 1st and 3,014 QTL in the 2nd experiment from 47,144 and 43,405 gene expression phenotypes applying a LOD cut-off of 3. From these QTL we could recover 179 QTL in both experiments on the same chromosome. A specific eQTL-hotspot could be attributed to two genetically related lines showing differential expression of 443 genes compared to other members of the introgression line population. A total of 67 molecular markers were developed from an intitial set of 480 eQTL-forming ESTs.
In collaboration with the Applied Biochemistry group (H.-P. Mock and K. Witzel) protein spot volumes derived from 2D-gel electrophoresis were used as quantitative phenotypes. The QTL analysis of 1,050 protein phenotypes from the 1st growing batch yielded 72 QTL with a LOD cut-off of 3. In the 2nd experiment, 68 QTL derived from 2,118 protein phenotypes. QTL for B hordeins, protein disulfide isomerase, α-amylase inhibitor BDAI, subtilisin chymotrypsin inhibitor and for peroxidase BP1 have been found in both experiments on the same chromosome, indicating a high heritability of the amount of these proteins in the ripe grain (C. Pietsch).

In the past years the **barley scald resistance gene *Rrs2*** was fine-mapped and the genomic region flanking the resistance gene was obtained by chromosome walking using a barley BAC library. Since a large genomic region co-segregates with the resistance gene in the mapping population, an association genetics approach was chosen to genetically delimit the genomic region containing the *Rrs2* gene by analysis of linkage disequilibrium. The sequencing of PCR-amplified genomic fragments in a set of 25 varieties recovered a number of haplotypes and SNPs, which are specific for the *Rrs2* carrying varieties and which were converted in **diagnostic molecular markers**

a)

b)

variety	SNP 1	2	3	4	5**	6	7	8**	9	10	11	12	13	14	15**	16**	17**	haplotype	resistance
Hendrix	A	A	T	T	C	G	C	G	C	C	T	C	G	A	C	A	G	H1	susc.
Steffi	A	A	T	T	C	G	C	G	C	C	T	C	G	A	C	A	G		susc.
Alexis	C	G	C	A	C	G	C	G	C	T	C	C	A	G	C	A	G	H2	susc.
Auriga	C	G	C	A	C	G	C	G	C	T	C	C	A	G	C	A	G		susc.
Barke	C	G	C	A	C	G	C	G	C	T	C	C	A	G	C	A	G		susc.
LaMesita	C	G	C	A	C	G	C	G	C	T	C	C	A	G	C	A	G		res.
Morex	C	G	C	A	C	G	C	G	C	T	C	C	A	G	C	A	G		susc.
Triton	C	G	C	A	C	G	C	A	T	T	C	C	A	G	C	A	G	H3	res.
CI1225	C	G	C	A	C	G	C	A	T	T	C	C	A	G	C	A	G		res.
CI3515	C	G	C	A	C	G	C	A	T	T	C	C	A	G	C	A	G		res.
CI5831	C	G	C	A	C	G	C	A	T	T	C	C	A	G	C	A	G		res.
Escald15	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C	H4**	*Rrs2*
GxH	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
CI2235	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
Osiris	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
Pewter	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
PI452395	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
Atlas46	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
AtlasPk	C	G	C	A	G	G	C	A	C	T	C	C	A	G	A	G	C		*Rrs2*
IPZ24727	C	G	C	A	C	G	C	G	C	T	C	T	A	G	C	A	G	H5	susc.
Birte	C	G	C	A	C	G	T	G	C	T	C	C	A	G	C	A	G	H6	susc.
CI8288	C	G	C	A	C	G	C	G	C	T	C	C	A	G	A	G	A	H7	res.
Prestige	C	G	C	A	C	G	C	G	C	T	C	C	G	G	C	G	G	H8	susc.
Opal	C	A	C	A	C	A	C	G	C	T	C	C	G	G	C	G	G	H9	susc.
11258W	C	A	C	A	C	A	C	G	C	T	C	C	G	G	C	G	G		res

** $p < 0,01$ statistical analysis carried out using the program TASSEL (version 2.0.1)
* $p < 0,05$ assuming the General Linear Model (GLM)

Fig. 27: A diagnostic molecular marker for the resistance gene *Rrs2* against scald in barley was developed and validated in a set of barley varieties. The marker can be applied by barley breeders for marker assisted selection of resistant genotypes. a) Barley leaf showing symptoms of infection with *Rhynchosporium secalis* (scald) (Photo: G. Schweizer, LfL Freising) b) *Rrs2* marker: overview of haplotype pattern and SNPs of a 325 bp sequence at the *Rrs2* locus on chromosome 7H; haplotype H4 is significantly correlated with the *Rrs2* mediated resistance phenotype (A. Hanemann).

that can be used by barley breeders for marker-assisted selection of genotypes resistant to *Rhynchosporium secalis* (A. Hanemann) (see Fig. 27).

The development of mapping populations for further genetic dissection of QTLs detected in advanced backcross populations of spring barley and winter wheat was continued. The **finemapping of a novel gene for grain weight** and plant height on wheat chromosome 7D was initiated by developing homozygous recombinant lines in the BC4F4 generation of the cross "Prinz" × "M6" (M. Röder). The gene for the enzyme ent-kaurenoic acid oxidase (Kao), which is part of the gibberellic acid biosynthesis pathway was investigated as potential candidate gene. Partial sequencing of three gene copies led to the discovery of SNPs suitable for mapping in the segregating population (E. Khlestkina).

The analysis of the recombinant inbred population "Yangmai6" × "Sonalika" segregating for **resistance to spot blotch** caused by the fungal pathogen *Bipolaris sorokiniana* was completed. By applying composite interval mapping four QTLs were identified. Some of these QTLs were verified in a second mapping population "Ning8201" × "Sonalika", which contains a different donor for resistance (U. Kumar). In collaboration with the Federal Biological Research Centre for Agriculture and Forestry (K. Flath) linkage mapping of three resistance genes against stripe rust in wheat from novel resistance donors was performed using molecular markers (W. Dawit).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Molecular Genetics, Research Group Gene Expression; Prof. U. Wobus, Dr. N. Sreenivasulu;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, S. Weise;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, K. Witzel.

Outside the Institute:

TraitGenetics GmbH, Gatersleben; Dr. M. Ganal;
Federal Biological Research Centre for Agriculture and Forestry, Kleinmachnow; Dr. K. Flath;
Bavarian State Research Centre for Agriculture (LfL), Freising; Dr. G. Schweizer;
Haifa University, Institute of Evolution, Haifa, Israel; Dr. T. Fahima;
Institute of Cytology and Genetics (ICG), Novosibirsk, Russia; Dr. E. Salina, Dr. E. Khlestkina;
Universidad Autonoma de Baja California Sur, La Paz, Mexico; Dr. J. de León.

Publications

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Al Khanjari, S., K. Hammer, A. Buerkert & M.S. Röder: Molecular diversity of Omani wheat revealed by microsatellites: I. Tetraploid landraces. Genet. Resour. Crop Evol. 54 (2007) 1291-1300.

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Bálint, A.F., M.S. Röder, R. Hell, G. Galiba & A. Börner: Mapping of QTLs affecting copper tolerance and the Cu, Fe, Mn and Zn contents in the shoots of wheat seedlings. Biol. Plant. 51 (2007) 129-134.

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Huang, X.-Q., M. Wolf, M.W. Ganal, S. Orford, R.M.D. Koebner & M.S. Röder: Did modern plant breeding lead to genetic erosion in European winter wheat varieties? Crop Sci. 47 (2007) 343-349.

Iqbal, N., F. Eticha, E.K. Khlestkina, A. Weidner, M.S. Röder & A. Börner: The use of SSR markers to identify and map alien segments carrying genes for effective resistance to leaf rust in bread wheat. Plant Genet. Resour. 5 (2007) 100-103.

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Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: "Genetical Genomics" der Gerstenkornentwicklung – von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomXPress 1 (2007) 12-16.

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Lectures, Posters and Abstracts

V81, P37, P79, P80, P117, P135, P146, P148, P149, P165, P178, P179, P182, P205, P231, P237, P238, P241.

Additional Funding

For further information see the survey page 210.

Research Group: Bioinformatics and Information Technology

Head: Dr. Uwe Scholz

Scientists

IPK financed
Lange, Matthias, Dr. (Annex ITB, till 30.06.2007; P, since 01.07.2007)

Grant Positions
Spies, Karl (various projects, since 15.08.2007)
Stephanik, Andreas (BMBF, till 31.10.2007)
Steuernagel, Burkhard (BMBF)
Weise, Stephan (BMBF)

Visiting Scientists
Chen, Ming, Prof. (DAAD, 16.09.-30.09.2007)
Künne, Christian (self-financed, 01.11.-31.12.2007)
Stephanik, Andreas (self-financed, 01.11.-31.12.2007)

Goals

Research activities and support IPK biologists with the development and maintenance of molecular biological databases, molecular biological data integration, implementation of bioinformatics tools for various *in silico* analysis tasks and bioinformatics consulting. Besides these research activities, the group is responsible for the IT infrastructure of the institute.

Research Report

In 2007 the BMBF funding of the Bioinformatics Centre Gatersleben-Halle (BIC-GH) ended. One result of the BIC-GH was the development of **BATEx**, an integration system for gene expression data. It consists of a data warehouse and several applications to support upload, curation and exploring of data. A last part, that was added, is a graphical analysis application framework for analysis modules. Further data from AFGC and SGED was integrated into this warehouse. BATEx is an open source system and is available at http://pgrc.ipk-gatersleben.de/batex (A. Stephanik, B. Steuernagel).

Malting quality is one of the most important traits in barley. In order to support association studies, we developed an association data mart in collaboration with the Gene and Genome Mapping group. Approximately 60,000 data points of phenotypic data and about 20,000 data points of genetic data have been integrated into that mart. A graphical user interface based on the Oracle Application Express technology was developed. It allows browsing data, matching phenotypic and genetic information and exporting that data in interchangeable formats (S. Weise).

Together with the Plant Bioinformatics group we developed **MetaCrop** (http://metacrop.ipk-gatersleben.de). It is based on the information system software Meta-All and is a database of crop plant metabolism. MetaCrop (see Fig. 28) currently contains manually curated information about six major crop plants. A web interface was developed using the Oracle Application Express technology. It supports easy exploration of the data. All information can be downloaded in SBML format and can be used with visualisation and simulation tools (S. Weise).

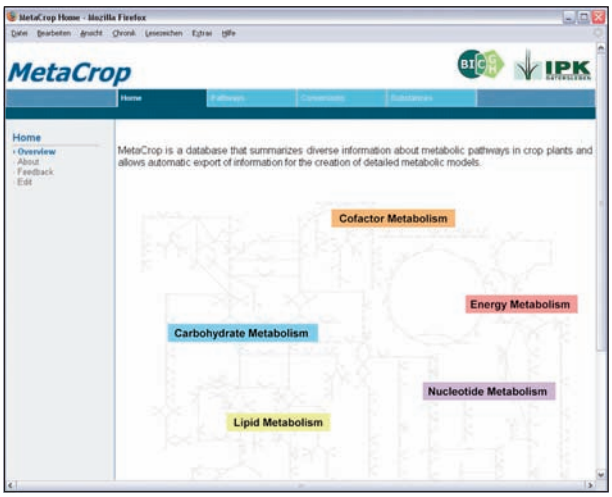

Fig. 28: MetaCrop: This figure shows the entry page of the MetaCrop database. Starting with an overview pathway the user is able to zoom through pathway information to the point of detailed parameters of certain substances or conversions, respectively (S. Weise).

The trilateral GABI project GENOSOME studies molecular processes during meristem development in Solanaceae. Last year's focus for the bioinformatics part was on comparative analysis of gene expression data derived from experiments of all working partners. Therefore, a visualisation tool (see Fig. 29) was set up to present the integrated data (B. Steuernagel).

In the frame of the GENOSOME project we contribute to the potato oligo chip initiative (**POCI**). This consortium introduced a new 44k microarray for *Solanum tuberosum*. We designed an information system to supply users of this chip with all necessary data, including sequence data, EST membership information, chip annotation and BLAST functionality to align own sequences to the POCI unigenes (B. Steuernagel).

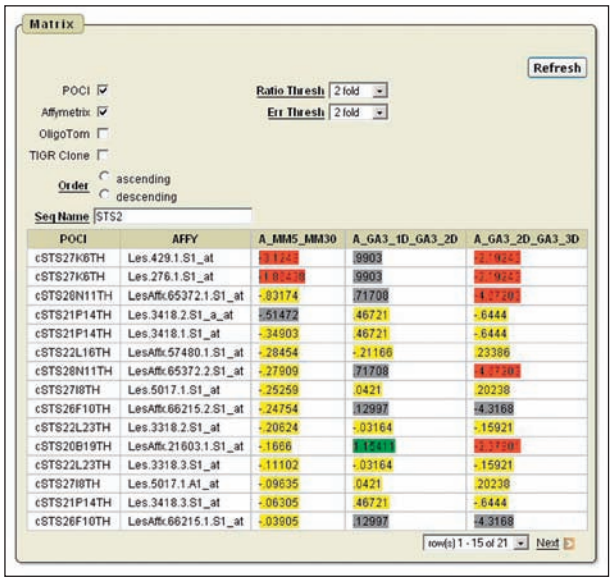

Fig. 29: Comparative Expression Analysis: This figure shows a matrix of processed gene expression data from different experiments. The values are ratios of selected materials. Coloration of the values denote difference of expression: red or green for different expression, yellow for no change and grey for data that was marked as "not reliable" during the integration process (B. Steuernagel).

In collaboration with the Genome Diversity group we enhanced the **Tilling database** application. New features have been added in order to provide more assistance to end users, e.g. the semi-automatic assembling of pool plates with DNA preps (J. Grässler, S. Weise).

Another joint activity with the Genome Diversity group is the **BAC-DB** application, which is developed in the frame of the physical mapping project. We developed the first part of the graphical user interface. It is intended to manage information about analysis pipelines, which consist of several steps and parameters. Further developments in the context of this application are subject to current work (S. Weise).

BioEscorte is a joint project with BASF Ludwigshafen for realising a search engine in life science databases. It is intended to investigate and implement new methods for increasing the specificity of text queries over integrated datasets. One year of the funding period of two years was co-financed by BASF (K. Spies, M. Lange).

The uniform function annotation of IPK EST sequences was promoted by the **Data Linkage Graph** approach. By using data integration methods a data network was derived. A classifying annotation of this network was performed using controlled vocabularies of IPK EST sequences. It was shown that a uniform annotation of EST clones is feasible this way (M. Lange).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Genome Diversity; Dr. S. Gottwald, Dr. D. Schulte, Dr. T. Sretenovic Rajicic, Dr. N. Stein;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann;
Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, C. Künne;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. I. Matthies, Dr. M. Röder;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber, Dr. B. Junker, E. Grafahrend-Belau, D. Koschützki, H. Schwöbbermeyer.

Outside the Institute:

Otto-von-Guericke University, ITI, Magdeburg; Prof. G. Paul;
University of Bielefeld, Research Group Bioinformatics/ Medical Informatics; Prof. R. Hofestädt;
Zhejiang University, Zhejiang, China; Prof. M. Chen;
INRA de Versailles, Research Group Laboratoire de Biologie Cellulaire, Versailles, France; Dr. P. Laufs;
Universidad Autonoma de Madrid Cantoblanco, Centro Nacional de Biotecnología CSIC, Madrid, Spain; Dr. S. Prat;
Rothamsted Research, Biomathematics and Bioinformatics Division, Rothamsted, UK; Dr. J. Köhler.

Publications

Peer Reviewed Papers

Lange, M., A. Himmelbach, P. Schweizer & U. Scholz: Data Linkage Graph: computation, querying and knowledge discovery of life science database networks. J. Integr. Bioinformatics 4 (2007) 68 Online Journal: http://journal.imbio.de/index.php?paper_id=68.

Weise, S., S. Harrer, I. Grosse, H. Knüpffer & E. Willner: The European *Poa* Database (EPDB). Plant Genet. Resour. Newsl. 150 (2007) 64-70.

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Senning, M., B. Steuernagel, A. Hartmann, U. Sonnewald & U. Scholz: Regulation der Keimruhe von Kartoffelknollen. GenomXPress 3 (2007) 7-10.

Electronic Publications

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop – A detailed database of crop plant metabolism. http://metacrop.ipk-gatersleben.de/ (2007).

Keller, E.R.J., C. Zanke & U. Scholz: EURALLIVEG – Vegetative Allium, Europe's Core Collection, Safe and Sound http://euralliveg.ipk-gatersleben.de/ (2007).

Scholz, U., C. Künne, M. Lange, H. Miehe & T. Funke: IPK Crop EST Database: CR-EST (Version 1.5). http://pgrc.ipk-gatersleben.de/cr-est/ (2007).

PhD and Diploma Theses

Heiss, S.: Entwicklung eines Data-Warehouses für pflanzengenetische Diversitätsstudien. (Diploma Thesis) Otto-von-Guericke-Universität Magdeburg, Fakultät für Informatik, Institut für Technische und Betriebliche Informationssysteme, Magdeburg (2007) 82 pp.

Klapperstück, M.: Konzeption und Umsetzung einer Graphanfragesprache zur nicht-materialisierten Integration biologischer Datenquellen. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Informatik, Halle/S. (2007) 98 pp.

Koopmann, J.H.: Integrierte plattformübergreifende Normalisierung von Expressionsdaten. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Informatik, Halle/S. (2007) 64 pp.

Spies, K.: Integration von Bioinformatikdatenbanken und -anwendungen des IPK Gatersleben mittels Web-Services in die internationale Bioinformatik-Infrastruktur. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Informatik, Halle/S. (2007) 126 pp.

Totz, J.: Workflow-supported Analysis of Gene Expression Data. (Diploma Thesis) Otto-von-Guericke-Universität Magdeburg, Fakultät für Informatik, Institut für Technische und Betriebliche Informationssysteme, Magdeburg (2007) 107 pp.

Xia, M.: Hierarchische Datenbankanfrage auf integrierte Datenbanken zur Funktionsklassifikation von molekularbiologischen Daten. (Diploma Thesis) Universität Bielefeld, Technische Fakultät, Bielefeld (2007) 85 pp.

Lectures, Posters and Abstracts

V134, V192, V193, V194, V255, V278, P11, P12, P42, P58, P67, P69, P72, P73, P127, P128, P148, P149, P173, P203, P204, P209, P227, P228.

Additional Funding

For further information see the survey page 211.

Abteilung Molekulare Genetik/ Department of Molecular Genetics

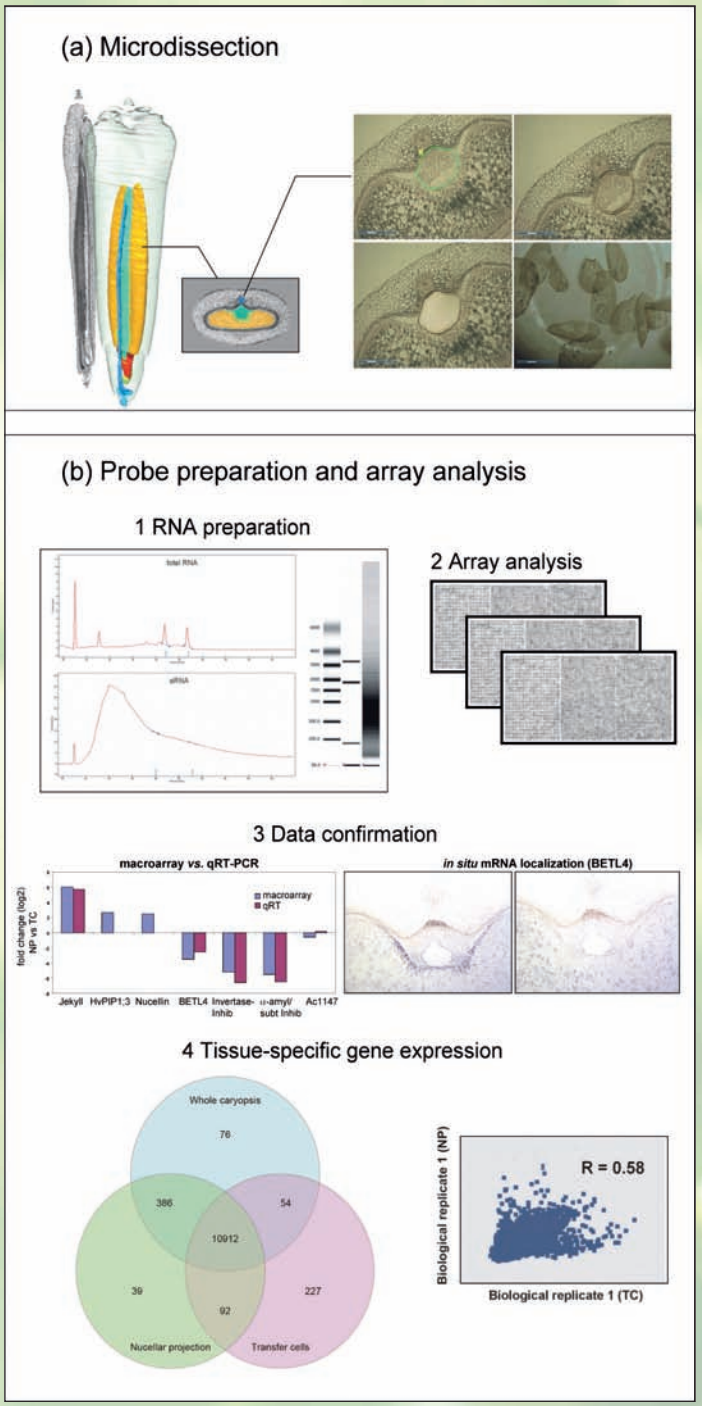

Fig. 30: Mikro-Dissektion sich entwickelnder Gerste-Samen und Array-Analyse der dissektierten Gewebe. (a) 3D-Modell eines sich entwickelnden Korns 7 DAF (links) rekonstruiert aus photographischen Aufnahmen von dünnen Querschnitten, die mit Osmiumtetroxid kontrastiert wurden (grau-schattiertes Modell; dargestellt ist ein virtueller Längsschnitt) und die dazugehörende farbige Markierung interessierender Gewebe (Segmentierung) der Schnitte (frontale Ansicht). Die Gewebe wurden automatisch segmentiert. Folgende Farben wurden für die Segmentierung verwendet: Hauptleitbündel: blau, nuzellare Projektion: grün, endospermale Transferzellen: hellgrün, Endosperm: gelb, Embryo-umgebende Region: rot. Schnitte aus dem oberen mittleren Bereich der Karyopse (rechts) wurden für die Mikrodissektion von nuzellarer Projektion und endospermalen Transferzellen verwendet.
(b) 25 – 50 Dissektate der jeweiligen Gewebe wurden gesammelt, die RNA wurde extrahiert, amplifiziert, mit ^{33}P-UTP markiert und als Probe für die Hybridisierung des 12K-Gerstenarrays verwendet. Das Expressionslevel ausgewählter Gene in den beiden Geweben wurde durch qRT-PCR ermittelt und mit den Ergebnissen der Array-Analyse verglichen; eine gute Übereinstimmung der Werte wurde registriert. Die korrekte Lokalisierung zweier mRNA-Spezies wurde mittels *in situ*-Hybridisierung überprüft. Auf der Grundlage eines vierfachen Unterschiedes im mRNA-Expressionslevel wurden 227 Transferzell-spezifische Gene detektiert und 39 Gene, die spezifisch in der nuzellaren Projektion exprimiert werden (J. Thiel, D. Weier, F. Bollenbeck, M. Strickert, N. Sreenivasulu).

Microdissection of developing barley grains and array analysis of selected tissues. (a) 3-D models of a developing grain 7 DAF (left) generated from photographs of cross sections contrasted by osmium tetroxide (gray-shaded model, virtual longitudinal cut) and the according histological mappings (segmentation) of sections (front view). During automatic segmentation tissues were labelled by the following colours: main vascular bundle, blue; nucellar projection, green; endosperm transfer cells, light green; endosperm, yellow; embryo-surrounding region, red. Sections from the upper middle part of caryopses were used for microdissection (right-hand side) of nucellar projection and endosperm transfer cells. (b) 25-50 dissected tissue regions were collected, RNA was isolated, amplified, labelled by ^{33}P-UTP and used as probe for hybridisation of the 12K barley cDNA array. Expression levels of selected genes in the two tissues were estimated by qRT-PCR and compared to array analysis results; correspondence was registered. mRNA localisation was revealed by *in situ* hybridisation. Based on an at least 4-fold difference in their expression level, 227 and 39 genes were detected exclusively transcribed in transfer cells and nucellar projection, respectively (J. Thiel, D. Weier, F. Bollenbeck, M. Strickert, N. Sreenivasulu).

Abteilung Molekulare Genetik

Leiter: Prof. Dr. Ulrich Wobus

Allgemeine Forschungsziele

Forschungsschwerpunkt der Abteilung Molekulare Genetik im Berichtsjahr war unverändert die molekulare Biologie und Physiologie von Embryogenese und Samenentwicklung, ergänzt durch verwandte, aber nicht auf Samen beschränkte Themen. Folgende zentralen Probleme wurden bearbeitet:

- Genexpressionsmuster in Entwicklungsprozessen, vornehmlich in Samen von Gerste, Erbse und *Arabidopsis*,
- Rolle und Wirkmechanismen von Transkriptionsfaktoren,
- Molekularphysiologie der Samenentwicklung unter besonderer Berücksichtigung der Speicherstoffsynthesen in Gerste und Erbse,
- Topografische Analyse von Entwicklungsprozessen im Samen,
- Asexuelle Formen der pflanzlichen Reproduktion (Apomixis und verwandte Prozesse), untersucht an *Poa pratensis*, *Hypericum* und Weizen,
- Umsetzung von Grundlagenerkenntnissen in angewandten Projekten: Verbesserung agronomischer Merkmale (Beispiel Weizen) und „Molecular Farming" in Samen,
- Analyse und Visualisierung von Daten sowie Prozess-Simulationen und Netzwerkanalyse, vornehmlich basierend auf den erarbeiteten experimentellen Daten.

Zentrales Ziel der Forschung ist ein systemisches Verständnis der Entwicklungsprozesse und Funktionszusammenhänge von der Determination des Fortpflanzungsmodus (sexuell *versus* asexuell) bis zum Abschluss der Samenentwicklung.

Entwicklung im Berichtsjahr

Im Berichtsjahr wurde die Abteilung durch eine Nachwuchsgruppe und zwei selbstständige Projektgruppen ergänzt: Nachwuchsgruppe Dateninspektion, Leiter Dr. Marc Strickert; Projektgruppe Hybridweizen, Leiter Dr. Mario Gils; Projektgruppe GABI-GRAIN, Leiter Dr. Nese Sreenivasulu (organisatorisch als Teil der Arbeitsgruppe Genwirkung geführt).

Im Folgenden werden, wie im Vorjahr, eine Reihe von im Berichtsjahr erzielten Forschungsergebnissen kurz dargestellt, gegliedert nach den eingangs erwähnten Arbeitsthemen. Einzelheiten und Publikationshinweise finden sich in den Berichten der Arbeitsgruppen.

Department of Molecular Genetics

Head: Prof. Ulrich Wobus

Research Goals

The major focus of research in the department is the molecular biology and physiology of plant embryogenesis and seed development. A few projects not devoted to seeds are also pursued. In the reporting year, research was focussed on the following topics:

- Global expression patterns underlying developmental processes, especially in seeds of barley, pea and *Arabidopsis*,
- Role and functional mechanisms of transcription factors, specific proteins and hormones in the seeds of said species,
- Molecular physiology of seed development in barley and pea with a focus on storage product synthesis,
- Topographical analysis of developmental processes in seeds,
- Asexual modes of plant reproduction (apomixis and related processes) studied in *Poa pratensis*, *Hypericum* and wheat,
- Transfer of basic knowledge into applied projects: the improvement of agronomical traits as exemplified in wheat and molecular farming in seeds,
- Analysis and visualisation of data as well as process simulation and network analysis, mainly based on the experimental data produced by the described projects.

The central goal of the department's efforts is a systemic understanding of the developmental processes and their functional relationships from the determination of the reproductive mode (sexual *versus* asexual) up to the developmental arrest at the end of seed maturation.

Developments during 2007

In the reporting year, three new groups funded by external money joined the department: the junior research group Data Inspection headed by Dr. Marc Strickert, the project group Hybrid Wheat headed by Dr. Mario Gils and the project group GABI-GRAIN headed by Dr. Nese Sreenivasulu (this group is organisationally embedded in the research group Gene Expression).

In the following, central aspects of research in the department are briefly summarised according to the

(1) Genexpressionsmuster in Entwicklungsprozessen. Expressionsanalysen mit Hilfe von verschiedenen Arrays sowie nachgeschalteten Northern- und RT-PCR-Analysen bilden den Kern vieler Teilprojekte. Fortgesetzt wurde die vergleichende Transkriptomanalyse von Gersten-Introgressionslinien und deren Eltern, abgeschlossen eine Affymetrix-Analyse von Kornentwicklung und -keimung bei der Sommergerste „Brenda" zwecks Herausarbeitung von Gemeinsamkeiten und Unterschieden beider Prozesse. Ebenso abgeschlossen wurde die Analyse der Transkriptionsmuster einer Gerstenkorn-Mutante, *seg8*. Ein Erbsen-Makroarray mit ca. 5.000 Unigenen wird routinemäßig bei der Analyse verschiedenster transgener Linien eingesetzt (Arbeitsgruppe Genwirkung). Weitere Beispiele enthalten die Berichte der Arbeitsgruppen.

(2) Rolle und Wirkmechanismen von Transkriptionsfaktoren (TF). Zielgene (bzw. deren Promotoren) eines der wichtigsten Regulatoren der Samenentwicklung, ABI3, wurden mit Hilfe der Chromatinimmunopräzipitation und anschließender Array-Hybridisierung der gefällten DNA-Fragmente (ChIP/chip-Analyse) identifiziert, darunter einige bislang nicht bekannte Targetgene (Arbeitsgruppe Phytoantikörper). Ein ähnlich bedeutender Entwicklungsregulator ist LEC1, dessen Zielgene ebenfalls mit Hilfe verschiedener Techniken einschließlich ChIP/chip-Analyse gesucht werden (Arbeitsgruppe Genregulation). Zur Rolle der RKD-TF-Familie siehe unter (5). Die Funktion von zwei Myb-Transkriptionsfaktoren, AtMYB44 und AtMYB77, wurde mit Hilfe von „gain- und loss-of-function"-Mutanten und deren Transkriptomanalyse näher untersucht (Arbeitsgruppe Phytoantikörper).

(3) Molekularphysiologie der Samenentwicklung unter besonderer Berücksichtigung der Speicherstoffsynthesen. Transgene Pflanzen werden weiterhin intensiv zur Aufklärung der Rolle von Schlüsselgenen in Stoffwechselwegen und regulatorischen Netzwerken genutzt. Überraschenderweise zeigten Erbsensamen, die einen ABA-Einzelketten-Antikörper exprimieren, einen erhöhten ABA-Gehalt, der als Ergebnis einer regulatorischen Überreaktion interpretiert wird. Die Wiederholung eines Freilandversuchs mit Erbsen, die samenspezifisch eine Aminosäurepermease exprimieren, bestätigte den erhöhten Proteingehalt auf Kosten von Stärke und Lipiden. Bei der Untersuchung der Rolle von Sauerstoff und Stickoxid in der Samenentwicklung wurde ein Autoregulationsmechanismus identifiziert und publiziert, der mit Hilfe transgener, ein nicht-symbiontisches Hämoglobin exprimierender *Arabidopsis*-Samen weiter aufgeklärt wird (Arbeitsgruppe Genwirkung).

(4) Topografische Analyse von Entwicklungsprozessen im Samen. Die räumliche Auflösung von Entwicklungsprozessen ist von großer Bedeutung für ein systembiologisches Verständnis der Samenentwicklung und deshalb auch seit Jahren Gegenstand intensiver Untersuchungen. Im Berichtsjahr wurde eine neue NMR-

main research areas described above. Details will be found in the group reports.

(1) Gene expression patterns underlying developmental processes. Expression analysis by means of different kinds of array analyses as well as follow-up Northern and RT-PCR analyses are at the centre of many projects. We continued the transcriptome analysis of barley introgression lines and their respective parents and finished an Affymetrix analysis of spring barley "Brenda" grain development and germination to delineate commonalities and differences of both processes. Likewise completed was the analysis of RNA expression patterns in the grain of the barley mutant *seg8*. A pea macroarray with about 5,000 unigenes is routinely used to analyse a variety of transgenic lines (research group Gene Expression). More examples are found in the group reports.

(2) Role and functional mechanisms of transcription factors (TF), specific proteins and hormones. Target promoters for one of the most important regulators of seed development, ABI3, were identified by chromatin immunoprecipitation and subsequent array hybridisation of precipitated DNA (ChIP/chip analysis). Among them are several that have not yet been described (research group Phytoantibodies). Of similar importance for seed development is the TF LEC1. Its target promoters are equally searched for by different methods including ChIP/chip analyses (research group Gene Regulation). The role of the RKF-TF-familiy is described below (5). Gain of function and loss of function mutants were investigated by transcript profiling and other methods to elucidate the function of the two Myb factors AtMYB44 and AtMYB77 (research group Phytoantibodies).

(3) Molecular physiology of seed development with a focus on storage product synthesis. Transgenic plants are still used extensively to elucidate the role of key genes in metabolic pathways and regulatory networks. Pea plants producing ABA single chain antibodies surprisingly revealed an increase of seed ABA content, explained as a regulatory overshoot reaction. A repeated field trial with transgenic peas overexpressing an amino acid permease confirmed an increased seed nitrogen content at the expense of starch and lipids. Studies on an autoregulatory loop involving oxygen and nitric oxid were published and will be further elucidated in transgenic *Arabidopsis* seeds expressing nonsymbiotic hemoglobins (research group Gene Expression).

(4) Topographical analysis of developmental processes in seeds. To analyse the spatial resolution of developmental processes is of outmost importance to understand the systemic properties of seed development. Therefore, we put much effort in method devel-

basierte Methode zur Analyse der Lipidverteilung publiziert. Entsprechende Methoden zur Visualisierung von Zuckern und Aminosäuren werden entwickelt. Speziell für die Analyse der räumlichen Verteilung von Metaboliten, aber auch von Transkripten und Proteinen werden Methoden der Computer-navigierten Cryo-Mikrodissektion ausgearbeitet (Arbeitsgruppe Genwirkung und Arbeitsgruppe Mustererkennung, Abteilung Cytogenetik und Genomanalyse).

(5) Asexuelle Formen der pflanzlichen Reproduktion (Apomixis und verwandte Prozesse). Die Arbeiten an sexuellen und parthenogenetischen Weizen-Eizellen haben zur Identifikation einer neuen, pflanzenspezifischen Transkriptionsfaktorfamilie geführt (RKD-Familie), deren umfassende Charakterisierung eine essenzielle Funktion in der Entwicklung des weiblichen Gametophyten nahelegt (Arbeitsgruppe Genregulation). Von besonderem Interesse ist die Initiation gametophytischer Entwicklungsprozesse nach ektopischer Expression von AtRKD1 und AtRKD2. Fortlaufende Arbeiten an *Hypericum* zur Isolation von Aposporie-gekoppelten Markersequenzen haben Marker-tragende BAC-Klone identifiziert, die gegenwärtig sequenziert werden (Arbeitsgruppe Genregulation).

(6) Umsetzung von Grundlagenerkenntnissen in angewandten Projekten. Das Berichtsjahr war gekennzeichnet durch große öffentliche Aufmerksamkeit und Auseinandersetzungen, ausgelöst durch den Freilandversuch mit transgenem Winterweizen zur Erhöhung des Proteingehalts. Der Versuch konnte bei Rund-um-die-Uhr-Bewachung zwecks Verhinderung von Zerstörungen erfolgreich beendet werden. Erste Ergebnisse enthält der Bericht der Arbeitsgruppe Genwirkung (s. S. 101). Fortgesetzt wurden die Arbeiten zur effizienten Produktion unterschiedlicher Spinnseidenproteine sowie von funktionalen Tuberkulose- und HIV-Antikörpern. Letztere wurden einer umfassenden Charakterisierung unterzogen. Um eine wirksame zytosolische Konzentration eines Gerstenvirus (BYDV)-Einzelkettenantikörpers zu erreichen, wurden eine Reihe von Mutanten erfolgreich getestet (Arbeitsgruppe Phytoantikörper). Die neugegründete Arbeitsgruppe Hybridweizen (s. o.) arbeitet ausschließlich anwendungsorientiert mit dem Ziel, auf relativ einfache Weise Weizen-Hybridsaatgut mit einem Gentechnik-basierten Verfahren herzustellen. Ein „proof-of-concept" wurde in *Arabidopsis* bereits erreicht.

(7) Analyse und Visualisierung von Daten, sowie Prozesssimulationen und Netzwerkanalyse. Viele der in der Abteilung erhobenen experimentellen Daten bedürfen einer umfangreichen bioinformatischen Analyse, die durch die Arbeitsgruppen Netzwerkanalyse und Dateninspektion im Rahmen gemeinsamer Projekte mit experimentellen Gruppen durchgeführt wurden. Neue Analysewerkzeuge wie MetaCrop wurden unter Nutzung aller verfügbaren Daten entwickelt und stehen über das Netz der Allgemeinheit zur Verfügung. Besonders bedeut-

opment and respective data acquisition during recent years. In the reporting year a new method to visualise lipid distribution was published and similar methods to visualise the distribution of sugars and amino acids are under development. To document the spatial distribution of especially metabolites but also transcripts and proteins a computer-navigated cryo-microdissection system is under development (research group Gene Expression in collaboration with the research group Pattern Recognition, Dept. of Cytogenetics and Genome Analysis).

(5) Asexual modes of plant reproduction (apomixis and related processes). Studies on sexual and parthenogenetic egg cells of wheat led to the identification of a new, plant-specific transcription factor family (RKD family). Thorough functional characterisation demonstrated an essential function during female gametophyte development. Most interestingly, ectopic expression of AtRKD1 and AtRKD2 initiated gametophytic processes. Continued research in *Hypericum* led to the identification of apospory-linked marker loci. Marker-carrying BAC clones have been identified and are presently sequenced (research group Gene Regulation).

(6) Transfer of basic knowledge into applied projects. The field trial with transgenic winter wheat exhibiting increased seed protein content received much public attention and disput. Mainly due to an around the clock surveillance the experimental field remained undestroyed. First experimental results of the trial are reported by the Gene Expression group (see p. 101). Attempts to efficiently produce different kinds of silk fibre proteins as well as functional tuberculosis and HIV antibodies were continued. HIV antibodies were extensively characterised. Several mutants of single chain antibody genes against a barley virus (BYDV) were produced and tested to increase necessary cytosolic concentrations (research group Phytoantibodies). The newly established project group Hybrid Wheat develops exclusively a comparatively simple system to produce hybrid wheat seeds by genetic engineering methods. Proof-of-concept was already achieved in *Arabidopsis*.

(7) Analysis and visualisation of data as well as process simulation and network analysis. Many of the experimentally achieved data sets demand extensive bioinformatic analyses, which is mainly carried out by the research groups Plant Bioinformatics and Data Inspection mostly within joined projects. New analysis tools like MetaCrop have been developed based on all available data and are publicly available through the internet. Of special importance is the start of a major BMBF-funded systems biology project called GABI-SysSEED aiming at a systemic understanding of the developing barley grain. Of special

sam ist der Einstieg in die Systembiologie des sich entwickelnden Gerstenkorns über ein im August angelaufenes, umfangreiches GABI-FUTURE-Projekt mit dem Akronym GABI-SysSEED. In diesem Zusammenhang ist die Entwicklung eines stöchiometrischen, kompartmentalisierten Modells, das über 250 Reaktionen des Primärmetabolismus der Gerste einschließt, besonders hervorzuheben.

Die folgenden Berichte der Arbeitsgruppen vermitteln einen detaillierten Einblick in die Forschungsaktivitäten der einzelnen Arbeitsgruppen.

Ulrich Wobus, Januar 2008

relevance to this approach is the development of a stoichiometric, compartmentalised model of the barley primary metabolism including about 250 reactions (research group Plant Bioinformatics).

The following group reports provide more detailed insights into the basic as well as applied research of the department.

Ulrich Wobus, January 2008

Research Group: Gene Expression

Head: Prof. Ulrich Wobus

Scientists

IPK financed
Borisjuk, Ljudmilla, Dr. (P)
Riebeseel, Erik (0,5 Annex, 15.01.-31.03.2007)
Rolletschek, Hardy, Dr. (P)
Sreenivasulu, Nese, Dr. (Annex, 01.07.-31.07.2007)
Staroske, Nicole (0,5 Annex, 15.06.-31.07.2007)
Tewes, Annegret, Dr. (P)
Weber, Hans, Dr. (P)
Weschke, Winfriede, Dr. (P)

Grant Positions
Harshavardhan, V. Tammegowda (0,5 BMBF, since 08.08.2007)
Müller, Martin, Dr. (BMBF)
Nguyen, Thuy Ha (0,5 DFG)
Radchuk, Ruslana (DFG)
Radchuk, Volodymyr, Dr. (BMBF)
Rajesh, Kalladan (0,5 BMBF, since 08.08.2007)
Riebeseel, Erik (0,5 DFG, till 14.01.2007; 0,5 EU, since 01.04.2007)
Seiler, Christiane (0,5 DFG, till 31.07.2007; 0,5 BMBF, since 01.08.2007)
Sreenivasulu, Nese, Dr. (BMBF)
Staroske, Nicole (0,5 BMBF, since 01.08.2007)
Thiel, Johannes, Dr. (DFG)
Weichert, Nicola, Dr. (Saxony-Anhalt)
Weier, Diana, Dr. (DFG)
Weigelt, Kathleen (0,5 EU)

Visiting Scientists
Gubatz, Sabine, Dr. (self-financed, 01.01.-22.06.2007)
Korkhovoy, Vitaly (DFG, 01.05.-31.07.2007)
Poulain, Eduardo (DAAD, 19.03.-30.03.2007)
Roscher, Albrecht, Dr. (DAAD, 24.04.-04.05.2007)

Goals

Regulatory networks operating during embryogenesis and seed development: genetic and metabolic control of developmental and metabolic processes.

Research Report

Our aim is to develop a holistic understanding of plant seed development and thus provide advanced strategies for plant seed improvement. In our experiments we mainly use the monocotyledonous barley plant (*Hordeum vulgare*) and the dicotyledonous pea plant (*Pisum sativum)*. In some projects relatives like wheat (*Triticum aestivum*) and other grain legumes like *Vicia narbonensis* are also used. During the reporting year, ongoing projects were continued and new ones started with the general aim to work out a detailed molecular understanding of seed developmental processes at several levels from gene expression to seed physiology and to gain increased knowledge on specific genes and processes, which play a major role in determining storage product accumulation and developing seed sink strength.

The achievements in 2007 are summarised as follows:
(1) Genomics of barley grain development (GABI SEED II project). Our work was focussed on expression profiling of developing grains of a set of 28 introgression lines selected from the BC3-DH population "Brenda" × Hs213. Among them 12 lines showed significant changes of the transcriptome in comparison to the elite parent line "Brenda". Based on the observed variances of transcript abundance, co-expressed gene sets of those lines were analysed to define pathway networks influencing seed traits. Changes in the abundance of the starch biosynthesis pathway transcripts correlated with starch content in a subset of lines (N. Sreenivasulu, M. Strickert, H. Rolletschek). Measurements of metabolites of the sucrose-to-starch pathway in these lines using HPLC- and LC/MS analysis are underway (H. Rolletschek). For a thorough analysis the MapMan and PageMan tools developed for *Arabidopsis* at the MPI-MP Golm were adapted to barley (N. Sreenivasulu in collaboration with B. Usadel/Golm) and further used for an in-depth comparative analysis of barley grain maturation and germination (Sreenivasulu et al., Plant Physiol. 2008).
Based on the work especially in the GABI I and II projects, two new projects were aquired and started in August 2007: GABI-SysSEED focussing on a systems biology approach to barley seed development and GABI-GRAIN with the aim to understand drought stress processes during grain development (project leader N. Sreenivasulu) in both of which group members are playing central roles.
Macroarray analysis was also used in combination with biochemical measurements to analyse the barley seg8 mutant (N. Sreenivasulu, V. Radchuk, L. Borisjuk, D. Weier, W. Weschke). Mutant grains are characterised by changed ABA levels, disturbed cellularisation of the endosperm coenocyte, lower endosperm ploidy levels and an altered transcriptome especially during the transition phase (manuscript in preparation).

(2) Barley grain 4-D modelling and 3-D cryodissection. Using a so-called warping tool (Pielot et al. 2007), 21 3-D NMR images of the developing barley grain are combined to get the "artificially growing barley grain". Methods for micro-dissection (D. Weier, L. Borisjuk) of specific tissues (e.g., transfer cells) and subsequent expression profiling (J. Thiel, N. Sreenivasulu, M. Strickert, W. Weschke) and metabolite analysis in the pmol scale (M. Müller, in collaboration with A. Matros/Applied Biochemistry group) are developed and allow high-throughput analysis (Thiel et al., in preparation). Calculation of volume ratios from the 3-D models and estimation of mRNA as well as metabolite levels out of the micro-dissected tissues will allow visualisation of developmental gradients at least in a median-throughput manner. Presently, analyses of ABA gradients in the developing barley grain are underway.
3-D images are also used to develop navigation tools (Fraunhofer Institute Magdeburg) and to navigate a 3-D laser (MMI) for cryo-microdissection (QUANT-PRO project). Cross-sectioning of individual caryopses and automated segmentation of five different tissues are prerequisite for the generation of average models, one for each of four different developmental stages. So-called minimal models derived thereof will define caryopsis regions relevant for each of the five tissues, but independent of individual variations within one of the four developmental stages (D. Weier, L. Borisjuk, W. Weschke in collaboration with F. Bollenbeck; for further details see Annual Report of the Pattern Recognition group p. 79).

(3) Functional analysis of selected genes and gene families. Expression levels and localisation patterns of all members of known gene families involved in starch biosynthesis and degradation were analysed. The study revealed that early pericarp serves as a transient storage organ for starch and that the gene machinery involved in starch biosynthesis/degradation in the pericarp is partially different from that of the developing endosperm, the germinating embryo and leaves (V. Radchuk, N. Sreenivasulu, L. Borisjuk; manuscript in preparation).
JEKYLL, a protein expressed primarily in the nucellar projection (Radchuk et al. 2006) is also expressed very late during anther development where it contributes to effective fertilisation of the barley floret (V. Radchuk, L. Borisjuk, manuscript in preparation). Based on its secondary protein structure, JEKYLL might belong to the group of glycine-rich proteins required for plant sexual reproduction. Based on this knowledge, two proteins (called JEKYLL2 and JEKYLL3) were identified showing sequence similarities to the original JEKYLL protein (JEKYLL1). The function of JEKYLL 2 and 3 and their possible interaction with JEKYLL1 are under investigation (V. Radchuk in collaboration with G. Hensel/Plant Reproductive Biology group).

(4) Transgenic winter wheat with increased grain protein content. Together with the five basic lines (see Annual Report 2006) and respective controls, 816 lines of the transgenic winter wheat breeding garden were planted in the field in 2006. 188 lines were selected by the co-operation partner Nordsaat based on plant and spike habitus, and harvested together with the basic lines and controls in August 2007. 73 of them (40 %) and the basic lines showed an increase in grain protein content (N. Weichert, W. Weschke). In a repetition of the field trial during 2007/2008 only the selected 188 lines were planted, but with higher numbers of individual plants per line to enable the estimation of parameters related to grain yield. Basic line HOSUT underwent an Affymetrix-based expression analysis (N. Weichert, M. Strickert, N. Sreenivasulu in collaboration with K. Krohn, University of Leipzig), metabolite profiling is underway (N. Weichert/H. Weichert, W. Weschke in collaboration with J. Kopka, MPI-MP Golm).

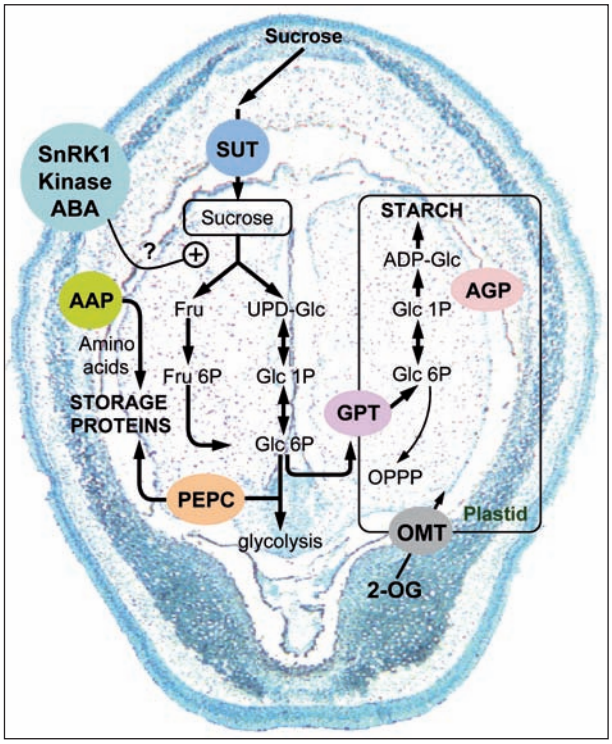

Fig. 31: Schematic overview of the assimilate uptake and the primary storage pathway in maturing legume seeds. Potential targets for the manipulation of metabolic pathways are highlighted by circles. Ectopic expression of transporters for sucrose and amino acids (SUT, AAP) could alter assimilates flux into the cotyledons. Increasing PEP carboxylase (PEPC) could increase flux into amino acid biosynthesis. Changing expression of genes of the sucrose to starch pathway (ADP) glucose pyrophosphorylase (AGP) and plastidic glucose-6-P translocator (GPT) could lead to a possible change in the production of seed components. OMT can control the uptake or carbon acceptors into plastids. SnRK1 kinase and ABA are major regulators of seed maturation (H. Weber, L. Borisjuk).

(5) Metabolites and seed development: the role of transporters/translocators, SnR kinases, abscisic acid and key metabolic enzymes analysed by transgenic approaches (see Fig. 31). After finishing the analysis of glucose-6-phosphate/phosphate translocator (GPT) antisense *Vicia narbonensis* plants (Rolletschek et

al. 2007) recent work focuses on investigating several sense and antisense oxoglutarate-malate translocator (OMT) and new phosphoenolpyruvate translocator pea lines (E. Riebeseel). Phenotypical analysis of transgenic pea seeds expressing either VfPTR1 (a peptide transporter) or VfAAP1 (an amino acid permease) under the phloem-specific SUC2-promoter from *Arabidopsis* has been performed for several homozygous lines. Seeds contain slightly higher nitrogen but effects are variable and dependent on environment. Similar results were seen in plants expressing two AAP1-genes under the control of either the Suc2- or the LeB4-promoter. Further analysis of the 2006 field trial (see Annual Report 2006) with AAP1 pea plants revealed an increased seed nitrogen content (8 %), which was mainly due to an increase in globulins (15 %) whereas albumins were 8 % lower. Sucrose, starch and lipids were decreased by approximately 5 to 10 % (C. Seiler, K. Weigelt, H. Weber, W. Weschke).

SnRK1-antisense pea seeds (Radchuk et al. 2006) have been further described and characterised. Growing embryos are deficient of ABA. Metabolic profiling data from SnRK1-repressed embryos (in collaboration with H. Vigeolas and P. Geigenberger/MPI-MP Golm) revealed lower levels of most of the metabolites, especially organic and amino acids indicating that metabolisation of sugars and conversion into amino acid synthesis is affected. The results corroborate that the kinase is a global regulator of seed maturation and interacts with ABA functions and sugar signalling (R. Radchuk).

In an attempt to influence the ABA content directly by expressing ABA-antibodies in pea seeds an improved USP-promoter (in contrast to earlier experiments with a LeB4 promoter) was used resulting in a clear phenotype (20 - 30 % increase in seed weight, decreased sucrose and starch content, higher globulin and albumin content). Surprisingly, ABA content in mature seeds dramatically increased by more than 70-fold. Possibly, the strong expression of anti-ABA antibodies at early maturation resulted in a depletion of free functional ABA and subsequently to a regulatory overshoot, i. e. a dramatic overproduction of ABA. However, more experiments are required (R. Radchuk, H. Weber).

Analysis of C/N partitioning of *V. narbonensis* plants overexpressing *Corynebacterium* PEPC (Radchuk et al. 2007) reveals higher uptake of carbon and nitrogen. Transcriptional profiling of embryos demonstrates a general up-regulation of seed metabolism, especially during the transition and late maturation phase, in terms of protein storage and processing, amino acid metabolism, primary metabolism and transport as well as mitochondrial activity. Apparently, activated organic and amino acid production leads to a wide-range activation of nitrogen metabolism. Activated stress tolerance genes indicate partial overlap between nutrient, stress and ABA signals and a common mechanism regulating nutrient, stress and ABA responses (R. Radchuk, H. Weber).

Pea seeds with repressed ADP-glucose-pyrophosphorylase (RNAi-plants) show reduced starch, stimulated protein storage, more soluble sugars and a wrinkled seed phenotype. Transcriptional profiling revealed a multitude of changes many of them can be explained by increased sugar levels and resulting osmotic stress (K. Weigelt, H. Weber).

(6) The role of oxygen and nitric oxide (NO) during seed development. Studies of localisation and functional characterisation of seed photosynthesis were continued. It was found that both light and photosynthetically-released oxygen affect caryopsis assimilate uptake and partitioning towards high energy-demanding storage compounds. Correspondingly, gene expression patterns changed. Photosynthetic oxygen supply was also found to affect sucrose but not glucose uptake into the non-green embryo. Interestingly, embryo-specific invertases were clearly up-regulated on both transcriptional and protein level. The investigation of important industrial oil producer seeds was continued in collaboration with partners from Bayer Crop Science (H. Rolletschek, L. Borisjuk). Collaborative studies on the role of oxygen distribution on fatty acid desaturation (Rolletschek et al. 2007) as well as on seed-specific transcription factors (Bäumlein et al. submitted) were finished.

Studies on the regulatory role of nitric oxide (NO) during seed development using isolated embryos of soybean and pea revealed that regular oxygen deficiency (hypoxia) triggers a nitrite-dependent increase in NO levels. NO, in turn, reduces the oxygen consumption of seeds, generating a localised decrease in both ATP availability and biosynthetic activity. Increasing oxygen availability in turn reduces endogenous NO levels, thereby abolishing mitochondrial and metabolic inhibition. Such auto-regulatory and reversible oxygen balancing avoids seed anoxia and suggests a key role for NO in regulating storage activity (Borisjuk et al. 2007; Borisjuk and Rolletschek submitted). Furthermore, NO effects on mitochondrial complexes were studied (Macherel et al., submitted). To manipulate NO metabolism, we used a transgenic approach with lines of *Arabidopsis* and pea overexpressing non-symbiotic hemoglobins. The generated lines are under study (H. Rolletschek, J. Thiel, L. Borisjuk).

(7) Topographical approaches to better understand seed development. A new lipid mapping tool (Neuberger et al. 2007) was coupled with macroarray expression analysis, biochemical measurements and electron microscopy to demonstrate tissue-specificity of oil storage *in vivo*. Development of a NMR-based method allowing *in vivo* quantitative visualisation of sucrose and amino acid is in progress (L. Borisjuk).

(8) Continued preservation and optimisation of cell cultures of different plant species was as in the past necessary to carry out transient gene expression/promoter analysis studies in collaboration with several IPK research groups (A. Tewes). Further improvement of the regeneration capacity of *Arabidopsis* tissue cultures was achieved and suspension cultures from mutant plants established. A culture system for 12 DAF barley caryopsis is under development (A. Tewes).

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner, Dr. N. Stein;
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert, Dr. I. Lermontova;
Dept. of Cytogenetics and Genome Analysis, Research Goup Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder, Dr. C. Pietsch;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert, Dr. R. Pielot, F. Bollenbeck, T. Czauderna;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, Dr. M. Lange;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber, C. Klukas, Dr. B. Junker;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology; Research Group Applied Biochemistry; Dr. H.-P. Mock, Dr. A. Matros, K. Witzel;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. I. Saalbach.

Outside the Institute:
Bavarian Julius Maximilians University Würzburg, Institute of Physics, Würzburg; Dr. P.M. Jakob, G. Melkus;
Konrad Zuse Centre, Berlin; Dr. V.J. Dercksen, Prof. H.-C. Hege;
Nordsaat Saatzucht GmbH, Böhnshausen; Dr. R. Schachschneider, Dr. L. Kuntze;
Lochow-Petkus GmbH, Bergen-Wohlde; Dr. V. Korzun;
University of Cologne, Institute of Botany, Cologne; Dr. R. Häusler, Dr. K. Fischer;
Humboldt University Berlin; Institute of Crop Science, Dept. of Crop Production in Tropical and Subtropical Areas, Berlin; Dr. K.-P. Götz;
Georg-August University Göttingen, Albrecht von Haller Institute for Plant Sciences, Plant Biochemistry, Göttingen; Prof. I. Feussner;
Molecular Machines and Industries GmbH, Eching; Dr. S. Niehren;
Max Planck Institute for Molecular Plant Physiology, Dept. of Metabolic Networks, Golm; Dr. P. Geigenberger, Dr. B. Usadel, Dr. Y. Gibon;
Fraunhofer Institute for Biomedical Techniques (IBMT), St. Ingbert/Saar; Dr. F. Volke;
Fraunhofer-Institut für Fabrikbetrieb und -automatisierung, Magdeburg; Dr. R. Mecke;
INRA, Dijon, France; Dr. R. Thompson, Dr. J. Burstin;
University of Vienna, Institute of Ecology and Protection of Nature, Vienna, Austria; Prof. A. Richter, Dr. T. Peterbauer;
Université d`Angers, France; Prof. D. Macherel;
Trent University, Plant Biology, Trent, Canada; Prof. R.J.N. Emery;
Pennsylvania State University, Dept. Bioengineering; Dr. T. Neuberger, A.G. Webb;
CICS, Sevilla, Spain; J.M. Martinez Rivas, M. Mancha;
University of Bern, Institute of Plant Science, Bern, Switzerland; Prof. D. Rentsch;
Bayer Crop Science, Ghent, Belgium.

Publications

Peer Reviewed Papers

Borisjuk, L., D. Macherel, A. Benamar, U. Wobus & H. Rolletschek: Low oxygen sensing and balancing in plant seeds: a role for nitric oxide. New Phytol. 176 (2007) 813-823.

Götz, K.P., N. Staroske, R. Radchuk, R.J. Emery, K.D. Wutzke, H. Herzog & H. Weber: Uptake and allocation of carbon and nitrogen in *Vicia narbonensis* plants with increased seed sink strength achieved by seed-specific expression of an amino acid permease. J. Exp. Bot. 58 (2007) 3183-3195.

Gubatz, S., V.J. Dercksen, C. Brüss, W. Weschke & U. Wobus: Analysis of barley (*Hordeum vulgare*) grain development using three-dimensional digital models. Plant J. 52 (2007) 779-790.

Radchuk, R., V. Radchuk, K.P. Götz, H. Weichert, A. Richter, R.J. Emery, W. Weschke & H. Weber: Ectopic expression of phosphoenolpyruvate carboxylase in *Vicia narbonensis* seeds: effects of improved nutrient status on seed maturation and transcriptional regulatory networks. Plant J. 51 (2007) 819-839.

Radchuk, V., N. Sreenivasulu, Y. Blume & W. Weschke: Distinct tubulin genes are differentially expressed during barley grain development. Physiol. Plant. 131 (2007) 571-580.

Rolletschek, H., L. Borisjuk, A. Sanchez-Garcia, C. Gotor, L.C. Romero, J.M. Martinez-Rivas & M. Mancha: Temperature-dependent endogenous oxygen concentration regulates microsomal oleate desaturase in developing sunflower seeds. J. Exp. Bot. 58 (2007) 3171-3181.

Rolletschek, H., T.H. Nguyen, R.E. Häusler, T. Rutten, C. Göbel, I. Feussner, R. Radchuk, A. Tewes, B. Claus, C. Klukas, U. Linemann, H. Weber, U. Wobus & L. Borisjuk: Antisense inhibition of the plastidial glucose-6-phos-

phate/phosphate translocator in *Vicia* seeds shifts cellular differentiation and promotes protein storage. Plant J. 51 (2007) 468-484.

Sreenivasulu, N., S.K. Sopory & P.B. Kavi Kishor: Deciphering the regulatory mechanisms of abiotic stress tolerance in plants by genomic approaches. Gene 388 (2007) 1-13.

Stark, M., B. Manz, A. Ehlers, M. Küppers, I. Riemann, F. Volke, U. Siebert, W. Weschke & K. König: Multiparametric high-resolution imaging of barley embryos by multiphoton microscopy and magnetic resonance micro-imaging. Microsc. Res. Techniq. 70 (2007) 426-432.

Strickert, M., N. Sreenivasulu, B. Usadel & U. Seiffert: Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. BMC Bioinformatics 8 (2007) 165.

Other Publications

Stark, M., B. Manz, I. Riemann, F. Volke, W. Weschke & K. König: Multiphoton and magnetic resonance imaging of barley embryos: comparing micro-imaging techniques across scale and parameter barriers. Multiphoton Microscopy in the Biomedical Sciences VII, P.T.C.SO, Proc. of SPIE. Vol. 6442 (2007) 644227.

Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: „Genetical Genomics" der Gerstenkornentwicklung – von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomXPress 1 (2007) 12-16.

Wobus, U., H.-P. Mock, C. Pietsch, V. Radchuk, M. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, W. Weschke & K. Witzel: GABI-SEED: Genetische Grundlagen komplexer agronomischer Merkmale im Getreidekorn entschlüsseln. GenomXPress Sonderausgabe März (2007) 19.

Lectures, Posters and Abstracts

V8, V15, V31, V32, V33, V34, V145, V176, V177, V178, V182, V270, V271, V275, V276, V277, V280, V281, V299, P18, P77, P98, P125, P141, P158, P161, P162, P165, P172, P173, P176, P180, P200, P205, P206, P210, P211, P212, P213, P224, P225, P226, P231.

Additional Funding

For further information see the survey page 212–213.

Research Group: Gene Regulation

Head: Dr. Helmut Bäumlein

Scientists

IPK financed
Koszegi, Dávid (0,5 Annex, 01.07.-14.09.2007)
Michael, Maria (0,5 Pakt für Forschung und Innovation, since 01.04.2007)
Mohr, Michaela (0,75 Annex, since 01.11.2007)
Schallau, Anna (0,5 Pakt für Forschung und Innovation)
Vorwieger, Astrid (0,5 Annex, since 01.09.2007)
Winter, Hendrik, Dr. (P)

Grant Positions
Koszegi, Dávid (0,5 BMBF, since 19.09.2007)
Vorwieger, Astrid (0,5 BMBF, till 21.05.2007)

Visiting Scientists
Le Hong, Diep (DAAD and Ministry of Education & Training Vietnam)

Goals

Analysis of gene expression during plant embryogenesis.

Research Report

The group deals with the characterisation of gene regulation during various forms of plant **embryogenesis** including zygotic, apomictic, somatic and androgenetic processes. Previous genetic studies in *Poa pratensis* suggest at least five loci as essential for the control of apomixis, challenging efforts to identify the corresponding genes at the molecular level. An **apospory** linked CAPS marker has been further characterised in *Hypericum* (A. Schallau, D. Koszegi). Several marker-containing BAC clones have been isolated and characterised. The sequencing of a selected BAC clone is close to be completed (collaboration with research group Expression Mapping). Ongoing histological studies aim to characterise the aposporous embryo sac formation in *Hypericum* (collaboration with research group Apomixis). Sexual and **parthenogenetic wheat egg** cells have been used to study molecular processes important for egg cell activation and parthenogenesis (A. Czihal). Complex subtractive approaches have identified candidate genes with egg cell-specific expression (collaboration with research group Expression Mapping and research group Plant Reproductive Biology). Work has been focussed on a novel class of **transcription factors** (TF), the RKD family (D. Koszegi). The strictly plant-specific RKD TF family of wheat consists of at least four different genes, with two of them being expressed. The genome of *Arabidopsis* contains at least five *RKD* genes. Consistent with a function as TFs, RKD gene products have been localised within the cell nucleus. Single cell RT-PCR, *in situ* hybridisations and the expression of promoter::GUS reporter gene fusions suggest RKD gene expression in the egg apparatus of the **female gametophyte** (collaboration with U. Großniklaus, A. Johnston) (see Fig. 32). This is further supported by whole mount *in situ* hybridisation (H. Winter). Promoter comparisons detect a common nonameric *cis*-motif shared by several egg cell expressed genes. Ectopic expression of *AtRKD1*, *AtRKD2* as well as *AtRKD1::GFP* and *AtRKD2::GFP* fusion constructs cause severe growth distortions and callus-like cell proliferation. RT-PCR reveals the expression of several gametophytic marker genes in this proliferating tissue, indicating that AtRKD1 and AtRKD2 trigger a gametophytic developmental pathway. Together, the data suggest a crucial role of RKD proteins for the development of the female gametophyte (D. Koszegi). Single and double mutants with T-DNA insertions in the genes *AtRKD1* and *AtRKD2* have been extensively analysed. However, the data reveal no linkage between the T-DNA insertion and the previously observed arrest at the functional megaspore stage (D. Koszegi, H. Bäumlein). Transgenic barley and wheat lines carrying RNAi constructs directed against *TaRKD* are currently under investigation (D. Koszegi, in collaboration with research group Plant Reproductive Biology). Ongoing work regarding the molecular characterisation of RKD factors aim at the identification of *cis*-motifs after expression in *E. coli*, the search for interacting proteins in yeast two hybrid systems and the hormone-regulated expression in transgenic plants (M. Michael, D. Koszegi).

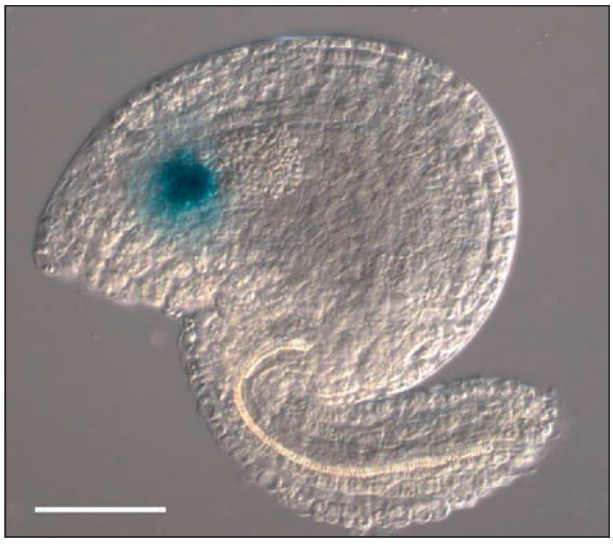

Fig. 32: Egg apparatus-specific activity of the AtRKD2 gene promoter of *Arabidopsis*. (bar=50 µm) (D. Koszegi).

A second research focus concerns the regulation of gene expression during **late embryogenesis** (A. Vorwieger, A. Czihal, Nguyen Thi TyetMinh). Participating in the Trilateral ArabidoSeed project (in collaboration with research group Phytoantibodies, research group Expression Mapping, research group Plant Data Warehouse) two experimental approaches for TF **gene regulation** have been applied: a) TF fusion to the glucocorticoid receptor (GR) domain and b) the estradiol-regulated XVE-system. Permanent induction of a *35::LEC1::GR* construct during germination leads to impaired growth of transgenic seedlings, ectopic embryo formation between root and hypocotyl and embryo-like structures on root tips similar to the *pkl* mutant. To isolate **downstream genes** involved in LEC1-dependent early embryogenesis induction, an array analysis has been performed based on inducible *35S::LEC1::GR* lines (in collaboration with J.P. Renou, INRA Evry). Candidate genes have been identified but the process of data validation is still ongoing. In addition first ChIP-on-chip experiments using a LEC1-specific antibody have been performed. Putative target gene candidates will be confirmed using transient assays. Two novel vectors have been constructed combining the possibility for GR-regulated expression of various transcription factor genes and their immunoprecipitation using antibodies directed against the HA or MYC-tag (Nguyen Thi TyetMinh, A. Vorwieger, H. Bäumlein). The molecular analysis of **ET factors** containing an UVRC-like domain putatively involved in gene regulation has been continued and includes the expression in *E. coli* and the hormone-regulated expression in transgenic plants as a prerequisite for the identification of target genes (D. Le Hong, A. Vorwieger). Work on the neomorphic nature of *fus3* splice site mutants has been finished.

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große, M. Mohr;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Expression Mapping; Dr. L. Altschmied, Dr. U. Hähnel;
Dept. of Molecular Genetics, Research Group Gene Expression; Prof. U. Wobus, Dr. A. Tewes;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, Dr. G. Mönke;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, Dr. A. Matros;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer, Dr. T. Rutten;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. I. Saalbach.

Outside the Institute:
Technical University, Brunswick; R. Hänsch;
Technical University, Brunswick; Prof. L. Beerhues;
University of Göttingen, Göttingen; Dr. W. Dröge-Laser;
University of Göteborg, Göteborg, Sweden; Dr. M. Ellerström;
University of Zurich, Zurich, Switzerland; Prof. U. Großniklaus, Dr. A. Johnston;
INRA, Versailles, France; Prof. M. Caboche, Dr. L. Lepiniec, Dr. B. Debreucq;
INRA, Evry, France; J.P. Renou.

Publications

Peer Reviewed Papers

Kotak, S., E. Vierling, H. Bäumlein & P. von Koskull-Döring: A novel transcriptional cascade regulating expression of heat stress proteins during seed development of *Arabidopsis*. Plant Cell 19 (2007) 182-195.

Perovic, D., P. Tiffin, D. Douchkov, H. Bäumlein & A. Graner: An integrated approach for the comparative analysis of a multigene family: The nicotianamine synthase genes of barley. Funct. Integr. Genomics 7 (2007) 169-179.

Vorwieger, A., C. Gryczka, A. Czihal, D. Douchkov, J. Tiedemann, H.-P. Mock, M. Jakoby, B. Weisshaar, I. Saalbach & H. Bäumlein: Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. Planta 226 (2007) 147-158.

Wang, H.Y., M. Klatte, M. Jakoby, H. Bäumlein, B. Weisshaar & P. Bauer: Iron deficiency-mediated stress regulation of four subgroup Ib BHLH genes in *Arabidopsis thaliana*. Planta 226 (2007) 897-908.

Book Chapters

Barcaccia, G., H. Bäumlein & T.F. Sharbel: Apomixis in St. John's wort (*Hypericum perforatum* L.): an overview and glimpse towards the future. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 259-280.

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Other Publications

Mönke, G., T.M. Linh, U. Conrad, U. Hähnel, L. Altschmied, M. Mohr, I. Grosse, A. Vorwieger, H. Bäumlein,

B. Weisshaar & P. Viehöver: GABI-ARABIDO-SEED: Wie steuern Transkriptionsfaktoren die Samenentwicklung bei Pflanzen? GenomXPress Sonderausgabe März (2007) 16.

Lectures, Posters and Abstracts

V22, V23, V24, V123, V285, P28, P29, P77, P84, P86, P125, P126, P153, P154, P155, P156, P157, P158, P159, P170, P171, P181, P183, P184, P197, P199, P220, P221, P235.

Additional Funding

For further information see the survey page 214.

Research Group: Phytoantibodies

Head: Dr. Udo Conrad

Scientists

IPK financed
Gahrtz, Manfred Dr. (0,5 Annex, till 31.05.2007)
Mönke, Gudrun, Dr. (P)
Nguyen, Lai Thanh (0,5 Annex, 15.01.-31.01.2007)
Rakhimova, Marziya (0,5 Annex, 01.05.-31.07.2007)
Tran My, Linh (0,5 Annex, since 16.02.2007)

Grant Positions
Floß, Doreen (0,5 EU)
Schallau, Kai (0,5 Saxony-Anhalt, since 01.08.2007)

Visiting Scientists
Hermann, Isabella (Martin Luther University Halle-Wittenberg)
Hoang, Phan Trong (DLR, 01.11.-31.12.2007)
Morandini, Francesca (Pharma-Planta, 02.05.-30.05.2007)
Nguyen, Lai Than (self-financed, 01.01.-14.01.2007)
Rakhimowa, Marziya (DAAD scholarship, till 30.04.2007; PhD scholarship, 01.08.-30.10.2007)

Goals

Tissue- and development-specific immunmodulation of phytohormone functions and of viral proteins in transgenic plants, development of the chromatin IP method with recombinant and classical antibodies for the molecular analysis of seed development as well as production of recombinant fiber proteins and recombinant therapeutic antibodies and vaccines in transgenic plants.

Research Report

Molecular Farming experiments were further performed with **recombinant spider silk proteins** to develop new materials for technical and medical purposes in plants. Transgenic plants expressing the spider silk protein FLAG with N-terminal spider silk fragment sequences and C-terminal constant sequences with and without cmyc-tag have been produced. Multimers of the FLAG protein dependent on the C-terminal constant sequences have been detected (M. Rakhimova, U. Conrad). Spider silk proteins containing the dimerisation tags have been produced in transgenic tobacco leaves and **dimerisation** experiments using **transglutaminase** have been successfully performed (K. Schallau).

In the frame of the **Pharma-Planta Project** production of two **neutralising anti HIV antibodies** (2G12 and 2F5) as ELP fusions in transgenic plants is studied. Complete anti HIV antibodies 2G12 and 2F5 as well as corresponding ELP fusion proteins have been produced in tobacco leaves and purified *via* protein A affinity chromatography (see Fig. 33). N-glycosylation patterns have been investigated. Mainly oligo-mannose type N-glycans were detected (D. Floß, J. Stadlmann, BOKU Vienna). The antigene binding parameters were studied by surface Plasmon resonance. The **affinity constants of the plant-produced antibodies** were **identical** both with and without ELP fusions compared to the **constants** of the **CHO-cell derived standard** (D. Floß, M. Sack, RWTH Aachen). Affinity purified **2G12 variants from plants** could **neutralise HIV** tested by a syncytium inhibition assay **comparable** to the **CHO cell-derived standard** or even **better** (D. Floß, G. Stiegler, Polymun Scientific, Vienna). Homozygous transgenic **double haploid tobacco plants** (USP promoter, CaMV35S promoter) have been produced using the double haploid technique. The expression level was increased regarding the gene dosage effect. The homozygosity was proven by offspring analysis (D. Floß, I. Saalbach, J. Kumlehn). Further work is dealing with the use of ELP to overexpress and to partly purify antigens for vaccina-

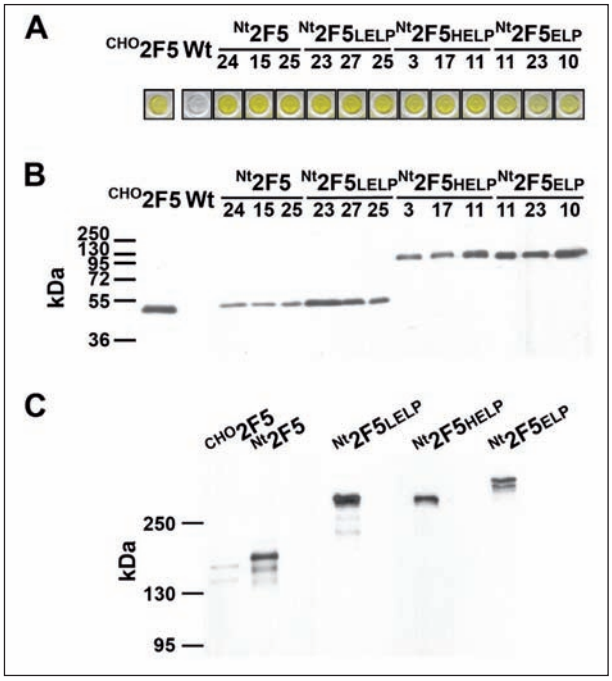

Fig. 33: Expression and assembly of anti HIV antibody 2F5 ELP fusion proteins in plants. **A**: Assembly of light and heavy chain variants detected in leaf extracts of different T_2 tobacco plants by protein L/protein A sandwich ELISA. **B**: Western blot analysis of different individual T_2 plants: 10 µg protein per lane was separated on a reducing 12 % SDS polyacrylamide gel, blotted and analysed with anti-human Fc specific IgG conjugated to HRP followed by ECL detection. ^{CHO}2F5: 34 ng per lane. Expression enhancement by ELP is shown. **C**: Western blot analysis of affinity-purified 2F5 derivatives from plants. Proteins were separated on a non-reducing 6 % SDS polyacrylamide gel, blotted and detected with anti-human Fc specific IgG conjugated to HRP followed by ECL detection. ^{CHO}2F5: 2 ng per lane; Wt: *N. tabacum* cv. SNN. The molecular weight of the assembled antibody-ELP is as expected (D. Floß).

tion from transgenic plants. **TB fusion antigens with ELP** have been produced in transgenic tobacco plants and partially purified. **Immune response** has been studied in mice and piglets. A humoral immune response against native antigens was achieved (D. Floß, L. Dedieu, CIRAD Montpellier, H. Salmon, INRA Nouzilly). **Antigens** from the **bird flue virus H5N1** with and without ELP have been stably expressed in tobacco leaves and seeds (Phan Trong Hoang, U. Conrad).

In *Arabidopsis thaliana* **seed-specific transcription factors** have key regulatory functions during the development of mature seeds. Chromatin from developing *Arabidopsis* seeds has been prepared and precipitation experiments have been performed with specific antibodies against the transcription factor ABI3. From a series of **chromatin immunoprecipitation experiments** including macroarray analysis **(ChIP/chip) 50** candidate **target promoters of ABI3** have been selected (G. Mönke, U. Hähnel, Expression Mapping group). Several of these promoters have been proven to be targets of ABI3 by transient GUS activation assays. Interesting **new targets** of ABI3 have been found by these experiments (G. Mönke, in collaboration with A. Tewes, Gene Expression group).

The functions of the **transcription factors AtMYB44** and **AtMYB77** have been studied by gain-of-function-experiments (a fragment of AtMYB77 in the cytosol) and by loss-of-function-experiments (KO-MYB44, KO-MYB77) using microarray. The 77-CY plants exhibited a strong stunted phenotype depending on the expression level. The up- or down-regulated genes belong to nearly all categories of plant life including development and stress response. Only a few genes were found to be up-regulated in a gain-of-function-plant (77-RY) and down-regulated in KO-plants (the *AtMYB77* transcript itself and two others). On the other hand, 23 genes are down-regulated in 77-CY and up-regulated either in 77-KO or 44-KO. This suggests that the **77fragC protein** may function in 77-CY plants as **a repressor** and down-regulates the expression of target genes. ChIP-on-chip experiments with the AtMYB44 transcription factor were done with wild-type plants and KO-MYB44 as negative controls. In one first trial with a cut-off of 1.5-fold enrichment, 20 promoters were selected as new putative candidate target of AtMYB44. Three of them belong to genes that were also up-regulated in 77-CY plants. Their promoters contain MYB-binding motifs and light responsive motifs. These results will be proven by GUS activation experiments in the future (Tran My Linh, G. Mönke, J.-P. Renou, UMR INRA Evry).

To enhance the stability of **anti BYDV scFv** in the plant cytosol, until six mutations have been introduced, detailed expression studies in *Nicotiana benthamiana* have been performed. **Stable improved cytosolic expression** have been shown in several lines expressing 5x and 6x mutated scFv as a thioredoxin fusion (M. Gahrtz in collaboration with I. Saalbach, Plant Reproductive Biology group).

Collaboration

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Expression Mapping; Dr. L. Altschmied, Dr. U. Hähnel;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke, Dr. A. Tewes;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. I. Saalbach.

Outside the Institute:

Federal Centre for Breeding Research on Cultivated Plants (BAZ), Aschersleben; Dr. J. Schubert;
IWM, Halle/S.; Dr. U. Spohn;
Martin Luther University Halle-Wittenberg, Institute of Pharmaceutical Biology, Halle/S.; Prof. W. Roos;
TITK, Rudolstadt; Dr. K. Heinemann;
Centre of Green Gene Technology, Neustadt a. d. Weinstraße; Dr. K. Bonrood, Dr. G. Krezal;
RWTH, Aachen; Dr. E. Stöger, M. Sack;
Fraunhofer IME, Aachen; Dr. S. Schillberg;
BOKU, Vienna, Austria; F. Altmann;
Polymun Scientific, Vienna, Austria; G. Stiegler;
CIRAD, Montpellier, France; Dr. L. Dedieu;
IBT, Hanoi, Vietnam; Prof. Le Tran Binh;
UMR INRA, Evry, France; J.-P. Renou;
INRA, Nouzilly; H. Salmon, J. Stadelmann.

Publications

Peer Reviewed Papers

Floss, D.M., D. Falkenburg & U. Conrad: Production of vaccines and therapeutic antibodies for veterinary applications in transgenic plants: an overview. Transgenic Res. 16 (2007) 315-332.

Ten Hoopen, P., A. Hunger, A. Muller, B. Hause, R. Kramell, C. Wasternack, S. Rosahl & U. Conrad: Immunomodulation of jasmonate to manipulate the wound response. J. Exp. Bot. 58 (2007) 2525-2535.

Other Publications

Mönke, G., T.M. Linh, U. Conrad, U. Hähnel, L. Altschmied, M. Mohr, I. Grosse, A. Vorwieger, H. Bäumlein, B. Weisshaar & P. Viehöver: GABI-ARABIDO-SEED: Wie steuern Transkriptionsfaktoren die Samenentwicklung bei Pflanzen? GenomXPress Sonderausgabe März (2007) 16.

PhD and Diploma Theses

Rakhimova, M.: Expression of spider silk and spider silk-like proteins in potato and tobacco. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2007) 93 pp.

Lectures, Posters and Abstracts

V43, V44, V45, V51, V52, V53, V160, V161, V266, P22, P45, P46, P47, P48, P59, P77, P87, P106, P107, P108, P153, P154, P155, P156, P157, P158, P159, P185, P186, P187, P197, P199.

Additional Funding

For further information see the survey page 214.

Research Group: Plant Bioinformatics

Head: Prof. Falk Schreiber

Scientists

IPK financed
Grafahrend-Belau, Eva (Annex, till 14.02.2007, since 01.11.2007)
Junker, Björn H., Dr. (BMBF, since 01.08.2007)
Klukas, Christian (Annex, since 01.11.2007)
Koschützki, Dirk (P, since 01.11.2007)
Schwöbbermeyer, Henning (BMBF, till 31.10.2007)

Grant Positions
Grafahrend-Belau, Eva (BMBF, 15.02.-31.10.2007)
Klukas, Christian (BMBF, till 08.06.2007; 08.08.-31.10.2007)
Koschützki, Dirk (BMBF, till 31.10.2007)
Schreiber, Falk, Prof. (BMBF, till 30.04.2007)

Visiting Scientists
Hamdi, Ines (BIC-GH, 12.03.-01.04.2007)

Goals

Modelling, analysis, simulation and visualisation of biochemical networks and related experimental data in the context of plant biological problems.

Research Report

In 2007 we continued the development of new and improved **methods for the analysis of experimental data in context of biological networks and classification hierarchies**. These advanced methods have been implemented in the freely available software system VANTED (visualisation and analysis of networks containing experimental data) (C. Klukas). The data integration methods, which allow the assignment of experimental data to different kinds of biochemical networks, have been extended to support different user-provided or database-derived identifier sets. Newly developed algorithms allow the flexible navigation within complex classification hierarchies such as GeneOntology and KEGG BRITE. Direct navigation between different pathway visualisations has been made possible. The analysis and visualisation of experimental data in the context of the underlying networks helps in understanding biological processes in plants. The methods have been developed in close collaboration with experimental groups and are used in collaborative projects (e. g. research groups Gene

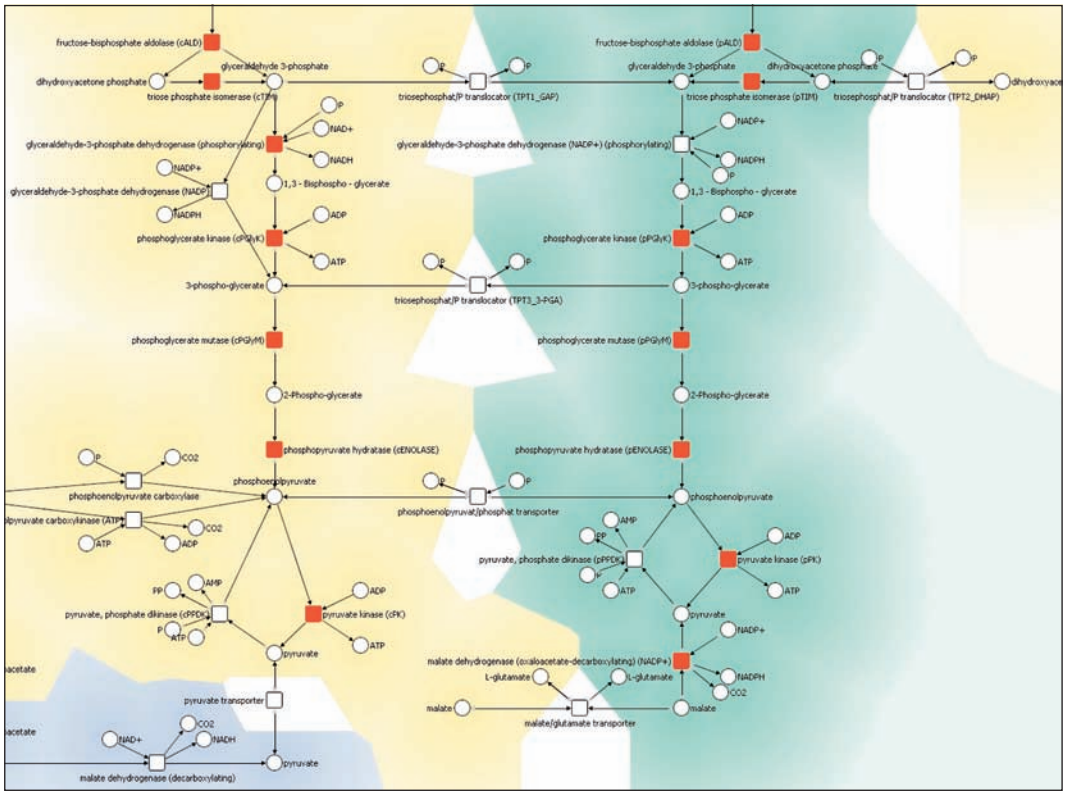

Fig. 34: Part of the glycolysis represented in the MetaCrop database. Additional experimental data (enzymes identified by proteomics analysis of plant parts shown in red, data from collaboration with the research group Applied Biochemistry) has been mapped onto the pathway. Data integration and visualisation has been done with the VANTED system (E. Grafahrend-Belau, C. Klukas).

Expression (H. Rolletschek, N. Sreenivasulu, W. Weschke) and Applied Biochemistry (H.-P. Mock, K. Witzel) as well as by many scientists outside the IPK.

Based on the previously developed information system Meta-All and in collaboration with the Bioinformatics and Information Technology group (U. Scholz, S. Weise), the **crop-specific metabolic pathway database** MetaCrop was created (E. Grafahrend-Belau, B.H. Junker). MetaCrop contains diverse hand-curated information about metabolic pathways of currently six crop plants (barley, wheat, rice, maize, potato, and canola) with special emphasis on the metabolism of agronomic important organs such as seed and tuber. It represents metabolic processes in an unprecedented resolution, containing information about pathway structure, reaction kinetics, localisation, transport, environmental circumstances and taxonomic relations at different levels of detail (see Fig. 34, p. 111). Furthermore, MetaCrop supports the direct export of prototypic metabolic models in the standard exchange format SBML by which these can be analysed and simulated with different tools.

Within the project GABI-SysSEED, which started in July 2007 with several partners inside and outside of the IPK (L. Borisjuk, J. Kumlehn, H.-P. Mock, V. Radchuk, U. Seiffert, N. Sreenivasulu, H. Weber, W. Weschke, P. Geigenberger (Max Planck Institute for Molecular Plant Biology Golm) K.-P. Götz (Humboldt University Berlin), P. Chandler (CSIRO Canberra) **structural and kinetic models of barley seed metabolism** will be developed in our research group. A first milestone will be reached soon by the completion of a stoichiometric, compartmented model containing more than 250 reactions of the central metabolism of *Hordeum vulgare* (E. Grafahrend-Belau, B.H. Junker). The model will be used to explore the general metabolic capabilities of barley seeds and to predict the effect of gene deletion and repression.

For the **structural analysis of molecular biological networks** we continued our efforts from previous years. Especially methods for ranking network elements (centrality analysis) were in the focus of our research and we developed methods specifically tuned towards the analysis of gene regulatory networks and metabolic pathways. For the first type of networks the development of a novel method called motif-based centrality was continued. This method allows the ranking of network elements based on underlying functional structures and yields interesting results about global regulators in gene regulatory networks (D. Koschützki, H. Schwöbbermeyer). For the second type of networks (metabolic pathways), we developed an analysis approach, which combines flux balance analysis with the concept of centralities and provides a new way to define important metabolites, the metabolic core as well as provides a clustering of metabolites into pathways (B.H. Junker, D. Koschützki).

Finding information about biological networks in the world wide web is, even by using powerful search engines, still a tedious task. To ease the **discovery of data structured as networks** we developed a community-based information system, the system BiNCo-Wiki, which allows to share information about biological networks, stores information about tools that can be used to analyse those networks and provides a portal to the community interested in the analysis of biological networks (D. Koschützki, M. Telgkamp).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Plant Data Warehouse; Prof. I. Große;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, Dr. M. Lange, S. Weise;
Dept. of Molecular Genetics, Research Group Gene Expression; Prof. U. Wobus, Dr. L. Borisjuk, Dr. H. Weber, Dr. V. Radchuk, Dr. H. Rolletschek, Dr. N. Sreenivasulu, Dr. W. Weschke;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, K. Witzel;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

University of Bielefeld, Research Group Bioinformatics/ Medical Informatics, Bielefeld; Prof. R. Hofestädt;
University of Passau, Faculty of Mathematics and Informatics, Passau; Prof. F.J. Brandenburg, Dr. C. Bachmaier;
Friedrich Alexander University Erlangen-Nuremberg, Institute of Biology, Erlangen; Prof. U. Sonnewald;
Brandenburg University of Technology, Institute for Informatics, Cottbus; Prof. W. Kurth, Prof. M. Heiner;
Humboldt University, Faculty of Agriculture and Horticulture, Berlin; Dr. K.P. Götz;
Humboldt University, Institute for Theoretical Biology, Berlin; Dr. R. Steuer;
University of Applied Sciences, Berlin; Prof. I. Koch;
Free University of Berlin, Berlin; Dr. B. Gemeinholzer;
Uniklinikum Göttingen; Dr. A. Potapov;
Max Planck Institute for Molecular Plant Physiology (MPI), Dept. of Metabolic Networks, Golm; Dr. P. Geigenberger, Dr. B. Usadel;

Martin Luther University Halle-Wittenberg, Institute of Bioinformatics, Halle/S.; Prof. S. Posch;
Leibniz Institute of Plant Biochemistry, Halle/S.; Dr. S. Neumann;
Monash University, Melbourne, Australia; Prof. K. Marriot, Dr. T. Dwyer;
NICTA, Sydney, Australia; Prof. P. Eades, Dr. S. Hong, Dr. K. Xu;
Teheran University, Teheran, Iran; Prof. A. Masoudi Nejad;
CSIRO Canberra, Australia; Dr. P. Chandler;
Brookhaven National Laboratory, Upton, USA; Dr. J. Schwender.

Publications

Peer Reviewed Papers

Junker, B.H., J. Lonien, L.E. Heady, A. Rogers & J. Schwender: Parallel determination of enzyme activities and *in vivo* fluxes in *Brassica napus* embryos grown on organic or inorganic nitrogen source. Phytochemistry 68 (2007) 2232-2242.

Klukas, C. & F. Schreiber: Dynamic exploration and editing of KEGG pathway diagrams. Bioinformatics 23 (2007) 344-350.

Koschützki, D., H. Schwöbbermeyer & F. Schreiber: Ranking of network elements based on functional substructures. J. Theor. Biol. 248 (2007) 471-479.

Rolletschek, H., T.H. Nguyen, R.E. Häusler, T. Rutten, C. Göbel, I. Feussner, R. Radchuk, A. Tewes, B. Claus, C. Klukas, U. Linemann, H. Weber, U. Wobus & L. Borisjuk: Antisense inhibition of the plastidial glucose-6-phosphate/phosphate translocator in *Vicia* seeds shifts cellular differentiation and promotes protein storage. Plant J. 51 (2007) 468-484.

Telgkamp, M., D. Koschützki, H. Schwöbbermeyer & F. Schreiber: Community-based linking of biological network resources: databases, formats and tools. J. Integr. Bioinformatics 4 (2007) 71 Online Journal: http://journal.imbio.de/index.php?paper_id=71.

Other Publications

Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: „Genetical Genomics" der Gerstenkornentwicklung – von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomXPress 1 (2007) 12-16.

Wobus, U., H.-P. Mock, C. Pietsch, V. Radchuk, M. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, W. Weschke & K. Witzel: GABI-SEED: Genetische Grundlagen komplexer agronomischer Merkmale im Getreidekorn entschlüsseln. GenomXPress Sonderausgabe März (2007) 19.

Electronic Publications

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop – A detailed database of crop plant metabolism. http://metacrop.ipk-gatersleben.de/ (2007).

Klukas, C.: VANTED – visualization and analysis of networks containing experimental data. http://vanted.ipk-gatersleben.de/ (2007).

Telgkamp, M., D. Koschützki, H. Schwöbbermeyer & F. Schreiber: BiNCo-Wiki – Community-based Linking of Biological Network Resources. http://pgrc.ipk-gatersleben.de/BiNCO-wiki (2007).

PhD and Diploma Theses

Telgkamp, M.: Generating networks from data sources. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2007) 59 pp.

Patents

Schreiber, F., D. Koschützki & H. Schwöbbermeyer: A device for and a method of evaluating a network related relevance of a network element linked to one or more further network elements in a network, a program element and a computer-readable medium. WO 2007/074172 A1, Anmeldetag: 29.12.2005, Anmelder: IPK, Offenlegung: 05.07.2007, IPK-Nr. 2005/04.

Lectures, Posters and Abstracts

V10, V89, V90, V107, V108, V109, V110, V120, V121, V122, V195, V196, V197, V198, V199, V200, V201, V202, V203, V204, V205, V206, V207, V208, P67, P68, P69, P70, P71, P72, P73, P98, P105, P119, P120, P121, P122, P124, P162, P227, P228, P231, P237, P238.

Additional Funding

For further information see the survey page 215.

Research Group: Data Inspection

(since 01.06.2007)

Head: Dr. Marc Strickert

Scientists

Grant Positions
Keilwagen, Jens (Saxony-Anhalt, since 01.10.2007)
Seifert, Michael (Saxony-Anhalt, since 01.10.2007)

Goals

Analysis of sequence data and multi-channel data from array and gel technologies using data-driven computer models.

Research Report

The junior research group Data Inspection was established in June 2007 for the continuation and enhancement of selected topics in **sequence analysis** and gene **expression analysis**, covered by the BIC-GH bioinformatics groups Plant Data Warehouse and Pattern Recognition at IPK until the discontinuation of BIC-GH on October 31, 2007. Fundamental aims are the design, development, and computer implementation of new algorithms for visual data inspection and analysis, especially **novelty detection**, for assisting in biological hypothesis generation and validation.

One focus of sequence analysis research is directed on extensions of Markov Random Fields for the integration of additional biological knowledge into models for improved **motif discovery** and identification. Ongoing research deals with a reassessment of binding sites in databases, trying to identify misannotated binding sites, shifted binding sites, and misassigned strand information. Furthermore, active distinction between motifs in treatment-specific sequences from less informative background sequences is currently under development (J. Keilwagen).

Another focus regarding the **linkage of sequence information to expression data** is realised by extensions of Hidden Markov Models. On one hand, the coupling of chromosomal distances between neighbouring genes and their transcript levels is used to improve the prediction accuracy of differential gene expression. On the other hand, ChIP/chip experiments are examined for predicting putative transcription factor target genes and their regulatory sequence motifs (M. Seifert in collaboration with ARABIDO-SEED project groups headed by L. Altschmied, H. Bäumlein, U. Conrad and I. Große).

Recently developed tools for the visualisation and analysis of gene expression data have been applied to barley transcript collections from 12k macroarrays. Particularly, the high throughput multidimensional scaling technique (HiT-MDS) allowed a **faithful visualisation** of developmental stages and an identification of starch-specific lines in *Hordeum spontaneum* (HS213) introgression experiments (in collaboration with N. Sreenivasulu, research group Gene Expression). Lines with differential starch regulation were compared on the level of individual genes by using a new method for **supervised attribute rating** (SARDUX, see Fig. 35). In contrast to traditional test statistics for the extraction of ranked gene lists only little assumptions on data distributions are needed, allowing small sample sizes, in principle, but producing dataset-specific truth rather than providing universal validity. The SARDUX method was also applied to a database containing protein expression levels from 2-D electrophoresis gels of Steptoe and Morex lines under salt stress for the isolation of candidate proteins (in collaboration with K. Witzel and H.-P. Mock, research group Applied Biochemistry).

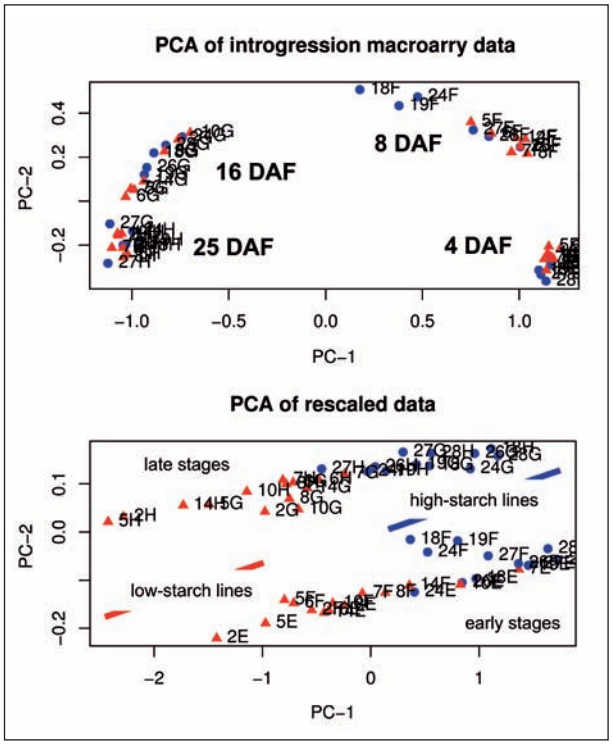

Fig. 35: PCA visualisations of barley introgression line transcript levels. Top panel: hybridisation experiments containing 4814 high-quality genes, showing a temporal clustering of the four considered developmental stages 4, 8, 16, and 25 days after flowering (DAF), and a mixture of phenotypes tentatively labelled by their high-starch (blue) and low-starch content (red). Bottom panel: same data as above, but rescaled by gene relevances using the new SARDUX method. The top five genes, responsible for the separation (HB11B03, HA07F02, HB32L20, HA13A12, and HZ57P03) are currently under investigation, hinting in combination with other genes particularly at starch-specific regulatory pathways (M. Strickert, N. Sreenivasulu).

Collaboration

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder, Dr. C. Pietsch;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert, T. Czauderna;
Dept. of Molecular Genetics, Research Group Gene Expression; Prof. U. Wobus, Dr. N. Sreenivasulu, Dr. W. Weschke, Dr. J. Thiel;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, K. Witzel.

Outside the Institute:
Martin Luther University Halle-Wittenberg, Halle/S.; Prof. I. Große, Prof. S. Posch, J. Grau;
Technical University, Clausthal; Prof. B. Hammer, A. Hasenfuß;
Bielefeld University, Centre for Biotechnology, Bielefeld; J. Baumbach, T. Kohl;
University of Leipzig; Dr. T. Villmann, Dr. F.-M. Schleif;
University of Groningen; Prof. M. Biehl, P. Schneider;
Max Planck Institute for Molecular Genetics, Berlin; Dr. A. Schliep.

Publications

Peer Reviewed Papers

Strickert, M., N. Sreenivasulu, B. Usadel & U. Seiffert: Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. BMC Bioinformatics 8 (2007) 165.

Book Chapters

Villmann, T., M. Strickert, C. Brüss, F.-M. Schleif & U. Seiffert: Visualization of fuzzy information in fuzzy-classification for image segmentation using MDS. In: Verleysen, M. (Eds.): Proc. 15th European Symposium on Artificial Neural Networks, ESANN 2007, Bruges/Belgium. D-Side Publications, Evere/Belgium (2007) 103-108.

Other Publications

Hammer, B., A. Hasenfuss, F. Rossi & M. Strickert: Topographic processing of relational data. Proceedings of the 6th International Workshop on Self-Organizing Maps (WSOM 2007), ISBN: 978-3-00-022473-7 (2007) DOI: 10.2390/biecoll-wsom2007-121.

Hammer, B., A. Hasenfuss, F.-M. Schleif, T. Villmann & M. Strickert: Intuitive clustering of biological data. Proc. of the International Joint Conference on Artificial Neural Networks (IJCNN 2007), 1877-1882 pp.

Strickert, M., F.-M. Schleif & U. Seiffert: Gradients of Pearson correlation for analysis of biomedical data. Proceedings of the Argentine Symposium on Artificial Intelligence (ASAI 2007), (2007) 139-150.

Strickert, M. & U. Seiffert: Correlation-based data representation. Online Proceedings of the Dagstuhl Seminar 07131, Similarity-based Clustering and its Application to Medicine and Biology, Dagstuhl. (2007) http://drops.dagstuhl.de/opus/volltexte/2007/1134/.

Strickert, M., K. Witzel, H.-P. Mock, F.-M. Schleif & T. Villmann: Supervised attribute relevance determination for protein identification in stress experiments. Proceedings of the International Workshop on Machine Learning in Systems Biology (MLSB 2007) (2007) 81-86.

Villmann, T., F.-M. Schleif, E. Merenyi, M. Strickert & B. Hammer: Class imaging of hyperspectral satellite remote sensing data using FLSOM. Proceedings of the 6th International Workshop on Self-Organizing Maps (WSOM 2007), ISBN: 978-3-00-022473-7 (2007) DOI: 10.2390/biecoll-wsom2007-110.

Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: „Genetical Genomics" der Gerstenkornentwicklung – von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomXPress 1 (2007) 12-16.

Wobus, U., H.-P. Mock, C. Pietsch, V. Radchuk, M. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, W. Weschke & K. Witzel: GABI-SEED: Genetische Grundlagen komplexer agronomischer Merkmale im Getreidekorn entschlüsseln. GenomXPress Sonderausgabe März (2007) 19.

Electronic Publications

Strickert, M.: High-Throughput Multidimensional Scaling (HiT-MDS-2). http://hitmds.webhop.net/ (2007).

Strickert, M.: Neural Gas Clustering with Pearson Correlation (NG-C). http://pgrc-16.ipk-gatersleben.de/~stricker/ng/ (2007).

Strickert, M. & U. Seiffert: Nonlinear gene expression analysis. http://pgrc-16.ipk-gatersleben.de/wgrp/mue/mue_projects7.php (2007).

PhD and Diploma Theses

Ante, M.: Datenanalyse von cDNA-Array-Experimenten zur Identifikation möglicher regulatorischer Zielgene des epigenetischen Seneszenz-Kontrollfaktors SUVH2 und der stressabhängigen HIPP-Kernproteine. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2007) 74 pp.

Lectures, Posters and Abstracts

V256, V257, V258, V259, V260, V261, V262, V263, P165, P205, P206, P210, P211, P212, P213, P215, P231, P239, P240.

Additional Funding

For further information see the survey page 215.

Research Group: Hybrid Wheat

(since 01.08.2007)

Head: Dr. Mario Gils

Scientists

IPK financed
Kempe, Katja (BMBF, since 01.08.2007)
Rubtsova, Myroslava, Dr. (BMBF, since 01.08.2007)

Grant Positions
Rubtsova, Myroslava, Dr. (Nordsaat, 01.05.-31.07.2007)

Goals

The goal of our group is the development of a gene technology-based method that provides a significant simplification of the hybrid seed production procedure in wheat.

Research Report

For industrial production of hybrid seed, the female partner must be male-sterile during the crossing process in order not to become self fertilised by its own pollen. For creating the female crossing line, a technology should be developed that will completely replace the (non-optimal) chemical gametocyte-sterilisation technology that is the conventional method used for wheat at present. It allows growing the female partners as male-sterile plants, whereas the hybrid progeny resulting from the pollination by a pollinator line is fully fertile. The conditional male sterility of the female line can be achieved by splitting a barnase gene that is controlled by a tapetum-specific promoter into two fragments. *In vivo* complementation of two inactive barnase fragments *via* intein-mediated *trans*-splicing should lead to a functional barnase protein produced in the tapetum and consequently to pollen ablation. By using an *in vivo* recombination system, the complementary barnase gene fragments will be located on the same locus on homologous chromosomes ("linked in repulsion", see Fig. 36). In the female crossing line both gene fragments are present, thus causing the plant to be male-sterile. As a result of the subsequent hybridisation step, each progeny inherits only one gene fragment, rendering all hybrid progenies fully fertile.

Project milestones that have been finished:

Proof of concept in a model species: The feasibility of the system was demonstrated in a study performed in *Arabidopsis thaliana* (M. Gils).
Stably expressing phiC31 integrase lines: T-DNA constructs containing a phage derived phiC31 integrase transgene were stably transformed into wheat plants using the ballistic bombardment technology (M. Rubtsova, M. Gils). A plant virus-based transient assay system (developed by Icon Genetics, Halle, Germany) was utilised to monitor the site-specific recombination activity of the integrase protein *in vivo* (M. Rubtsova, K. Kempe). Doubled haploid (DH) inbred lines were produced that

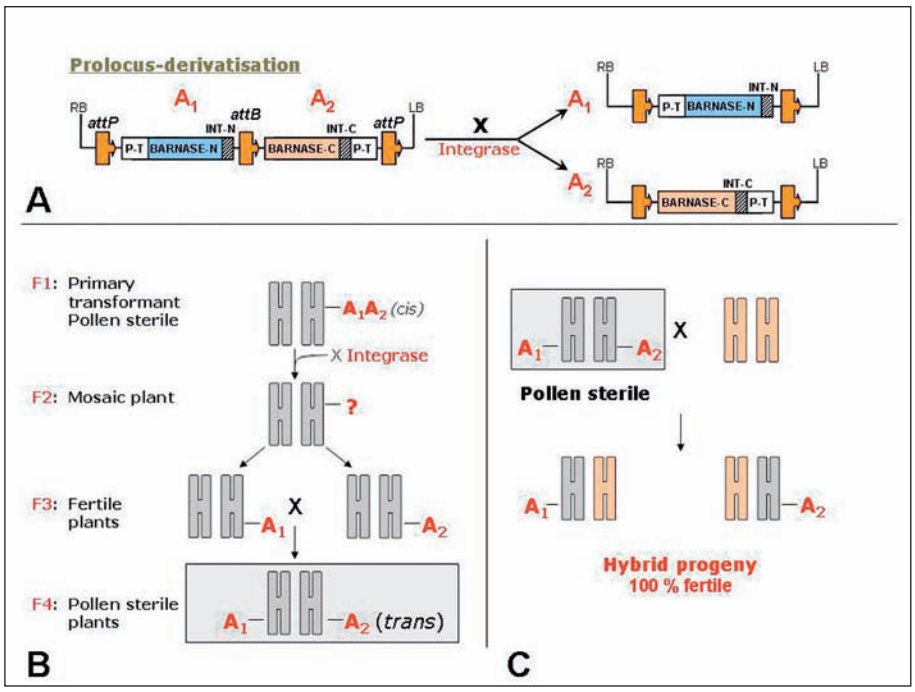

Fig. 36: A: Provector-derivatisation. Recombination between *attB* and *attP* leads to the deletion of one of the two vectors parts A_1 or A_2. Abbreviations: LB, RB: DNA left and right borders; P-T: Tapetum-specific promoter osg6B from rice; Int-N, Int-C: N- and C-terminal Intein sequences; *attP*, *attB*: *Streptomyces* phage phiC31 recombinase attachment sites; phiC31: Phage phiC31 recombinase (M. Gils).

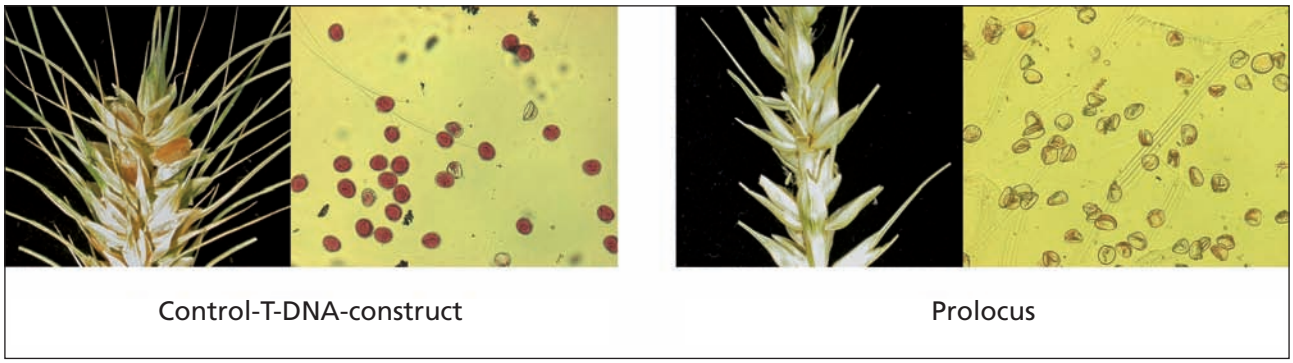

Fig. 37:
Pollen ablation in transgenic wheat caused by a tapetum-specific expression of a toxic barnase protein from a prolocus construct (M. Gils).

constitutively express an active phiC31 integrase enzyme over several generations. Lines were selected, that contain a single copy of the integrase gene (K. Kempe, M. Gils). They will be used as the recombination source for the prolocus derivatisation according to Fig. 37.

Our current work is mainly aimed at the **establishment of wheat lines that contain functional prolocus-constructs**. Wheat lines carrying different prolocus vector constructs with split barnase gene have been established (M. Rubtsova). Some of these lines display a male-sterile phenotype (K. Kempe, M. Rubtsova, see Fig. 37). First results indicate, that the functional complementation of two barnase fragments *via* intein-mediated *trans*-splicing can create a pollen-sterile phenotype in wheat. Currently, molecular experiments are performed in order to analyse the integrity and copy number of the integrated proloci. First progeny plants derived from crosses between pollen-sterile prolocus plants and DH-integrase lines are under analysis (K. Kempe, M. Gils).

Collaboration

Outside the Institute:
Nordsaat Saatzucht GmbH, Saatzucht Langenstein, Böhnshausen; W. von Rhade;
Saaten-Union Resistenzlabor GmbH, Leopoldshöhe; Dr. J. Weyen.

Publications

Other Publications

Gils, M., K. Kempe, M. Rubtsova & R. Schachschneider: Der „Split Gene Approach" für Pflanzen: Mit geteilten Genen zum vollen Ertrag. GABI-FUTURE-Brückenprojekt „Hybridweizen": Die Etablierung eines neuartigen transgenen Systems zur Erzeugung von Hybridweizensaatgut. GenomXPress 4 (2007) 7-10.

Lectures, Posters and Abstracts

V57, P63.

Additional Funding

For further information see the survey page 215.

Abteilung Molekulare Zellbiologie/ Department of Molecular Cell Biology

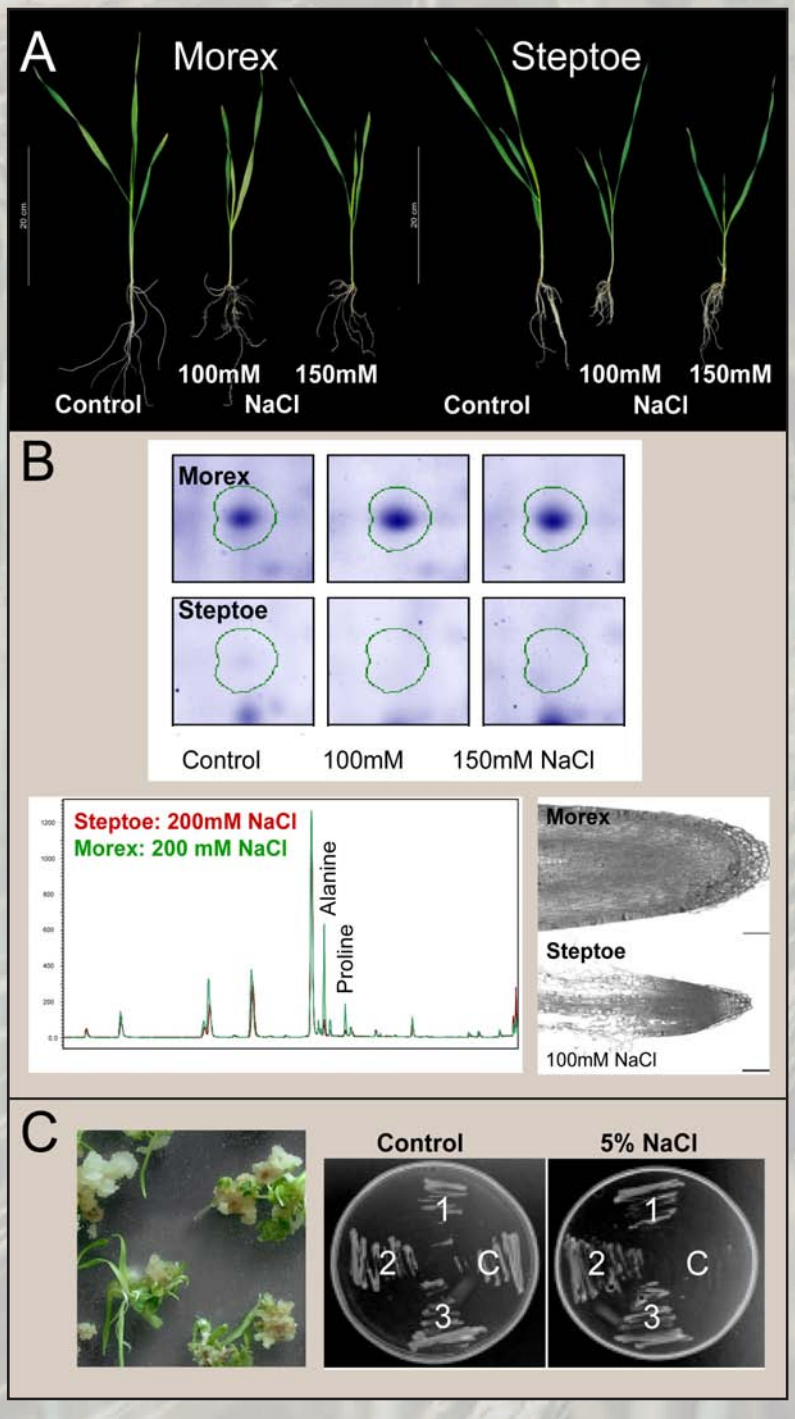

Fig. 38
Molekularbiologische und biochemische Untersuchungen zur Salztoleranz bei Gerste unter Verwendung von Kartierungspopulationen. (A) Die Elternlinien der Steptoe-Morex-Kartierungspopulation zeigen ein gegensätzliches Verhalten gegenüber Salzstress. Untersuchungen zur Keimfähigkeit unter Stressbedingungen und in Langzeitstressexperimenten ergaben eine erhöhte Toleranz von Morex gegenüber Salzstress im Vergleich zu Steptoe. (B) Zur umfassenden Analyse von Salzstressmechanismen in beiden Gerstenlinien werden Methoden zur Ermittlung und Identifizierung differenziell exprimierter Proteine, zur Bestimmung von Verbindungen des Primärmetabolismus, sowie für die Analyse der Morphologie und Ultrastruktur von behandeltem Gewebe verwendet. (C) Kandidatengene, die zu einer erhöhten Toleranz gegenüber Salzstress beitragen könnten, werden mittels Überexprimierung in Gerste und heterologer Expression in Hefe genauer charakterisiert (K. Witzel, G. Hensel, M. Hajirezaei, A. Weidner, T. Rutten, A. Börner, M. Strickert, M. Melzer, J. Kumlehn, H.-P. Mock, G. Kunze).

Complementary molecular and biochemical analysis of salt tolerance mechanisms in barley using mapping populations. (A) The parental lines of the Steptoe-Morex mapping population display contrasting salt tolerance that was revealed by germination tests and long-term stress experiments. Based on biometric measurements, the Morex parent showed higher tolerance towards salinity as the Steptoe parent. (B) The comprehensive investigation of salt stress response in both barley lines included the detection and identification of differentially regulated proteins, the determination of primary metabolites as well as the analysis of morphology and ultrastructure of stressed tissue. (C) Candidate genes are further characterised by over-expression studies in barley and by heterologous expression in yeast (K. Witzel, G. Hensel, M. Hajirezaei, A. Weidner, T. Rutten, A. Börner, M. Strickert, M. Melzer, J. Kumlehn, H.-P. Mock, G. Kunze).

Abteilung Molekulare Zellbiologie

Leiter: Prof. Dr. Gotthard Kunze
(kommissarisch)

Allgemeine Forschungsziele

Die Forschungsarbeiten der Abteilung Molekulare Zellbiologie konzentrieren sich auf die Themenkomplexe Molekulare Pflanzenbiochemie und -physiologie. Diese umfassen Studien in folgenden Bereichen:

- Untersuchungen zur photosynthetischen Bindung von anorganischem Kohlenstoff und dessen Nutzung für die Bildung von nieder- und hochmolekularen Stoffwechselprodukten des Primär- und Sekundärmetabolismus,
- Beeinflussung pflanzlicher Reaktionen auf biotische und abiotische Umwelteinflüsse,
- Analyse regulatorischer Netzwerke zur Koordination simultan ablaufender Stoffwechselprozesse,
- Untersuchung und Beeinflussung reproduktionsbiologischer Prozesse.

Ziel ist es, Verfahren zur biotechnologischen Erzeugung und Erfassung wertvoller zellulärer Inhaltsstoffe und Ansätze zur Herstellung von Nutzpflanzen mit verbesserten agronomischen Eigenschaften zu entwickeln (molecular engineering, molecular farming). Dafür wurden Methoden für die Metabolit- und Proteomanalytik etabliert und für die moderne Pflanzenzüchtung bereitgestellt (metabolic profiling). Neben pflanzlichen Zellkulturen und transgenen Pflanzen werden Hefen als zelluläre Expressionssysteme zur Aufklärung der molekularen Grundlagen spezifischer Stoffwechselleistungen, Resistenzen und Mechanismen, die bei der Stressregulation essenziell sind, genutzt bzw. als Biosensoren zur Erfassung biologisch wirksamer Substanzen und Mykorrhiza-Pflanzen-Interaktionen eingesetzt.

Zusätzlich wurde in der Abteilung, eine arbeitsgruppenübergreifende Plattform für die molekulare Analyse der Salztoleranz von Gersten-Akzessionen etabliert. Hier werden die in der Abteilung entwickelten Technologien für die molekulare, biochemische und strukturelle Analyse auf Gerste übertragen und mit anderen am IPK etablierten Techniken wie Transkriptprofilierung und QTL-Analysen kombiniert. Ziel ist das bessere Verstehen der Regulation von Stoffwechselwegen, um gezielt die agronomische Leistungsfähigkeit von Gerste verbessern zu können. So wurden im Berichtszeitraum anhand Salztoleranter (Morex) bzw. Salz-sensitiver Gerstenlinien (Steptoe) erste Proteomanalysen durchgeführt, die unter NaCl-Stress in Wurzel und Blatt akkumulierten kompa-

Department of Molecular Cell Biology

Head: Prof. Gotthard Kunze
(temporary)

Research Goals

The research focus of the Department is concentrated on basic molecular plant biochemistry and physiology, with an emphasis on photosynthetic carbon fixation and its exploitation for:

- the synthesis of primary and secondary metabolites,
- the regulation of plant metabolism by biotic and abiotic stimuli,
- the elaboration of regulatory networks acting to integrate parallel metabolic pathways,
- the regulation of key processes during reproduction.

We are attempting to develop strategies for the enhancement of the yield of valuable compounds in plants (molecular engineering, molecular pharming) and for the optimisation of crop productivity. Tools which aid in the analysis of metabolic and proteomic data are being developed and applied in the context of modern plant breeding (metabolic profiling). In addition to the use of plant cell culture and transgenesis in plants, cellular expression systems in yeast have been established to elucidate the molecular basis of particular metabolic pathways, stress resistances and stress regulation. Other areas of research include the development of biosensors to detect biologically active compounds, and the analysis of mycorrhiza plant interactions.

The inter-group research project "Molecular analysis of salt tolerance in barley" has been established to exploit in barley some of the molecular biological, biochemical and structural analysis techniques developed within the Department. These are being combined with transcript profiling and QTL analysis, techniques in which other IPK Departments have developed expertise. The overall aim of the project is gain a more profound understanding of the regulation of critical metabolic pathways in barley, and to use this knowledge to generate strategies to improve the agronomic performance of the crop. We have analysed proteomic fingerprints of the contrasting varieties "Morex" (salt tolerant) and "Steptoe" (salt sensitive), identified solutes which are preferentially accumulated in the roots and leaves of salt-stressed plants, and recorded morphological adaptations to the stress. At the same time, a cDNA library has been generated from each of these varieties, to facilitate the isolation of genes whose products affect the level of salt tolerance.

tiblen Solute analysiert, die dabei auftretenden morphologischen Veränderungen dokumentiert und mit der Etablierung entsprechender cDNA-Banken die Voraussetzung zur Isolation von Genen geschaffen, deren Produkte einen Einfluss auf die Salztoleranz ausüben.

Entwicklung im Berichtsjahr

Im Berichtsjahr gab es keine wesentlichen strukturellen Änderungen in der Abteilung. Die bereits im Vorjahr etablierten Schwerpunkte Regulation des Primär- und Sekundärstoffwechsels, pflanzliche Reproduktionsbiologie, zelluläre Expressionssysteme und strukturelle Zellbiologie wurden aufrechterhalten.

Trotz der verringerten Personalstärke war die Publikationsleistung der Abteilung, gemessen an eingeladenen Vorträgen (10), erschienenen oder im Druck befindlichen Artikeln (37) und Patentanmeldungen (2) ebenso hoch wie im Vorjahr. So konnten im Berichtszeitraum Fortschritte in den verschiedenen Forschungsschwerpunkten erzielt werden, von denen einige im Folgenden hervorgehoben sind. Einzelheiten und Publikationshinweise sind den Berichten zu den Arbeitsgruppen zu entnehmen.

(1) Bildung von nieder- und hochmolekularen Stoffwechselprodukten des Primär- und Sekundärmetabolismus

Um herauszufinden, welche molekularbiologischen und biochemischen Prozesse während der Adventivwurzelbildung bei Petunien eine Rolle spielen, wurden in der Arbeitsgruppe Molekulare Pflanzenphysiologie verschiedene Entwicklungsstadien der Wurzelbildung untersucht. Anhand der erzielten Ergebnisse konnte ein charakteristischer Drei-Phasen-Mechanismus postuliert werden: (1) Expression verwundungsinduzierter Gene und Spaltung der Assimilate innerhalb des Apoplasten in den früheren Phasen der Wurzelbildung, (2) apoplastischer Transport der entstandenen Monosaccharide ins Zytosol und deren Umwandlung zu Speichersubstanzen, und (3) symplastischer Transport von Saccharose und Resynthese von Intermediaten wie Zuckerphosphate und organischen Säuren bzw. Proteinen in den späteren Stadien der Wurzelbildung.
Die Funktion sekundärer Inhaltsstoffe für die pflanzliche Stressabwehr und ihre Bedeutung für die menschliche Ernährung wird in mehreren Projekten der Arbeitsgruppe Angewandte Biochemie untersucht. Hierbei konnte u. a. die protektive Wirkung von Anthocyanen experimentell belegt werden.
Im Rahmen eines Projektes zur internationalen Zusammenarbeit in Bildung und Forschung mit Indien, (Molecular Biology Division des Bhabha Atomic Research Center in Mumbai) und einer Diplomarbeit wurden in der Arbeitsgruppe Strukturelle Zellbiologie Untersuchungen zur molekularen Architektur des Photosyntheseapparates durchgeführt. Hierbei standen zellbiologische Untersuchungen zur zellulären Lokalisation von fünf Enzymen

Developments during 2007

During the reporting period no significant structural and organisational changes affected the Department. Our publication record (ten invited lectures, 37 peer-reviewed publications and two patent applications) remained at a similar level to that achieved in 2006. Substantial progress in the various research areas has been made, as outlined below. For more detail, refer to the reports of each individual research group.

(1) Synthesis of primary and secondary metabolism components

To identify which molecular and biochemical processes play a role in adventitious root development in *Petunia*, various developmental stages during root formation were studied by the Molecular Plant Physiology research group. Molecular and biochemical evidence suggested that a characteristic three-phase-mechanism operated, in which at an early developmental stage, wound-responsive genes are induced, and translocated assimilates are mobilised within the apoplast; later, the monosaccharides produced in the cytosol are transported into the apoplast, where they are converted to storage compounds; finally at a later developmental stage, sucrose is transported through the symplast, and intermediates such as sugar phosphates and organic acids (as well as proteins) are regenerated and resynthesised.

Based on outputs of completed projects, the Applied Biochemistry group investigated the function of secondary substances generated as part of the defence response of plants to stress, and their relevance for human food. In particular, the protective effect of anthocyanins was experimentally proven.

As part of the Indo-German project IND 05/009, in collaboration with the Molecular Biology Division of the Bhabha Atomic Research Centre in Mumbai, the molecular architecture of the photosynthetic apparatus was investigated, with a focus on the localisation of Calvin cycle enzymes in the thylakoids of the cyanobacterium *Synechocystis* 6803. This was achieved using high-pressure frozen cells and isolated thylakoid membranes. Immuno-labelling was successfully applied to demonstrate the physical association of five sequential Calvin cycle enzymes (phosphoriboisomerase, phosphoribulokinase, ribulose-1,5-bisphosphate carboxylase/oxygenase, 3-phosphoglyceratekinase and glyceraldehyde-3-phosphate dehydrogenase). The likelihood is that these soluble enzymes are arrayed along the thylakoid membranes. Such an arrangement would allow for efficient channelling of the light reaction products, as well as of Calvin cycle intermediates, thereby facilitating the synchronisation of the light and dark reactions.

des Calvin-Zyklus (Pentosephosphat-Isomerase, Phosphoribulokinase, Ribulose-1,5-bisphosphat Carboxylase, Phosphoglycerat-Kinase, Glycerinaldehydphosphat-Dehydrogenase) im Mittelpunkt. Die Ergebnisse zeigten eine Membranassoziation dieser Enzyme zu den Thylakoiden, was Voraussetzung für ein effizienteres Channelling von Produkten der Lichtreaktion und Intermediaten des Calvin-Zyklus und somit die optimierte Synchronisation von Licht- und Dunkelreaktion ist.

(2) Reaktionen auf biotische und abiotische Umwelteinflüsse

Die Nutzung von Hefen als Modellorganismen zur Analyse der Osmotoleranz und als zelluläre Expressionssysteme zur Aufklärung der molekularen Grundlagen spezifischer Stoffwechselleistungen, sowie stressregulierter Resistenzen und Mechanismen steht im Mittelpunkt der Arbeiten in der Arbeitsgruppe Hefegenetik. Dazu werden neben *Saccharomyces cerevisiae* bevorzugt nicht-*saccharomycete* Hefen wie *Arxula adeninivorans* und *Hansenula polymorpha* eingesetzt. Am Beispiel der osmotoleranten Hefe *A. adeninivorans* konnte gezeigt werden, dass im Gegensatz zu osmosensitiven Hefen die Aktivierung des sog. HOG-Pathways neben der Phosphorylierungsreaktion über eine induzierbare Expression der entsprechenden Gene erfolgt. Die phosphorylierte MAP-kinase Hog1p induziert wiederum die Expression von Genen, die für die Synthese von kompatiblen Soluten wie Glycerol, Erythritol und Mannitol notwendig sind. Die Synthese von Mannitol erfolgt dabei sowohl über eine NaCl induzierbare Mannitol-Dehydrogenase als auch über eine nicht-NaCl induzierbare Mannitol-1-phosphat-Dehydrogenase.

(3) Regulatorische Netzwerke zur Koordination simultan ablaufender Stoffwechselprozesse

Zur weiteren Proteomanalyse von Stressabwehrmechanismen von Pflanzen wurde in der Arbeitsgruppe Angewandte Biochemie eine LC-basierte, markierungsunabhängige Quantifizierungsmethode etabliert und damit die Änderung des Proteoms von Epidermis und Blättern der Gerste nach UV-Behandlung untersucht. Die Analyse von Kontrollpflanzen zeigte zunächst, dass die LC-basierte Methodik komplementär zu den vorher durchgeführten Untersuchungen per 2-D Gelelektrophorese war. Beide Datensätze wurden genutzt, um eine Übersicht über die in der Epidermis ablaufenden Stoffwechselvorgänge zu gewinnen. Die UV-Behandlung rief eine Änderung im epidermalen Proteom hervor, nicht jedoch im restlichen Blattgewebe. Dieser Befund spiegelt wider, dass der Epidermis bei moderater UV-Exposition eine wesentliche Schutzfunktion zukommt. Die funktionelle Charakterisierung des Stress-induzierten Proteins At1g62740 und des homologen Proteins in Tabak zeigte eine duale Lokalisierung im Kern und Cytosol. Gelfiltrationsexperimente bestätigten, dass in Tabakgeweben das Protein sowohl als Dimer als auch als Bestandteil eines hochmolekularen Komplexes vorliegt. Seine Funktion für die Stressabwehr wurde mit Hilfe von RNAi-Konstrukten in Tabak unter-

(2) Regulation of plant metabolism by biotic and abiotic stimuli

Yeasts have been used by the Yeast Genetics group as models for the analysis of osmo-tolerance and as cellular expression systems to elucidate the molecular basis of specific pathways, stress resistances and stress regulation mechanisms. The species chosen have included both *Saccharomyces cerevisiae* and non-*Saccharomyces* yeasts such as *Arxula adeninivorans* and *Hansenula polymorpha*. In the osmo-tolerant *A. adeninivorans*, the so-called HOG pathway is activated by inducible gene expression as well as by phosphorylation. The phosphorylated MAP kinase Hog1p induces the expression of genes necessary for the synthesis of compatible solutes, such as glycerol, erythritol and mannitol. The synthesis of mannitol is achieved by a NaCl-inducible mannitol dehydrogenase in conjunction with a non-NaCl-inducible mannitol-1-phosphate dehydrogenase.

(3) Regulatory networks acting to integrate parallel metabolic pathways

LC-based, label-free quantification has been established as part of the proteomic analysis of the plant stress defence response, and particularly has been applied to analyse the response of the barley leaf epidermis and the leaf in general to UV stress. LC analysis generated data, which was consistent with, but complementary to those generated by 2D gel electrophoresis. Joint data sets derived from the two methods were used to identify metabolic pathways active in the plant epidermis. Treatment with UV perturbed the epidermis proteome, but did not affect the proteome in the rest of the leaf. This outcome clearly demonstrated the role of the epidermis as a protectant against UV exposure. Functional characterisation of the stress-induced protein At1g62740 and its tobacco homologue showed that it was present both in the cytoplasm and the nucleus. Gel filtration experiments confirmed that in tobacco, the protein is present as a dimer, and is a component of a high molecular weight complex. Its function in stress defence was investigated by RNAi methods in tobacco The constructs exhibited effects of the growth behaviour during exposure to cold and drought, but none at heat treatment.

(4) Regulation of key processes in plant reproduction

The Plant Reproductive Biology research group has been developing plant cell culture, genetic transformation and micro-dissection techniques, which are useful for the elucidation and modulation of cellular mechanisms operating during plant reproduction and the plant-pathogen interaction. In collaboration with the Transcriptome Analysis group, a set of generic binary vectors tailored for the transformation of cereal species has been generated, and vector functionality comprehensively tested. These IPKb vectors are compatible with GATEWAY system with respect to both over-expression and knock-down, offer a range of constitutive and tissue-specific promoters for

sucht. Dabei zeigte sich bei Kälte- und Trockenstress im Vergleich zu Kontrolllinien ein Effekt auf das Wachstum.

(4) Untersuchung und Beeinflussung reproduktionsbiologischer Prozesse

In der Arbeitsgruppe Pflanzliche Reproduktionsbiologie werden Methoden zur pflanzlichen Zellkultur, zur genetischen Transformation sowie zur Mikrodissektion entwickelt und für die Aufklärung und Beeinflussung zellbiologischer Mechanismen z. B. im Kontext von reproduktionsbiologischen Prozessen und Pflanze-Pathogen-Interaktionen angewendet. In Kooperation mit der Arbeitsgruppe Transkriptomanalyse wurde ein Set generischer Binärvektoren für die genetische Transformation von Getreidearten fertiggestellt und erfolgreich einer umfassenden funktionellen Überprüfung unterzogen. Diese IPKb-Vektoren stehen für nichtkommerzielle Arbeiten frei zur Verfügung und stellen aufgrund ihrer Modularität eine einzigartige Basis für die komfortable Herstellung verschiedenster Transformationsvektoren dar. Die Besonderheiten der IPKb-Vektoren umfassen die GATEWAY-Kompatibilität sowohl der Überexpressions- als auch der *knock-down*-Vektorderivate, die Verfügbarkeit von Vektoren mit verschiedenen konstitutiven und spezifischen Getreide-kompatiblen Promotoren für die Expression von Effektorgenen sowie der Möglichkeit der einfachen Integration weiterer Promotoren und Selektionsmarker der Wahl. Die bezüglich einheimischer Getreidearten bereits seit einigen Jahren außerordentlich leistungsfähige Transformationsplattform der Arbeitsgruppe wurde durch die Entwicklung neuer Methoden auf den agronomisch bedeutenden Mais sowie auf *Hypericum perforatum* (Johanniskraut), eine wichtige Modellart der Apomixisforschung, erweitert. Darüber hinaus wurde auch für Mais eine neuartige Methode zur Herstellung doppelhaploider Pflanzen etabliert, die vielfältige Möglichkeiten der Anwendung für biotechnologische Ansätze bietet. Als Beispiel der Anwendung von Haploidentechnologien wurde eine Methode entwickelt, die auf außerordentlich effiziente Weise die Herstellung reinerbig transgener, Selektionsmarker-freier Gerstenlinien gestattet. Diese Methode basiert auf der Co-Integration unabhängiger DNA-Fragmente mit Effektor- bzw. Markergen und der nachfolgenden Segregation dieser ungekoppelten Gene in Populationen doppelhaploider Pflanzen, die mittels embryogener Pollenkulturen hergestellt werden.

(5) Biosensoren zur Erfassung biologisch wirksamer Substanzen

Im Biosensorlabor der Arbeitsgruppe Hefegenetik wurden mikrobielle Biosensoren entwickelt und validiert, mit denen östrogene Aktivitäten in Abwasser, Urin, Blut und Milch messbar sind. Der auf *A. adeninivorans* basierende Sensor ist mit einer Nachweisgrenze für 17 ß-Estradiol (E2) von 6 bis 8 ng l^{-1} und einem Messbereich von 10 bis 80 ng l^{-1} Östrogenizität äquivalent zu E2, der derzeit sensitivste Sensor zur Bestimmung von östrogenen Aktivitäten.

the expression of effector genes, and facilitate the introduction of further promoters or selectable markers. The transformation platform, which was already optimised for the temperate cereals, has now been extended to maize and *Hypericum perforatum* (St. John's Wort), an important experimental model for apomixis research. We have established a novel method of generating maize haploids, which opens a number of new research avenues. We have also been able to combine a simple *Agrobacterium*-based barley transformation system with doubled haploid production, such that the plants emerging from embryogenic pollen culture segregate independently for the effector gene and the selection marker. This represents an efficient system for generating true-breeding transgenic, selectable marker-free barley.

(5) Biosensors for detection of biologic active substances

The Yeast Genetics biosensor laboratory has developed and validated microbial biosensors, based on the yeast *A. adeninivorans*, designed to detect estrogenic activity in samples of urine, blood and milk. The detection limit was 6-8 ng l^{-1} for 17 ß-estradiol (E2), with a dynamic range of 10-80 ng l^{-1}. This level of sensitivity is higher than that of other products on the market for the detection of endocrine-disrupting substances.

In addition to the collaborations described above, the Department continues to operate a core facility for electron and light microscopy (Structural Cell Biology research group) and proteomic analysis (Applied Biochemistry and Molecular Plant Physiology). Efficient transformation systems have been elaborated for the cereals, the Solanaceae (tomato, potato, eggplant and pepper) and various yeast species (Plant Reproductive Biology, Molecular Plant Physiology and Yeast Geneticsgroups).

Gotthard Kunze, January 2008

Neben einer zentralen Einrichtung für Licht- und Elektronenmikroskopie (Arbeitsgruppe Strukturelle Zellbiologie) verfügt die Abteilung zusätzlich über leistungsfähige Plattformen für Proteom- und Metabolitanalysen (Arbeitsgruppe Angewandte Biochemie, Arbeitsgruppe Molekulare Pflanzenphysiologie). Darüber hinaus stehen in den Arbeitsgruppen Pflanzliche Reproduktionsbiologie, Molekulare Pflanzenphysiologie und Hefegenetik effiziente Transformationssysteme für Getreide, Körnerleguminosen, Nachtschattengewächse (Solanaceae) und Hefen zur Verfügung.

Gotthard Kunze, Januar 2008

Research Group: Molecular Plant Physiology

Head: Dr. Mohammad R. Hajirezaei
(temporary)

Scientists

Grant Positions
Ahkami, Amir Hossein (0,5 Pakt für Forschung und Innovation)
Kim, Young-Min (0,5 DFG, since 01.05.2007)
Mockwitz, Ines (0,5 DFG, since 15.02.2007)

Visiting Scientists
Junker, Björn H., Dr. (US Department of Energy, 31.01.-30.06.2007)
Kronberg, Kristin (self-financed, 01.02.-30.06.2007)
Mohsen, Saiedi (Iran, since 25.10.2007)
Peisker, Martin, Dr. (self-financed, 15.01.-14.06.2007)
Rastgar-Jazii, Ferdous (self-financed, 15.07.-30.09.2007)
Torabi, Sepideh (University of Teheran, 18.10.-31.12.2007)
Vazan, Saeed, Dr. (University of Karaj, 18.10.-31.12.2007)

Goals

This group's research centers on basic aspects of molecular plant biochemistry and physiology. This includes photosynthetic carbon fixation and its use for the synthesis of low and high molecular weight primary metabolism compounds; an investigation of the identity of the rate-limiting steps within **carbohydrate metabolism**; and the regulation of plant metabolism by environmental stimuli, both **biotic and abiotic**. The overall aim is to contribute towards the improvement of biotechnological strategies for the production of valuable compounds in plants (molecular engineering, molecular farming) and to optimise the agronomic performance of crop plants. In addition, we are developing analytical tools to help in the interpretation of metabolomic data (metabolic profiling).

Research Report

The major current foci of the Molecular Plant Physiology group include photo-assimilate partitioning within the **primary metabolism**, and regulation of plant responses to environmental challenges. We have established a number of analytical methods for metabolite detection and for the measurement of various photosynthetic parameters. These include IC-MS, and several additional HPLC- and photometry-based detection systems.

The elucidation of the rate-limiting steps within the primary metabolism is aimed at the identification of the key primary metabolism enzymes, and the exploitation of substrate channeling to increase the amount of the end product (Y.-M. Kim). To instance, different isoforms of **hexokinases**, a key step within the glycolysis, of **tobacco plants** have been isolated and characterised. Transgenic plants for individual isoforms have been created and are currently under investigation to elucidate the individual function of the hexokinase isoforms (I. Mockwitz). In addition, specific promoters of different isoforms have been isolated (Y.-M. Kim).

In an investigation of the molecular and physiological events during **adventitious root development of *Petunia***,

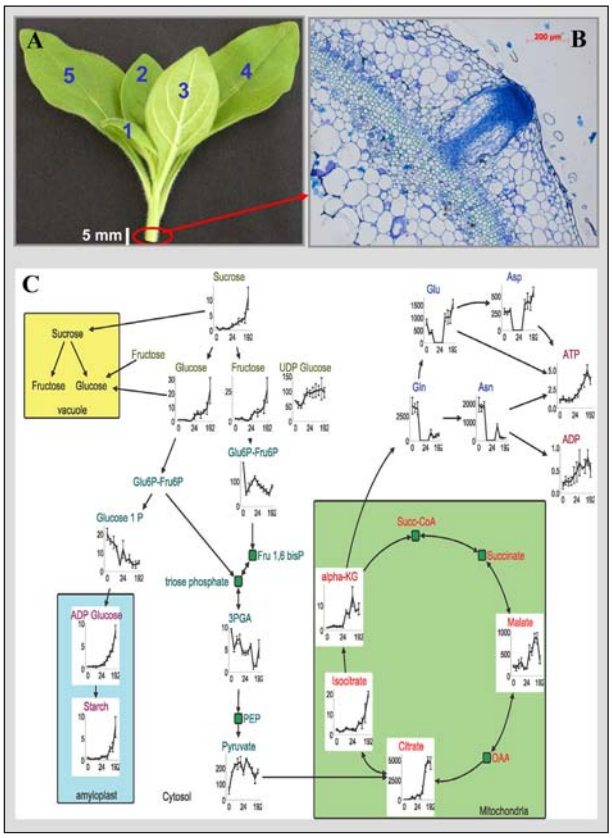

Fig. 39: Regulation of plant metabolism by pathogenic bacteria. The compatible interaction between *Xanthomonas campestris* pv. *vesicatoria* (*Xcv*) and tobacco (Petit havana) plants was established as a model system to study the regulation of plant metabolism by pathogenic bacteria. A bacterial flavodoxin was expressed in the plastids (PFLD) and in the cytosol (CFLD) of tobacco plants. After transfer into the greenhouse plants were infected with *Xanthomonas campestris.* Samples were harvested after 19 hours for microscopical analysis.
Light microscopy comparison between non-transformed (A) and flavodoxin-expressing (B) tobacco plants showed a strong disorganisation of cellular structure in non-transformed plant whereas cellular structure of flavodoxin-containing plants were not affected by the infection.
The bacterial infection resulted in a strong phenotypic alteration of non-transformed (C) and cytosolic-targeted (D, E) plants while plastidic-targeted plants were slightly affected (F) or showed no visible symptoms (G) (M. Melzer, M. Wiesner, N. Carrillo, M. Zurbriggen).

various developmental stages of the root formation in cuttings are to be cytologically (in collaboration with IGZ in Erfurt, Dr. U. Drüge) and biochemically characterised. Detailed biochemical analysis of different developmental stages revealed that specific enzymes such as invertases, phosphofructokinase, glc-6-P dehydrogenase and fructose-1,6-bis phosphatase and intermediates like soluble and insoluble sugars as well as malate and citrate play a crucial role during root formation in *Petunia*. A specific cDNA library has been prepared from the cutting ends at which new roots are formed. The cDNA library contains 4,700 EST's with an average sequence length of 495 bp (A.H. Ahkami, M.R. Hajirezaei – Fig. 39, p. 124).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. H. Rolletschek;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Molecular Cell Biology, Research Group Yeast Genetics; Prof. G. Kunze.

Outside the Institute:

Friedrich Alexander University Erlangen-Nuremberg, Department of Biochemistry, Erlangen; Prof. U. Sonnewald, Dr. R. Börnke;
University of Kaiserslautern, Department of Plant Physiology, Kaiserslautern; Prof. E. Neuhaus, Dr. T. Möhlmann, M. Flörchinger, Dr. T. Tjaden;
University of Heidelberg, Department of Molecular Biology of Plants, Heidelberg; Prof. R. Hell, M. Wirtz;
Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Plant Cell Line, Brunswick; Dr. H.-M. Schumacher;
Institute of Vegetable and Ornamental Crops (IGZ), Department Plant Propagation, Erfurt; Dr. U. Drüge;
Instituto de Biología Molecular y Celular de Rosario (IBR), CONICET, Department of Microbiology, Universidad Nacional de Rosario, Rosario, Argentina; Prof. A. Viale;
Instituto de Biología Molecular y Celular de Rosario (IBR), CONICET, División Biología Molecular, Facultad de Ciencias Bioquímicas y Farmacéuticas, Universidad Nacional de Rosario, Rosario, Argentina; Prof. N. Carrillo;
Agricultural Biotechnology Research Institute of Iran (ABRII), Department of Molecular and Cellular Biology, Karaj, Iran; G. Hosseini Salekdeh;

Publications

Peer Reviewed Papers

Abbasi, A.-R., M. Hajirezaei, D. Hofius, U. Sonnewald & L.M. Voll: Specific roles of α- and γ-tocopherol in abiotic stress responses of transgenic tobacco. Plant Physiol. 143 (2007) 1720-1738.

Ding, L., D. Hofius, M.-R. Hajirezaei, A.R. Fernie, F. Börnke & U. Sonnewald: Functional analysis of the essential bifunctional tobacco enzyme 3-dehydroquinate dehydratase/shikimate dehydrogenase in transgenic tobacco plants. J. Exp. Bot. 58 (2007) 2053-2067.

Kronberg, K., F. Vogel, T. Rutten, M.R. Hajirezaei, U. Sonnewald & D. Hofius: The silver lining of a viral agent: increasing seed yield and harvest index in *Arabidopsis* by ectopic expression of the potato leaf roll virus movement protein. Plant Physiol. 145 (2007) 905-918.

Rodriguez, R.E., A. Lodeyro, H.O. Poli, M. Zurbriggen, M. Peisker, J.F. Palatnik, V.B. Tognetti, H. Tschiersch, M.-R. Hajirezaei, E.M. Valle & N. Carrillo: Transgenic tobacco plants overexpressing chloroplastic ferredoxin-NADP(H) reductase display normal rates of photosynthesis and increased tolerance to oxidative stress. Plant Physiol. 143 (2007) 639-649.

Tognetti, V.B., M.D. Zurbriggen, E.N. Morandi, M.F. Fillat, E.M. Valle, M.-R. Hajirezaei & N. Carrillo: Enhanced plant tolerance to iron starvation by functional substitution of chloroplast ferredoxin with a bacterial flavodoxin. Proc. Natl. Acad. Sci. USA 104 (2007) 11495-11500.

Lectures, Posters and Abstracts

V76, V77, V78, V79, P6, P7, P152, P240, P245.

Additional Funding

For further information see the survey page 216.

Research Group: Applied Biochemistry

Head: Dr. Hans-Peter Mock

Scientists

IPK financed
Döll, Stefanie (0,5 Annex)
Matros, Andrea, Dr. (P)
Witzel, Katja (0,5 Annex, since 01.07.2007)

Grant Positions
Hedtmann, Christiane (0,5 Industry project, since 01.11.2007)
Kaspar, Stephanie (BMBF)
Lippmann, Rico (0,5 BMBF, since 15.11.2007)
Peterek, Silke, Dr. (EU)
Tandron Moya, Yudesly, Dr. (BMBF, since 01.09.2007)
Witzel, Katja (0,5 BMBF, till 30.06.2007)

Visiting Scientists
Capanoglu, Esra (DAAD, 01.01.-04.05.2007)
Mazzucotelli, Elisabetta (EMBO fellowship, 03.09.-20.12.2007)
Ogunwolu, Semiu Olalekan (University Ibadan, 05.03.-02.06.2007)

Goals

The group works on aspects of secondary metabolism in plants with respect to protective functions against abiotic and biotic stresses and also to their potential health effects as a part of the human diet. A number of plant systems are studied with the ultimate goal to gain further insights into regulatory programmes and mechanism of allocation into different branches of secondary metabolism. Proteome approaches as well as HPLC-, HPLC-MS and GC-MS-based profiling of secondary compounds are major tools of research.

Research Report

The characterisation of tobacco varieties with contrasting **trichome morphology and phytochemistry** has been continued (C. Hedtmann, collaboration with Dr. T. Rutten, research group Structural Cell Biology). From a set of twenty-two accessions, leaf exudates were collected to characterise the profiles of secondary compounds secreted from glandular trichomes. In addition to the phenylpropanoid analysis, profiles of terpenoids and sucrose esters will be gained. To this end, a GC-MS-based method for the analysis of these classes of secondary compounds has been established.
The **functional characterisation** of the trichome-enriched protein termed **STINT,** earlier identified by its homology with a stress-induced protein of *Arabidopsis,* has been continued. Transgenic plants harbouring GUS constructs demonstrated strong expression in trichomes under control conditions, consistent with the previous proteome data. GFP constructs revealed the dual localisation of the protein in the cytosol as well as in nuclei (C. Hedtmann). The functional significance of STINT gene expression was tested with RNA_i-plants using different stress conditions. Impaired growth relative to control plants was observed in RNA_i-plants when applying cold or drought stress, whereas heat stress had similar morphological impact on all lines (C. Hedtmann).

Analysis of *Arabidopsis* mutant lines with modified responses to cold stress in their phenylpropanoid profiles has been continued (S. Peterek). The evaluation of large datasets was supported by the interactive visualisation and inspection tool ChromaViIns3D (collaboration with T. Czauderna, research group Pattern Recognition). For several selected lines, a map-based cloning of candidate genes was initiated.

Seed **proteome analysis of a barley mapping population** has been continued in the GABI-SEED II project (coordinator: Prof. U. Wobus; collaboration with W. Weschke, U. Seiffert, F. Schreiber). A second large set of samples has been analysed. Data on protein abundance were visualised with the help of the VANTED software (K. Witzel, A. Matros, collaboration with F. Schreiber and C. Klukas) and subsequently used for QTL mapping (collaboration with C. Pietsch and M. Röder).

A genetical proteomics approach has been initiated for the evaluation of **salt stress responses in barley mapping populations** (K. Witzel, A. Matros; collaboration with A. Börner and all groups of the Molecular Cell Biology department). The seed proteome of parental lines and selected offsprings of two mapping populations have been analysed and putative candidates related to salt tolerance in the germination assay were selected. For several of these candidates, full-length clones were obtained and used to generate constructs with a seed-specific as well as a ubiquitous promoter. Transgenic lines obtained in the Plant Reproductive Biology group are now available for functional characterisation. Analysis of the genetic resources has been extended using a hydroponics system. Biometric analysis and proteome analysis were performed for root and leaf tissues of plants grown under different salt concentrations. A kinetic study has been initiated for selected conditions to monitor the patterns of changes in the proteome over time. For the analysis of protein

expression in this high-dimensional dataset, a new algorithm with parallel attribute weighting was applied to reduce the complexity of data and enhance statistical analysis of 2-D gels (K. Witzel, collaboration with M. Strickert).

The project on the **epidermal proteome of barley** and its responses to the inoculation with powdery mildew (E. Metzner, collaboration with P. Schweizer and W. Knogge) has been continued. Changes in the proteome have been monitored at several stages after inoculation using DIGE technology. Complementary to the proteome approach, transcript profiling will now be performed in the laboratory of P. Schweizer on the same material for a comprehensive view on cellular responses during plant-pathogen interaction. In parallel, a map of the barley epidermal proteome has been established and identified spots have been related to biochemical pathways (S. Kaspar, collaboration with F. Schreiber). Recent experiments demonstrate a clear change in the epidermal proteome in response to UV stress, whereas the overall leaf proteome remained unaffected. For this analysis, a quantitative and label-free LC-based proteome approach was established on our Nano-HPLC ESI-MS/MS platform (S. Kaspar, A. Matros) (Fig. 40). This novel approach will also be applied to **kinetic studies of developing barley grains** within the QuantPro project (coordinator: U. Seiffert; collaboration with W. Weschke; MMI, Munich and IFF, Magdeburg). Analyses of proteome changes in full grains of several developmental stages have already been started and will be accomplished by investigation of separated tissues. Complementary to the proteome approach, metabolite and transcript profiling will be performed on the same material in this project.

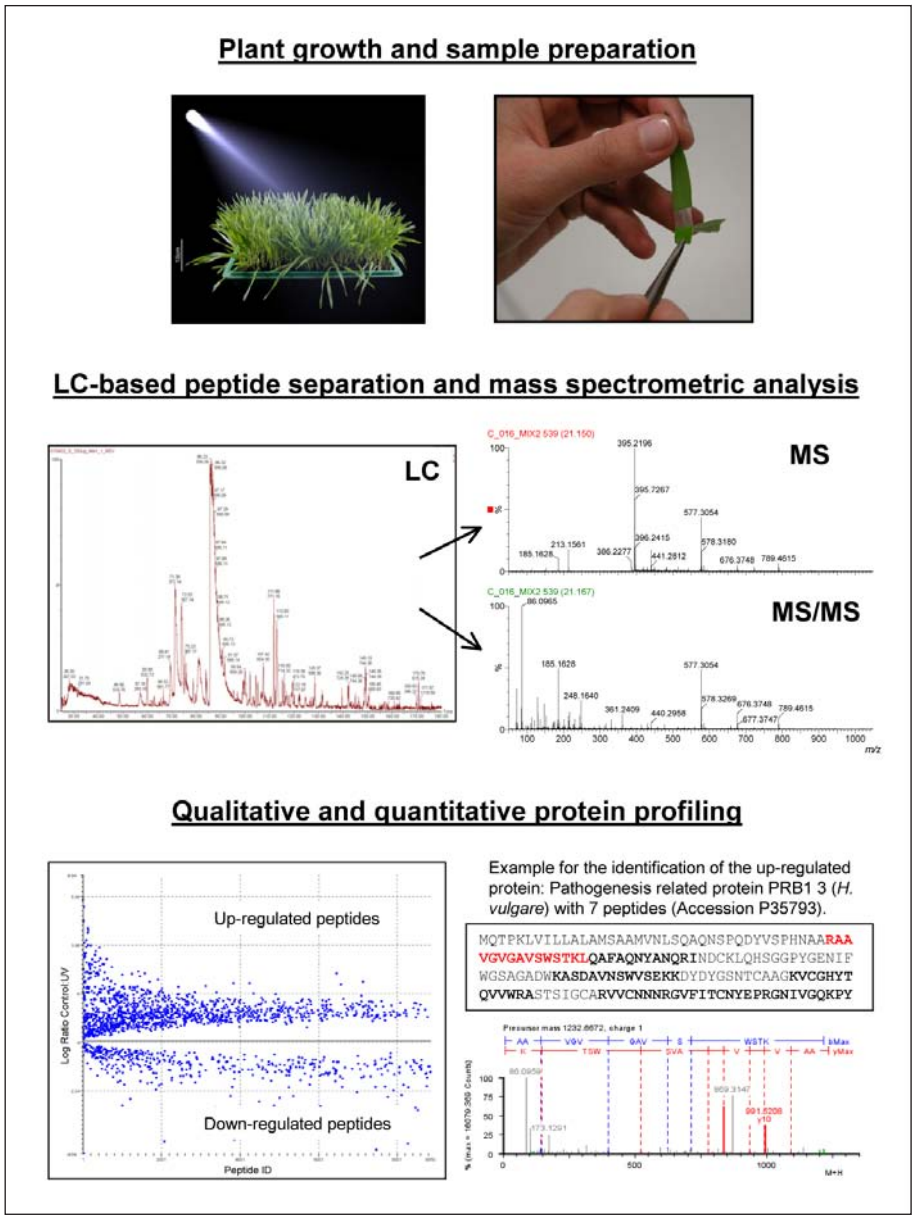

Fig. 40: Scheme for label-free quantitative LC-based proteome approach. Proteins were extracted from epidermal tissue of *H. vulgare* cultivated under regular conditions or exposed to UV-B radiation. Protein extracts were digested with trypsin and equal amounts of peptide mixtures were used for separation and analysis on a nano-HPLC ESI-MS/MS system. Quantitative protein profiling (Expression software, Waters) revealed peptides with increased as well as reduced abundance during UV-stress conditions. Identification of corresponding proteins was done by database search against *Viridiplantae* protein index of the nrNCBI database or HvGI of TIGR EST sequences based on the fragment ion spectra of the various peptides (S. Kaspar, A. Matros, H.-P. Mock).

In the EU FLORA project dealing with the **potential beneficial health effects of flavonoids,** the group performs the phytochemical characterisation of plant material. Material of transgenic *Arabidopsis* lines with modified expression of transcription factors in combination with varying environmental conditions provided by a partner lab has been analysed by HPLC-MS. In addition, seeds from corn lines with ectopic expression of transcription factors were profiled for the elevated levels of phenylpropanoids. In particular, anthocyanins were purified and their composition determined (Fig. 41). Phytochemical composition has been related with data from mice feeding studies demonstrating a protective effect of anthocyanin rich diet in the animal test system (S. Peterek, Y. Tandron Moya, A. Matros).

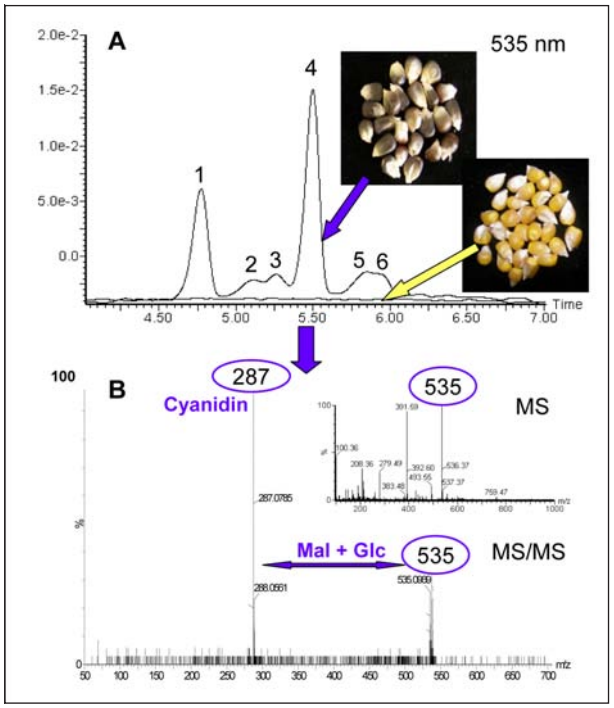

Fig. 41:
Profiling and identification of anthocyanins from the corn line "ACR". A: UV chromatogram at absorption wavelength 535 nm. A: Preparative HPLC was used for the separation of individual compounds. The fractions were collected and subjected to an analytical UPLC column (Acquity UPLC™ BEH C18, 1.7 µm, 4.1 x 50 mm, Waters) in combination with a mass spectrometer for initial characterisation. For the further identification the purified substances were analysed by ESI-MS/MS (Q-TOF Premier, Waters). B: MS/MS fragmentation pattern of one purified anthocyanin with ions at *m/z* at 535 and 287 is presented. The mass spectrum of the molecular ion with *m/z* 535 is depicted in the embedded graph. This anthocyanin was identified as cyanidin malonyl-glucoside (S. Peterek, A. Matros, H.-P. Mock).

Collaboration

Within the Institute:

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Pattern Recognition; Dr. U. Seiffert;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber;
Dept. of Molecular Genetics, Junior Research Group Data Inspection; Dr. M. Strickert;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Molecular Cell Biology, Research Group Yeast Genetics; Prof. G. Kunze.

Outside the Institute:

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Leibniz Institute of Plant Biochemistry, Halle/S.; Dr. W. Knogge, Dr. K. Naumann;
Fraunhofer Institute for Factor Operation and Automation (IFF), Department Virtual Prototyping, Magdeburg; Dr. R. Mecke;
Molecular Machines & Industries GmbH (MMI), CTO Instruments, Eching; Dr. S. Niehren;
Georg August University Göttingen, Institute of Botany, Göttingen; Prof. I. Feußner;
Justus Liebig University Gießen, Department of Botany, Giessen; Prof. A.J.E. van Bel;
Friedrich Alexander University Erlangen-Nuremberg, Department of Biochemistry, Erlangen; Prof. U. Sonnewald, Dr. F. Börnke;
Institute of Biochemical Plant Pathology (BIOP), GSF Neuherberg; Dr. W. Heller;
Christian Albrechts University Kiel; Institute of Botany, Kiel; Prof. K. Krupinska;
Sperimentale per l'Agrumicoltura, Catania, Italy; Dr. G. Reforgiato;
Technical University of Denmark, Institute BioCentrum, Copenhagen, Denmark; Prof. J.B. Svensson;
John Innes Centre, Norwich, UK; Dr. C. Martin;
Plant Research International, Wageningen, The Netherlands; Dr. R. Hall, Dr. J. Beekwilder;
Waters, Application Centre, Manchester, UK; Dr. J. Langridge, Dr. H. Vissers.

Publications

Peer Reviewed Papers

Bartels, A., H.-P. Mock & J. Papenbrock: Differential expression of *Arabidopsis* sulfurtransferases under various growth conditions. Plant Physiol. Biochem. 45 (2007) 178-187.

Böer, E., G. Steinborn, A. Matros, H.-P. Mock, G. Gellissen & G. Kunze: Production of interleukin-6 in *Arxula adeninivorans*, *Hansenula polymorpha* and *Saccharomyces cerevisiae* by applying the wide-range yeast vector (CoMed™) system to simultaneous comparative assessment. FEMS Yeast Res. 7 (2007) 1181-1187.

Gigolashvili, T., B. Berger, H.-P. Mock, C. Müller, B. Weisshaar & U.I. Flügge: The transcription factor HIG1/MYB51 regulates indolic glucosinolate biosynthesis in *Arabidopsis thaliana*. Plant J. 50 (2007) 886-901.

Vorwieger, A., C. Gryczka, A. Czihal, D. Douchkov, J. Tiedemann, H.-P. Mock, M. Jakoby, B. Weisshaar, I. Saalbach & H. Bäumlein: Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. Planta 226 (2007) 147-158.

Witzel, K., G.K. Surabhi, G. Jyothsnakumari, C. Sudhakar, A. Matros & H.-P. Mock: Quantitative proteome analysis of barley seeds using ruthenium(II)-tris-(bathophenanthroline-disulphonate) staining. J. Proteome Res. 6 (2007) 1325-1333.

Book Chapters

Mock, H.-P.: Tocopherol composition of plants and their regulation. In: Preedy, V.R. & R.R. Watson (Eds.): The Encyclopedia of Vitamin E. CAB International, Wallingford (2007) 112-121.

Other Publications

Strickert, M., K. Witzel, H.-P. Mock, F.-M. Schleif & T. Villmann: Supervised attribute relevance determination for protein identification in stress experiments. Proceedings of the International Workshop on Machine Learning in Systems Biology (MLSB 2007), (2007) 81-86.

Toufektsian, M.C., F. Boucher, P. Salen, M. de Lorgeril, L. Giordano, M.B. Donati, S. Peterek, H.-P. Mock, R. Pilu, K. Petroni & C. Tonelli: Long-term dietary intake of flavonoids induces protection against *ex vivo* myocardial infarction in rats. Abstracts of the 10th European Nutrition Conference, 10.-13.07.2007, Paris. Ann. Nutr. Metab. 51 (suppl. 1) (2007) 273.

Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: „Genetical Genomics" der Gerstenkornentwicklung – von der Genexpression zu landwirtschaftlich bedeutsamen Merkmalen. GenomXPress 1 (2007) 12-16.

Wobus, U., H.-P. Mock, C. Pietsch, V. Radchuk, M. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, W. Weschke & K. Witzel: GABI-SEED: Genetische Grundlagen komplexer agronomischer Merkmale im Getreidekorn entschlüsseln. GenomXPress Sonderausgabe März (2007) 19.

PhD and Diploma Theses

Hedtmann, C.: Charakterisierung von einem Stress-induzierten Protein aus *Nicotiana tabacum* mit Homologie zum Gen At1g62740. (Master) Universität Hannover, Hannover (2007) 71 pp.

Poblenz, T.: Etablierung einer Methode zur Anreicherung und Trennung phosphorylierter Proteine aus Gesamtblattproteinextrakten von *Arabidopsis thaliana*. (Diploma Thesis) Hochschule Anhalt (FH), Köthen (2007) 110 pp.

Lectures, Posters and Abstracts

V143, V144, V154, V155, V156, V286, P27, P35, P36, P99, P103, P104, P105, P147, P231, P237, P238, P239, P240.

Additional Funding

For further information see the survey page 216.

Research Group: Structural Cell Biology

Head: Dr. Michael Melzer

Scientists

IPK financed
Rutten, Twan, Dr. (P)

Grant Positions
Daghma, Diaa El-Din (0,5 BMBF, since 01.11.2007)

Visiting Scientists
Agarwal, Rachna (BMBF/DLR, 01.06.-28.07.2007)
Chittela, Ragini Kaut (BMBF, 28.09.-24.11.2007)
Sainis, Jayashree, Prof. (BMBF, 28.09.-24.11.2007)

Goals

As the **central facility for light and electron microscopy** at the institute, the research group Structural Cell Biology provides services and theoretical advice to understand biological structure and functional relationships in plant cells and tissues. Our main focus is **ultrastructural characterisation**, **monitoring cell dynamic processes** and spatial **distribution of macromolecules**. The microscopy facility is equipped with the following state-of-the-art microscopy imaging systems and instruments: **Transmission electron microscope** FEI Tecnai G2-Sphera 200 KV, field emission scanning electron microscope Hitachi S 4100, **confocal laser scanning microscope** Zeiss LSM 510 META, fluorescence microscopes Zeiss Axioskop and Axiovert 135 each with an AxioCam HRc camera system.

Research Report

In the past year, several ongoing projects, internal and external collaboration have been continued or completed. The Indo-German collaborative project about the investigation of the **molecular architecture of the apparatus of photosynthesis and DNA recombination** with the Bhabha Atomic Research Centre was continued (S. Ortleb, R. Agarwal, R. Chittela and J. Sainis). We successfully established **high pressure freezing** for cells of the Cyanobacteria *Synechococcus* sp. PCC 7942 and *Synechocystis* 6803. Immunogold studies of the cryofixed cells showed predominant labelling of the thylakoid membranes and confirmed our previous data about the **organisation of Calvin cycle enzymes along isolated thylakoids** (see Fig. 42). In the second part of the project we continued the characterisation of **DNA-protein interactions** of the isolated homologous **recombination proteins Rad51 and Dmc1** from rice. MALDI-TOF analysis of purified OsRad51 confirmed its identity as a member of Rad51 group of proteins. Additional experiments using cytochrome C spreading technique, show complex joint molecules when linear dsDNA and ssDNA were incubated in presence of recombinase. This first report on DNA binding properties of Rad51 from crop plants supports that **OsRad51 promotes the renaturation of complementary single strands.** In a joint project of the Molecular Cell Biology department the **salt tolerance mechanisms** in barley are investigated using the genetic variation of mapping populations. First comparative morphological and ultrastructural studies of root and leaf tissue of the salt-tolerant line Morex and the salt-sensitive line Steptoe have been carried out. While the leaf morphology seems to be more or less unaffected after salt treatment (100 mM and 200 mM NaCl), significant differences can be detected in the root tissue. At 100 mM NaCl the root tip of Morex is unaffected, yet the sensitive line Steptoe shows a **significant reduction of the meristematic tissue**, an increased number of root hairs in the elongation zone and a disordered cell arrangement. Exposure to 200 mM NaCl affects both lines but Steptoe more severely.

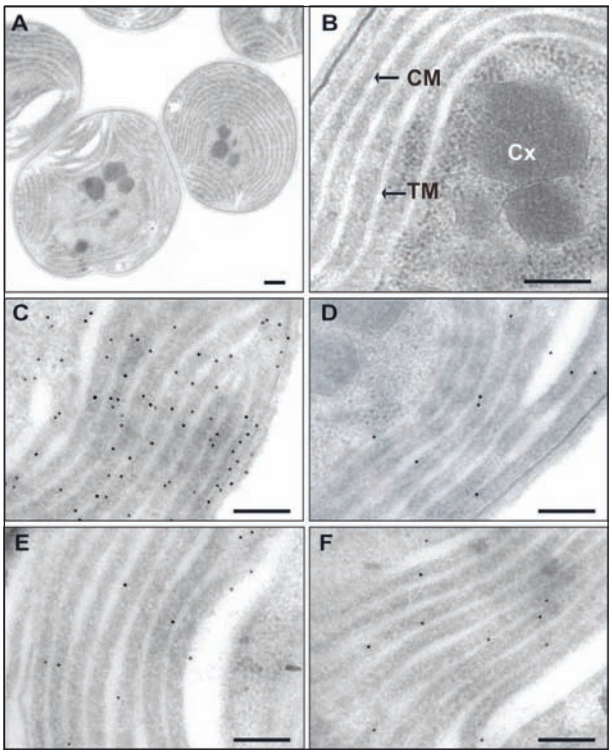

Fig. 42: Immunogold labelling of *Synechocystis* 6803. (A-B) Ultrastructure of cells after high pressure freezing. Immunogold localisation with specific polyclonal anti-rabbit antibodies and 10 nm protein-A gold of the catalytic portion of the chloroplast H^+-ATP synthase (C), phosphoglycerate kinase (D), ribose-5-phosphate isomerase (E) and ribulose-1,5-bisphosphate carboxylase/oxygenase (F). All enzymes were localised predominantly at the thylakoid membranes. CM, cytoplasmic membrane, Cx, carboxysome; TM, thylakoid membrane. Bar = 100 nm (S. Ortleb, R. Agarwal, J. Sainis, M. Melzer).

In collaboration with the Department of Forest Genetics and Plant Physiology of the Swedish University of Agricultural Science in Umeå (G. Wingsle and V. Srivastava) the **cell biological characterisation of hipI-Superoxide Dismutase (SOD)** in poplar antisense plants was completed. Immunolocalisation studies showed the enzyme to be localised extracellular, in the secondary cell wall of xylem vessels and phloem fibres. The up-regulation of selected genes involved in lignin biosynthesis was verified by real time (RT) PCR. These results and additional histological examinations confirmed that in the transgenic plants, a **premature transition into maturation** occurs and that **reduced expression of hipI-SOD** during development and differentiation leads to **increased ROS production.** First characterisations of *Arabidopsis* hipi-SOD mutants and plants with expression of a hipI-SOD-GFP fusion protein confirm these results so far.

A number of studies on **mitosis-affecting factors** were carried out in collaboration with the Dept. of Cytogenetics and Genome Analysis. Post-translational modifications of conserved N-terminal residues in histones regulate many aspects of chromosome activity. Haspin, a member of a distinctive group of protein kinases present in diverse eukaryotes, is known to phosphorylate H3 at Thr 3 *in vitro*. Recently, **haspin kinase** has also been found in plants and its role in *Arabidopsis thaliana* is studied in collaboration with the research group Chromosome Structure and Function (R. Karimi). Both overexpression under control of the 35S promoter and suppression by means of RNAi have **profound effects on the plant morphology**. The typical vascular distribution that we found, however, suggests that in plants haspin has functions different from that in non-plant eukaryotes. Nim-A kinase ("never in mitosis") from *Aspergillus nidulans* also affects the phosphorylation of histone H3 and thus the organisation of chromosomes. In another collaboration (F. Agueci), **morphological aspects of a nim-A kinase** in *Arabidopsis* were examined. The homologue to the kinase from *Aspergillus nidulans* also affects the phosphorylation of histone H3 and the organisation of chromosomes. Downregulation by RNAi has no obvious effect on plant phenotype, but **significantly changes leaf architecture** causing a strong reduction in cell number. Interestingly, other organs like the stem, appear less affected.

In collaboration with the research group Karyotype Evolution (I. Lermontova) morphological studies of *Arabidopsis* with downregulation of CENH3, which substitutes histone H3 in the nucleosome of active centromeres, was carried out. Downregulation of CENH3, which plays a crucial role in chromosome segregation and thus cell division, leads to dwarf-growth and early flowering. However, despite their smaller sizes, leaf architecture and overall cell size appear remarkably similar to that of the WT. Obviously, cell number is reduced, underlining the prediction of a **reduced mitosis in CENH3-RNAi plants.** In this case, however, leaf architecture has not been disrupted as happened in case of nim-A. In collaboration with the research group Applied Biochemistry (C. Hedtmann) research on **Stint**, a stress-induced *Nicotiana tabacum* protein, was continued. Although this protein has now been identified as a **co-chaperone of Hsp70**, its role is still unclear. Plants with downregulated Stint expression and grown under cold stress, appear dwarf-like and **show significant morphological and ultrastructural changes**. In a series of experiments the most significant changes were found in the tissue of the stem including **reduced lignification and vacuolar depositions** in the pith. In collaboration with the research group Gene Regulation (A. Vorwieger) expression studies of **LEAFY COTELYDON1 (LEC1)**, a major regulator of the embryonic state, were performed. In normal germinating plants, LEC1 is suppressed. Experimental conditions have been established to allow the induction of LEC1 in seedlings as old as 10 days after germination. The most obvious structural change is **the transformation of all non-differentiated tissues into storage compartments** (Fig. 43).

As part of GABI-POEM project "Comparative structural cell biological studies of gametophytic pollen development vs. **initiation of pollen embryogenesis**" started with first **histological and ultrastructural** experiments of isolated microspores from barley (D. Daghma).

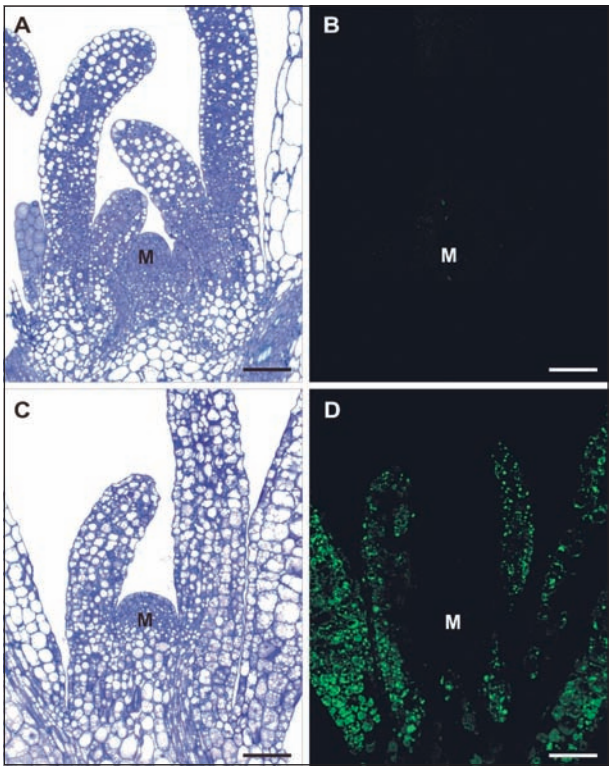

Fig. 43: Morphology and immuncytochemistry of *Arabidopsis thaliana* LEC1::GR seedlings. Ten day-old seedlings of *Arabidopsis thaliana* were transferred onto inducing medium containing ABA and dexamethasone and incubated on this medium for another four days. Whereas WT seedlings continued growing (A), it stopped in the LEC1::GR seedlings (C). Following harvesting the apical parts of the stems were processed for immunofluorescence microscopy and labelled for the presence of the storage protein cruciferin. WT seedlings remained negative for the presence of cruciferin (B). In transgenic LEC1::GR seedlings cruciferin had accumulated in the young, not yet fully differentiated leaves (D). M: meristem. Bar = 50 µm (T. Rutten, A. Vorwieger).

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Molecular Genetics, Research Group Gene Expression; Prof. U. Wobus;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Molecular Cell Biology, Research Group Yeast Genetics; Prof. G. Kunze.

Outside the Institute:
Max Planck Institute for Molecular Plant Physiology, Golm; Dr. P. Dörrmann;
Humboldt University Berlin, Faculty of Mathematics and Natural Sciences I, Berlin; Prof. B. Grimm;
Biologische Bundesanstalt, Institut für Pflanzenvirologie, Mikrobiologie und biologische Sicherheit, Brunswick; Dr. K. Richert-Pöggeler;
Friedrich Alexander University Erlangen-Nuremberg, Dept. of Molecular Plant Physiology, Erlangen; Prof. N. Sauer;
University of Freiburg, Institute of Biology II, Freiburg; Prof. K. Palme;
University of Kaiserslautern, Dept. of Plant Physiology, Kaiserslautern; Prof. E. Neuhaus;
University of Karlsruhe, Institute of Botany II, Karlsruhe; Prof. H. Puchta;
Swedish University of Agricultural Science, Dept. of Forest Genetics and Plant Physiology, Umeå, Sweden; Prof. G. Wingsle;
University of Aalborg, Dept. of Life Sciences, Aalborg, Denmark; Prof. K. Grasser;
University of Stockholm, Dept. of Plant Physiology, Stockholm, Sweden; Prof. S. Karpinski;
Russian Academy of Sciences, Institute of Basic Biological Problems, Pushino, Russia; Prof. I. Prokhorenko;
Bhabha Atomic Research Centre, Molecular Biology and Agriculture Division, Mumbai, India; Prof. J. Sainis.

Publications

Peer Reviewed Papers

Gernand, D., H. Golczyk, T. Rutten, T. Ilnicki, A. Houben & A.J. Joachimiak: Tissue culture triggers chromosome alterations, amplification, and transposition of repeat sequences in *Allium fistulosum*. Genome 50 (2007) 435-442.

Kronberg, K., F. Vogel, T. Rutten, M.R. Hajirezaei, U. Sonnewald & D. Hofius: The silver lining of a viral agent: increasing seed yield and harvest index in *Arabidopsis* by ectopic expression of the potato leaf roll virus movement protein. Plant Physiol. 145 (2007) 905-918.

Reinhold, T., A. Alawady, B. Grimm, K.C. Beran, P. Jahns, U. Conrath, J. Bauer, J. Reiser, M. Melzer, W. Jeblick & H.E. Neuhaus: Limitation of nocturnal import of ATP into *Arabidopsis* chloroplasts leads to photooxidative damage. Plant J. 50 (2007) 293-304.

Rolletschek, H., T.H. Nguyen, R.E. Häusler, T. Rutten, C. Göbel, I. Feussner, R. Radchuk, A. Tewes, B. Claus, C. Klukas, U. Linemann, H. Weber, U. Wobus & L. Borisjuk: Antisense inhibition of the plastidial glucose-6-phosphate/phosphate translocator in *Vicia* seeds shifts cellular differentiation and promotes protein storage. Plant J. 51 (2007) 468-484.

Srivastava, V., H. Schinkel, J. Witzell, M. Hertzberg, M. Torp, M.K. Srivastava, B. Karpinska, M. Melzer & G. Wingsle: Downregulation of high-isoelectric-point extracellular superoxide dismutase mediates alterations in the metabolism of reactive oxygen species and developmental disturbances in hybrid aspen. Plant J. 49 (2007) 135-148.

Book Chapters

Voigt, M.-L., M. Melzer, T. Rutten, T. Mitchell-Olds & T.F. Sharbel: Gametogenesis in the apomictic *Boechera holboellii* complex: the male perspective. In: Hörandl, E., U. Grossniklaus & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 235-257.

PhD and Diploma Theses

Ortleb, S.: Untersuchungen zur Architektur des Photosyntheseapparates von *Synechococcus* sp. PCC 7942 und *Synechocystis* sp. PCC 6803 (Cyanobacteria: Chroococcales). (Diploma Thesis) Hochschule Anhalt (FH), Köthen (2007) 88 pp.

Lectures, Posters and Abstracts

V146, V147, V148, V149, V150, V151, P2, P3, P6, P7, P25, P32, P126, P151, P162, P181, P220, P221, P226, P236, P240.

Additional Funding

For further information see the survey page 217.

Research Group: Plant Reproductive Biology

Head: Dr. Jochen Kumlehn

Scientists

IPK financed
Bruchmüller, Astrid (0,5 Annex)
Gahrtz, Manfred, Dr. (0,5 Annex, till 31.05.2007)
Hensel, Götz, Dr. (0,5 P)
Plasun, Katarzyna (0,5 Pakt für Forschung und Innovation, 01.07.-30.09.2007)
Rizzo, Paride (0,5 Pakt für Forschung und Innovation, since 01.04.2007)
Saalbach, Isolde, Dr. (0,5 P)
Zimmermann, Grit (0,5 Annex, since 01.07.2007)

Grant Positions
Goedeke, Stefanie (0,5 Industry, till 02.11.2007)
Hensel, Götz, Dr. (0,5 Industry)
Kapusi, Eszter (0,5 BMBF)
Kastner, Christine (0,5 DFG)
Kugelmann, Eszter (BMBF, since 01.09.2007)
Levy-Guarda, Nathalie, Dr. (Industry, 01.09.-31.12.2007)
Plasun, Katarzyna (0,5 BMBF, since 01.10.2007)
Riechen, Jan (0,5 EU)
Zierold, Uwe, Dr. (DFG)

Visiting Scientists
Bakos, Ferenc, Dr. (DAAD, 01.07.-31.12.2007)
Ombori, Omwoyo (DAAD, till 24.01.2007)
Varshney, Alok, Dr. (self-financed, 01.01.-30.06.2007)

Scholars
Jin, Kim Song (InWEnt, 02.05.-14.09.2007)

Goals

The research focus of the group is to develop and implement technologies for plant cell culture, genetic transformation and microdissection in application-oriented investigations on asexual and sexual plant reproduction, on plant-pathogen interactions as well as on the production of recombinant proteins in plants.

Research Report

Transformation vector systems, which work well for many dicotyledonous species are, unfortunately, of only limited use in the monocotyledons, largely because commonly used promoter sequences and/or selectable markers are ineffective in a monocotyledonous host. In collaboration with the Transcriptome Analysis group, a set of **modular binary vectors (the IPKb series), specifically tailored for cereal transformation** and targeted to either **over-expression or RNA-interference** (RNAi)-mediated gene knock-down was generated. In both types, the insertion of effector sequences is facilitated by the exploitation of **GATEWAY destination cassettes**, which permit the site-specific and efficient exchange of DNA fragments between plasmids (Fig. 44, p. 134). This is particularly advantageous in the context of RNAi vectors. The IPKb vector set includes derivatives both of the over-expression (pIPKb002 to pIPK005) and RNAi types (pIPKb007 to pIPK010), in which various promoters (Fig. 44) have been inserted to drive transgene expression. Any other established or *de novo* isolated promoter sequence can be readily inserted upstream of the GATEWAY destination cassette of either the over-expression vector pIPKb001, or the RNAi vector pIPKb006, thereby increasing the versatility of the IPKb vector set. Moreover, the IPKb vectors allow for the ready introduction of further marker gene expression cassettes. This can be accomplished via the exchange of the selectable marker-containing *Sfi*I fragment with those of compatible vectors. The functionality of pIPKb002 to pIPKb005 was tested by introducing the *gus* gene into the GATEWAY destination site, followed by *Agrobacterium*-mediated transformation of barley and subsequent expression analysis of stable transgenic plants. Resultant T1 seedlings expressed GUS, with the strongest expression present in the leaves of lines transformed with pIPKb002_GUS (driven by the maize *Ubi1* promoter), followed by pIPKb003_GUS (rice *Act1* promoter), pIPKb005_GUS (wheat *GstA1* promoter) and pIPKb004_GUS (doubled enhanced CaMV*35S* promoter). For the transgenic lines obtained using pIPKb005_GUS, fluorescence spectroscopy revealed that the GUS activity in isolated abaxial epidermis was, on average, about ten times stronger than in the remaining leaf tissue. The functionality of the RNAi-vectors was verified via the biolistic delivery into barley leaf tissue of vector derivatives targeted against *Mlo*, a negative regulator of resistance against the causal pathogen of barley powdery mildew. All of the plasmids tested (pIPKb007_Mlo to pIPKb010_Mlo) produced a phenocopy of the loss-of-function *mlo* resistance, indicating that the presence *in planta* of the *Mlo*-RNAi constructs acted to reduce the transcription of MLO, and hence increased the level of resistance to powdery mildew. In addition to the generation of numerous stable transgenic barley and wheat plants using derivatives of IPKb destination vectors, pIPKb002_GUS and pIPKb004_GUS proved also effective for the stable transformation of tobacco (U. Zierold, G. Hensel, J. Riechen, H. Büchner, C. Marthe, J. Schellwat).

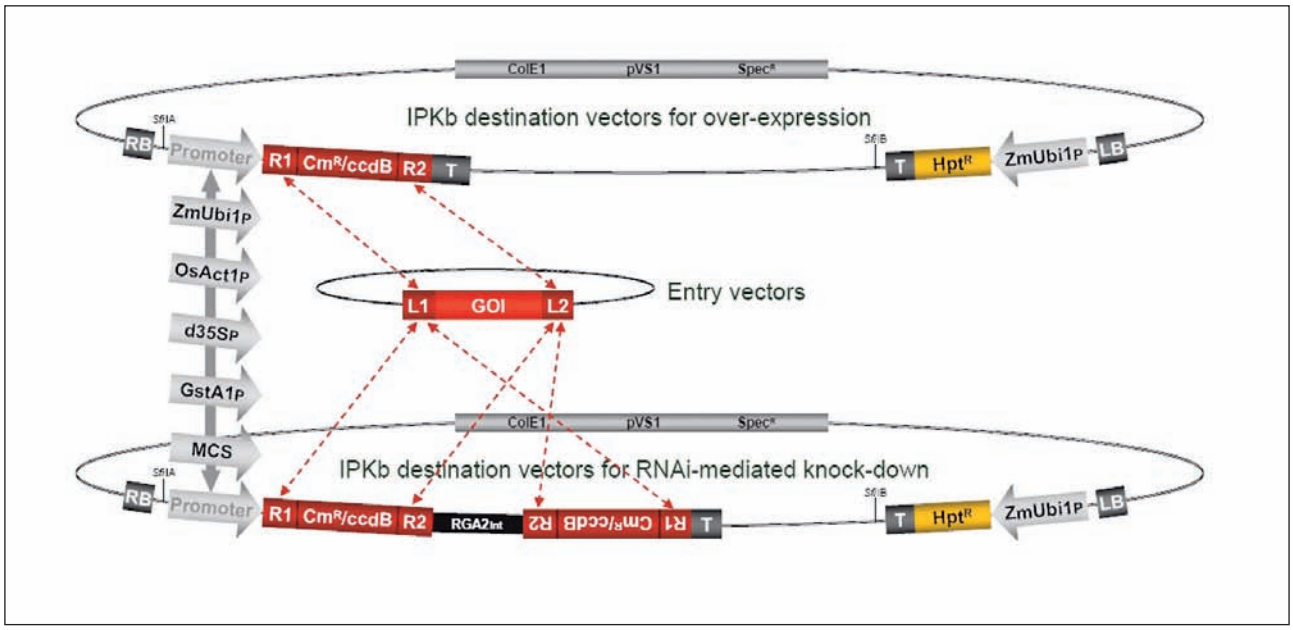

Fig. 44: Schematic representation of the IPKb over-expression and RNAi-mediated gene knock-down binary plasmid types. A gene sequence of interest (GOI) can be exchanged between an appropriate entry vector and an IPKb destination vector using the GATEWAY recombination system, as indicated by the attL and attR recombination sites (L1, L2, R1 and R2) and the dashed arrows. Derivatives are available for both plasmid types, involving any of the four promoters shown, or with a multiple cloning site (MCS) allowing the integration of further promoters. Cm^R: chloramphenicol resistance gene for selection of bacteria; ccdB: toxin gene for negative selection of bacteria; RGA2Int: intron of wheat *RGA2* gene; RB and LB: right and left T-DNA borders; ColE1: *E. coli* origin of replication; pVS1: *Agrobacterium* origin of replication; $Spec^R$: spectinomycin resistance gene for selection of bacteria; T: transcription termination sequence; Hpt^R: hygromycin resistance gene for plant selection; ZmUbi1P: maize ubiquitin 1 promoter; OsAct1P: rice actin 1 promoter; d35SP: doubled enhanced CaMV 35S promoter; GstA1P: wheat glutathione-S-transferase 1 promoter; *Sfi*IA and *Sfi*IB: *Sfi*I restriction sites (J. Kumlehn).

Stable genetic transformation of maize is of vital importance to enable detailed functional analyses of genes involved in plant-pathogen interaction. However, efficient maize transformation is still difficult to perform since only a few exotic genotypes are well amenable to this method and published protocols are only hardly reproducible in other labs. To provide a powerful technical platform within the DFG-Forschergruppe 666, we have developed a reproducible method of ***Agrobacterium*-mediated transformation of maize** using immature zygotic embryos. Following step-wise optimisation of the protocol, a number of transgenic maize lines were obtained for which stable genomic integration of the recombinant DNA as well as expression of the transgene has been verified (Ch. Kastner, C. Bollmann, H. Büchner).

In recent years, haploid technology has enormously contributed to plant breeding progress and proved to be one of the most successful biotechnological approaches. Following implementation of a novel principle of rendering isolated microspores competent to undergo pollen embryogenesis, **haploid plant formation has been established in maize**. In particular, freshly isolated microspores are pre-treated in a medium with limited metabolisable carbohydrate and nitrogen to perturb normal pollen maturation, followed by culture in a rich medium that supports embryogenic development. Further improvements of the basic method were achieved through optimised population density and co-cultivation of heterologous feeder tissues (F. Bakos, Ch. Kastner, S. Wolf, H. Büchner).

The generation of marker-free transgenic plants is regarded as a prerequisite for the successful implementation of genetic engineering in crop breeding. We have provided experimental evidence that selectable marker genes can be eliminated in an exceedingly efficient manner from transgenic **barley** using *Agrobacterium*-mediated co-transformation followed by the separation of unlinked effector and marker genes through genetic segregation in populations of pollen-derived doubled haploids. In a project funded by the BMBF, fourteen different methods of co-transfer of independent T-DNAs have been tested. The so far highest proportion of unlinked integration of marker and effector genes has been obtained upon the employment of a bacterial clone carrying the two different T-DNAs on two separate binary vectors. By this method, more than 7 percent of the embryos inoculated with agrobacteria lead to the formation of primary transgenic plants, from which **marker-free, homozygous transgenic lines** have been **instantly obtained through embryogenic pollen culture** (E. Kapusi, G. Hensel, S. Wolf, N. Levy-Guarda).

As a member of the PRO-GABI consortium we have produced more than 1,500 transgenic barley and 200 **transgenic wheat lines using 37 promoter-reporter gene constructs and 17 promoter-effector gene constructs**. These plants constitute a valuable basis for the ongoing characterisation of novel promoters or promoter elements and their use in approaches to the genetic engineering of cereals (G. Hensel, C. Marthe, E. Grützemann).

In the context of a collaboration with the Gene Expression group, transgenic winter wheat lines that over-express either an amino acid or a sucrose transporter have been generated. This project aims at the creation of **wheat lines with increased grain protein content**. For both constructs, selectable marker-free transgenic lines have been generated, which now permit a comprehensive characterisation under field conditions (I. Saalbach, S. Knüpffer, P. Hoffmeister).

As a regulator of a number of transcription factors, the phytohormone abscisic acid (ABA) is implicated in many developmental processes in the context of seed formation, such as embryo differentiation, storage protein synthesis and seed dormancy. In collaboration with the Novoplant GmbH and the Gene Expression group we have produced **transgenic pea lines with high seed-specific expression of an ABA-specific single-chain antibody**. The preliminary characterisation of these lines revealed a remarkable modulation of ABA-content and a **significant increase in the albumin and globulin fractions of seeds** as well as of the individual seed weight (I. Saalbach, S. Knüpffer, P. Hoffmeister).

To provide a technological platform for future functional gene analyses in the **apomictic model species *Hypericum perforatum***, we have developed a method of **stable *Agrobacterium*-mediated transformation** using stem segments of seedlings as gene transfer target for the generation of transgenic plants (S. Freist, G. Hensel).

Collaboration

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. N. Stein;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. F.M. Mette;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Expression Mapping; Dr. L. Altschmied;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Gene Expression; Dr. W. Weschke, Dr. H. Weber, Dr. N. Sreenivasulu;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein, D. Koszegi;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, D. Floß;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer.

Outside the Institute:
Novoplant GmbH, Gatersleben; Dr. D. Falkenburg;
SunGene GmbH, Gatersleben; Dr. J. Lerchl, Dr. B. Tschiersch, Dr. Ch. Biesgen;
BASF Plant Science, Ludwigshafen; Dr. T. Wetjen, Dr. S. Bieri;
Humboldt University Berlin, Institute of Biology, Berlin; K. Rosner;
Nordsaat Saatzucht GmbH, Böhnshausen; Dr. R. Schachschneider;
Saaten-Union, Resistenzlabor, Hovedissen; Dr. J. Weyen;
Federal Centre for Breeding Research on Cultivated Plants (BAZ), Quedlinburg; Dr. J. Schubert, Dr. A. Habekuss, Dr. V. Fomitcheva;
Justus Liebig University Gießen, Institute of Phytopathology and Applied Zoology (IPAZ), Gießen; Prof. K.-H. Kogel, Dr. G. Langen;
Friedrich Alexander University Erlangen-Nuremberg, Institute of Biochemistry, Erlangen; Prof. U. Sonnewald, Dr. L. Voll;
University of Regensburg, Department of Cell Biology and Plant Physiology, Regensburg; Prof. T. Dresselhaus, Dr. M. Gahrtz;
Technical University Munich, Institute of Phytopathology, Munich; Prof. R. Hückelhoven;
Christian Albrechts University Kiel, Institute of Botany, Kiel; Prof. K. Krupinska;
University of Zurich, Institute of Biochemistry, Zurich, Switzerland; Dr. A. Honegger;
Scottish Crop Research Institute, Genome Dynamics Department, Invergowrie, UK; Dr. D. Leader, Dr. C. Lacomme, J. Middlefell-Williams;
Thomas Jefferson University, Jefferson Medical College, Department of Cancer Biology, Philadelphia, USA; Dr. N. Borisjuk.

Publications

Peer Reviewed Papers
Goedeke, S., G. Hensel, E. Kapusi, M. Gahrtz & J. Kumlehn: Transgenic barley in fundamental research and biotechnology. Transgenic Plant J. 1 (2007) 104-117.
Himmelbach, A., U. Zierold, G. Hensel, J. Riechen, D. Douchkov, P. Schweizer & J. Kumlehn: A set of modular binary vectors for transformation of cereals. Plant Physiol. 145 (2007) 1192-1200.
Vorwieger, A., C. Gryczka, A. Czihal, D. Douchkov, J. Tiedemann, H.-P. Mock, M. Jakoby, B. Weisshaar, I. Saalbach &

H. Bäumlein: Iron assimilation and transcription factor controlled synthesis of riboflavin in plants. Planta 226 (2007) 147-158.

Book Chapters

Hensel, G., V. Valkov, C. Marthe & J. Kumlehn: *Agrobacterium*-mediated transformation of various barley (*Hordeum vulgare* L.) genotypes. In: Xu, Z. (Eds.): Biotechnology and sustainable agriculture 2006 and beyond. Springer, Dordrecht/The Netherlands (2007) 143-145.

Matzk, F., S. Prodanovic, A. Czihal, J. Tiedemann, F. Arzenton, F.R. Blattner, J. Kumlehn, L. Altschmied, I. Schubert, A. Johnston, U. Grossniklaus & H. Bäumlein: Genetic control of apomixis: preliminary lessons from *Poa*, *Hypericum* and wheat egg cells. In: Hörandl, E., U. Grossniklaus, P.J. van Dijk & T.F. Sharbel (Eds.): Apomixis: evolution, mechanisms and perspectives. Regnum Veg. 147, A. R. G. Gantner Verlag, Rugell/Liechtenstein (2007) 159-166.

Other Publications

Kumlehn, J., P. Schweizer, G. Langen, S. Bieri & T. Wetjen: PROGABI: Pflanzliche Abwehrmechanismen gegen Pilzbefall gezielt einschalten. GenomXPress Sonderausgabe März (2007) 24.

PhD and Diploma Theses

Michael, M.: Untersuchungen zur Etablierung eines Selektionsmarkersystems auf der Grundlage der Phosphomannose-Isomerase aus *E. coli* für die Transformation von Gerste. (Master) Leibniz-Universität Hannover, Naturwissenschaftliche Fakultät, Hannover (2007) 57 pp.

Lectures, Posters and Abstracts

V7, V83, V129, V302, P19, P20, P21, P22, P23, P28, P29, P46, P47, P59, P64, P74, P83, P84, P85, P86, P88, P89, P100, P101, P102, P106, P107, P108, P125, P126, P136, P137, P166, P167, P173, P177, P201, P202, P219, P224, P225, P226, P240, P242, P243, P244.

Additional Funding

For further information see the survey page 217.

Research Group: Yeast Genetics

Head: Prof. Gotthard Kunze

Scientists

IPK financed
Böer, Erik, Dr. (Annex, 01.09.-31.10.2007)
Florschütz, Kristina, Dr. (0,75 P, 01.01.-31.03.2007)
Körner, Martina, Dr. (Annex, since 01.09.2007)
Scholz, Anja (0,5 Annex)
Steinborn, Gerhard, Dr. (P, till 28.02.2007; Annex, 01.04.-30.09.2007)

Grant Positions
Böer, Erik, Dr. (Industry, till 31.08.2007, since 01.11.2007)
Florschütz, Kristina, Dr. (AIF, since 01.04.2007)
Kaiser, Christian (Saxony-Anhalt)
Körner, Martina, Dr. (AiF, till 31.08.2007)

Visiting Scientists
Adholeya, Alok, Dr. (BMBF, 16.07.-26.07.2007)
Baronian, Keith, Dr. (DLR, 10.06.-01.07.2007)
Kumar, Sanjeev (BMBF/DLR, 01.09.- 12.10.2007)
Prasad, Gandham Satyanarayana, Dr. (DFG, 30.07.-27.10.2007)
Steinborn, Gerhard, Dr. (self-financed, 09.03.-31.03.2007)

Scholars
Knobloch, Peggy (self-financed, PhD scholarship, 15.06.-30.11.2007)
Perez, Vanessa Bou (COMEAST scholarship, 15.01.-14.04.2007)
Sedzielewska, Kinga (COMEAST scholarship, since 19.11.2007)
Watzke, Katja (DBU scholarship)

Goals

The major objective of the research group is the development of yeast as a model organism for the analysis of **osmo-tolerance**, and as an expression platform for **heterologous gene expression**. The latter is being exploited for **functional gene analysis** in plants and microbes, as well as for the production of heterologous proteins. The yeast species used include both *Saccharomyces cerevisiae* and **non-*Saccharomyces* yeasts** such as *Arxula adeninivorans*. Yeasts and filamentous fungi also constitute a source of genes, which could be used for metabolic redesign of plants, in order to engineer improved quality of end products, or to develop recombinant microbes for use as biosensors for detection of environmental pollution.

Research Report

Yeasts like *A. adeninivorans* with extremely high levels of **osmo-tolerance** are particularly suitable as model organisms for detailed analyses of this phenomenon in plants and yeasts. The programme, which includes the intergroup project "Molecular analysis of salt tolerance in barley" as well as the analysis of this tolerance in the osmo-tolerant yeast *A. adeninivorans,* is focussed on the analysis of the key pathways that underlie this tolerance, and the identification of compatible solutes. cDNA sequences of barley and *A. adeninivorans* encoding for products improving osmo-tolerance are identified after transformation of the osmo-sensitive yeast *S. cerevisiae*. The analysis of the first selected *A. adeninivorans* genes including gene products demonstrates that in contrast to organisms with moderate osmo-resistance, which activate the **HOG pathway** by the phosphorylation of the relevant enzymes, highly osmo-resistant yeasts additionally induce the expression of genes in this pathway, such as the MAPKK kinase *ASTE11* and the MAP kinase *AHOG1*. Phosphorylated Ahog1p induces the expression of genes encoding the synthesis of **compatible solutes**, such as glycerol, erythritol and mannitol. Whereas the levels of glycerol and erythritol correlate directly with the osmolarity of the culture media, intracellular mannitol is accumulated to a very high extent and relatively independent of the osmolarity of the medium. This effect, in conjunction with the combination of phosphorylation and gene induction, seems to provide a better adaptation during transition from low to high osmolarity conditions. In addition biochemical analysis has shown that *A. adeninivorans* is able to synthesise mannitol by two pathways (1) fructose can be converted to mannitol by using a NaCl-inducible mannitol dehydrogenase and (2) fructose-6-phosphate is converted via mannitol-1-phosphate to mannitol with the enzymes mannitol-1-phosphate-dehydrogenase (not NaCl-inducible) and an unspecific phosphatase. Since both enzymes are encoded by different genes and use different coenzymes, we postulate the function of these two pathways as a conversion of NADH ↔ NADPH and the use of mannitol as carbon source and compatible solute. Analysis of gene expression level including the construction of the respective gene disruption mutants is in progress to clarify this phenomenon (E. Böer, G. Steinborn, M. Hajirezaei; Molecular Plant Physiology group).

A. adeninivorans is able to assimilate and ferment many compounds as its sole source for energy and carbon. This includes tannin, pyrogallol, protocatechuic acid, purine and uric acid. The metabolism of these compounds is based on pathways that are either completely unknown or only partially characterised (e.g., tannin and purine biodegradation). The first steps in **tannin metabolism** were

identified by means of the isolation and characterisation of the genes involved and their respective gene products. It is hydrolysed to gallic acid by the enzyme tannase, and subsequently converted to pyrogallol by gallate decarboxylase. The third step is the conversion of pyrogallol to 2-hydroxy mucoic acid by catechol-1.2 dioxygenase. All these genes are of biotechnological interest – the gene encoding tannase may be useful as a means to reduce the amount of tannin present in animal feedstock and agricultural waste water, or may serve to improve biogas production based on plant materials (E. Böer, G. Steinborn, H.-P. Mock; Applied Biochemistry group, M.R. Hajirezaei; Molecular Plant Physiology group; see Fig. 45).

The exploitation of yeasts and fungi as a source for genes encoding proteins of biotechnological interest has been targeted predominantly at those, which may have an impact on the quality of plant products. Some specific examples are the *A. adeninivorans*-derived genes encoding enzymes with broad substrate specificity such as **tannase**, phytase, gallat decarboxylasae and **mannitol dehydrogenase**. These may be of future value as feed and food additives, for development of biocatalytic processes, and may also play a role in biogas production since the presence of mixtures of these enzymes has been shown to significantly improve biogas yield (E. Böer). Based on differences in their substrate specificity, both native and recombinant **anthocyanases**

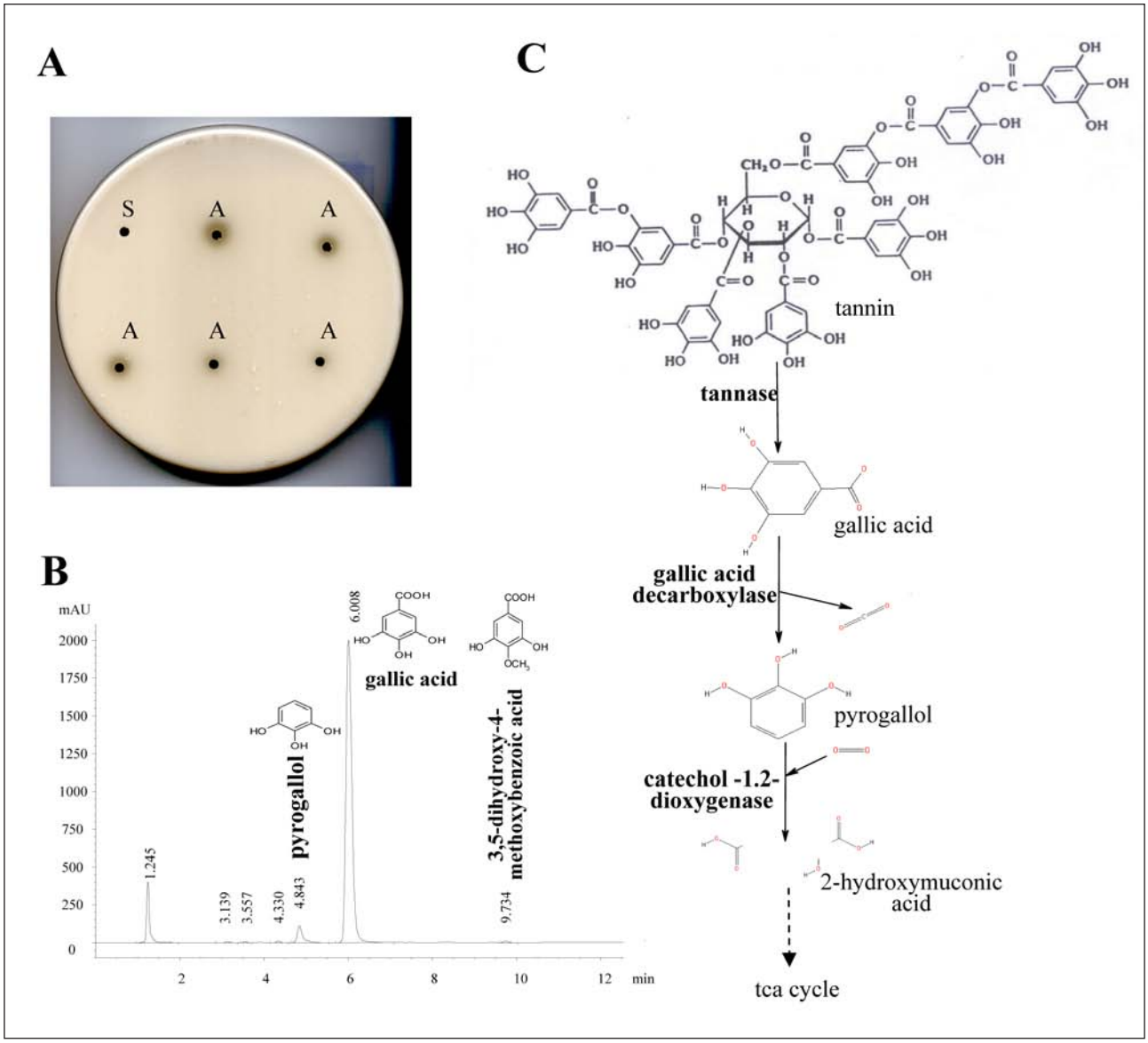

Fig. 45: Tannin degradation by *A. adeninivorans*. (A) Screening of different *A. adeninivorans* wildtype strains as putative gene donors for tannase genes. For this purpose media of various yeast cultures were dropped onto agar plates containing tannin. During incubation (18 h, 30 °C) the enzyme tannase cleaves tannin in gallic acid which causes clear zones. Using this method *A. adeninivorans* wildtype strains (A) were screened which synthesise and accumulate tannase in the culture medium. *S. cerevisiae* (S) as tannase negative yeast was used as a control.
(B) Degradation of gallic acid to pyrogallol. *A. adeninivorans* LS3 was cultured for 48 h in yeast minimal medium with gallic acid as carbon source. After harvesting, protein extracts were prepared and used for bioconversion of 0.1 mg ml^{-1} gallic acid. MS analyses have been demonstrated that pyrogallol and not 3.5-dihydroxy-4-methoxybenzoic acid is accumulated as reaction product of gallat decarboxylase.
(C) Tannin degradation pathway. Tannin is digested to gallic acid by secreted tannase. Subsequently intracellular localised gallic acid decarboxylase converted gallic acid to pyrogallol which is again converted to 2-hydroxy mucoic acid by catechol-1,2 dioxygenase (E. Böer, R. Sietmann: Univ. of Greifswald).

from *Candida molischiana* and *Schizosaccharomyces pombe* have been further analysed. Both enzymes are particularly suitable for decolorising anthocyanin-containing products such as grape extract (P. Knobloch, G.S. Prasad).

The **wide-range integrative yeast expression vector system** based on *A. adeninivorans*-derived plasmids has been further refined. A set of new cassettes with inducible promoters have been involved in the system. All promoters that are induced by the nitrogen source allow the expression of genes encoding toxic gene products. For example the *ATAN* gene encoding for tannase has been expressed for the first time at a very high level in *A. adeninivorans* by using the *AYNI* promoter (from the *nitrite reductase* gene) as expression element. In combination with the multicopy integration system based on auxotrophic selection markers with deleted stable promoter integration of high-copy numbers of expression cassettes with inducible promoters and an increased expression level in *A. adeninivorans, S. cerevisiae* and *Hansenula polymorpha* are possible under inducible conditions (G. Steinborn, E. Böer, N. Straube, A. Schröter). In addition it has been used to express bacterial genes from *Ralstonia euthropha* and *Methylobacterium extorquens* in order to synthesise **polyhydroxyalkanoate** (PHA), a biodegradable plastic (A. Scholz, H.-P. Mock; Applied Biochemistry group).

Another established direction in the research group involves the development of yeast biosensors (mainly *A. adeninivorans*) for the detection of estrogenic activities in environmental samples, i.e., urine, blood and milk. The sensor is based on recombinant *A. adeninivorans* cells, which includes the human estrogen receptor α (hERα) and is designed as estrogen screen assay with biochemical measurement as well as microbial biosensor with amperometric detection method. The **estrogen screen assay** has been validated for its suitability to measure estrogens and estrogen-like substances in samples of different wastewater treatment plants that exhibits high matrix effects. With a detection limit between 6 and 8 ng l^{-1} for 17 β-estradiol (E2), an in-house reproducibility lower than 5 ng l^{-1} the assay is applicable for a range of 10 to 80 ng l^{-1} effective E2 concentration. Based on these parameters the sensor is currently the most sensitive available for endocrine-disrupting substances (M. Körner, C. Kaiser, K. Florschütz, K. Baronian; see Fig. 46).

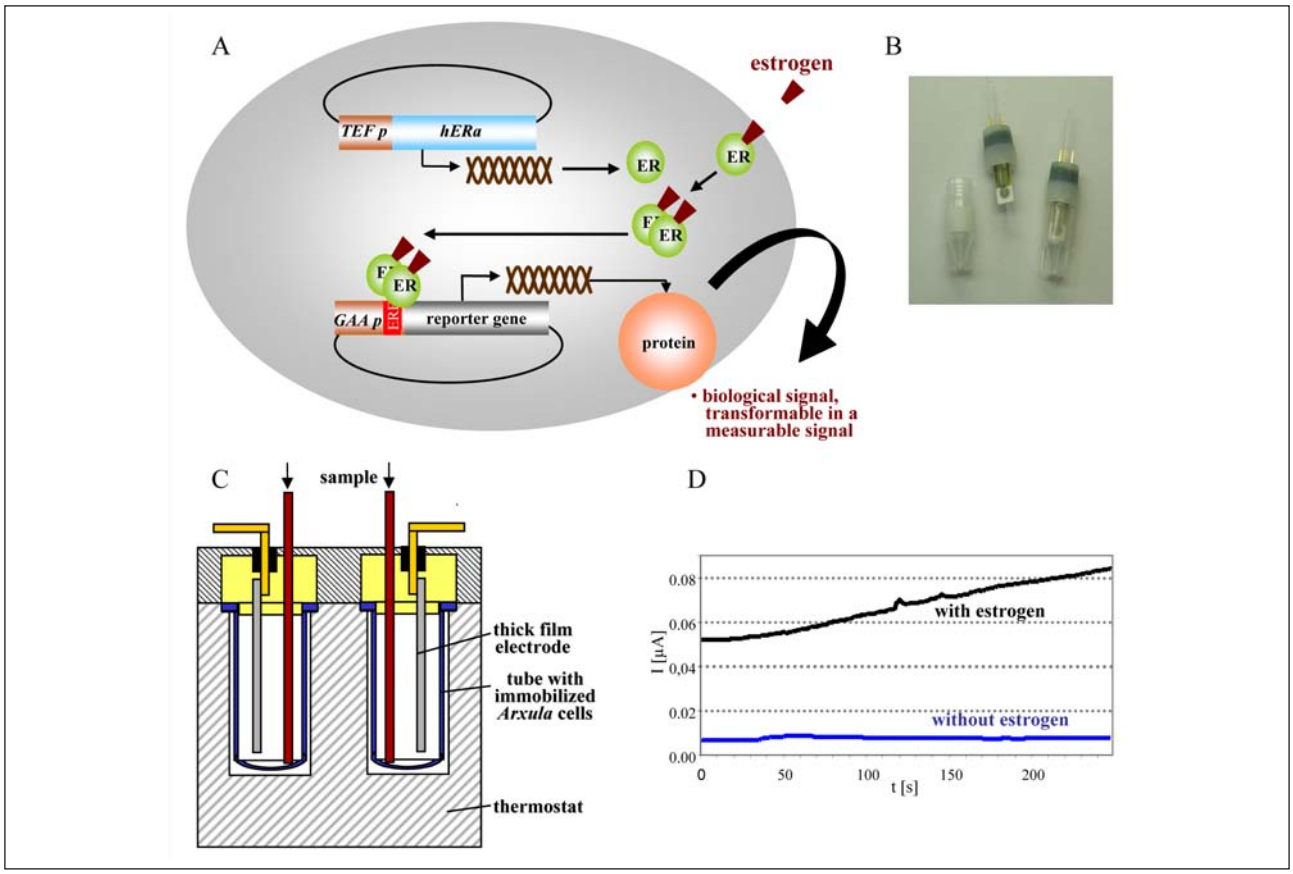

Fig. 46: Microbial biosensor for amperometric detection of estrogens and estrogen derivates. (A) Measuring principle. As microbial sensor component recombinant *A. adeninivorans* strains are used harboring two heterologous expression cassettes with *human estrogen receptor* α and the *phyK* reporter gene. In the presence of estrogens the estrogen receptor, which is constitutively expressed from the first cassette interacts with these components and is able to bind the estrogen response element (ERE) region in the *GAA* promoter localised on the second cassette. This results in the activation of the *phyK* gene which expresses phytase. The concentration of the recombinant secreted enzyme correlates with the concentration of estrogens. (B) Measuring chamber with immobilised *A. adeninivorans* cells and thick film electrode. (C) Measuring system (Estr-A monitor) with two measuring chambers and thermostat. (D) Measuring curves of estrogen and estrogen free samples. Aminophenylphosphate as substrate is hydrolysed by the recombinant phytase in p-chinominin and phosphate. p-Chinominin as electrochemical active substance is amperometric measured by the thick-film electrode (M. Körner, C. Kaiser).

A second biosensor project has been developed and adapted **DNA biosensors** for the taxonomic analysis of fungi (arbuscular mycorrhiza) as well as for the identification and classification of mycorrhiza residing at plant roots. Based on piezo-crystals plus genera and species-specific mycorrhiza rDNA sequences, the sensor is able to analyse the mycorrhizal content in plant populations. The sensor has been validated and applied in the analysis of the mycorrhizal content in a *Vetiveria zizanioides* population growing under extreme conditions (K. Florschütz, K. Watzke, K. Sedzielewska, V. Bou Perez, G. Oswald).

Collaboration

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Molecular Cell Biology, Research Group Molecular Plant Physiology; Dr. M. Hajirezaei;
Dept. of Molecular Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Molecular Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Molecular Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
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ARTES Biotechnology GmbH, Düsseldorf; Dr. M. Piontek;
ASA Spezialenzyme GmbH, Braunschweig; Dr. A. Cordes;
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Bundesanstalt für Materialforschung und -prüfung (BAM), Berlin; Dr. G. Kley, Dr. C. Piechotta;
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Christchurch Polytechnic Institute, Christchurch, New Zealand; Dr. K. Baronian;
c-LEcta GmbH, Leipzig; Dr. M. Struhalla;
Institut für Automation und Kommunikation e.V. Magdeburg (ifak), Magdeburg; Dr. A. Auge;
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PharmedArtis GmbH, Aachen; Prof. G. Gellissen;
Baumschulen Oberdorla GmbH, Oberdorla; Dr. H. Dembny, Prof. E. Arand;
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University of Delhi, Department of Microbiology, New Delhi, India; Prof. T. Satyanarayana;
Energy and Resources Institute (teri), Delhi, India; Dr. A. Adholeya;
University of Greifswald, Institute of Genetics and Biochemistry, Greifswald; Prof. R. Bode, Prof. R. Schauer.

Publications

Peer Reviewed Papers

Böer, E., G. Steinborn, G. Kunze & G. Gellissen: Yeast expression platforms. Appl. Microbiol. Biotechnol. 77 (2007) 513-523.

Böer, E., G. Steinborn, A. Matros, H.-P. Mock, G. Gellissen & G. Kunze: Production of interleukin-6 in *Arxula adeninivorans*, *Hansenula polymorpha* and *Saccharomyces cerevisiae* by applying the wide-range yeast vector (CoMed™) system to simultaneous comparative assessment. FEMS Yeast Res. 7 (2007) 1181-1187.

El Fiki, A., G.E. Metabteb, C. Bellebna, T. Wartmann, R. Bode, G. Gellissen & G. Kunze: The *Arxula adeninivorans ATAL* gene encoding transaldolase-gene characterization and biotechnological exploitation. Appl. Microbiol. Biotechnol. 74 (2007) 1292-1299.

Kaur, P., G. Kunze & T. Satyanarayana: Yeast phytases: present scenario and future perspectives. Crit. Rev. Biotechnol. 27 (2007) 93-109.

Kaur, P., A. Lingner, B. Singh, E. Böer, J. Polajeva, G. Steinborn, R. Bode, G. Gellissen, T. Satyanarayana & G. Kunze: *APHO1* from the yeast *Arxula adeninivorans* encodes an acid phosphatase of broad substrate specificity. Anton. Leeuw. Int. J. G. 91 (2007) 45-55.

Minocha, N., P. Kaur, T. Satyanarayana & G. Kunze: Acid phosphatase production by recombinant *Arxula adeninivorans*. Appl. Microbiol. Biotechnol. 76 (2007) 387-393.

Steinborn, G., G. Gellissen & G. Kunze: A novel vector element providing multicopy vector integration in *Arxula adeninivorans*. FEMS Yeast Res. 7 (2007) 1197-1205.

Steinborn, G., T. Wartmann, G. Gellissen & G. Kunze: Construction of an *Arxula adeninivorans* host-vector system based on *trp1* complementation. J. Biotechnol. 127 (2007) 392-401.

Tag, K., K. Riedel, H.J. Bauer, G. Hanke, K.H.R. Baronian & G. Kunze: Amperometric detection of Cu^{2+} by yeast biosensors using Flow Injection Analysis (FIA). Sensors Actuators B 122 (2007) 403-409.

PhD and Diploma Theses

Heide, K.: Etablierung und Validierung eines *online*-Analysators zur Erfassung östrogen-wirksamer Substanzen mittels Hefezellen-Dickschichtsensors. (Diploma Thesis) Hochschule Anhalt (FH) Köthen (2007) 76 pp.

Müller, I.: *Arxula adeninivorans* als Produzent von Polyhydroxyalkanoaten (PHA) – Expression der Gene *phbA* und *phbB* von *Ralstonia euthropha*. (Diploma Thesis) Hochschule Anhalt (FH), Köthen (2007) 72 pp.

Straube, N.: Synthese und Analyse von rekombinanter Anthocyanase aus *Schizosaccharomyces pombe* in *Arxula adeninivorans*. (Diploma Thesis) Hochschule Anhalt (FH), Köthen (2007) 70 pp.

Tulke, D.: Hefezellen als Produzenten von rekombinanten Anthocyanasen. (Bachelor) Hochschule Anhalt (FH), Köthen (2007) 91 pp.

Lectures, Posters and Abstracts

V119, V130, V131, V132, V191, P16, P43, P44, P123, P222.

Additional Funding

For further information see the survey page 218.

Pflanzengenom-Ressourcen-Centrum (PGRC)

Koordinator: Dr. habil. Patrick Schweizer

Das Pflanzengenom-Ressourcen-Centrum (PGRC; http://pgrc.ipk-gatersleben.de/) des IPK erbrachte als Forschungs- und Dienstleistungsplattform im Jahr 2007 Serviceleistungen für interne Nutzer und koordinierte internationale Kooperationen und Forschungsnetzwerke im Bereich Genomforschung der Gerste. Grundlegend hat sich an der Organisation des PGRC nichts geändert. Allerdings ist zu erwarten, dass die erfolgte Fusion der Arbeitsgruppen „Bioinformatik" und „Informationstechnologie" unter der Leitung von Dr. Uwe Scholz auch für das PGRC positive Auswirkung haben wird, indem sich die Bereitstellung von Werkzeugen der Genomforschung und die Aufrechterhaltung respektive Erweiterung der dafür notwendigen technischen Infrastruktur nun in einer Hand befinden.

Für den wissenschaftlichen Fortschritt der zum PGRC gehörenden Arbeitsgruppen wird auf die Jahresberichte der jeweiligen Gruppen verwiesen.

1. PGRC-Service:
Die in-Haus-Sequenzierung auf dem ABI 3730-System hat sich bewährt, was sich in einer deutlich erhöhten Anzahl Auftragssequenzierungen niederschlug (von 39.041 in 2006 auf 63.600 in 2007). Die hohe Qualität der Sequenzdaten erlaubt nun z. B. PCR-Fragment Sequenzierung für SNP (single nucleotide polymorphism)-Analysen ohne wesentlichen Editieraufwand. Vorbereitungen wurden getroffen für den neuen „Genotyping"-Service, der ab 2008 verfügbar sein wird. Dieser Service bietet den Nutzern DNA-Fragmentanalysen auf dem MegaBACE1000 System mit 96 Kapillaren an, das dadurch einer neuen Bestimmung zugeführt werden konnte. Erste Erfahrungen bezüglich Datenqualität waren positiv. Der „Arraying"- und Klonservice wurde stärker nachgefragt als in den vergangenen Jahren, vor allem für „spotting" von Kolonie-filtern von Genbanken und für die Erstellung von Sicherheitskopien. Die Unterstützung des TILLING-Projektes der Gerste im Haus wurde weiterhin fortgeführt mit dem Ziel einer späteren Umwandlung in einen PGRC-Service.

2. Netzwerke:
Zwei vom BarleyGenomeNet, einem vom PGRC koordinierten Europäischen Netzwerk von Institutionen, eingereichte ERA-PG-Anträge wurden bewilligt, und die Projekte sollen 2008 auch am IPK anlaufen. In den Projekten soll Assoziationsgenetik im großen Umfang (Pro-

Plant Genome Resources Centre (PGRC)

Coordinator: Dr. Patrick Schweizer

The Plant Genome Resources Centre (PGRC; http://pgrc.ipk-gatersleben.de/) of the IPK is a research and service platform and has provided service to users in-house in 2007, besides continuing to coordinate international cooperations and networks in the field of crop plant genomics, especially barley genomics. Generally, the organisation of the PGRC has not changed in 2007. However, PGRC is expected to benefit from the fusion of the group "Bioinformatics" with "Information Technology" leading to the new group "Bioinformatics and Information Technology" because the build-up of bioinformatics tools and providing of the necessary information technology is now managed by the same unit.

Scientific progress within research groups that belong to the PGRC is not presented here. Please refer to the annual reports of the corresponding groups.

1. PGRC Service:
In-house sequencing service on the ABI 3730 instrument has proven to be highly efficient, which is reflected by an increased ordering (63,600 sequences in 2007 compared to 39,041 in 2006). For instance, data quality now allows to sequence PCR fragments for SNP (single nucleotide polymorphism) detection without much manual editing of raw sequence data. Preparations for the new PGRC service "Genotyping" have been done, which will be available from 2008 on. This service offers DNA fragment analysis on the MegaBACE1000 system to users. Thus, the MegaBACE instrument could be allocated to a new function. First experience regarding data quality was positive. The arraying and clone services were used more intensively than in previous years, mainly because of enhanced requests for colony spotting of DNA libraries and for establishment of backup-copies of libraries. Support of the TILLING project of barley that is running at the IPK was continued aiming at a transformation into a PGRC service.

2. Networks:
Two ERA-PG projects submitted by BarleyGenomeNet, a European network of institutions that is coordinated by the PGRC, were successful and should start up also at IPK in 2008. In project "EXBARDIV" (for "EXploiting BARley DIVersity"), large-scale association mapping is planned whereas in project "BARCODE" morphological mutants

jekt Akronym „EXBARDIV"), Mutationskartierung und BAC-Endsequenzierung (Projekt Akronym „BARCODE") durchgeführt werden. Ein weiteres, vom PGRC initiiertes bilaterales deutsch-ungarisches Netzwerk „PlantResource" wird nun auch in Ungarn gegenfinanziert, nachdem es in Deutschland bereits seit 2005 vom Land Sachsen-Anhalt gefördert wird. „PlantResource" hat vor allem die Verbesserung der abiotischen Stressresistenz von Getreide zum Ziel. Weitere für das PGRC bedeutsame Netzwerke wurden gegründet oder weiterentwickelt, mit maßgeblicher Beteiligung von PGRC-Mitgliedern (z. B. Dr. N. Stein). Zu erwähnen ist insbesondere das Internationale Gerstengenom-Sequenzierungs-Konsortium (IBSC) und die COST-Aktivität „TritiGen".

Patrick Schweizer, Januar 2008

will be mapped, also by the help of massive and BAC-end sequencing. "PlantResource", a bilateral German-Hungarian network initiated by the PGRC has also received funding in Hungary in 2007 after it has been funded by the State of Saxony-Anhalt since autumn 2005. "PlantResource" mainly aims at the development of cereals with enhanced tolerance to abiotic stress. Last but not least, further networks of high relevance to the PGRC were initiated or extended with strong commitment from PGRC members (e. g. Dr. N. Stein). Of special interest are the International Barley Genome Sequencing Consortium (IBSC) and the COST action "TritiGen".

Patrick Schweizer, January 2008

Die Entwicklung der Bioinformatik am IPK

Koordinator: Prof. Dr. Falk Schreiber

Neben der schon vor Jahren am IPK etablierten Arbeitsgruppe Bioinformatik (jetzt Bioinformatik und Informationstechnologie) ist es besonders der umfassenden Förderung durch das BMBF im Rahmen des Bioinformatik-Centrums Gatersleben-Halle (BIC-GH) zu verdanken, dass in den vergangenen Jahren eine vielseitige und kompetente Bioinformatik am Institut aufgebaut werden konnte. Im Rahmen von BIC-GH wurden die Arbeitsgruppen Mustererkennung, Netzwerkanalyse und Plant Data Warehouse gefördert. Für den wissenschaftlichen Forschritt der vier genannten Arbeitsgruppen im Jahr 2007 wird auf die Jahresberichte der jeweiligen Gruppen verwiesen. Hier sei nur kurz zusammengefasst: Die Gruppen haben ausgezeichnete Arbeit geleistet. Dies zeigt sich an Publikationen, nicht nur in führenden Bioinformatik-Zeitschriften (beispielsweise „Bioinformatics" und „BMC Bioinformatics"), sondern auch, entsprechend der Interdisziplinarität des Faches, in wichtigen Zeitschriften der Biologie, Informatik und Physik. Dies zeigt sich ebenso in erfolgreich eingeworbenen Drittmittelprojekten mit integralem Bioinformatik-Teil von der Sequenzierung bis zur Systembiologie. Und schließlich wurden mehrere Wissenschaftler der Bioinformatik des IPK in 2007 zu Professoren ernannt: zum 1. Oktober 2007 Dr. Ivo Große zum Professor für Bioinformatik an der Martin-Luther-Universität (MLU) Halle-Wittenberg, zum 1. November 2007 Dr. Falk Schreiber zum Professor für Pflanzliche Bioinformatik an der MLU Halle-Wittenberg (als gemeinsame Professur der MLU und dem IPK Gatersleben) und zum 1. März 2008 Dr. Dirk Koschützki zum Professor für Informatik an der Fachhochschule Furtwangen. Ohne die umfangreiche Förderung durch das BMBF wären diese Ergebnisse nicht möglich gewesen, und dem BMBF sei hier nochmals herzlich gedankt.

Das Jahr 2007 war für die Bioinformatik am IPK ein Jahr mit weitreichenden Veränderungen. Das Auslaufen der umfangreichen Förderung des BIC-GH durch das BMBF per 31. Oktober 2007 und der damit verbundene Wegfall der Arbeitsgruppen Plant Data Warehouse, Netzwerkanalyse sowie Mustererkennung (letzte zum 29. Februar 2008) machte eine Neustrukturierung der Bioinformatik erforderlich. So wurde die durch das Institut finanzierte Bioinformatik ausgebaut: Die bisherige Arbeitsgruppe Bioinformatik wurde um den Teil Informationstechnologie erweitert und die bisher durch das BMBF finanzierte Arbeitsgruppe Netzwerkanalyse als Arbeitsgruppe Pflanzliche Bioinformatik weitergeführt. Positiv war in diesem Umbruchprozess auch das erfolgreiche Einwerben einer

The Development of Bioinformatics at IPK

Coordinator: Prof. Falk Schreiber

Complementary to the research group Bioinformatics (now research group Bioinformatics and Information Technology), which has been long established, it is thanks in particular to the extensive support of the Federal Ministry of Education and Research (BMBF) in the context of the Bioinformatics Centre Gatersleben-Halle (BIC-GH), that such a diverse and competent bioinformatics presence has been established at the institute. Within the framework of the BIC-GH the research groups Pattern Recognition, Network Analysis and Plant Data Warehouse have been funded. The 2007 scientific successes of the four mentioned research groups are detailed in the annual reports for each group. In brief summary: the research groups have achieved excellent work. This is indicated in publications not only in leading bioinformatics journals (for example, "Bioinformatics" and "BMC Bioinformatics"), but also, in keeping with the interdisciplinarity of the field, in important journals in biology, computer science, and physics. It is also indicated by the successful attainment of external funding for projects with bioinformatics aspects, from sequencing to systems biology. In addition, several IPK scientists were appointed to professor positions in 2007: on October 1, 2007 Prof. Ivo Große as Professor of Bioinformatics at the Martin Luther University (MLU) Halle-Wittenberg, on November 1, 2007 Prof. Falk Schreiber as Professor for Plant Bioinformatics at the MLU Halle-Wittenberg (as a joint professorship of MLU and IPK Gatersleben), and on March 1, 2008 Dirk Koschützki as Professor for Computer Science at the Furtwangen University of Applied Sciences. Without the comprehensive support of the BMBF, these results would not have been possible, and we sincerely thank the BMBF once again.

The year 2007 was one of extensive changes for bioinformatics at the IPK. The expiry of the generous funding of the BIC-GH by the BMBF on October 31, 2007, and the associated phasing out of the research groups Plant Data Warehouse, Network Analysis and Pattern Recognition (the latter by February 29, 2008), made the restructuring of bioinformatics at the IPK necessary. IPK-funded bioinformatics was thus strengthened: the former research group Bioinformatics has been extended with an information technology direction, and the previously BMBF-funded research group Network Analysis has been continued as research group Plant Bioinformatics. In this process of upheaval it is also positive to see success in procuring Saxony-Anhalt State funding for a new junior

durch das Land Sachsen-Anhalt finanzierten Nachwuchsgruppe (Arbeitsgruppe Dateninspektion) sowie mehrere Drittmittelprojekte, besonders im Förderprogramm GABI-FUTURE.

Um die wissenschaftliche Arbeit der Gruppen langfristig zu stärken und besser zu koordinieren, wurde am IPK die Position des Koordinators Wissenschaftliche Bioinformatik geschaffen, die als gemeinsame Professur mit der MLU Halle-Wittenberg gestaltet wurde. Seine Aufgabe ist, die durch die interne und nationale Förderung am IPK initiierte Bioinformatik zu verstetigen und langfristig eine international anerkannte Plattform für die pflanzliche Bioinformatik sowie die computergestützten und theoretischen Aspekte der Systembiologie der Pflanze zu schaffen. Dazu soll die Bioinformatik-Forschung am IPK in enger Zusammenarbeit von biologisch orientierten und Bioinformatik-Arbeitsgruppen erhalten und ausgebaut, die Abstimmung der wissenschaftlichen Arbeit der Bioinformatik-Arbeitsgruppen intensiviert, und die Außenwirkung und internationale Sichtbarkeit der Bioinformatik gestärkt werden. In die Koordination sind die Arbeitsgruppen Bioinformatik und Informationstechnologie, Dateninspektion, Genbank-Dokumentation, Mustererkennung und Pflanzliche Bioinformatik eingeschlossen.

Im Jahr 2008 wird ein Höhepunkt für die Bioinformatik am IPK das „International Symposium on Integrative Bioinformatics" (IB 2008) sein, welches das IPK vom 20. bis 22. August 2008 in der Leucorea Wittenberg veranstalten wird. Neben Experten aus den Gebieten integrative Bioinformatik und Systembiologie wie Dr. Peter Karp (SRI), Prof. Dr. Roland Eils (DKFZ Heidelberg) und Prof. Dr. Dietmar Schomburg (TU Braunschweig) werden Fachbeiträge, Software-Demonstrationen und Poster einen umfassenden Überblick zum aktuellen Stand der Forschung in der integrativen Bioinformatik geben. Weitere Informationen finden sich unter http://meetings.ipk-gatersleben.de/ib08/.

Falk Schreiber, Januar 2008

research group (research group Data Inspection), and external funding for multiple projects, in particular within the GABI-FUTURE Programme.

In order to strengthen and better coordinate the scientific work of the research groups in the long term, the position of a Bioinformatics Coordinator was created as a joint professorship with the MLU Halle-Wittenberg. The role of this coordinator is to perpetuate and strengthen the bioinformatics at the IPK, which was initiated by internal and national funding, and in the long term to create an internationally recognised platform for plant bioinformatics as well as for the computer-supported and theoretical aspects of plant systems biology. To this purpose, bioinformatics research at the IPK must be maintained and extended in close collaboration between biology-oriented and bioinformatics research groups, the coordination of scientific work between the bioinformatics research groups must be intensified, and the public perception and international visibility of bioinformatics at the IPK must be strengthened. The research groups Bioinformatics and Information Technology, Data Inspection, Genebank Documentation, Pattern Recognition, and Plant Bioinformatics are included in the sphere of coordination.

The highlight of 2008 for bioinformatics at the IPK will be the "International Symposium on Integrative Bioinformatics" (IB 2008), which will be held by the IPK at the Leucorea Wittenberg from August 20 to 22. In addition to experts in the fields of integrative bioinformatics and systems biology such as Dr. Peter Karp (SRI), Prof. Roland Eils (DKFZ Heidelberg), and Prof. Dietmar Schomburg (TU Brunswick); scientific presentations, software demonstrations, and posters will provide a comprehensive survey of the state-of-the-art in integrative bioinformatics. All those interested in participating are warmly invited to attend, and may find more information at http://meetings.ipk-gatersleben.de/ib08/.

Falk Schreiber, January 2008

Kolloquien, Seminare/ Colloquia and Seminars

Gatersleben Lectures

11. Januar 2007
Dr. K. Kalantidis, IMBB-FORTH, Vassilika Vouton, Crete, Greece: Unravelling systemic silencing in plants.

18. Januar 2007
Dr. I. Holme, Danish Institute of Agricultural Sciences, Research Centre Flakkebjerg, Dept. of Genetics and Biotechnology, Slagelse, Denmark: Transformation of barley by *Agrobacterium tumefaciens* infection of *in vitro* cultured ovules.

19. Februar 2007
Prof. G. Galili, Weizmann Institute of Science, Dept. of Plant Sciences, Rehovot/Israel: Lysine: a minor amino acid within a multiple functional, super regulated metabolic pathway.

21. Februar 2007
Dr. R. de Vos, Plant Research International, Wageningen, The Netherlands: Untargeted metabolomics as tool in plant biology and genetics.

26. Februar 2007
Prof. J. Fajkus, Masaryk University, Brno, Czech Republic: Evolution of plant telomeres and telomerases.

8. März 2007
Prof. H. Mertsching, Fraunhofer-Institut für Grenzflächen- und Bioverfahrenstechnik (IGB), Stuttgart, Germany: Tissue engineering: State of the art and new developments.

26. April 2007
Dr. M. Frank, BASF, Limburgerhof, Germany: Genetic engineering of late blight resistance in potato.

22. Mai 2007
Prof. G. Jürgens, Lehrstuhl Entwicklungsgenetik, ZMBP, Eberhard-Karls-Universität Tübingen, Germany: Regulation of membrane trafficking in *Arabidopsis*: section, endocytosis, recycling and cytokinesis.

26. Juni 2006
Dr. A. Johnston, University of Zurich, Switzerland: No longer the forgotten generation: The female gametophyte and gene regulation in *Arabidopsis.*

20. September 2007
Dr. P. Rabinowicz, The Institute of Genome Sciences, School of Medicine, University of Maryland, Baltimore, MD, USA: Plant genome sequencing: Shotgun, BACs, gene-enrichment or all of the above.

7. November 2007
Prof. C.E. Lawrence, Division of Applied Mathematics, Center for Computational Molecular Biology, Brown University, Providence, USA: Abuse of the mode in genomics and an ensemble based alternative.

7. Dezember 2007
Prof. F. Uhlmann, Chromosome Segregation Laboratory, Cancer Research UK, London Research Institute, London, UK: Mitotic chromosome structure and segregation.

Abteilungsseminare/ Seminars of the Departments Vavilov- und PGRC-Seminare/ Vavilov and PGRC Seminars

31. Januar 2007
Prof. DI Dr. H. Grausgruber, Department of Applied Plant Sciences and Plant Biotechnology, University of Natural Resources and Applied Life Sciences, Vienna, Austria: Neue Chancen für wenig genutzte Getreidearten durch funktionelle Lebensmittel?

14. Februar 2007
PD Dr. F. Asch, Rheinische Friedrich-Wilhelms-Universität Bonn, Institut für Nutzpflanzenwissenschaften und Ressourcenschutz, Bereich Pflanzenernährung, Bonn, Germany: A "natural lab" approach for salinity research.

28. Februar 2007
Dr. S. Stracke, IPK, Abteilung Genbank, Gatersleben, Germany: Impact of gene interactions and population structure on association studies for flowering time in barley.

25. April 2007
Dr. J. Ahlemeyer, Institut für Pflanzenbau und Pflanzenzüchtung I, Justus-Liebig-Universität, Gießen, Germany: Yield gained, diversity ventured? – Changes in agronomics traits and genome composition during 40 years of winter barley breeding.

13. Juni 2007
D. T.F. Endresen, Nordic Gene Bank, Alnarp, Sweden: Prediction of agricultural traits in plant genetic resources with ecological parameters.

20. Juni 2007
Dr. Y. Yan, Internationales Institut für Biophysik (IIB), Neuss, Germany: Biophoton emission of barley seeds.

1. August 2007
Dr. A. Giura, National Agricultural Research and Development Institute (INCDA), Fundulea, Romania: Development of wheat genetics stocks and their use at NARDI – Fundulea.

29. August 2007
G. M. Zubieta, PROINPA Foundation, Genetic Ressources, Cochabamba, Bolivia: PROINPA Foundation: Working to maintain the agrobiodiversity in Bolivia.

5. September 2007
M. Nagel, Abteilung Genbank, IPK, Gatersleben, Germany: Langlebigkeit von Saatgut unter ambienten Lagerungsbedingungen in der *ex situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen in Gatersleben.

12. September 2007
Dr. A. Bálint und Dipl-Ing. F. Szira, Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvásár, Hungary: Genetic and physiological studies of drought tolerance in barley.

10. Oktober 2007
Dr. K. Kowalczyk, Institute of Plant Genetics, Breeding and Biotechnology, Lublin, Poland: Current status of cereals research in the Institute of Plant Genetics, Breeding and Biotechnology in Lublin.

30. Oktober 2007
Dr. G. Barcaccia, University of Padova, Department of Environmental Agronomy and Crop Production, Legnaro, Italy: Using molecular markers for assessing and preserving genetic diversity in maize landraces: A case study.

7. November 2007
Dr. K. Baghalin, Department of Horticulture, Faculty of Agriculture, Azad University, Karaj Branch, Iran: Domestication approaches for Iranian natural resources of medicinal plants.

8. November 2007
Dr. U. Radelof und Dr. F. Wagner, ATLAS Biolabs GmbH, Berlin/Cologne, Germany: High performance gene expression profiling at ATLAS Biolabs.

14. November 2007
Prof. J. Puchalski, Botanical Garden, Center for Biological Diversity Conservation, Polish Academy of Sciences, Warsaw, Poland: Long-term seed storage of crop and native plants in the Botanical Garden of the Polish Academy of Sciences – research studies and practical issues.

10. Dezember 2007
Dr. H. Knüpffer, Abteilung Genbank, IPK, Gatersleben: The Mansfeld Database and the Encyclopedia of Life – report from the EoL Plant Species Pages Workshop (St. Louis, Missouri) and possible implications for biodiversity informatics at IPK.

18. Dezember 2007
Dr. S. P. Landjeva, Institute of Genetics, Bulgarian Academy of Sciences, Sofia, Bulgaria: Genetic variability of seed longevity after long-term storage in wheat.

Vavilov-Vortragsabende/ Vavilov Evening

13. Februar 2007
Dr. S. Jakob, Abteilung Genbank, IPK Gatersleben, Germany: Patagonien – Am Ende der Welt.

24. April 2007
Prof. M. Fischer, Dresden, Germany: Nepal – dem Mount Everest ein Stück näher.

Genetische Seminare/ Genetics Seminars

5. März 2007
Dr. T. Schwarzacher, University of Leicester, Leicester, UK: Evolution and function of repetitive sequences in cereal plant species.

9. März 2007
Prof. B.N. Prasad, Tribhuvan University, Kathmandu, Nepal: Prospect of biofertiliser for sustainable crop productivity.

2. April 2007
Dr. E. Albertini, University of Perugia, Perugia, Italy: In planta production of foreign proteins of pharmaceutical interest.

4. April 2007
Prof. D. Segal, Department of Molecular Microbiology & Biotechnology, Tel Aviv University, Tel Aviv, Israel: The COP9 signalosome – a plant regulator of photomorphogenesis assumes novel roles in animals – lessons from *Drosophila*.

14. Mai 2007
Dr. O. Mittelsten Scheid, Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria: Epigenetic changes in polyploid *Arabidopsis*.

4. Juni 2007
Dr. B. Rotter, GenXPro GmbH, Frankfurt am Main, Germany: Super TAG-reaping the high-hanging fruits of gene expression.

3. Juli 2007
Dr. S. Crockett, Institute of Pharmaceutical Chemistry, Graz, Austria: Impact of polyploidy on phytochemistry in medicinal plants: What is known?

5. Juli 2007
Dr. O. Calderini, CNR-IGV Perugia, Italy: Apomixis in *Paspalum simplex*: Physical mapping efforts.

31. August 2007
D. Kurihara, Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan: Functional analysis of plant Aurora kinases in chromosome segregation during mitosis.

4. September 2007
Dr. I. Grunwald, Fraunhofer-Institut für Fertigungstechnik und Angewandte Materialforschung, Bremen, Germany: First Aid by Sea Life – biological glues for medical applications.

11. September 2007
Dr. J. Scheller, Biochemisches Institut, Christian-Albrechts-Universität, Medizinische Fakultät, Kiel, Germany: IL-6 Transsignaling: Soluble cytokine receptors in control of acute and chronic inflammation.

24. September 2007
Prof. W.-H. Shen, IBMP-CNRS, Strasbourg, France: SETing epigenetic marks by histone methyltransferases.

9. Oktober 2007
Dr. W. Aufsatz, Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria: Elucidation of the role of the Rpd3-type histone deacetylase HDA6 in RNA-mediated silencing processes.

29. Oktober 2007
A. Sepsi, Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvásár, Hungary: Characterisation of a leaf rust resistant wheat – *Thinopyrum ponticum* partial amphidiploid using sequential multicolour GISH and FISH.

6. November 2007
Dr. B. Kilian, Max-Planck-Institut für Züchtungsforschung, Köln, Germany: Genetic diversity, evolution, and domestication of Triticeae in the fertile crescent.

14. November 2007
Prof. D. Collinge, LIFE Department, University of Copenhagen, Copenhagen, Denmark: Roles for a NAC transcription factor and DUF26 receptor-like protein kinase in *Blumeria-Arabidopsis* and barley interactions.

15. November 2007
Prof. X.F. Cao, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China: Biochemical and genetic analysis of histone modification in plants.

16. November 2007
Dr. E. Potokina, School of Biosciences, University of Birmingham, Birmingham, UK: Cis-regulatory mutations and limited pleiotropy in barley.

21. November 2007
Dr. S. Greiner, Botanisches Institut, Ludwig-Maximilians-Universität, München, Germany: *Oenothera*: Non-Mendelian inheritance and speciation.

27. November 2007
S. de Nooijer, University of Wageningen, Laboratory of Molecular Biology, Wageningen, The Netherlands: Organisation through aspecific interactions in plant nuclei.

4. Dezember 2007
Prof. H. Loxdale, Max-Planck-Institut für Chemische Ökologie, Jena, Germany: Here today, gone tomorrow: the strange life, times and population genetics of specialist cyclical parthenogens (tansy aphids).

10. Dezember 2007
Dr. H. Vogel, Max-Planck-Institut für Chemische Ökologie, Jena, Germany: Plant defenses and insect counter defenses.

11. Dezember 2007
Dr. S. Nasuda, Laboratory of Plant Genetics, Graduate School of Agriculture, Kyoto University, Kyoto, Japan: Do chromosomes 7HS* and 7HS** carry neocentromeres?: analysis of the telocentric barley chromosomes 7HS without centromeric repeats.

Zellbiologische Seminare/ Cell Biology Seminars

23. Januar 2007
Prof. W. Roos, Institut für Pharmazeutische Biologie und Pharmakologie, Halle/S., Germany: pH-Signaturen führen zur Expression des pflanzlichen Sekundärstoffwechsels.

16. April 2007
Dr. J. Beekwilder, PRI Wageningen, The Netherlands: Enzymes for modification of tomato flavonoids during processing.

24. Mai 2007
Prof. N. Carrillo, Instituto de Biología Moleculary Cellular De Rosario (IBR), Universidad Nacional de Rosario, Rosario, Argentinia: Genetic manipulation of electron distribution in chloroplasts: its effect on stress tolerance.

2. Juli 2007
Dr. S. Neumann, Leibniz-Institut für Pflanzenbiochemie, Halle/S., Germany: MetWare: A mass spectrometry storage and processing system.

18. Juli 2007
Dr. A. Adholeya, Biotechnology & Management of Bioresources, The Energy and Resources Institute, New Delhi, India: Application and *in vitro* studies in Mycorrhiza.

25. Oktober 2007
Dr. G. S. Prasad, Institute of Microbial Technology, Chandigarh, India: How close is close, and how far is far, do define a species in yeasts.

6. November 2007
Prof. J. K. Sainis, Molecular Biology Division, Bhabha Atomic Research Centre, Mumbai, India: Digital imaging technology in variety identification of wheat.

29. November 2007
Prof. D. Honys, Czech Academy of Sciences, Institute of Experimental Botany, Department of Pollen Biology, Prague, Czech Republic: Pollen transcriptomics; chips and tricks.

Waterman-Seminare/ Waterman Seminars

26. Januar 2007
Dr. T. Villmann, Universität Leipzig, Leipzig, Germany: Fuzzy classification of BIO-medical data using FLSOM.

1. Februar 2007
J. Baumbach, Universität Bielefeld, Bielefeld, Germany: CoryneRegNet – An ontology-based systems biology platform for data integration, analysis, and visualization of corynebacterial gene regulatory networks.

8. Februar 2007
Dr. B. Kersten, RZPD – Deutsches Ressourcenzentrum für Genomforschung GmbH, Berlin, Germany: GABI-primary databases: current content and future targets.

22. Februar 2007
Dr. H. Schoof, Max-Planck-Institut für Züchtungsforschung, Köln, Germany: Network matters: integrating plant genomic data.

20. März 2007
R. Winnenburg, Rothamsted Research, Biomathematics and Bioinformatics Division, Hertfordshire, UK: ONDEX in action – a data integration platform and its application.

4. Mai 2007
Dr. A. Kel, BIOBASE GmbH, Wolfenbüttel, Germany: Gene regulation code.

2. Juli 2007
A.O. Schmitt, Humboldt-Universität zu Berlin, Landwirtschaftlich-Gärtnerische Fakultät, Institut für Nutztierwissenschaften, Berlin, Germany: Long chromosomal deletions in fifteen inbred mouse lines and their implications for quantitative traits.

18. September 2007
Dr. O. Ebenhöh, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Golm, Germany: Structural and functional analysis of metabolism with the method of network expansion.

28. September 2007
Prof. M. Chen, College of Life Sciences, Zhejiang University, Hangzhou, China: Rice chip annotation system and gene regulatory sub-network inference.

18. Oktober 2007
Dr. P. Neuvial, Institut Curie, Service de Bioinformatique and Université Paris VII, Laboratoire de Probabilités et Modèles Aléatoires, Paris, France: Tools and Methods for analysis of DNA copy number microarrays.

25. Oktober 2007
M.M. Hoffmann, EMBL – European Bioinformatics Institute, Cambridge, UK: Predicting selection in promoters by simulating the effects of mutations.

26. Oktober 2007
Dr. G. Buck-Sorlin, Crop and Weed Ecology Group, University of Wageningen, Wageningen, The Netherlands: Genericness, modularity, and mutual embedding of programming paradigms for improved functional-structural plant modelling.

7. November 2007
Dr. J. Kopka, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Golm, Germany: GC-TOF-MS based metabolite profiling: recent developments and new potentials.

13. November 2007
B. Sommer, Universität Bielefeld, Bielefeld, Germany: CELLmicrocosmos – building and environment for the information center cell.

Wissenschaft trifft Wirtschaft/ Science meets Business

7. Februar 2007
Dr. M. Struhalla, c-LEcta GmbH, Leipzig, Germany: Entdeckung, Optimierung und Produktion von Enzymen für industrielle Anwendungen – Strategien und Technologien der c-LEcta GmbH.

Vorträge und Poster/ Lectures and Posters

Eingeladene Vorträge auf internationalen Tagungen (Auswahl)/ Invited Lectures at International Conferences (Selection)

Vorträge/Lectures

V1. Blattner, F.R.: Analysis of speciation processes in *Hordeum* (Poaceae) – evidence for sympatric speciation? – "New Horizons in Evolutionary Biology", University of Haifa, Haifa/Israel, 23.-25.01.2007.

V2. Graner, A.: The International Barley Sequencing Consortium, a global effort towards one goal. – Aaronsohn-ITMI Conference, Tiberias/Israel, 16.-20.04.2007.

V3. Graner, A.: Playing the gamut of diversity: association mapping in barley. – International Workshop "Molecular Plant Breeding", Beijing/China, 22.09.2007.

V4. Houben, A., R. Pickering, D. Gernand & T. Rutten (vorgetragen von Houben, A.): Mechanisms of selective chromosome elimination in embryos of interspecific crosses. – Symposium "Molecular Basis of Plant Breeding", Ch. Charan Singh University, Meerut/India, 26.-28.02.2007.

V5. Houben, A.: Elimination of chromosomes as a result of an intergenomic conflict. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

V6. Keller, E.R.J., A. Kaczmarczyk & A. Senula (vorgetragen von Keller, E.R.J.): Cryopreservation for plant genebanks. A matter between high expectations and cautious reservation. – Annual SLTB(Soc. Low Temp. Biol.)-Meeting "Validation, Safety and Ethical Issues Impacting the Low Temperature Storage", Derby/UK, 13.-14.09.2007.

V7. Kumlehn, J.: Coupling *Agrobacterium*-mediated transformation and haploid technology. – International Conference on Plant Transformation Technologies, Vienna/Austria, 04.-07.02.2007.

V8. Rolletschek, H., U. Wobus & L. Borisjuk (vorgetragen von Rolletschek, H.): Mechanism for low oxygen sensing in crop seeds. – 9th Conference of the International Society for Plant Anaerobiosis (ISAP), Matsushima, Sendai/Japan, 18.-23.11.2007.

V9. Schmid, K.: Genetic population structure of *Arabidopsis thaliana* populations from glacial refugia in Southern Europe. – 4th Tri-National Arabidopsis Meeting (TNAM 2007), Vienna/Austria, 12.-15.09.2007.

V10. Schreiber, F.: Analysis and visualisation of high-throughput data in the context of relevant networks. – 3rd International Rauischholzhausen Conference on Analysis of Compatibility Pathways in Plant-Microbe-Interactions, Gießen, 04.-06.03.2007.

V11. Schubert, I., K. Watanabe & A. Pecinka (vorgetragen von Schubert, I.): HR versus NHEJ at the chromosomal level. – EMBO Workshop "Plant DNA Repair Recombination", Presqu'ile de Giens/France, 31.05.-03.06.2007.

V12. Schweizer, P.: Functional genomics and gene-technology for biotic-stress resistance in wheat and barley. – Gordon Research Conference on Agricultural Science, Ventura/USA, 11.-16.03.2007.

V13. Sharbel, T.F.: The genomics and transcriptomics of natural apomictic populations: Sifting through variation and focusing in on apomixis factors. – 3rd International Conference on Apomixis, Wernigerode, 27.06.-01.07.2007.

V14. Stein, N.: Patterns of allelic diversity at *Hv-EIF4E* based virus resistance in barley. – Plant and Animal Genome XV. Conference, San Diego/USA, 13.-17.01.2007.

V15. Weber, H. & R. Radchuk (vorgetragen von Weber, H.): Modulating seed maturation by transgenic approaches: Understanding metabolic regulation of seed development and transcriptional regulatory networks. – Seed Symposium "Translational Seed Biology: From Model Systems to Crop Improvement", Davis/USA, 18.09.2007.

V16. Wobus, A.M.: Stem cell differentiation into the hepatic and pancreatic lineage. – DASCDOC & DASC Joint Meeting, Sønderborg/Denmark, 04.02.2007.

V17. Wobus, A.M.: Stem Cell Biology – Embryonic stem cells as model system to study embryotoxic effects. – HESI Workshop "Alternative Assays for Developmental Toxicology", Cary/USA, 27.-28.02.2007.

Weitere Vorträge

V18. Achigan-Dako, G.E.: The evolution of the ITS sequences supports the new upgrading of the *Luffinae* sub-tribe and the relocation of the *Cucumerinae*. – 19th Congress of the Association for African Plant's Taxonomy, AETFAT, Yaoundé/Cameroon, 26.02.-04.03.2007.

V19. Aliyu, O.M. & T.F. Sharbel (vorgetragen von Aliyu, O.M.): A high-throughput system for rapid ploidy analysis and seed screening for reproductive pathways in plants. – 17th Annual Meeting of the German Society of Cytometry (DGfZ), Regensburg, 10.-13.10.2007.

V20. Baier, C.: First analyses of the genetic structure of two Southeast Asian tropical ant-plants – *Macaranga winkleri* and *M. tanarius*. – PhD Student Course "Molecular marker analysis of

plant population structure and processes", University of Copenhagen, Copenhagen/Denmark, 21.-25.05.2007.

V21. Balint, A., F. Szira, R. Varshney, A. Börner & G. Galiba (vorgetragen von Balint, A.): Mapping of QTLs for drought tolerance in barley at different developmental stages. – 1st Workshop on TritiGenCOST action FA0604 "Triticeae genomics for the advancement of essential European crops", Tenerife/Spain 02.10.2007.

V22. Bäumlein, H.: ARABIDOSEED – Establishing the network of seed gene expression and analysis of its biodiversity. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V23. Bäumlein, H.: Regulated expression of transcription factors. – Annual Meeting of the Trilateral Project "ARABIDOSEED", Sevilla/Spain, 09.-10.03.2007.

V24. Bäumlein, H.: Novel transcription factors involved in the gametophyte-sporophyte transition in wheat and *Arabidopsis*. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V25. Ben-Gal, I., S. Arviv, A. Shani, A. Smilovici, A. Kel, O. Kel-Margoulis, A. Gohr, J. Grau, S. Posch, J. Keilwagen, M. Mohr & I. Grosse (vorgetragen von Grosse, I.): Computational recognition of cis-regulatory elements. – TRANSISTOR bioinformatics course at Biobase, Wolfenbüttel, 23.03.2007.

V26. Bieri, S., I. Ciolkowski, G. Hensel, A. Himmelbach, J. Kumlehn, G. Langen, L. Liu, P. Schweizer & T. Wetjen (vorgetragen von Bieri, S.): A GABI network to identify, characterise and optimise novel promoters from monocotyledonous plants for the genetic engineering of fungal resistance. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V27. Blattner, F.R.: Phylogeographic analyses and ecoclimatic niche modeling reveal speciation processes in *Hordeum*. – Botanisches Kolloquium, Zurich/Switzerland, 04.06.2007.

V28. Blattner, F.R.: Analysis of speciation processes in sympatric species of *Hordeum* (Poaceae) from southern South America. – Botanikertagung 2007 der Deutschen Botanischen Gesellschaft, Universität Hamburg, Hamburg, 03.-07.09.2007.

V29. Bollenbeck, F.: Quantifying biodiversity in histological cross-sections towards fast tissue prediction for inter-individual 3D models. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V30. Bollenbeck, F.: Quantifizierung von Biodiversität in virtuellen Karyopsen zur robusten Gewebevorhersage für VR unterstützte 3-D-Mikrodissektion. – 10. Wissenschaftstage, Fraunhofer IFF, Magdeburg, 28.06.2007.

V31. Borisjuk, L., T. Neuberger, U. Wobus & H. Rolletschek (vorgetragen von Borisjuk, L.): Quantitative imaging for storage metabolism in crop seeds. – "Secondary Metabolism in Plant Seeds: Current Status and Future Applications", Potsdam, 21.-24.02.2007.

V32. Borisjuk, L.: Functional embryogenesis of *Brassica* seeds: experimental design. – Meeting Bayer-CropScience, Ghent/Belgium, 14.03.2007.

V33. Borisjuk, L., U. Wobus & H. Rolletschek (vorgetragen von Borisjuk, L.): Mechanisms for oxygen sensing and balancing in naturally hypoxic crop plant seeds. – ASPB-Meeting, Chicago/USA, 07.-11.07.2007.

V34. Borisjuk, L.: Spatial analysis of seed storage. – Monsanto, Davis/USA, 25.08.2007.

V35. Borisjuk, N., G. Hensel, J. Kumlehn, M. Golovkin, S. Spitsin, S. Andrianov, N. Pogrebnyak, Y. Smirnov, R. Brodzik, P. Matyszczuk & H. Koprowski (vorgetragen von Borisjuk, N.): Expression of avian flu antigen for bird immunization. – Plant Biology & Botany Joint Congress, Chicago/USA, 07.-11.07.2007.

V36. Börner, A., M.-L. Graichen & U. Lohwasser (vorgetragen von Börner, A.): Management, conservation and characterisation of genetic resources of the leafy vegetables at the IPK Gatersleben. – Wageningen/The Netherlands, 14.02.2007.

V37. Börner, A.: Erhaltung und Nutzbarmachung pflanzengenetischer Ressourcen im 21. Jahrhundert – Die Kulturpflanzenbank in Gatersleben. – Aachener Gesellschaft für Gartenkultur, Aachen, 20.03.2007.

V38. Börner, A., V. Korzun, E.K. Khlestkina, O.B. Dobrovolskaya, T.A. Pshenichnikova, M.R. Simon & M.S. Röder (vorgetragen von Börner, A.): Genetic stocks in wheat research – Examples of successful cooperation. – 14th International EWAC Conference, Istanbul/Turkey, 06.-10.05.2007.

V39. Börner, A.: Management and evaluation of *ex situ* collections – the Gatersleben genebank. – 18th EUCARPIA Genetic Resources Section Meeting "Plant Genetic Resources and their Exploitation in the Plant Breeding for Food and Agriculture", Pieštany/Slovak Republic, 23.-26.05.2007.

V40. Börner, A., A. Weidner, K. Neumann & K.F.M. Salem (vorgetragen von Börner, A.): Abiotic stress tolerance in cereals: Evaluation and molecular gene mapping. – Conference of Siberian Department of the Russian Academy of Science "Resistance of Plants to Environmental Stresses", Irkutsk/Russia, 16.-19.09.2007.

V41. Carchilan, M.: Transcription analysis of rye B chromosomes. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

V42. Chebotar, S.V., A. Börner, Y. Sivolap & M. Sivolap (vorgetragen von Chebotar, S.V.): Pyramiding of dwarfing genes in the bread wheat varieties from the South of Ukraine. – 14th International EWAC Conference, Istanbul/Turkey, 06.-10.05.2007.

V43. Conrad, U.: Production of therapeutic antibodies and antigens and immunomodulation of physiological functions in transgenic plants. – Kolloquium, Gregor Mendel Institute of Molecular Plant Biology, Vienna/Austria, 08.02.2007.

V44. Conrad, U. & D. Floss (vorgetragen von Conrad, U.): Expression of TB antigen variants in transgenic plants. – Meeting "Recombinant protein synthesis, assembly and stability", Milano/Italy, 23.-25.05.2007

V45. Conrad, U.: ELP fusions – tools for molecular farming. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V46. Daniel, I.O.: Evaluating maize seed deterioration and longevity during storage under various relative humidity conditions at simulated tropical storage temperature. – 28th International Seed Testing Association Congress, Iguassu Falls/Brazil, 07.-09.05.2007.

V47. Dehmer, K.J., A. Graner, I. Grosse, C. Kuenne, U. Scholz, E. Willner & T. Sretenovic-Rajicic (vorgetragen von Dehmer, K.J.): SNP genotyping of a large *Lolium* genetic resources collection and data analysis via a Diversity Studies Toolkit. – Copenhagen/Denmark, 21.08.2007.

V48. Demidov, D.: Characterisation of aurora-like kinases in plants. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

V49. Dittbrenner, A.: Phytochemische und molekulargenetische Untersuchungen an *Papaver somniferum* L. (Papaveraceae) im Kontext zur bestehenden infraspezifischen Klassifikation. – Botanischer Garten und Botanisches Museum Berlin-Dahlem, Berlin, 16.04.2007.

V50. Dittbrenner, A., U. Lohwasser, H.-P. Mock & A. Börner: Molecular and phytochemical studies of *Papaver somniferum* L. in the context of intraspecific classification. – 5th International Symposium on the Taxonomy of Cultivated Plants, Wageningen/The Netherlands, 15.-19.10.2007.

V51. Floss, D.: Anti-HIV antibody ELP fusion proteins derived from tobacco plants. – PharmaPlanta Meeting, Vienna/Austria, 03.02.2007.

V52. Floss, D.: Plantibodies against HIV: A proof of concept study. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V53. Floss, D.: ELP-Fusionen: Werkzeuge zur Expressionssteigerung in transgenen Pflanzen. – Gesellschaft für Pflanzenbiotechnologie Workshop „Neue Impulse aus der Grundlagenforschung für angewandte Pflanzenbiotechnologie", RLP AgroScience, Neustadt/Weinstraße, 12.-13.07.2007.

V54. Fritsch, R.M.: Taxonomy of *Allium* L. species in Iran, Tajikistan, and Uzbekistan. – 1st Kazbegi Workshop "Botany, taxonomy and phytochemistry of wild *Allium* L. species of the Caucasus and Central Asia", Kazbegi/Georgia, 04.-08.06.2007.

V55. Fritsch, R.M.: Critical *Allium* L. (Alliaceae) taxa of Southwest and Central Asia – International Symposium: 7th Plant Life of South West Asia (7th PLoSWA), Eskişehir/Turkey, 25.-29.06.2007.

V56. Galla, G., G. Barcaccia & T.F. Sharbel (vorgetragen von Galla, G.): Apospory in *Hypericum perforatum*: from a cytohistological analysis of sporogenesis and gametogenesis to the transcriptome. – 51st SIGA (Societa Italiana Genetica Agraria) Annual Congress, Riva del Garda/Italy, 23.-26.09.2007.

V57. Gils, M., M. Rubtsova & K. Kempe (vorgetragen von Gils, M.): A novel hybrid seed system for plants. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V58. Graner, A. & N. Stein (vorgetragen von Graner, A.): Towards sequencing the barley genome. – Barley Workshop, Plant and Animal Genome XV. Conference, San Diego/USA, 13.-17.01.2007.

V59. Graner, A., N. Stein & T. Thiel (vorgetragen von Graner, A.): Comparative genomics between barley and rice: options and limitations. – The Otto Warburg Minerva Center Symposium "Comparative Genomics", The Hebrew University of Jerusalem, Jerusalem/Israel, 21.02.2007.

V60. Graner, A.: Genomforschung: Vom Erkenntnisgewinn zur züchterischen Nutzung pflanzengenetischer Ressourcen. – Ehrenkolloquium für Prof. E. Weber, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 23.02.2007.

V61. Graner, A.: Von den molekularen Grundlagen zu molekularen Markern (GABI smart breeding). – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V62. Graner, A.: The federal *ex situ*-genebank at the interface of conservation management, service and research. – Inauguration of the Israeli Gene Bank Center, Bet Dagan/Israel, 15.04.2007.

V63. Graner, A.: Vom Gen zum Phän am Beispiel der Gelbmosaikvirusresistenz der Gerste. – Ehrenkolloquium zum 70. Geburtstag von Prof. G. Proeseler, BAZ Quedlinburg, 25.04.2007.

V64. Graner, A.: Comparative genomics of barley and rice: promises kept and pending. – Seminarvortrag, University of Wageningen, Wageningen/The Netherlands, 10.05.2007.

V65. Graner, A.: Genetische Ressourcen und Ressortforschung. – GPZ-Veranstaltung „Züchtungsforschung im neuen Haus", BAZ Quedlinburg, 15.05.2007.

V66. Graner, A.: The federal *ex situ*-genebank: facts and figures. – 3. Europäische Saatgut-Tagung, BAZ Quedlinburg, 18.-20.5.2007.

V67. Graner, A.: Aufbau der bundeszentralen *ex situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen. – BIOTECHNICA 2007, Hannover, 09.-11.10.2007.

V68. Graner, A.: From diversity to function – running the gamut of genomics research at IPK. – Semi-

narvortrag, BASF Plant Science, Limburgerhof, 03.12.2007.

V69. Grosse, I.: Recognition of DNA binding sites with Variable Order Bayesian networks. – Berlex Bioscience, Redmond/USA, 19.01.2007.

V70. Grosse, I.: Network reconstruction with Variable Order Bayesian networks. – Berlex Bioscience, Redmond/USA, 19.01.2007.

V71. Grosse, I.: Datenanalyse mit dem Plant Data Warehouse. – BMBF-Evaluierung der Nationalen Bioinformatik Kompetenzzentren, Berlin, 01.-02.03.2007.

V72. Grosse, I.: Overview on WP4. – Annual Meeting of the Trilateral Project "ARABIDOSEED", Sevilla/Spain, 09.-10.03.2007.

V73. Grosse, I.: Recognition of transcription factor binding sites with Variable Order Bayesian networks. The European Bioinformatics Institute, Hinxton/UK, 10.10.2007.

V74. Gurushidze, M., F.R. Blattner & R.M. Fritsch (vorgetragen von Gurushidze, M.): Phylogeny of *Allium* subg. *Melanocrommyum* and taxonomic position of the red dye containing species. – 1st Kazbegi Workshop "Botany, taxonomy and phytochemistry of wild *Allium* L. species of the Caucasus and Central Asia", Kazbegi/Georgia, 04.-08.06.2007.

V75. Gurushidze, M., F.R. Blattner & R.M. Fritsch (vorgetragen von Gurushidze, M.): Phylogeny of *Allium* subg. *Melanocrommyum* – evidence from molecular data. – International Symposium: 7th Plant Life of South West Asia (7th PLoSWA), Eskişehir/Turkey, 25.-29.06.2007.

V76. Hajirezaei, M.-R.: Genes, proteins and metabolites: Comprehensive investigation of plant metabolism to better understand plant development. – Workshop "Raps – eine Pflanze für die Zukunft", Leucorea, Wittenberg, 18.-20.06.2007.

V77. Hajirezaei, M.-R.: Fundamentals of primary metabolism and its potential for biotechnological applications. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V78. Hajirezaei, M.-R.: Fundamentals of primary metabolism and its potential for biotechnological applications. – Symposium on "Integrated molecular approach to enhance lime tolerance to witches' broom", Teheran/Iran, 28.-31.10.2007.

V79. Hajirezaei, M.-R., I. Mockwitz, Y.M. Kim, A. Ahkami, V. Tognetti, M. Zurbriggen & N. Carrillo (vorgetragen von Hajirezaei, M.-R.): Fundamentals of primary metabolism: Molecular and biochemical attempts to identify key steps. – 43th Annual Meeting, Argentine Society for Biochemistry and Molecular Biology (SAIB), Mar del Plata/Argentina, 17.-20.11.2007.

V80. Hamilton, N.: Understanding apomixis in *Hypericum perforatum* L. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V81. Hanemann, A.: Towards the map-based cloning of the scald resistance gene *Rrs2* in barley (*Hordeum vulgare* L.). – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V82. Haseneyer, G., S. Stracke, C. Einfeldt, A. Broda, C. Paul, S. Sauer, A. Graner & H.H. Geiger (vorgetragen von Haseneyer, G.): Association between sequence polymorphism and trait variation in a spring barley collection. – 6th Plant Genomics European Meeting, Tenerife/Spain, 03.-06.10.2007.

V83. Hensel, G., C. Marthe, A. Kusserow, I. Otto, A. Himmelbach, N. Borisjuk, G. Goedeke, E. Kapusi, S. Broeders, T. Czauderna, N. Stein, I. Saalbach, P. Schweizer & J. Kumlehn (vorgetragen von Hensel, G.): Transgenic barley in applied research and biotechnology. – Gesellschaft für Pflanzenbiotechnologie Workshop "Neue Impulse aus der Grundlagenforschung für angewandte Pflanzenbiotechnologie", RLP AgroScience, Neustadt/Weinstraße, 12.-13.07.2007.

V84. Höffken, M.: Population structure of *Arabidopsis thaliana* based on genome-wide SNP-data. – Workshop "Estimating demographic parameters from genetic data", Fouly/Schweiz, 08.06.2007.

V85. Houben, A., D. Demidov & D. Gernand (vorgetragen von Houben, A.): Cell cycle dependent histone phosphorylation and mechanisms of selective chromosome elimination. – Jammu University, Dept. Biotechnology, Jammu/India, 29.02.2007.

V86. Houben, A.: Mechanisms of uniparental chromosome elimination in wide crosses. – Tagung der GPZ-AG Cytogenetik und Chromosomenanalyse, IPK Gatersleben und SWSeed Hadmersleben GmbH, 05.-06.07.2007.

V87. Houben, A.: Intergenomic conflicts in plants. – Kolloquium, Universität Kassel, 20.12.2007.

V88. Jedelská, J., R.M. Fritsch & M. Keusgen (vorgetragen von Jedelská, J.): Bioactivity and cysteine sulphoxides of some wild *Allium* species from Central Asia. – Abstracts, International Congress and 55th Annual Meeting of the Society of Medicinal Plant Research, Graz/Austria, 02.-06.09.2007.

V89. Junker, B.H.: MetaCrop – an information system for crop plant metabolism. – 6th Plant Genomics European Meeting, Tenerife/Spain, 03.-06.10.2007.

V90. Junker, B.H.: Integrated quantitative analysis and mathematical modelling of seed central metabolism. – Humboldt-Universität zu Berlin, Berlin, 12.12.2007.

V91. Kaczmarczyk, A. & M. Grübe (vorgetragen von Kaczmarczyk, A.): Kartoffel-Kryokonservierung im IPK. – COST Minisymposium „15 Jahre erfolgreiche Kryokonservierung von Kartoffel", IPK, Gatersleben, 25.-26.01.2007.

V92. Kaczmarczyk, A., M. Grübe & E.R.J. Keller (vorgetragen von Kaczmarczyk, A.): Cryopreservation

of potato: New Results from the IPK Gatersleben, Germany. – VI. International Congress on Biotechnology and Agriculture (BioVeg 2007), Ciego De Avila/Cuba, 07.-12.05.2007.

V93. Kaczmarczyk, A., M. Grübe & E.R.J. Keller (vorgetragen von Kaczmarczyk, A.): Thermal analysis of the water status in explants of potato (*Solanum tuberosum* L.) comparing two cryopreservation methods. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V94. Kaczmarczyk, A., M. Grübe & E.R.J. Keller (vorgetragen von Kaczmarczyk, A.): Cryopreservation of potato: New results from the IPK Gatersleben. – N. I. Vavilov All-Russian Research Institute of Plant Industry (VIR), Puschkin/Russia, 28.06.2007.

V95. Kaczmarczyk, A., M. Grübe & E.R.J. Keller (vorgetragen von Kaczmarczyk, A.): Influence of alternating cold preculture on cryopreservation results for potato shoot tips. – Annual SLTB (Soc. Low Temp. Biol.)-Meeting "Validation, Safety and Ethical Issues Impacting the Low Temperature Storage", Derby/UK, 13.-14.09.2007.

V96. Keilwagen, J., P. Azhaguvel, S. Stracke, A. Graner, N. Stein & I. Grosse (vorgetragen von Keilwagen, J.): Predicting the number of haplotypes by an integration of marker, passport, and phenotypic data. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V97. Keilwagen, J.: Zur Gumbel- und Gammaverteilung. – Oberseminar Stochastik, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 22.11.2007.

V98. Keller, E.R.J.: Kryokonservierung von *Allium*. – COST Minisymposium „15 Jahre erfolgreiche Kryokonservierung von Kartoffel", IPK, Gatersleben, 25.-26.01.2007.

V99. Keller, E.R.J.: The tripartite cryobank philosophy. – EURALLIVEG First Project Coordination Meeting, IPK, Gatersleben, 12.-13.04.2007.

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V214. Schubert, I.: News about plant centromeres. – Seminar, Centre National de la Recherche Scientifique (C.N.R.S.), Institut de Biologie Moléculaire des Plantes, Strasbourg/France, 30.05.2007.

V215. Schubert, I.: Chromosome painting elucidates karyotype evolution (in Brassicaceae). – Tagung der GPZ-Ag Cytogenetik und Chromosomenanalyse, IPK Gatersleben and SWSeed Hadmersleben GmbH, 05.-06.07.2007.

V216. Schubert, I.: Evolution pflanzlicher Chromosomenbestände. – Kolloquium, Institut für Pflanzenbau und Pflanzenzüchung, Georg-August-Universität Göttingen, Göttingen 01.11.2007.

V217. Schubert, I.: DNA and protein components of plant centromeres. – Kolloquium, University of Ghent, Ghent/Belgium, 19.-21.12.2007.

V218. Schubert, V.: Sister chromatid arrangement in plant interphase nuclei. – Tagung der GPZ-Ag Cytogenetik und Chromosomenanalyse, IPK Gatersleben and SWSeed Hadmersleben GmbH, 05.-06.07.2007.

V219. Schulte, D.: Status of the barley physical map project. – 1st Workshop on TritiGenCOST action FA0604 "Triticeae genomics for the advancement of essential European crops", Tenerife/Spain, 01.10.2007.

V220. Schumacher, H.M. & E.R.J. Keller (vorgetragen von Keller, E.R.J.): Pflanzliche Kryokonservierung in Deutschland. Entwicklung einer angewandten wissenschaftlichen Disziplin. Kartoffel-Kryokonservierung im IPK. – COST Minisymposium „15 Jahre erfolgreiche Kryokonservierung von Kartoffel", IPK, Gatersleben, 25.-26.01.2007.

V221. Schweizer, P.: A high-throughput, automated phenomics screen in barley reveals genes required for durable disease resistance. – Plant and Animal Genome XV. Conference, San Diego/USA, 13.-17.01.2007.

V222. Schweizer, P.: An automated phenomics screen in barley reveals genes required for resistance or disease. – Universität Konstanz, Konstanz, 29.01.2007.

V223. Schweizer, P.: Functional genomics and gene-technology for biotic-stress resistance in wheat and barley. – KWS SAAT AG, Einbeck, 12.06.2007.

V224. Schweizer, P.: A high-throughput phenomics approach in barley reveals genes required for durable disease resistance: An entry point for targeted trait improvement. – EPSO Workshop "The European Feed Value Chain", University of Copenhagen, Copenhagen/Denmark, 26.-27.06.2007.

V225. Schweizer, P.: A phenomics screening in barley reveals gene-neofunctionalization affecting plant-pathogen interactions. – 6th Plant Genomics European Meeting, Tenerife/Spain, 03.-06.10.2007.

V226. Schweizer, P.: Funktionelle Genomforschung und Gentechnik für biotische Stressresistenz in Gerste und Weizen. – Resistenztagung GFP & DPG, Fulda, 11.12.2007.

V227. Seifert, M. & I. Grosse (vorgetragen von Seifert, M.): Genome-wide detection of ABI3 target genes in *Arabidopsis thaliana* from ChIP/chip data using Hidden Markov Models. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V228. Seiffert, U.: Machine Learning Techniken zur Bildverarbeitung in der Pflanzenbioinformatik. – Kolloquium Fakultät für Informatik, Technische Universität, Chemnitz, 19.01.2007.

V229. Seiffert, U.: Anwendungen künstlicher neuronaler Netze zur Bildverarbeitung in der Pflanzenbioinformatik. – Institutskolloquium, Institut für Elektronik, Signalverarbeitung und Kommunikationstechnik, Otto-von-Guericke-Universität, Magdeburg, 06.02.2007.

V230. Seiffert, U.: Recognition of spatio-temporal development patterns. – BMBF-Evaluierung der Nationalen Bioinformatik Kompetenzzentren, Berlin, 01.-02.03.2007.

V231. Seiffert, U.: Machine learning techniques in Bioinformatics. – Kolloquium, IDSIA, Lugano/Switzerland, 14.05.2007.

V232. Seiffert, U.: Image processing in Bioinformatics. – ETH Zurich, Zurich/Switzerland, 03.07.2007.

V233. Seiffert, U.: Machine learning techniques in Plant Bioinformatics. – Plant Bioinformatics Symposium, Halle/S., 24.-25.09.2007.

V234. Seiffert, U.: Fuzzy image processing in Plant Bioinformatics. – Alpen-Adria-Universität, Klagenfurt/Austria, 16.10.2007.

V235. Senula, A.: Kryokonservierung von Minze. – COST Minisymposium „15 Jahre erfolgreiche Kryokonservierung von Kartoffel", IPK, Gatersleben, 25.-26.01.2007.

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V237. Senula, A.: *In vitro* Langzeiterhaltung – Erfahrungen und Probleme. – Tagung Arbeitsgruppe Langzeitlagerung und Kryokonservierung des Arbeitskreises Deutsche *In-vitro*-Kulturen (ADIVK), Hillscheid, 04.05.2007.

V238. Sharbel, T.F. & E. Albertini (vorgetragen von Albertini, E.): Apomixis and sexual reproduction. Are they as different as people think? – Plant and Animal Genome XV. Conference, San Diego/USA, 13.-17.01.2007.

V239. Sharbel, T.F., E. Albertini, G. Galla, S. Ancillotti, J.-M. Corral, M. Falcinelli, F. Matzk & G. Barcaccia (vorgetragen von Barcaccia, G.): Development and mapping molecular markers in *Hypericum perforatum* L. for investigating apomixis. – Plant and Animal Genome XV. Conference, San Diego/USA, 13.-17.01.2007.

V240. Sharbel, T.F.: Why do some plants choose not to have sex? – Max-Planck-Institut für Chemische Ökologie, Jena, 02.03.2007.

V241. Sharbel, T.F.: Why do some plants choose not to have sex? – Department of Applied Biology, University of Helsinki, Helsinki/Finland, 05.03.2007.

V242. Sharbel, T.F.: Molecular signatures of apomictic ovules. – Naturwissenschaftliche Fakultät III Biologie und Vorklinische Medizin, Universität Regensburg, Regensburg, 08.11.2007.

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V244. Sharbel, T.F.: Molecular signatures of apomictic ovules. – Departamento de Genetica, Universidad de Granada, Granada/Spain, 27.11.2007.

V245. Sharbel, T.F.: From populations to transcriptomics: understanding the evolution of asexual reproduction in angiosperms. – Fachbereich 10: Biologie, Johannes Gutenberg-Universität Mainz, Mainz, 13.12.2007.

V246. Staginnus, C., F. Noreem, R. Akbergenov, T. Schwarzacher, M.F. Mette, T. Hohn & K. Richert-Pöggeler (vorgetragen von Richert-Pöggeler, K.): Endogene Pararetroviren: „Hitchhiker" im Pflanzengenom. – DPG-Arbeitskreis „Pflanzenvirologie", Jahrestagung BAZ Quedlinburg, 29.-30.03.2007.

V247. Stein, N.: GABI-TILL – Establishment of a central platform for testing lead gene function in crops based on TILLING. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V248. Stein, N.: Fortschritte in der Gräsergenomforschung und ihre Bedeutung für Entwicklungen in der Futtergräserzüchtung. – Öffentliche Sitzung der Abteilung Futterpflanzen, GFP, Steinach, 24.-25.04.2007.

V249. Stein, N.: Barley genomics fast forward – from gene isolation to genome sequencing. – Institutskolloquium, Max-Planck-Institut für Züchtungsforschung (MPIZ), Köln, 12.09.2007.

V250. Stein, N.: Integrative genomics in the *Triticeae* – promises kept and pending. – BIC-GH Symposium 'Plant Bioinformatics', Martin-Luther-Universität Halle-Wittenberg, Halle/S., 24.-25.09.2007.

V251. Stein, N.: BARCODE – Genomics-assisted dissection of barley morphology and development. – ERA-PG First Grant-Holders Workshop, 6th Plant Genomics European Meeting, Tenerife/Spain, 03.-06.10.2007.

V252. Stein, N.: IBSC – the International Barley genome Sequencing Consortium: progress towards sequencing the barley genome. – Workshop "Coordinating Plant Genomics at International Level, Current Activities and Future Opportunities", 6th Plant Genomics European Meeting, Tenerife/Spain, 03.-06.10.2007.

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V254. Stein, N.: Linking physical and genetic maps. – Course "Current Challenges in Plant Biology-Genomics", University of Helsinki, FGSPB, Helsinki/Finland, 10.-11.12.2007.

V255. Stephanik, A.: BATEx – integration of gene expression data into the Plant Data Warehouse. – BIC-GH Symposium 'Plant Bioinformatics', Martin-Luther-Universität Halle-Wittenberg, Halle/S., 24.-25.09.2007.

V256. Strickert, M.: Browsing temporally regulated gene expressions in correlation maximizing space. – 3rd International Rauischholzhausen Conference on Analysis of Compatibility Pathways in Plant-Microbe-Interactions, Gießen, 04.-06.03.2007.

V257. Strickert, M.: Correlation-based data processing and its application to biology. – Seminar No. 07131: Similarity-based Clustering and its Application to Medicine and Biology, Schloss Dagstuhl, 25.-30.03.2007.

V258. Strickert, M.: Reconstructing similarity relationships for intuitive data inspection. – Workshop "Raps – eine Pflanze für die Zukunft", Leucorea, Wittenberg, 18.-20.06.2007.

V259. Strickert, M., F.-M. Schleif & U. Seiffert (vorgetragen von Strickert, M.): Gradients of Pearson correlation for the analysis of biomedical data.

– IX. Argentine Symposium on Artificial Intelligence (ASAI 2007), Mar del Plata/Argentina, 27.-28.08.2007

V260. Strickert, M.: Supervised attribute relevance determination for protein identification in stress experiments. – International Workshop on Machine Learning in Systems Biology (MLSB 2007), Evry/France, 24.-25.09.2007

V261. Strickert, M.: Attribute rating and rapid embedding of biological high-throughput data. – Max-Planck-Institut für Physik komplexer Systeme, Dresden, 10.10.2007.

V262. Strickert, M.: Finding relevant differential features in gene expression data and protein data. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V263. Strickert, M.: Was tun mit hochdimensionalen biomedizinischen Daten? – 14. Systemwissenschaftliches Kolloquium, Universität Osnabrück, Osnabrück, 01.11.2007.

V264. Thiel, T., N. Stein, A. Graner & I. Grosse (vorgetragen von Thiel, T.): Inferring barley genome duplications using the synteny to rice. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

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V266. Tran, M.L.: AtMYB44 and AtMYB77 – Analysis of transgenic plants and chromatin immunoprecipitation. – Annual Meeting of the Trilateral Project "ARABIDOSEED", Sevilla/Spain, 09.-10.03.2007.

V267. Voigt, M.L., M. Piwczynski, H. Vogel, T. Mitchell-Olds, A. Varshney, J. Kumlehn, B. Rotter & T.F. Sharbel (vorgetragen von Voigt, M.L.): From a phenotype to transcriptomics. – 3rd International Conference on Apomixis, Wernigerode, 27.06.-01.07.2007.

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V269. Watanabe, K.: Positional sister chromatid alignment in a mutant of the *Arabidopsis* homolog of Structural Maintenance of Chromosome 5 (SMC5). – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

V270. Weber, H. & W. Link (vorgetragen von Weber, H.): Genetics and molecular physiology of seed heterosis in *V. faba*. – DFG-Project Meeting, Bonn, 06.02.2007.

V271. Weber, H., R. Radchuk & K. Weigelt (vorgetragen von Weber, H.): Systems approaches to seed composition. – Project Meeting "The EU GRAIN LEGUMES Integrated Project" (GLIP), Paris/France, 22.02.2007.

V272. Weidner, A., V. Schubert, F. Eticha, N. Iqbal, E.K. Khlestkina, M.S. Röder & A. Börner (vorgetragen von Weidner, A.): Symptom expression and chromosomal location of leaf rust resistance from *Aegilops markgrafii* introgressed into hexaploid wheat background. – 14th International EWAC Conference, Istanbul/Turkey, 06.-10.05.2007.

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V274. Weidner, A., R.K. Varshney, G.H. Buck-Sorlin, N. Stein, A. Graner & A. Börner (vorgetragen von Weidner, A.): Salzstresstoleranz bei Gerste: Assoziationskartierung kontra klassische QTL-Kartierung. – GPZ-Vortragstagung „Klimawandel als Herausforderung", Halle/S., 04.-05.10.2007.

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V276. Weigelt, K., H. Küster, I. Saalbach & H. Weber (vorgetragen von Weigelt, K.): Manipulation of seed metabolism in transgenic pea plants to increase protein content. – Gesellschaft für Pflanzenbiotechnologie Workshop „Neue Impulse aus der Grundlagenforschung für angewandte Pflanzenbiotechnologie", RLP AgroScience, Neustadt/Weinstraße, 12.-13.07.2007.

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V278. Weise, S.: Meta-All: a system for managing metabolic pathway information. – International Workshop "Storage and Annotation of Reaction Kinetics Data", Heidelberg, 21.-23.05.2007.

V279. Weising, K., D. Guicking, B. Fiala & F.R. Blattner (vorgetragen von Weising, K.): Phylogeography and population structure of SE Asian ant plants of the genus *Macaranga*, sect. *Pruinosae* (Euphorbiaceae). – Botanikertagung 2007 der Deutschen Botanischen Gesellschaft, Universität Hamburg, Hamburg, 03.-07.09.2007.

V280. Weschke, W.: GABI-SEED 2 – Barley as a model and a crop: Gene expression networks determining

seed traits. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V281. Weschke, W.: Analysis of seed development in legumes and barley – towards a Systems Biology approach. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V282. Willner, E.: Fodder crops in the German *ex situ*-collection at the IPK Genebank – Developments since 2003. – 9th ECPGR Meeting "Working Group on Forages", Pieštany/Slovak Republic, 23.-25.10.2007.

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V285. Winter, H., A. Diestel, S. Gärtig, N. Krone, K. Sterenberg & M.D. Sacristan (vorgetragen von Winter, H.): Transfer of mono- and oligogenic blackleg resistances into oilseed rape. – 12th International Rapeseed Congress, Wuhan/China, 26.-30.03.2007.

V286. Witzel, K. & H.-P. Mock (vorgetragen von Witzel, K.): Proteomic approaches to evaluate agronomic traits in crop and model plants. – COST Meeting FA0603 "Plant Proteomics in Europe", München, 20.-21.09.2007

V287. Wobus, A.M.: Aktuelle Fortschritte der Stammzellforschung. – BBAW Arbeitsgruppe „Gentechnologiebericht", Berlin, 15.02.2007.

V288. Wobus, A.M.: Pancreatic and hepatic differentiation of ES cells and adult progenitor cells. – NIH Bethesda/USA, 26.02.2007.

V289. Wobus, A.M.: Stand der Forschung mit humanen embryonalen Stammzellen. – Konferenz der Friedrich-Ebert-Stiftung „Stammzellforschung in Deutschland", Berlin, 19.03.2007.

V290. Wobus, A.M.: Stammzellforschung – Potentiale und Probleme. – 4. Kollegwoche des Lebenswissenschaftlichen Kollegs der Studienstiftung, Bonn, 18.-23.03.2007.

V291. Wobus, A.M.: Gegenwärtige Situation der Forschung an pluripotenten humanen Zellen in Deutschland. – Novartis Ethics Advisory Board, Basel/Switzerland, 27.04.2007.

V292. Wobus, A.M.: Pancreatic and hepatic differentiation of embryonic stem and adult progenitor cells. – Faculty of Life Sciences, The University of Manchester, Manchester/UK, 30.05.2007.

V293. Wobus, A.M.: Pancreatic differentiation of embryonic stem cells. – BMBF Network of Competence Initiative on Diabetes, Medizinische Fakultät Carl Gustav Carus, Technische Universität Dresden, Dresden, 25.06.2007.

V294. Wobus, A.M.: Aktuelle Aspekte der Stammzellforschung. – Veranstaltung „Fünf Jahre ZES – Forschung und ethische Kriterien im Rahmen des Stammzellgesetzes", Berlin, 17.09.2007.

V295. Wobus, A.M.: Differentiation analysis of embryonic stem cells into the pancreatic lineage. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

V296. Wobus, A.M.: Die Zukunft bioethischer Debatten in Europa. – Tagung „Das Kreuz mit den Stammzellen" – Die Bedeutung kultureller und religiöser Traditionen für biopolitische Entscheidungen, Evangelische Akademie Sachsen-Anhalt e.V., Lutherstadt Wittenberg, 02.-04.11.2007.

V297. Wobus, A.M.: Embryonic stem cell differentiation into the pancreatic lineage. – EMBL Conference "Functional Genomics with Embryonic Stem Cells", Heidelberg, 24.-26.11.2007.

V298. Wobus, A.M.: Aktuelle Aspekte der Stammzellforschung. – Klassensitzung der Biowissenschaftlich-Medizinischen Klasse der BBAW, Berlin, 14.12.2007.

V299. Wobus, U.: From gene to phene: concepts of genome wide scientific approaches utilizing barley grain as a model. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

V300. Wulfert, I., J. Kruse & K.J. Dehmer (vorgetragen von Wulfert, I.): Surveillance of genebank material for quarantine viruses. – 13th EAPR Virology Section Meeting, Edinburgh/UK, 19.06.2007.

V301. Zaynali Nezhad, K., U. Lohwasser, M.S. Röder & A. Börner (vorgetragen von Zaynali Nezhad, K.): Post-anthesis drought tolerance assessment on bread wheat. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

V302. Zierold, U., A. Himmelbach, G. Hensel, J. Riechen, P. Schweizer & J. Kumlehn (vorgetragen von Zierold, U.): A versatile set of generic vectors for *Agrobacterium*-based transformation of monocotyledonous plants. – International Conference on Plant Transformation Technologies, Vienna/Austria, 04.-07.02.2007.

V303. Zurbriggen, M., V. Tognetti, M.-R. Hajirezaei, E. Valle & N. Carrillo (vorgetragen von Carrillo, N.): Replacement of chloroplast ferredoxin with a bacterial flavodoxin leads to enhanced tolerance to iron starvation in tobacco. – 19th FAOBMB Seoul Conference (Federation of Asian and Oceanian Biochemists and Molecular Biologists), Seoul/Republic of Korea, 27.-30.05.2007.

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Poster/Posters

P1. Achigan-Dako, G.E., J. Fuchs & F.R. Blattner: Genome size differences correlate with usage types (bottle gourds vs. seed consumption) and growing elevation in *Lagenaria siceraria* (Cucurbitaceae). – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P2. Agarwal, R., J. Sainis & M. Melzer: Locating calvin cycle enzymes in high pressure fixed cells and isolated thylakoids of *Synechocystis* 6803. – Microscopy & Microanalysis 2007, Ft. Lauderdale/USA, 05.-09.08.2007.

P3. Agarwal, R., J. Sainis & M. Melzer: Locating calvin cycle enzymes in high pressure fixed cells and isolated thylakoids of *Synechocystis* 6803. – National Conference on Electron Microscopy and Allied Fields, New Delhi/India, 26.-28.11.2007.

P4. Agueci, F.: Characterisation of NIMA-like kinases of *Arabidopsis thaliana*. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P5. Agueci, F., R. Karimi & A. Houben: Characterisation of NIMA- and Haspin-like kinases in *Arabidopsis thaliana*. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

P6. Ahkami, A.H., U. Druege, K.T. Haensch, M. Bucher, P. Franken, S. Gianinazzi, B. Hause, S. Porfirova, M. Melzer & M.R. Hajirezaei: The role of invertases in phloem unloading of sucrose in *Petunia* during adventitious root development. – "Plant Vascular Biology", Taipei/Taiwan, 07.-11.05.2007.

P7. Ahkami, A.H., U. Druege, K.T. Haensch, M. Bucher, P. Franken, S. Gianinazzi, B. Hause, S. Porfirova, M. Melzer & M.R. Hajirezaei: Molecular and physiological analysis of adventitious root development (ARD) in *Petunia*. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P8. Aliyu, O.M. & T.F. Sharbel: A high-throughput system for rapid ploidy analysis and seed screening for reproductive pathways in plants. – 3rd International Conference on Apomixis, Wernigerode, 27.06.-01.02.2007.

P9. Athmer, B., G. Kocsy, G. Galiba & N. Stein: Expression profiling of cold responsive genes in barley, wheat and rye. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P10. Bach, K., E. Dietrich & R. Schmidt: GABI-BRIDGE: Analysis of genetic diversity in candidate genes for oil content traits in rapeseed (*Brassica napus* L.). – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

P11. Bachmann, H., T. Funke, C. Kuenne, E. Langer, M. Mohr, A. Stephanik, T. Thiel, U. Scholz, S. Weise & I. Grosse: The Plant Bioinformatics Portal. – BMBF-Evaluierung der Nationalen Bioinformatik Kompetenzzentren, Berlin, 01.-02.03.2007.

P12. Bachmann, H., I. Grosse, C. Kuenne, E. Langer, A. Stephanik, U. Scholz & S. Weise: Architecture of the Plant Data Warehouse. – BMBF-Evaluierung der Nationalen Bioinformatik Kompetenzzentren, Berlin, 01.-02.03.2007.

P13. Baier, C. & F.R. Blattner: Analysis of the genetic structure of two Southeast Asian tropical ant-plants – *Macaranga winkleri* and *M. tanarius*. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P14. Banaei, A., V. Colot, M.F. Mette & A. Houben: Heterosis and chromatin structure: Does intraspecific hybridisation trigger epigenetic changes? – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

P15. Banaei, A., M.F. Mette, V. Colot & A. Houben: Analysis of the relationship between heterosis and epigenetic modifications of DNA and histones in *Arabidopsis thaliana*. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P16. Böer, E., G. Steinborn, A. Scholz & G. Kunze: *Arxula adeninivorans* – host for expression of biotechnologically interesting gene products. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P17. Bollenbeck, F., R. Pielot & U. Seiffert: New insights into barley grain development: 3D/4D models of spatio-temporal dynamics. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P18. Borisjuk, L., T. Neuberger, N. Sreenivasulu, U. Wobus & H. Rolletschek: Quantitative imaging of lipid storage in the developing seed. – ASPB-Meeting, Chicago/USA, 07.-11.07.2007.

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P214. Thiel, T., A. Graner, S. Posch, N. Stein, R.K. Varshney & I. Grosse: Computational mapping of barley ESTs. – BMBF-Evaluierung der Nationalen Bioinformatik Kompetenzzentren, Berlin, 01.-02.03.2007.

P215. Villmann, T., M. Strickert, C. Brüss, F.-M. Schleif & U. Seiffert: Visualization of fuzzy information in fuzzy-classification for image segmentation using MDS. – 15th European Symposium on Artificial Neural Networks (ESANN 2007), Bruges/Belgium, 25.-27.04.2007.

P216. Vlasenko, L. & A. Houben: Identification of plant Aurora regulators and substrates. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P217. Vlasenko, L. & A. Houben: Identification of plant Aurora regulators and substrates. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

P218. Vogt, A., J. Jedelská, R.M. Fritsch & M. Keusgen: Sulphurpyrrols – a new class of substances of medicinally used *Allium* species growing in Central Asia. – 1st Kazbegi Workshop "Botany, taxonomy and phytochemistry of wild *Allium* L. species of the Caucasus and Central Asia", Kazbegi/Georgia, 04.-08.06.2007.

P219. Voigt, M.-L., M. Piwczynski, H. Vogel, T. Mitchell-Olds, A. Varshney, J. Kumlehn, B. Rotter & T.F. Sharbel: From a phenotype to transcriptomics. – 3rd International Conference on Apomixis, Wernigerode, 27.06.-01.07.2007.

P220. Vorwieger, A., T. Rutten, J. Tiedemann & H. Bäumlein: Regulated expression of *lec1* in *Arabidopsis thaliana* seedlings gives rise to *pkl* root phenotype. – 4th Tri-National Arabidopsis Meeting (TNAM 2007), Vienna/Austria, 12.-15.09.2007.

P221. Vorwieger, A., T. Rutten, T.M. Nguyen Thi & H. Bäumlein: Regulated induction of embryogenesis by LEC1. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P222. Watzke, K., A. Spindler, R. Watzke, K. Tag & G. Kunze: Differential expression of *Glomus intraradices* genes during the presymbiotic and symbiotic phase of the fungus. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P223. Weidner, A., F. Asch, G.H. Buck-Sorlin & A. Börner: QTLs for salt resistance vary with development stage in field grown barley. – Tropentag 2007 "Utilisation of diversity in land use systems: Sustainable and organic approaches to meet human needs", Witzenhausen, 09.-11.10.2007.

P224. Weigelt, K., H. Küster, K.-P. Götz, I. Saalbach & H. Weber: Over-expression of a *Vicia faba* amino acid permease in developing seeds of transgenic pea (*Pisum sativum*) changes protein metabolism. – Botanikertagung 2007 der Deutschen Botanischen Gesellschaft, Universität Hamburg, Hamburg, 03.-07.09.2007.

P225. Weigelt, K., H. Küster, I. Saalbach & H. Weber: Over-expression of a *V. faba* amino acid permease in developing seeds of transgenic pea (*Pisum sativum*) changes protein metabolism. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P226. Weigelt, K., T. Rutten, H. Küster, K.-P. Götz, I. Saalbach & H. Weber: Repression of ADP-glucose pyrophosphorylase in developing embryos affects seed metabolism. – 6th European Conference on Grain Legumes, Lisbon/Portugal, 12.-16.11.2007.

P227. Weise, S., B.H. Junker, C. Klukas, D. Koschützki, I. Grosse, F. Schreiber & U. Scholz: Meta-All: a system for managing metabolic pathway information. – 3rd International Rauischholzhausen Conference on Analysis of Compatibility Pathways in Plant-Microbe-Interactions, Gießen, 04.-06.03.2007.

P228. Weise, S., B.H. Junker, C. Klukas, D. Koschützki, I. Grosse, F. Schreiber & U. Scholz: Meta-All: a system for managing metabolic pathway information. – International Workshop "Storage and Annotation of Reaction Kinetics Data", Heidelberg, 21.-23.05.2007.

P229. Weissleder, A., V. Schubert, I. Lermontova & I. Schubert: YFP-CenH3/H2B-DsRed double transformants do not stably express both constructs simultaneously in *Arabidopsis* interphase nuclei. – 3rd Plant Science Student Conference, IPB, Halle/S., 05.-08.06.2007.

P230. Weissleder, A., V. Schubert, I. Lermontova & I. Schubert: YFP-CenH3/H2B-DsRed double transformants do not stably express both constructs simultaneously in *Arabidopsis* interphase nuclei. – 16th International Chromosome Conference (ICC), Amsterdam/The Netherlands, 25.-29.08.2007.

P231. Weschke, W., H.-P. Mock, C. Pietsch, V. Radchuk, M.S. Röder, F. Schreiber, U. Seiffert, N. Sreenivasulu, M. Strickert, K. Witzel & U. Wobus: Barley as a model and a crop: Gene expression networks determining seed traits (GABI-SEED 2). – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

P232. Wiese, C., T. Nikolova, I. Zahanich, U. Ravens, K.R. Boheler & A.M. Wobus: Differentiation induction of embryonic stem cells into sinoatrial node-like cells by Suramin. – Symposium "Reprogramming of somatic cells for the therapy of heart disorders", Düsseldorf, 09.-10.10.2007.

P233. Wiese, C., T. Nikolova, I. Zahanich, U. Ravens, K.R. Boheler & A.M. Wobus: Differentiation induction of embryonic stem cells into sinoatrial node-like cells by Suramin. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P234. Willner, E. & K.J. Dehmer: Most original samples, primary holders and sharing of responsibilities: *Poa* as an example for rationalization of European genebank collections. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P235. Winter, H., A. Diestel, S. Gärtig, N. Krone, K. Sterenberg & M.D. Sacristan: Transfer of mono- and oligogenic blackleg resistances into oilseed rape. – 12th International Rapeseed Congress, Wuhan/China, 26.-30.03.2007.

P236. Witucka-Wall, H., M. von Korff, A. Blacha, M. Melzer, R.C. Meyer, O. Toerjek & T. Altmann: Morphological, metabolite and transcript analysis of heterosis in *Arabidopsis*. – 4th Tri-National *Arabidopsis* Meeting (TNAM 2007), Vienna/Austria, 12.-15.09.2007.

P237. Witzel, K., C. Klukas, F. Schreiber, C. Pietsch, M. Röder, U. Seiffert, A. Matros & H.-P. Mock: Proteome analysis of a barley mapping population. – 7th GABI Status Seminar, Potsdam, 06.-08.03.2007.

P238. Witzel, K., C. Klukas, F. Schreiber, C. Pietsch, M. Röder, U. Seiffert, A. Matros & H.-P. Mock: Proteome analysis of a barley mapping population. – 40. Jahrestagung der Deutschen Gesellschaft für Massenspektrometrie (DGMS), Bremen, 11.-14.03.2007.

P239. Witzel, K., M. Strickert, A. Weidner, A. Börner & H.-P. Mock: Proteomic investigation of salt tolerance mechanisms of barley using the genetic variation of mapping populations. – COST Meeting FA0603 "Plant Proteomics in Europe", München, 20.-21.09.2007.

P240. Witzel, K., G. Hensel, M.-R. Hajirezaei, A. Weidner, T. Rutten, A. Börner, M. Strickert, M. Melzer, J. Kumlehn, H.-P. Mock & G. Kunze: Molecular and biochemical analysis of salt stress responses in barley mapping populations. – Institutstag IPK, Gatersleben, 22.-23.10.2007.

P241. Zaynali Nezhad, K., U. Lohwasser, M.S. Röder & A. Börner: Assessment of post-anthesis drought tolerance in bread wheat. – GPZ-Vortragstagung "Klimawandel als Herausforderung", Halle/S., 04.-05.10.2007.

P242. Zierold, U., A. Himmelbach, G. Hensel, J. Riechen, P. Schweizer & J. Kumlehn: A versatile set of generic vectors for *Agrobacterium*-based transformation of monocotyledonous plants. – 3rd International Rauischholzhausen Conference on Analysis of Compatibility Pathways in Plant-Microbe-Interactions, Gießen, 04.-06.03.2007.

P243. Zierold, U., U. Sonnewald & J. Kumlehn: Establishment of cell-specific ethano-inducible expression systems in monocotyledonous plants. – 3rd International Rauischholzhausen Conference on Analysis of Compatibility Pathways in Plant-Microbe-Interactions, Gießen, 04.-06.03.2007.

P244. Zierold, U., D. Douchkov, J. Kumlehn & P. Schweizer: Overexpression and gene silencing of HvSNAP34 and HvThioredoxin in the susceptible barley line Golden Promise. – XIII. International Congress on Molecular Plant-Microbe Interactions, Sorrento/Italy, 21.-27.07.2007.

P245. Zurbriggen, M., V. Tognetti, M.-R. Hajirezaei, E. Valle & N. Carrillo: Development of multiple stress tolerance in crop plants by introduction of a cyanobacterial flavodoxin. – 43th Annual Meeting, Argentine Society for Biochemistry and Molecular Biology (SAIB), Mar del Plata/Argentina, 17.-20.11.2007.

Vom Institut organisierte Tagungen und Veranstaltungen/ Meetings and Conferences organised by IPK

COST-Minisymposium „Kryokonservierung von Pflanzengenetischen Ressourcen in Deutschland – 15 Jahre Kartoffel-Kryobank. Neue Chancen der Europäischen Zusammenarbeit durch COST“
25. - 26. Januar 2007, Gatersleben
25 Teilnehmer

Festliche Veranstaltung anlässlich der Verabschiedung von Prof. Dr. Ulrich Wobus und der Einführung von Prof. Dr. Andreas Graner als Geschäftsführender Direktor
30. März 2007, Gatersleben
ca. 200 Teilnehmer

Fig. 47: Nutzen die Möglichkeit zum Gedankenaustausch bei der Festveranstaltung am 30. März 2007: Der Direktor des Leibniz-Instituts für Neurowissenschaften, Magdeburg, Prof. Scheich, der Rektor der Martin-Luther-Universität Halle-Wittenberg, Prof. Diepenbrock, der Kultusminister des Landes Sachsen-Anhalt, Prof. Olbertz, und der ehemalige Wirtschaftsminister des Landes Sachsen-Anhalt, Dr. Rehberger (v.l.n.r.) (Foto: B. Schäfer)./ A discussion of the Acting Director of the Leibniz Institute for Neurobiology, Magdeburg, Prof. Scheich, the President of the Martin Luther University Halle-Wittenberg, Prof. Diepenbrock, the Minister of Education and Cultural Affairs of Saxony-Anhalt, Prof. Olbertz, and the former Minister of Economic Affairs of Saxony-Anhalt, Dr. Rehberger at the celebratory event on 30th March 2007 (sorting left) (Photo: B. Schäfer).

Start-up-Meeting des EU-Projekts EURALLIVEG
12. - 13. April 2007, Gatersleben
15 Teilnehmer

Treffen für trilaterales GABI-Projekt „Vergleichende Genomforschung zur Regulation der Meristemaktivität bei Nachtschattengewächsen (Solanaceae)“
15. - 17. April 2007, Gatersleben, Meisdorf
15 Teilnehmer

Tag der offenen Tür in der Genbank-Außenstelle „Nord“
5. Mai 2007, Malchow
ca. 200 Teilnehmer

Fig. 48: Eine Mitarbeiterin mit „kleinen Gästen“ – unter ihnen die Rapsblütenkönigin – während des Tages der offenen Tür am Standort Malchow (Foto: E. Willner)./ An employee amongst “little guests” – including the Rapsblütenkönigin – on the occasion of the Open Day at the External Branch in Malchow (Photo: E. Willner).

Fig. 49: Bei strahlendem Sonnenschein fanden wiederum zahlreiche interessierte Besucher den Weg zum Tag der offenen Tür auf dem Biotech-Campus Gatersleben (Foto: H. Ernst)./ Many interested visitors came to the Open Day at the Biotech Campus Gatersleben, as in the years before (Photo: H. Ernst).

Fig. 50: Unter Anleitung von Mitarbeitern der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung konnten Besucher selbst mit Pflanzenmaterial, hier Kartoffeln, arbeiten (Foto: H. Ernst)./ Visitors could prepare potato tissue under the guidance of employees of the *In vitro* Storage and Cryopreservation group (Photo: H. Ernst).

Tag der offenen Tür
9. Juni 2007, Gatersleben
ca. 1.000 Teilnehmer

Workshop BIC-GH
"Raps – eine Pflanze für die Zukunft"
Analyse, Repräsentation, Modellierung, Simulation und Visualisierung metabolischer Netzwerke in Raps zur Verbesserung agronomischer Merkmale
18. - 20. Juni 2007, Leucorea, Wittenberg
25 Teilnehmer

3rd International Conference on APOMIXIS and 9th Gatersleben Research Conference
27. Juni - 2. Juli 2007, Gatersleben und Wernigerode
140 Teilnehmer

Tagung der GPZ-Ag 3 „Cytogenetik und Chromosomenanalyse"
5. - 6. Juli 2007, Gatersleben und Hadmersleben
48 Teilnehmer

Plant Bioinformatics – A BIC-GH-Symposium Bioinformatics Centre Gatersleben-Halle
24. - 25. September 2007, MLU Halle-Wittenberg, Halle/S.
55 Teilnehmer

Institutstag
Vortragsveranstaltung, Posterpräsentation aller wissenschaftlichen Arbeitsgruppen
22. - 23. Oktober 2007, Gatersleben
200 Teilnehmer

Beteiligung an der Organisation externer Veranstaltungen/ Participation in Organising External Meetings

Thema	Zeitpunkt der Veranstaltung Ort Land	Veranstalter/Mitorganisatoren (beteiligte Einrichtungen)	Anzahl Teilnehmer
Workshop "Specialized chromosomes"; 16th International Chromosome Conference (ICC)	25.-29.08.2007 Amsterdam Niederlande	Prof. H. de Jong (Wageningen) Prof. H. Tanke (Leiden) Prof. P. Fransz (Amsterdam) Prof. I. Schubert	100
Stem Cells and Tumourigenesis (3rd World Congress on Regenerative Medicine)	19.10.2007 Leipzig	Symposium organised by the ETCS Prof. Anna M. Wobus	100
International Workshop Integrative Bioinformatics 4th Annual Meeting	10.-12.09.2007 University of Ghent Belgien	Scientific Committee Dr. M. Lange Dr. U. Scholz	137

Ehrungen, Preise/ Honours, Awards

Aufgrund seiner vielfältigen Verdienste bei der Zusammenführung der deutschen, europäischen und weltweiten Pflanzenforschung und dem Ausbau des IPK zu einem weltweit anerkannten Pflanzenforschungsinstitut wird **Professor Dr. Ulrich Wobus** am 30. März 2007 im Rahmen der Festveranstaltung der Übergabe der Institutsführung das Bundesverdienstkreuz am Bande durch den Kultusminister Professor Dr. Jan-Hendrik Olbertz überreicht.

In Anerkennung seiner großen Verdienste um die Entwicklung der molekularbiologischen Forschung an Kulturpflanzen in Deutschland und um den Ausbau des Instituts für Pflanzengenetik und Kulturpflanzenforschung in Gatersleben zu einer Forschungsstätte von internationalem Rang und einem Ort der Begegnung von Wissenschaftlern und Praktikern in der Pflanzenzüchtung ernannte die Gesellschaft für Pflanzenzüchtung e.V. Herrn **Professor Dr. Ulrich Wobus** zu ihrem **Ehrenmitglied**.

Anlässlich der 1st EU Summer School in Proteomic Basics wurde das Poster zum Thema „Proteome analysis of the effect of UV-radiation on barley leaf tissue using a 2-D approach and LC-based separation techniques" von **Stephanie Kaspar** mit einem **Posterpreis** ausgezeichnet. Die Veranstaltung fand vom 12. bis 18. August 2007 im Kloster Neustift, Brixen, Italien, statt.

Während der 17. Jahrestagung der Deutschen Gesellschaft für Zytometrie (DGfZ) vom 10. bis 13. Oktober 2007 in Regensburg wurde das Poster von **Dr. Jörg Fuchs** mit dem Titel „Flow-sorted nuclei are valuable subjects to investigate the structural and functional nuclear architecture in *Arabidopsis*" mit dem **Posterpreis** ausgezeichnet.

Auf dem 7. GABI Statusseminar wurde das Poster von **Dr. Marc Strickert** zum Thema „Correlation-based mining of gene expression patterns in introgression lines of *Hordeum spontaneum* ('HS213') back-crossed with genetic background of spring barley ('Brenda')" ebenfalls mit dem **Posterpreis** ausgezeichnet. Das Statusseminar fand vom 6. bis 8. März 2007 in Potsdam statt.

Arbeitsaufenthalte von Gästen im IPK/Guest Researchers at the IPK

(ab einer Woche, ohne InWEnt-Stipendiaten, Schüler, Praktikanten, Studenten)

Abteilung Genbank

Wilma Sabetta, Universität Bari, Italien, 09.03.2007 bis 31.12.2007, PhD-Student, Finanzierung durch Universität Bari (Dr. S. Gottwald/Arbeitsgruppe Genomdiversität).

Dr. Delfina Barabaschi, Centre for Genomic Research (CRA), Fiorenzuola d'Adra, Italien, 15.06.2007 bis 31.12.2007, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Dragan Perovic, Bundesanstalt für Züchtungsforschung Quedlinburg, Quedlinburg, 07.06.2007 bis 31.12.2007, Finanzierung durch BAZ Quedlinburg (Prof. A. Graner/Arbeitsgruppe Genomdiversität).

Dr. Udda Lundqvist, Nordic Gene Bank, Alnarp, Schweden, 20.06.2007 bis 26.06.2007, Finanzierung durch IPK (Dr. S. Gottwald/Arbeitsgruppe Genomdiversität).

Prof. Ivo Große, Martin-Luther-Universität Halle-Wittenberg, 01.10.2007 bis 31.12.2007, Finanzierung durch Martin-Luther-Universität Halle-Wittenberg (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Sven Mielordt, 01.05.2007 bis 30.06.2007, Eigenfinanzierung (Prof. I. Große/Arbeitsgruppe Plant Data Warehouse).

Dr. Oxana Dobrovolskaya, Institute of Cytology and Genetics, Nowosibirsk, Russland, 15.07.2007 bis 12.10.2007, Finanzierung durch DFG (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Svetlana Landjeva, Institute of Genetics, Sofia, Bulgarien, 22.09.2007 bis 22.12.2007, Finanzierung durch DFG (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Marta Olas, Research Institute of Vegetable Crops, Warschau, Polen, 11.04.2007 bis 27.04.2007, Finanzierung durch ein EU-Projekt (Dr. J. Keller/*In vitro*-Erhaltung und Cryo-Lagerung).

Dr. Luciana Altieri, Fakultät der Agrarwissenschaften der Universität Potenza, Potenza, Italien, 20.05.2007 bis 01.06.2007, Finanzierung durch EU-Projekt (Dr. J. Keller/Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung).

Korinna Esfeld, Naturkundemuseum Stuttgart, 16.04.2007 bis 11.05.2007; 28.08.2007 bis 28.09.2007, Finanzierung durch SMNC und Universität Heidelberg (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Dr. Violetta Kotseruba, Komarov Botanical Institute, St. Petersburg, Russland, 20.09.2007 bis 19.11.2007, Finanzierung durch DAAD und 20.11.2007 bis 26.12.2007, Eigenfinanzierung (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Guiseppe Puglia, Tuscia University, Viterbo, Italien, 29.11.2007 bis 31.12.2007, PhD-Student, Finanzierung über FIDAF Stipendium (Dr. K. Schmid/Arbeitsgruppe Quantitative Evolutionsgenetik).

Abteilung Cytogenetik und Genomanalyse

Dr. Ludmilla Malysheva-Otto, 01.01.2007 bis 14.02.2007; 15.06.2007 bis 31.12.2007, Eigenfinanzierung (Prof. I. Schubert/Arbeitsgruppe Karyotypevolution).

Dr. Fritz Matzk, 01.07.2007 bis 31.12.2007, Eigenfinanzierung (Prof. I. Schubert/Arbeitsgruppe Karyotypevolution).

Prof. Takashi R. Endo, University Kyoto, Japan, 30.08.2007 bis 04.09.2007, Finanzierung durch IPK (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Dr. Richard Pickering, Institute for Crop Research, Christchurch, Neuseeland, 16.05.2007 bis 16.07.2007 Finanzierung durch DFG (Prof. I. Schubert/Arbeitsgruppe Karyotypevolution).

Navina Hamilton, Max-Planck-Institut, Jena, 01.01.2007 bis 31.07.2007, Finanzierung durch ein Promotionsstipendium (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Giulio Galla, Universität Padua, Italien, 05.03.2007 bis 31.12.2007, Finanzierung über ein Stipendium der Universität Padua (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Marta Puente Molins, 24.04.2007 bis 31.05.2007, Eigenfinanzierung (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Manrique Inmaculada Poyato, Universität Granada, Spanien, 05.09.2007 bis 22.12.2007, PhD-Student, Finanzierung durch die Universität Granada (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Thomas Thiel, Max-Planck-Institut, Jena, 01.11.2007 bis 31.12.2007, Finanzierung über ein Doktorandenstipen-

dium der Max-Planck-Research-School (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr.-Ing. Alexander Ihlow, 01.05.2007 bis 31.05.2007, Eigenfinanzierung (Dr. U. Seiffert/Arbeitsgruppe Mustererkennung).

Nina Zellerhof, Rheinisch-Westfälische Technische Hochschule (RWTH), Aachen, 15.07.2007 bis 03.08.2007, Finanzierung über Peter u. Traudl Engelhorn Stiftung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Dr. Jorrit-Jan Krijger, Institut für Phytopathologie und Pflanzenschutz, Halle/S., 24.09.2007 bis 19.10.2007, Finanzierung durch SFBbu und Martin-Luther-Universität Halle-Wittenberg (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Ralph Horbach, Institut für Phytopathologie und Pflanzenschutz, Halle/S., 24.09.2007 bis 19.10.2007, Finanzierung durch SFBbu und Martin-Luther-Universität Halle-Wittenberg (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Simona Urso, Centre for Genomic Research (CRA), Fiorenzuelo d'Arda, Italien, 24.10.2007 bis 14.11.2007, PhD-Studentin, (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Dawit Bedane Woubit, Biologische Bundesanstalt für Land- und Forstwirtschaft (BBA), Kleinmachnow, 05.03.2007 bis 30.03.2007; 02.07.2007 bis 30.07.2007, Finanzierung durch DAAD (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Shailendra Sharma, Alexander von Humboldt-Stiftung, Bonn, 26.07.2007 bis 31.12.2007, Finanzierung über ein Forschungsstipendium der Humboldt-Stiftung (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Elena Khlestkina, Institute of Cytology and Genetics, Nowosibirsk, Russland, 02.06.2007 bis 28.08.2007, Finanzierung durch DFG (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. José de Leon Alvarez, Universidad Autónoma de Baja California Sur, La Paz, Mexiko, 03.08.2007 bis 28.08.2007, Finanzierung durch PROMEP-SEP (Mexico) (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Yifru Teklu Woldemariam, Alemaya University, Dire Dawa, Äthiopien, 06.09.2007 bis 31.12.2007, Finanzierung durch Stipendium der Humboldt-Stiftung (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Elena Salina, Institute of Cytology and Genetics, Nowosibirsk, Russland, 05.11.2007 bis 17.11.2007, Finanzierung durch BMBF (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Andreas Stephanik, 01.11.2007 bis 31.12.2007, Eigenfinanzierung (Dr. U. Scholz/Arbeitsgruppe Bioinformatik und Informationstechnologie).

Prof. Ming Chen, College of Life Sciences, Zhejiang University, Hangzhou, China, 16.09.2007 bis 30.09.2007, Finanzierung durch DAAD (Dr. U. Scholz/Arbeitsgruppe Bioinformatik und Informationstechnologie).

Abteilung Molekulare Genetik

Dr. Mario Gils, 11.05.2007 bis 31.07.2007, Eigenfinanzierung (Dr. W. Weschke/Arbeitsgruppe Genwirkung).

Eduardo Poulain, Universität Amiens, Frankreich, 19.03.2007 bis 30.03.2007, Finanzierung durch DAAD, (Dr. H. Rolletschek/Arbeitsgruppe Genwirkung).

Dr. Albrecht Roscher, Universität Amiens, Frankreich, 24.04.2007 bis 04.05.2007, Finanzierung durch DAAD (Dr. H. Rolletschek/Arbeitsgruppe Genwirkung).

Vitaliy Korkhovoy, Institute of Cell Biology and Genetic Engineering, Kiew, Ukraine, 01.05.2007 bis 31.07.2007, Finanzierung durch DFG (Dr. V. Radchuk/Arbeitsgruppe Genwirkung).

Nguyen Lai Thanh, 01.01.2007 bis 14.01.2007, Eigenfinanzierung (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Francesca Morandini, 02.05.2007 bis 30.05.2007, Finanzierung durch Pharma-Planta (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Phan Trong Hoang, Institute of Biotechnology, Hanoi, Vietnam, 01.11.2007 bis 31.12.2007, PhD-Student, Finanzierung durch ein DLR-Projekt (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Marziya Rakhimova, 01.01.2007 bis 30.04.2007, Finanzierung durch ein DAAD-Forschungsstipendium (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper) und 01.08.2007 bis 30.10.2007, PhD-Student, Eigenfinanzierung (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Ines Hamdi, National Institute of Computer Science, Manouba University, Tunis, Tunesien, 12.03.2007 bis 01.04.2007, Finanzierung durch BIC-GH (Prof. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Henning Schwöbbermeyer, 01.11.2007 bis 31.12.2007, Eigenfinanzierung (Prof. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Dr. Myroslava Rubtsova, Nordsaat Saatzuchtgesellschaft mbH, Böhnshausen, 01.05.2007 bis 31.07.2007, Finanzie-

rung durch Nordsaat (Dr. M. Gils/Arbeitsgruppe Hybridweizen).

Abteilung Molekulare Zellbiologie

Dr. Martin Peisker, 15.01.2007 bis 14.06.2007, Eigenfinanzierung (Dr. M.R. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenphysiologie).

Ferdous Rastar Jazii, National Research Center for Genetic Engineering and Biotechnology (NRCGEB), Teheran, Iran, 15.07.2007 bis 30.09.2007, Eigenfinanzierung (Dr. M.R. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenphysiologie).

Dr. Björn Junker, Brookhaven National Laboratory, Upton (New York), USA, 31.01.2007 bis 30.06.2007, Finanzierung durch U.S. Department of Energy (Dr. M.R. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenphysiologie).

Dr. Saeed Vazan, Faculty of Agriculture, Azad University Karaj, Iran, 18.10.2007 bis 31.12.2007, Finanzierung durch Islamic Azad University Karaj (Dr. M.R. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenphysiologie).

Sepideh Torabi, Agricultural Biotechnology Research Institute, Karaj, Iran, 18.10.2007 bis 31.12.2007, Finanzierung durch University Teheran (Dr. M.R. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenphysiologie).

Esra Capanoglu, Istanbul Technical University, Istanbul, Turkey, 10.12.2006 bis 04.05.2007, Finanzierung durch DAAD (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Semiu Olalekan Ogunwolu, Cocoa Research Institute of Nigeria, Ibadan, Nigeria, 05.03.2007 bis 02.06.2007, Finanzierung durch University Ibadan (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Ricco Scheibel, Technische Fachhochschule Berlin, 05.03.2007 bis 04.09.2007, Finanzierung durch *SunGene* (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Kristin Kronberg, 01.02.2007 bis 30.06.2007, Eigenfinanzierung (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Joanna Melonek, Universität Kiel, Botanisches Institut, Kiel, 04.06.2007 bis 15.06.2007, Selbstfinanzierung (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Ernst Metzner, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.12.2005 bis 31.12.2007, Finanzierung durch Universität Halle über Graduiertenkolleg des Landes Sachsen-Anhalt (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie und Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Dr. Elisabetta Mazzucotelli, Experimental Institute of Cereal Research, Fiorenzuola d'Arda, Italien, 03.09.2007 bis 30.11.2007, Finanzierung durch EMBO-Stipendium (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Sandra Zimmermann, Universität Kaiserslautern, Pflanzenphysiologie, Kaiserslautern, 05.02.2007 bis 11.02.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Simon Kirchberger, Universität Kaiserslautern, Pflanzenphysiologie, Kaiserslautern, 05.02.2007 bis 11.02.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Dr. Alexander Dovzhenko, Albert-Ludwigs-Universität Freiburg, Biologie II, Freiburg, 26.02.2007 bis 04.03.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Dr. Francesco Pinosa, Albert-Ludwigs-Universität Freiburg, Biologie II, Freiburg, 26.02.2007 bis 04.03.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Vaibhav Srivastava, Swedish University of Agricultural Science, Umeå, Schweden, 16.03.2007 bis 29.03.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Rachna Agarwal, Bhaba Atomic Research Center, Molecular Biology and Agriculture Division, Bombay, Indien, 01.06.2007 bis 28.07.2007, PhD-Studentin, Finanzierung durch BMBF/DLR (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Rajani Kant Chittela, Bhaba Atomic Research Center, Molecular Biology and Agriculture Division, Bombay, Indien, 28.09.2007 bis 24.11.2007, Finanzierung durch BMBF/DLR (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Prof. Jayashree Sainis, Bhaba Atomic Research Center, Molecular Biology and Agriculture Division, Bombay, Indien, 28.09.2007 bis 24.11.2007, Finanzierung durch BMBF/DLR (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Prof. Gunnar Wingsle, Swedish University of Agricultural Science, Umeå, Schweden, 14.12.2007 bis 20.12.2007, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Omwoyo Ombori, Kenyatta University, Department of Biochemistry and Biotechnology, Nairobi, Kenya,

01.01.2007 bis 24.01.2007, Finanzierung durch DAAD (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Alok Varshney, 01.01.2007 bis 30.06.2007, Eigenfinanzierung (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Ferenc Bakos, Agricultural Research Institute of HAS, Plant Cell Biology Department Martonvasar, Ungarn, 01.07.2007 bis 31.12.2007, Finanzierung durch DAAD (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Katja Watzke, Firma Amykor GmbH, Wolfen, 01.09.2005 bis 31.12.2008, Finanzierung durch DBU-Stipendium (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Vanessa Bou Perez, University Valencia, Valencia, Spanien, 15.01.2007 bis 14.04.2007, Finanzierung durch EU (Leonardo-Stipendium) (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Gerhard Steinborn, 09.03.2007 bis 31.03.2007, Eigenfinanzierung (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Keith Baronian, Christchurch Polytechnic Institute of Technology, Neuseeland, 10.06.2007 bis 01.07.2007, Finanzierung durch BMBF/DLR (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Peggy Knobloch, 15.06.2007 bis 30.11.2007, Eigenfinanzierung (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Alok Adholeya, The Energy and Resources Institute, Neu Delhi, Indien, 16.07.2007 bis 26.07.2007, Finanzierung durch BMBF/DLR (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Gandham Satyanarayana Prasad, Institute of Microbial Technology (IMTECH), Chandigarh, Indien, 30.07.2007 bis 27.10.2007, Finanzierung durch DFG (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Sanjeev Kumar, The Energy and Resources Institute, Neu Delhi, Indien, 01.09.2007 bis 12.10.2007, Finanzierung durch BMBF/DLR (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Kinga Sedzielewska, Wroclaw University of Technology, Wroclaw, Polen, 19.11.2007 bis 18.04.2008, Finanzierung durch EU (Leonardo-Stipendium) (Prof. G. Kunze/Arbeitsgruppe Hefegenetik).

Arbeitsaufenthalte von Wissenschaftlern in anderen Einrichtungen/ Stays of IPK Researchers at other Institutes

Abteilung Genbank

Grit Haseneyer/Arbeitsgruppe Genomdiversität, Universität Stuttgart-Hohenheim, 29.01.2007 bis 03.02.2007, Finanzierung durch BMBF.

Grit Haseneyer/Arbeitsgruppe Genomdiversität, Universität Stuttgart-Hohenheim, 03.09.2007 bis 07.09.2007, Finanzierung durch BMBF.

Abteilung Cytogenetik und Genomanalyse

Alexander Ihlow/Arbeitsgruppe Transkriptomanalyse, University of Waterloo, Ontario, Kanada, 02.06.2007 bis 27.09.2007, Finanzierung durch Grundhaushalt.

Alexander Ihlow/Arbeitsgruppe Transkriptomanalyse, Universität Zürich – Institut für Pflanzenbiologie, Schweiz, 04.11.2007 bis 17.11.2007, Finanzierung durch Grundhaushalt.

Annika Johrde/Arbeitsgruppe Transkriptomanalyse, National Institute of Agriculture Botany, Cambridge, Großbritannien, 04.11.2007 bis 17.11.2007, Finanzierung durch Grundhaushalt.

Ali M. Banaei Moghadam/Arbeitsgruppe Chromosomenstruktur und -funktion, Ecole Normale Supérieure, Paris, Frankreich, 06.11.2007 bis 31.01.2008, Finanzierung durch DFG.

Abteilung Molekulare Genetik

Dr. Ljoudmilla Borisjuk/Arbeitsgruppe Genwirkung, Universität Würzburg, 27.03.2007 bis 01.04.2007, Finanzierung durch DFG.

Doreen Floß/Arbeitsgruppe Phytoantikörper, Rheinisch-Westfälische Technische Hochschule, Aachen, 11.04.2007 bis 25.04.2007, Finanzierung durch EU.

Dr. Ljoudmilla Borisjuk/Arbeitsgruppe Genwirkung, Penn State University, USA, 24.05.2007 bis 04.06.2007, Finanzierung durch DFG.

Dr. Hardy Rolletschek/Arbeitsgruppe Genwirkung, Penn State University, USA, 24.05.2007 bis 04.06.2007, Finanzierung durch DFG.

Dr. Ljoudmilla Borisjuk/Arbeitsgruppe Genwirkung, Université de Picardie Jules Verne, Amiens, Frankreich, 18.06.2007 bis 29.06.2007, Finanzierung durch DAAD.

Dr. Hardy Rolletschek/Arbeitsgruppe Genwirkung, Université de Picardie Jules Verne, Amiens, Frankreich, 18.06.2007 bis 29.06.2007, Finanzierung durch DAAD.

Dr. Ljoudmilla Borisjuk/Arbeitsgruppe Genwirkung, Universität Würzburg, 11.09.2007 bis 15.09.2007, Finanzierung durch D1010157.

Kathleen Weigelt/Arbeitsgruppe Genwirkung, INRA, Dijon, Frankreich, 15.10.2007 bis 03.11.2007, Finanzierung durch Grundhaushalt.

Abteilung Molekulare Zellbiologie

Dr. Amir Hossein Ahkami/Arbeitsgruppe Molekulare Pflanzenphysiologie, Wissenschaftspark Golm, 08.07.2007 bis 26.07.2007, Finanzierung durch Pakt für Forschung und Innovation.

Katja Watzke/Arbeitsgruppe Hefegenetik, The Energy and Resources Institute, Neu Delhi, Indien, 15.10.2007 bis 29.10.2007, Finanzierung durch BMBF/DLR.

Katja Witzel/Arbeitsgruppe Angewandte Biochemie, Technische Universität, Lyngby, Dänemark, 15.10.2007 bis 22.12.2007, Finanzierung durch EU COST.

Prof. G. Kunze/Arbeitsgruppe Hefegenetik, Christchurch Polytechnic Institute of Technology, Christchurch, Neuseeland, 09.11.2007 bis 18.11.2007, Finanzierung durch BMBF/DLR.

Lehrtätigkeit/Teaching

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Priv.-Doz. Dr. A. Börner (GB) Dr. J. Keller (GB) Dr. U. Lohwasser (GB) Dr. A. Weidner (GB) Dr. A. Senula (GB)	„Management und Evaluierung pflanzengenetischer Ressourcen“ (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	2
Prof. Dr. I. Große (GB)	„Sequenzanalyse I“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	5
Prof. Dr. I. Große (GB)	„Expressionsdaten-analyse I“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	3
Prof. Dr. I. Große (GB)	„Sequenzanalyse II“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	3
Prof. Dr. I. Große (GB)	„Expressionsdaten-analyse II“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	3
Prof. Dr. I. Große (GB)	„Algorithmen der Bioinformatik II“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	5
Prof. Dr. I. Große (GB)	„Molekulare Phylogenie“ (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	3
Prof. Dr. I. Große (GB)	„Phylogenetic Footprinting“ (Literaturseminar)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	2
Dr. K. Schmid (GB)	Aktuelle Arbeiten aus der Populationsgenetik – Domestikation von Tieren und Pflanzen (Seminar)	Friedrich-Schiller-Universität Jena	Fakultät für Pharmazie und Biologie	2
Dr. K. Schmid (GB)	Einführung in die Populationsgenetik mit Übungen (Vorlesung)	Friedrich-Schiller-Universität Jena	Fakultät für Pharmazie und Biologie	3
Dr. K. Schmid (GB)	Evolutionsgenetik und -genomik (Vorlesung)	Friedrich-Schiller-Universität Jena	Fakultät für Pharmazie und Biologie	2
Dr. K. Schmid (GB)	Aktuelle Arbeiten aus der Populationsgenetik (Seminar)	Friedrich-Schiller-Universität Jena	Fakultät für Pharmazie und Biologie	2
Prof. Dr. I. Schubert (CYT) Dr. J. Fuchs (CYT)	„Klassische und molekulare Cytogenetik“ (Komplexpraktikum)	Universität Kassel	Fachbereich Genetik	7

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Priv.-Doz. Dr. V. Schubert (CYT) Dr. G. Jovtchev (CYT) Dr. J. Fuchs (CYT) Dr. M. Melzer (MZB) B. Claus (MZB)	„Moderne Techniken der Mikroskopie und Cytogenetik“ (Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Landwirtschaftliche Fakultät	2
Priv.-Doz. Dr. V. Schubert (CYT)	„Pflanzenzüchtung“ (Vorlesung)	Hochschule Anhalt Bernburg	FB Landwirtschaft	1
Dr. A. Houben (CYT)	„Biotechnologie in der Pflanzenproduktion“ (Vorlesung und Praktikum)	Hochschule Anhalt Bernburg	FB Landwirtschaft	7
Priv.-Doz. Dr. R. Schmidt (CYT)	„Einblicke durch Genomprojekte: Was machen Pflanzen anders?“ (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Priv.-Doz. Dr. R. Schmidt (CYT)	„Struktur-/Funktionsbeziehungen in Eukaryontengenomen“ (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Prof. Dr. A. M. Wobus (CYT)	MD/PhD Programm Molecular Medicine: „Stem Cells“	Medizinische Hochschule Hannover	-	0,5
Prof. Dr. A. M. Wobus (CYT)	Kurs „Grundlagen der Säuger-Zell- und Gewebekultur und aktuelle Aspekte der Stammzellforschung“ (Vorlesungen, Seminare und praktische Übungen)	Martin-Luther-Universität Halle-Wittenberg	Medizinische Fakultät	1,5
Dr. U. Seiffert (CYT)	„Genetische Algorithmen“ (Vorlesung)	Otto-von-Guericke-Universität Magdeburg	Fakultät für Elektrotechnik und Informationstechnik	2
Dr. U. Seiffert (CYT)	„Künstliche neuronale Netze“ (Vorlesung)	Otto-von-Guericke-Universität Magdeburg	Fakultät für Elektrotechnik und Informationstechnik	5
Dr. L. Altschmied (CYT)	Pflanzenphysiologisches Praktikum	Friedrich-Schiller-Universität Jena	Institut für Pflanzenphysiologie	4
Dr. U. Scholz (CYT) Dr. M. Lange (CYT)	„Einführung in die Bioinformatik“ (Vorlesung und Übung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	6
Dr. U. Scholz (CYT) Dr. M. Lange (CYT) S. Weise (CYT)	„Einführung in die Bioinformatik“ (Vorlesung und Übung)	Otto-von-Guericke-Universität Magdeburg	Fakultät für Verfahrens- und Systemtechnik	4
Dr. U. Scholz (CYT) Dr. M. Lange (CYT)	„Einführung in die Bioinformatik“ (Vorlesung und Übung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	4

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Prof. Dr. U. Wobus (MOG) Dr. habil. H. Bäumlein (MOG)	„Ausgewählte Aspekte der pflanzlichen Molekular- und Entwicklungsbiologie“ (Vorlesung und Praktikum)	Friedrich-Schiller-Universität Jena und Martin-Luther-Universität Halle-Wittenberg	Biologisch-Pharmazeutische Fakultät und Mathe–matisch-Naturwissenschaftlich-Technische Fakultät	je 6,5
Dr. habil. H. Bäumlein (MOG)	„Biotechnologie in der Pflanzenproduktion“ (Vorlesung)	Hochschule Anhalt Bernburg	FB Landwirtschaft	7
Priv.-Doz. Dr. H.-P. Mock (MZB)	„Proteomanalyse von Pflanzen“ (Praktikum)	Martin-Luther-Universität Halle-Wittenberg	FB Biologie	4
Priv.-Doz. Dr. H.-P. Mock (MZB)	„Pflanzenphysiologie“ (Grundpraktikum)	Martin-Luther-Universität Halle-Wittenberg	FB Biologie	4
Prof. Dr. G. Kunze (MZB)	„Molekulargenetik Teil I“ (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (MZB)	„Molekulargenetik Teil II“ (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (MZB)	„Molekulargenetik-Gentechnik“ (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	2
Prof. Dr. G. Kunze (MZB)	„Biosensoren für die Umweltkontrolle“ (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	2
Prof. Dr. G. Kunze (MZB)	„Hefegenetik“ (Praktikum)	Ernst-Moritz-Arndt-Universität Greifswald	Mathematisch-Naturwissenschaftliche Fakultät, FB Biologie	4
Semesterwochenstunden (SWS) insgesamt:				**118,5**

Mitarbeit an wissenschaftlichen Zeitschriften/ Editing Scientific Journals

Mitarbeiter des Leibniz-Instituts für Pflanzengenetik und Kulturpflanzenforschung sind Herausgeber bzw. Mitherausgeber folgender Zeitschriften:

Botanical Journal of Iran, Rostaniha, Tehran, Iran (R. Fritsch, Associate Editor).

Cell Biology and Toxicology, Kluwer Academic Publisher, Dordrecht, The Netherlands (Anna M. Wobus, Consulting Editor).

Cells Tissues Organs, Karger AG, Basel, Switzerland (Anna M. Wobus, Associate Editor).

Chromosoma, Springer, New York, USA (I. Schubert, Associate Editor).

Chromosome Research, Springer, Dordrecht, The Netherlands (A. Houben, Editorial Advisory Board).

Cytogenetics & Genome Research (CGR), Karger AG, Basel, Switzerland (I. Schubert, Editorial Board).

Electronic Wheat Information Service, Shizuoka, Japan (A. Houben, Editorial Advisory Board).

Genetic Resources and Crop Evolution (GRACE), Springer, Dordrecht, The Netherlands (K. Pistrick, Managing Editorial Board; F.R. Blattner, Editorial Board).

Genetics and Breeding, Bulgarian Academy of Sciences for the Bulgarian Genetical Society, Sofia, Bulgaria (I. Schubert, Editorial Board).

International Journal of Knowledge-based Intelligent Engineering Systems, KES International, Brighton, UK (U. Seiffert, Editorial Advisory Board).

Journal of Integrative Bioinformatics, IMBio, Bielefeld (F. Schreiber, Associate Editor).

Journal of Plant Physiology, Elsevier, Amsterdam, The Netherlands (J. Kumlehn, Editorial Board).

Journal of Stem Cells, Nova Science Publishers, Inc., New York, USA (Anna M. Wobus, Editorial Advisory Board Member).

Journal of Tissue Engineering and Regenerative Medicine, John Wiley & Sons, Ltd., UK (Anna M. Wobus, Editorial Board Member).

Molecular Breeding, Springer, Dordrecht, The Netherlands (A. Graner, Editorial Board).

Plant Biotechnology Journal, Blackwell Publishing, Bristol, UK (R. Schmidt, Advisory Board).

Plant Cell Reports, Springer, Berlin-Heidelberg (R. Schmidt, Editorial Board).

Plant Molecular Biology, Springer, Berlin-Heidelberg (R. Schmidt, Editorial Board).

Plant Systematics and Evolution, Springer, Berlin-Heidelberg (F.R. Blattner, Editorial Board).

Stem Cells, AlphaMed Press, Durham, USA (Anna M. Wobus, Editorial Board Member).

The International Journal of Developmental Biology, The University of the Basque Country Press, Bilbao, Spain (Anna M. Wobus, Editorial Advisory Board).

The Open Mycology Journal, Bentham Science Publishers Ltd. (G. Kunze, Editorial Advisory Board).

The Plant Journal, Blackwell Publishing, Oxford, UK (U. Wobus, Advisory Board).

Theoretical and Applied Genetics, Springer, Berlin-Heidelberg (A. Graner, Editorial Board).

Tätigkeit in Gremien/ Activities in Boards

Geschäftsführender Direktor (bis 31.03.2007)

Prof. Dr. U. Wobus
- Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA;
- Ordentliches Mitglied der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);
- Korrespondierendes Mitglied der Nordrhein-Westfälischen Akademie der Wissenschaften;
- Mitglied im Ausschuss „Landwirtschaftliche Biotechnologie" des DECHEMA-Fachausschusses Biotechnologie;
- Mitglied des Wissenschaftlichen Beirates der Bundesanstalt für Züchtungsforschung an Kulturpflanzen (BAZ), Quedlinburg;
- Mitglied des Wissenschaftlichen Beirates der Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung (GFP), Bonn;
- Mitglied des Fachbeirates des Max-Planck-Instituts für Molekulare Pflanzenphysiologie, Golm;
- Mitglied des Vorauswahlkomitees der Karl Heinz Beckurts-Stiftung;
- Stellv. Vorsitzender der InnoPlanta e.V. Pflanzenbiotechnologie Nordharz/Börde;
- IPK-Repräsentant in der European Plant Science Organization (EPSO) (bis 31.03.2007);
- Mitglied der *WGL*-Jury Wissenschaftspreis des Stifterverbandes „Gesellschaft braucht Wissenschaft";
- Mitglied des Kuratoriums der Sparkassenstiftung Aschersleben-Staßfurt;
- Vorsitzender des Fördervereins des Schülerlabors „Grünes Labor Gatersleben";
- Vergleichender Berichterstatter (Rapporteur) der Max-Planck-Gesellschaft im Rahmen der erweiterten Fachbeiratsbegutachtung für Forschungsfeld 3 der Biologisch-Medizinischen Sektion (Tätigkeitszeitraum 2007/2008).

Geschäftsführender Direktor (ab 01.04.2007)

Prof. Dr. A. Graner
- Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA;
- Mitglied des Aufsichtsrates der Deutschen Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ);
- Mitglied des Vorstandsrates der Gesellschaft für Pflanzenzüchtung e.V. (GPZ);
- Mitglied des Scientific Coordination Committee (SCC) des BMBF-Forschungsverbundes „Genomanalyse am Biologischen System Pflanze (GABI)";
- Mitglied des Beirates für nachwachsende Rohstoffe, Ministerium für Landwirtschaft und Umwelt des Landes Sachsen-Anhalt;
- Stellvertretender Vorsitzender des Scientific Advisory Boards des Max-Planck-Instituts für Züchtungsforschung, Köln;
- Mitglied des „Beratungs- und Koordinierungsausschusses (BEKO) des Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen landwirtschaftlicher und gartenbaulicher Kulturpflanzen", BMELV, Bonn;
- Mitglied des Wissenschaftlichen Beirates Otto Warburg Center for Agricultural Biotechnology, Hebrew University, Jerusalem;
- Mitglied des Wissenschaftlichen Beirates des BMBF im Forschungsprogramm „Beiträge zur biologischen Sicherheit gentechnisch veränderter Pflanzen";
- SCRI Honorary Fellow;
- Steering Committee, International Barley Sequencing Consortium (Vorsitzender);
- Stellvertretender Vorsitzender der Gemeinschaft zur Förderung der Kulturpflanzenforschung Gatersleben e.V.;
- Advisory Board, EU Forschungsprojekt 7 "TriticeaeGenome";
- Berufungskommissionen:
  W3 Professur für Pflanzenzüchtung (MLU Halle);
  W3 Professur Molekulare Pflanzengenetik (IPK, MLU-Halle); W3 Professur Molekulare Physiologie und Zellbiologie der Pflanzen (IPK, MLU-Halle); W2 Professur Pflanzliche Bioinformatik (IPK, MLU-Halle);
  Leiterstelle, Institut für Sicherheit in der Gentechnik bei Pflanzen (Julius Kühn-Institut, Quedlinburg).

Abteilung Genbank

Dr. N. Stein
- International Barley Genome Sequencing Consortium (IBSC) (Co-chair);
- (ETGI, http://www.etgi.org);
- COST-Action Tritigen FA0604 (National Representative).

Priv.-Doz. Dr. A. Börner
- Koordinator der European Wheat Aneuploid Co-operative;
- Vorstandsmitglied und Schriftführer der Gemeinschaft zur Förderung der Kulturpflanzenforschung Gatersleben e.V.;
- Mitglied des Scientific Committee des EUCARPIA Genetic Resources Meetings 2007, Piestany, Slowakische Republik.

Dr. J. Keller
- Mitglied der Koordinierungsgruppe des ECPGR Vegetables Network und Vice-Chairman der *Allium*-Arbeitsgruppe;
- Vorstandsmitglied der Gesellschaft für Pflanzenbiotechnologie e.V.;
- Vorstandsmitglied in der Internationalen Gesellschaft für Tieftemperaturbiologie (Society of Low Temperature Biology);
- Mitglied im Lenkungsausschuss und National Representative der europäischen COST Action 871 „Kryokonservierung in Europa".
- Mitglied der Ag zum Europäischen Kooperationsprogramm Pflanzengenetischer Ressourcen (ECPGR) des Beratungs- und Koordinierungsausschusses (BeKo) von Bund und Ländern (Leiter des BMELV).

Dr. H. Knüpffer
- Koordinator des Cereals Network sowie Chairman der Barley Working Group des European Co-operative Programme for Plant Genetic Resources (ECPGR);
- Mitglied der Network Coordinating Group des Documentation and Information Network des ECPGR;
- Mitglied der Arbeitsgruppe zum Europäischen Kooperationsprogramm pflanzengenetischer Ressourcen (ECPGR) des Beratungs- und Koordinierungsausschusses für pflanzengenetische Ressourcen (BeKo) von Bund und Ländern (unter Leitung des BMELV);
- Mitglied des International Barley Core Collection Committee (Bioversity International);
- Mitglied der Arbeitsgruppe Biodiversity Information Standards (TDWG – ehem. Taxonomic Databases Working Group).

Dr. K.J. Dehmer
- Mitglied in der ECP/GR Working Group on Potato.

E. Willner
- Mitglied (Vice chairperson) in der ECP/GR Working Group on Forages.

Dr. K. Pistrick
- Mitglied im Nomenclature Committee of the International Seed Testing Association (ISTA);
- Mitglied der Arbeitsgruppe zum Modell- und Demonstrationsvorhaben „Beispielhafte Erfassung und Charakterisierung der genetischen Ressourcen an Zierpflanzen anhand der Rose – Errichtung eines Genbanknetzwerkes für die Rose" der Bundesanstalt für Landwirtschaft und Ernährung, Bonn.

Dr. K. Schmid
- Member of Management Committee COST Action FA 604 "Triticeae genomics".

Abteilung Cytogenetik

Prof. Dr. I. Schubert
- Mitglied im Advisory Board of the Centre of Excellence in Plant Agrobiology and Molecular Genetics (PAGEN).

Dr. U. Seiffert
- Mitglied der Fachgruppe 8.4.9 – Mikroelektronik neuronaler Netze im Rahmen der Informationstechnischen Gesellschaft (ITG) des VDE.

Dr. habil. P. Schweizer
- Koordinator des BarleyGenomeNet;
- Mitglied im Projekt Management Team BIOEXPLOIT (EU FP6).

Prof. Dr. A. M. Wobus
- Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA;
- Ordentliches Mitglied der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);
- Mitglied der Zentralen Ethik-Kommission für Stammzellforschung (ZES) am Robert-Koch-Institut, Berlin;
- Council Member of the European Tissue Culture Society (ETCS);
- Koordinatorin des Schwerpunktprogramms 1109 der DFG „Embryonale und gewebespezifische Stammzellen - Regenerative Zellsysteme für einen Zell- und Gewebeersatz";
- Mitglied des Novartis Ethics Advisory Board von NOVARTIS Pharma International, Basel, Schweiz;
- Mitglied der Arbeitsgruppe „Stammzellforschung" der Senatskommission für Genforschung der DFG;
- Mitglied der Arbeitsgruppe „Gentechnologiebericht" der Berlin-Brandenburgischen Akademie der Wissenschaften;
- Mitglied des Programmbeirats des Wissenschaftszentrums Sachsen-Anhalt (WZW).

Abteilung Molekulare Genetik

Prof. Dr. F. Schreiber
- Mitglied in der Fachgruppe 4.0.2 – Informatik in den Biowissenschaften im Rahmen der Gesellschaft für Informatik (GI).
- Mitglied im German/Russian Virtual Network on Bioinformatics.

Abteilung Molekulare Zellbiologie

Prof. Dr. G. Kunze

– Mitglied im wissenschaftlichen Beirat der Fa. ARTES Biotechnology GmbH.

Öffentlichkeitsarbeit/ Public Relations

Informationsveranstaltungen und Führungen/ Informative Events and Guided Tours

1. Januar – 30. Juni 2007
Wöchentliche Treffen von Schülern der 5. Klasse im Rahmen der Gesamtschule Kirchdorf zum Thema „Bunte Pflanzenwelt", je 5 Schüler, insgesamt 12 Nachmittage (V. Miehe).

9. Januar 2007
Besuch der Bundestagsabgeordneten Frau Katherina Reiche (CDU/CSU), Vorstellung des Leibniz-Instituts, Gespräch über aktuelle Fragen zur Grünen Gentechnik sowie über Möglichkeiten und Chancen in der Region, Gewächshausbesichtigung anlässlich des Freisetzungsantrags „Winterweizen" und Besichtigung des Genomzentrums (Prof. Dr. U. Wobus, B. Eise, Prof. Dr. A. Graner, Dr. habil. P. Schweizer, Dr. W. Weschke).

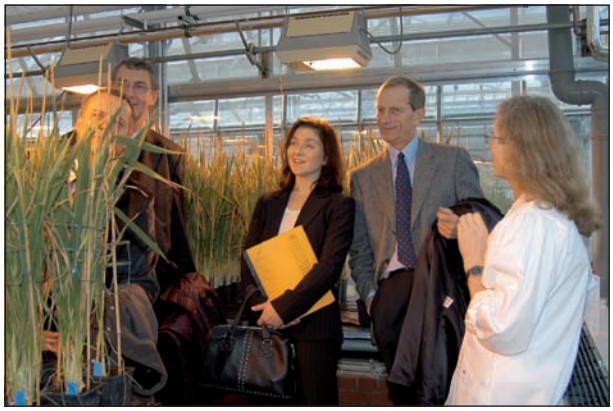

Fig. 51: Die Bundestagsabgeordenten der CDU/CSU-Fraktion Ulrich Petzold und Katherina Reiche erhalten von Prof. Ulrich Wobus und Dr. Winfriede Weschke (v.l.n.r.) im Gewächshaus Einblicke in die laufenden Arbeiten der Arbeitsgruppe Genwirkung (Foto: H. Ernst)./ The members of the parliamentary group of the CDU/CSU in the Federal Parliament, Ulrich Petzold and Katherina Reiche in discussion with Prof. Ulrich Wobus and Dr. Winfriede Weschke (from left to right) about current research of the Gene Expression group in a greenhouse (Photo: H. Ernst).

11. Januar 2007
Besuch von Teilnehmern eines Senioren-Colleges, 30 Personen, Vorstellung des Leibniz-Instituts sowie der Aufgaben der Genbank, Besichtigung des Samenkühllagers und anschließendem Rundgang zum Genomzentrum mit Blick auf den Biopark und Informationen über die Ausgründungen aus dem IPK (W. Mühlenberg, Priv.-Doz. Dr. A. Börner).

19. Januar 2007
Besuch von Studenten im Fach Pflanzenbiotechnologie der Hochschule Anhalt, Bernburg, 30 Personen, Vorstellung des Leibniz-Instituts, Information über die Arbeit der Gruppe Chromosomenstruktur und -funktion mit anschließendem Laborrundgang, Vorstellung der Arbeitsgruppe Genregulation und Besichtigung der Pflanzenkulturräume sowie Information über die Arbeit der Genbank und Besuch der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung (W. Mühlenberg, Dr. A. Houben, Dr. habil. H. Bäumlein, Dr. J. Keller).

25. Januar 2007
Besuch der Interessengemeinschaft für gentechnikfreie Saatgutarbeit, Hannover, 7 Personen, Vortrag über den Weizenversuch und Informationen über das Genbankmanagement, Feldbesichtigung (Prof. A. Graner, Dr. W. Weschke, Priv.-Doz. Dr. A. Börner, P. Schreiber).

16. Februar 2007
Besuch einer Gruppe von Künstlern zum Initiativprojekt der Kunststiftung des Landes Sachsen-Anhalt Artist-in-Lab, 18 Personen, Vorstellung des Leibniz-Instituts, Besichtigung eines *Arabidopsis*-Labors sowie eines Experimental-Gewächshauses, Kurzvortrag und Demonstration über Verfahren zur genetischen Veränderung von Pflanzen, Vorstellung der Genbank und Besichtigung des Samenkühllagers, Demonstration der Vielfalt von Getreide (Prof. U. Wobus, Dr. habil. H. Bäumlein, Dr. W. Weschke, Dr. J. Kumlehn, Priv.-Doz. Dr. A. Börner).

20. Februar 2007
Besuch von Mitarbeitern des Pflanzenzuchtunternehmens RAGT 2N, Vorstellung des Instituts sowie Informationen und Führungen über die Aufgaben der Genbank (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, Dr. A. Weidner, K. Neumann).

23. Februar 2007
Besuch einer Gruppe Biologiestudenten der Universität Kassel, 10 Personen, Begrüßung und Informationen über die Aufgaben der Genbank und Besichtigung (Priv.-Doz. Dr. A. Börner).

2. März 2007
Besuch einer Ausbildungsgruppe des Kolpingwerkes Hettstedt (Garten- und Landschaftsbauer), 10 Personen, Besichtigung des Staudengartens und eines Gewächshauses (K. Menzel).

16. März 2007
Besuch von Herrn MdEP Dr. Horst Schnellhardt und Herrn Dr. Rudolf Strohmeier, Kabinettschef der Kommissarin Vivian Reding (Informationsgesellschaft und Medien), 3 Personen, Information über den Biotech-Campus Gatersleben, Vorstellung der Arbeit des Instituts, Information über die geplante Einbindung des Instituts in das 7. Rahmenprogramm, Gespräche mit dem Leiter der Abteilung Genbank sowie der Arbeitsgruppen *In vitro*-Erhaltung und Cryo-Lagerung und Pflanzliche Reproduktionsbiologie (Prof. U. Wobus, Prof. A. Graner, Dr. J. Keller, Dr. J. Kumlehn).

29. März 2007
Besuch von Herrn Prof. Diter von Wettstein, Washington State University, Informationen über die Bereiche im Institut (Prof. U. Wobus, Prof. A. Graner, Dr. N. Stein, Dr. F. Blattner, Dr. W. Weschke, Dr. M. Röder, Dr. A. Houben, Prof. I. Schubert, Priv.-Doz. Dr. A. Börner, Dr. A. Senula, Prof. G. Kunze).

30. März 2007
Durchführung eines Projekttages für die 2. Klasse der Grundschule Kirchdorf, 12 Personen, Basteln mit Naturmaterial (V. Miehe).

2. April 2007
Besuch des Staatssekretärs Gerd Lindemann (BMELV) und der Landrätin Frau Heike Brehmer, 4 Personen, Vorstellung des Leibniz-Instituts, Gespräche über Novellierung des Gentechnikgesetzes im Zusammenhang mit GVO-Freilandversuchen, neue Materialabgabeordnung für die IPK-Genbank und über Genbank und Gentechnik am IPK, anschließend Besuch der Genbank (Prof. U. Wobus, Prof. A. Graner, B. Eise).

10. April 2007
Besuch von Herrn Bischof Axel Noack, 6 Personen, Information über die Aufgaben der Genbank und Rundgang zum Ährensaal, Herbar und Samenkühllager (Prof. A. Graner, Prof. U. Wobus, Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick).

11. April 2007
Führung einer Gruppe von Mitarbeitern des Finanzamtes Quedlinburg durch die Botanischen Vergleichssammlungen (Herbarium, Samen- und Frucht- sowie Ährensammlung) der Abteilung Genbank (Dr. K. Pistrick).

17. April 2007
Besuch von Teilnehmern des trilateralen GABI-Treffens (aus Frankreich, Deutschland und Spanien), 15 Personen, Vorstellung der Arbeit der Genbank, Information über Methoden zur *In vitro*-Erhaltung und Cryo-Lagerung, Besichtigung der Ähren- und Samensammlung sowie des Herbariums (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. K. Pistrick).

4. Mai 2007
Besuch von Herrn William Gerardo Gamboa, Costa Rica, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

10. Mai 2007
Besuch der Bioinformatikgruppe des Max-Planck-Instituts für Molekulare Pflanzenphysiologie, 14 Personen, Information über die Aufgaben des Instituts, Vorstellung der Aufgaben der Kulturpflanzenbank und Besichtigung des Samenkühllagers (Prof. U. Wobus, Dr. U. Lohwasser).

14. Mai 2007
Besuch des Direktors der Südkoreanischen Genbank, Vorstellung der Arbeit in der Genbank, Aufgaben der Botanischen Vergleichssammlungen (Prof. A. Graner, Dr. K. Pistrick, Dr. J. Keller, Dr. H. Knüpffer, Dr. F. Blattner, Priv.-Doz. Dr. A. Börner).

15. Mai 2007
Besuch einer Gruppe der Landesseniorenvereinigung Stendal, 50 Personen, Vorstellung des Instituts, Information über die Aufgaben der Kulturpflanzenbank, Besichtigung des Samenkühllagers, Herbars und der Ährensammlung, Information über die Aufgaben der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung und Feldführung (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, Dr. K. Pistrick, Dr. A. Senula).

23. Mai 2007
Besuch von Lehrlingen der Beruflichen Schule des Landkreises Nordwestmecklenburg, Zierow, 26 Personen, Führung durch die Teilsammlungen Malchow der IPK-Genbank und Durchführung von Übungen zur Pflanzenbestimmung und Herbaranlage (V. Miehe, H. Weiß, E. Willner).

24. Mai bis 31. August 2007
Betreuung der Arbeiten von M.-L. Meyer in den Botanischen Vergleichssammlungen im Rahmen des Programms „Artist in Lab" der Kunststiftung des Landes Sachsen-Anhalt (Dr. K. Pistrick).

31. Mai 2007
Besuch von Studenten der Fachhochschule Weihenstephan, 40 Personen, Vorstellung des Instituts sowie der Aufgaben der Genbank, Klimakammer- und Gewächshausbesichtigung sowie Versuchsfeldbesichtigung (Prof. A. Graner, E. Geyer, P. Schreiber).

1. Juni 2007
Besuch einer Gruppe von Gartenbaustudenten der Fachhochschule Wiesbaden, Fachbereich Geisenheim, 12 Personen, Vorstellung des Instituts sowie der Aufgaben der Genbank, Besichtigung des Samenkühllagers, des Herbariums und der Samensammlung, Erläuterung der *in vitro*-Erhaltung und Kryolagerung, Analyse der Biodiversität mit molekularen Methoden, Feldführung (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, Dr. K. Pistrick, Dr. A. Senula, Dr. F. Blattner).

1. Juni 2007
Besuch von Mitgliedern der Deutschen Gesellschaft für Technische Zusammenarbeit GmbH (GTZ), 6 Personen, Information über die Aufgaben des Instituts, Vorstellung der Aufgaben der Genbank, Besichtigung des Samenkühllagers, Information über die Aufgaben der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung, Vorstellung des Genomzentrums, Abschlussgespräch (Prof. U. Wobus, Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. habil. P. Schweizer).

3. Juni 2007
Führung durch die Einrichtung und Erläuterung der Arbeit einer Genbank und Schaugarten der HS Wismar im Rahmen eines Klassentreffens, 10 Personen (V. Miehe).

5. Juni 2007
Besuch von Lehrlingen der Beruflichen Schule des Landkreises Nordwestmecklenburg, Zierow, 31 Personen, Führung durch die Teilsammlungen Malchow der IPK-Genbank und Durchführung von Übungen zur Pflanzenbestimmung und Herbaranlage (C. Paetsch, H. Weiß, E. Willner).

6. Juni 2007
Besuch einer Gruppe von Wirtschafts- und Handelsräten in Sachsen-Anhalt, 25 Personen, Vorstellung des Instituts sowie der Aufgaben der Genbank, Besichtigung des Samenkühllagers, Erläuterung der *in vitro*-Erhaltung und Kryolagerung (Prof. A. Graner, Priv.-Doz. Dr. A. Börner, Dr. J. Keller).

10. Juni 2007
Führung durch die Einrichtung und Erläuterung der Arbeit einer Genbank und Schaugarten der Hochschule Wismar für die Gartenfreunde e.V. aus Schwerin-Mueß, 15 Personen (V. Miehe).

14. Juni 2007
Versuchsfeldführung für Institutsmitarbeiter (Priv.-Doz. Dr. A. Börner, P. Schreiber).

19. Juni 2007
Besuch von Lehrlingen der Beruflichen Schule des Landkreises Nordwestmecklenburg, Zierow, 21 Personen, Führung durch die Teilsammlungen Malchow der IPK-Genbank und Durchführung von Übungen zur Pflanzenbestimmung und Herbaranlage (C. Paetsch, H. Weiß, E. Willner).

19. Juni 2007
Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank für Schüler des Geschwister-Scholl-Gymnasiums, Bützow, 9 Personen (Dr. K.J. Dehmer).

20. Juni 2007
Besuch von Herrn Dr. Karl-Heinz Weege, Ministerium für Landwirtschaft und Umwelt des Landes Sachsen-Anhalt) sowie von zwei Expertinnen des estnischen Landwirtschaftsministeriums, Büro für Pflanzenproduktion, Frau Kristiina Digryte und Renata Tsaturjan, 3 Personen, Vorstellung des Instituts, Feldführungen Winterweizen, Genbankfelder und Erbse, Vorstellung der Aufgaben der Genbank, Besichtigung des Samenkühllagers, Abschlussdiskussion (Prof. U. Wobus, Dr. W. Weschke, Priv.-Doz. Dr. A. Börner, Dr. J. Kumlehn, P. Schreiber, Dr. M. Giersberg/Firma Novoplant).

25. Juni 2007
Besuch von Mitgliedern des Deutschen Bundestages, Ausschuss für Umwelt, Naturschutz und Reaktorsicherheit, CDU/CSU, 25 Personen, Begrüßung durch den Geschäftsführenden Direktor des IPK, der Ministerin für Landwirtschaft und Umwelt, Frau Petra Wernicke, und der Bürgermeisterin der Gemeinde Gatersleben, Frau Dr. E. Hüttner, Vorstellung des Instituts, Gespräch über aktuelle Fragen zur Grünen Gentechnik am Beispiel des Instituts, Information über den Stand des Freisetzungsversuchs „Winterweizen", Besichtigung des Erhaltungsanbaus der Genbank und des Samenkühllagers (Prof. A. Graner, Prof. U. Wobus, B. Eise, Dr. habil. P. Schweizer, Dr. W. Weschke, Dr. J. Freitag).

26. Juni 2007
Besuch von Mitgliedern der Agrargenossenschaft Warnstedt, 15 Personen, Vorstellung des Instituts und der Genbank, Besichtigung des Samenkühllagers und Versuchsfeldes (Priv.-Doz. Dr. A. Börner).

27. Juni 2007
Führung eines Thüringer Anbauberaters durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (M. Angeli, U. Behrendt, K. Göhrke, M. Vandrey).

2. Juli 2007
Führung von Herrn Ehrich, Lübeck, durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (M. Angeli, U. Behrendt, K. Göhrke, M. Vandrey).

4. Juli 2007
Führung von Frau Prof. Inge Broer, Universität Rostock, und Herrn Lorenz Bahlsen durch die Groß Lüsewitzer Wildkartoffel-Sortimente (M. Vandrey).

9. Juli 2007
Besuch von Studenten des Fachbereichs Ökologische Agrarwissenschaften, Universität Kassel-Witzenhausen, 8 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

13. Juli 2007
Besuch von Studenten der Hochschule Wismar, Fachbereich Verfahrens- und Umwelttechnik, 3 Personen, Führung durch die Einrichtung und Erläuterung des Genbank-Managements für Öl- und Futterpflanzen (E. Willner).

16. Juli 2007
Besuch von Mitgliedern des Fördervereins LAGA 2010, 15 Personen, Vorstellung des Instituts, insbesondere der Aufgaben der Genbank, Besichtigung des Samenkühllagers, Feldführung einschließlich Staudengarten (Priv.-Doz. Dr. A. Börner, P. Schreiber).

17. Juli 2007
Besuch einer Gruppe von Saatgutproduzenten der Firma Satimex Quedlinburg und Agro Cartu/Tbilisi, 4 Personen, Vorstellung des Instituts, Führung durch die Botanischen Vergleichssammlungen und Erfahrungsaustausch über die Situation pflanzengenetischer Ressourcen in Georgien (Prof. A. Graner, Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick).

18. Juli 2007
Besuch einer Gruppe von Studenten des Instituts für Biowissenschaften und Pflanzengenetik der Universität Rostock, ca. 20 Personen, Rundgang durch das Herbarium, die Samen- und Frucht- sowie die Ährensammlung des Bereiches Taxonomie und Evolution (Dr. K. Pistrick).

19. Juli 2007
Besuch von Mitarbeitern der Tschechischen Genbank aus Olomouc, 2 Personen, Vorstellung der Genbank sowie Besichtigung im Samenkühllager, Keimlabor und Ährensaal (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. C. Zanke).

24. Juli 2007
Besuch von Mitarbeitern des Priekuli Plant Breeding Institute, Lettland, 4 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

28. Juli 2007
Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank, 2 Personen (U. Behrendt).

30. Juli – 10. August 2007
Führung und Betreuung von Praktikantin S. Sawall in den Teilsammlungen Malchow der IPK-Genbank (E. Willner).

1. August 2007
Besuch einer Gruppe von Mitarbeitern des Europa-Rosariums Sangerhausen, 5 Personen, Erläuterungen zur Bedeutung der Dokumentation von Pflanzenmaterial in Botanischen Vergleichssammlungen für die praktische Arbeit mit pflanzengenetischen Ressourcen (Dr. K. Pistrick).

22. August 2007
Besuch einer königlichen Delegation (Staatsbesuch des Königs von Bunyoro) aus Uganda, 10 Personen, Vorstellung des Instituts, Besichtigung des Genomzentrums und der Genbank (Prof. A. Graner, Dr. L. Altschmied, B. Eise, R. Schnee).

23. August 2007
Führung von Herrn Jin Song Kim, InWEnt-Stipendiat, Nord-Korea, durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt, M. Vandrey).

23. August 2007
Besuch von Mitarbeitern des Dreschflegel e.V., Lübeck, Führung durch das Herbarium, die Ährensammlung sowie Frucht- und Samensammlung (Dr. K. Pistrick).

4. September 2007
Visit of Mr. Sando Bonow (Brazilian Agricultural Research Cooperation, Embrapa), Resources genetics and reproduction, long term seed storage, visiting of genebank multiplications, *In vitro* Storage and Cryopreservation, Research Group Genome Diversity, Taxonomy (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. N. Stein, Dr. K. Schmid).

11. September 2007
Besuch von Mitarbeitern der Landwirtschaftsverwaltung Hamburg, 11 Personen, Vorstellung des Instituts sowie Information über die Unternehmen am Campus, Information über Aufgaben der Genbank, Besichtigung von Samenkühllager, Trockenräumen und Dreschhalle, Gewächshaus- und Feldbesichtigung (P. Schreiber, R. Schnee).

12. September 2007
Visit of Chinese officials of the provinces Hunan and Hainan organised by the GTZ in Berlin, 10 Personen, Introduction to IPK and the objectives and tasks of the Federal *ex situ*-Genebank, Visit to collections of the Federal *ex situ*-Genebank (Prof. A. Graner, Priv.-Doz. Dr. A. Börner, R. Schnee).

14. September 2007
Besuch von Teilnehmern eines Studienjahrestreffens (zumeist Theologen), Berlin, 25 Personen, Vorstellung der Aufgaben des Instituts, Information über die Unternehmen am Campus, Information über die Aufgaben der Genbank und Gewächshausbesichtigung (Priv.-Doz. Dr. A. Börner, E. Geyer, R. Schnee).

17. September 2007
Recherche-Reise von Journalisten der Wissenschaftspressekonferenz in Forschungseinrichtungen der Region Braunschweig, 11 Personen, Vorstellung des Instituts und der Standortinitiative „Green Gate Gatersleben", Weizenversuch zur Steigerung des Proteingehaltes im Korn mit anschließenden Diskussionen, Besichtigung der Samenaufbereitung von gv-Pflanzen, Vorstellung der Aufgaben der Genbank und Besichtigung von Dreschhalle, Samenkühllager, Herbarium und Saatgutaufbereitung (Prof. A. Graner, Dr. W. Weschke, Dr. N. Weichert, Dr. F. Blattner, Dr. J. Freitag, R. Schnee).

Fig. 52: Dr. Nicola Weichert (l.) und Dr. Winfriede Weschke (2.v.l.) präsentieren den Journalisten der Wissenschaftspressekonferenz Getreidekörner ihres Freilandversuches (Foto: H. Ernst)./ Dr. Nicola Weichert (l.) and Dr. Winfriede Weschke (2nd left) show participants of the Conference of Science Journalists grains of their field trial (Photo: H. Ernst).

18. September 2007
Besuch der Landseniorenvereinigung Wolmirstedt, 35 Personen, Vorstellung der Aufgaben des Instituts sowie Informationen über die Unternehmen am Campus und die Aufgaben der Genbank, Besichtigung des Samenkühllagers, des Gewächshauses bzw. Feldbesichtigung (R. Schnee).

18. September 2007
Besuch des Landesamtes für Landwirtschaft und Forsten (Ostdeutschland und Niedersachsen), 7 Personen, Vorstellung des Instituts, Information über die Aufgaben der Genbank mit anschließender Besichtigung (R. Schnee).

20. September 2007
Besuch einer INRA-Delegation der Leibniz-Gemeinschaft Berlin, 10 Personen, Vorstellung des Instituts, Besichtigung des PGRC und der Genbank, Diskussion über Ideen und Möglichkeiten einer vertieften Zusammenarbeit mit INRA (Prof. U. Wobus, Dr. habil. H. Bäumlein, Dr. L. Altschmied, Dr. habil. P. Schweizer, Dr. N. Stein, Dr. F. Blattner, Dr. J. Kumlehn, Dr. J. Freitag).

22. September 2007
Besuch von Gästen (Baustoffhändler aus Deutschland) der Firma Große und Sohn GmbH, Aschersleben, 25 Personen, Vorstellung der Aufgaben des Instituts, Information über die Aufgaben der Genbank, Besichtigung des Samenkühllagers und des Gewächshauses einschließlich der Phytokammern (R. Schnee, E. Geyer).

26. September 2007
Besuch einer Studentengruppe der Bioverfahrenstechnik aus dem Hauptstudium der Universität Rostock, 20 Personen, Vorstellung des Instituts und der Aufgaben der Genbank mit anschließender Besichtigung (R. Schnee, Dr. U. Lohwasser).

27. September 2007
Durchführung eines Projekttages für die 6. Klasse der Realschule Kirchdorf zum Kennenlernen einer Genbank, 21 Personen (V. Miehe).

10. Oktober 2007
Besuch von Schülern einer 6. Klasse der Realschule Kirchdorf, 21 Personen, Durchführung eines Projekttages zum Thema „Rund um die Kartoffel" (V. Miehe).

11. Oktober 2007
Durchführung eines Projekttages für die 6. Klasse der Realschule Kirchdorf zum Kennenlernen einer Genbank im Allgemeinen und speziell die Erhaltungsarbeiten bei der Kartoffel, 20 Personen, (V. Miehe).

13. Oktober 2007
Teilnahme an der Aktion des Landfrauenvereins Nordwestmecklenburg, MEZ Gägelow, ca. 200 Personen, Stand zum Thema „Rund um die Kartoffel – Vielfalt, Erhaltung, Nutzung" (V. Miehe).

13. Oktober 2007
Ausstellung von alten Sorten der GLKS-Sammlung auf dem Aktionstag „Rund um die Kartoffeln" des Kreisvereins Bad Doberan des Landfrauenverbandes Mecklenburg-Vorpommern in Kröpelin, ca. 200 Personen, (Dr. K.J. Dehmer).

19. Oktober 2007
Durchführung eines Projekttages für die 3. Klasse der Realschule Kirchdorf zum Thema „Rund um die Kartoffel" – Vielfalt, Erhaltung, Nutzung, 12 Personen, (V. Miehe).

29. Oktober 2007
Besuch von Frau Ximena Cadima, Stiftung Proinpa aus Cochabamba, Bolivien, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (M. Vandrey).

30. Oktober 2007
Besuch von Studenten der Landesanstalt für Landwirtschaft und Gartenbau, Fachschule Quedlinburg, Fachbereich Gartenbau, 10 Personen, Vorstellung des Instituts, Erläuterung der *in vitro*-Erhaltung und Kryokonservierung von Kulturpflanzen, Besichtigung des Herbars sowie der Samensammlung, Gewächshausbesichtigung (R. Schnee, Dr. A. Senula, Dr. K. Pistrick, J. Marlow).

1. November 2007
Besichtigung der Genbank und der Züchtung (NPZ) im Rahmen der Arbeitsgemeinschaft Berufsvorbereitung der Realschule Grevesmühlen, 5 Personen (V. Miehe).

1. November 2007
Besuch von russischen Professoren der Pflanzenzucht in Begleitung von Monika Kühne (Hochschule Anhalt), 3 Personen, Vorstellung des Instituts und Green Gate Gatersleben, Besuch der Arbeitsgruppe Genregulation, Information über die Aufgaben der Genbank und Besichtigung des Samenkühllagers (R. Schnee, Dr. habil. H. Bäumlein).

7. November 2007
Durchführung einer Veranstaltung im Rahmen der Arbeitsgemeinschaft Berufsvorbereitung zur Kartoffelvielfalt in der Gesamtschule Neuburg, 5 Personen (V. Miehe).

7. November 2007
Besuch von Herrn Dr. Marcus Girnau, Geschäftsführer der Geschäftsstelle Berlin des Bundes für Lebensmittelrecht und Lebensmittelkunde e. V. (BLL) in Begleitung von Herrn Carsten Klein, Geschäftsführer der FDP-Fraktion im Landtag von Sachsen-Anhalt, 6 Personen, Vorstellung des Instituts und Informationen über die Aufgaben der Genbank, Besichtigung der Genbank (Prof. A. Graner, Priv.-Doz. Dr. A. Börner).

12. November 2007
Führungen durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank für Schüler des Gymnasiums Reutershagen, ca. 65 Personen (Dr. K.J. Dehmer).

12. - 16. November 2007
Führungen anlässlich der Schulaktionswoche am Biotech-Campus Gatersleben, ca. 300 Personen, Samenkühllager, Trocknung, *In vitro*-Erhaltung und Kryolagerung, Besichtigung der Sammlungen der Taxonomie, Computerdemo, TILLING-Projekt, Physische Karte Gerste, PCR, Vererbung, DNA-Isolierung, Einfärbeversuche DNA, Pflanzengenen mit Kanonen, Robotern und Goldstaub zu Leibe gerückt (R. Schnee, A. Kaczmarczyk, Dr. K. Pistrick, Dr. C. Zanke, Dr. U. Scholz, Dr. S. Gottwald, D. Schulte, Dr. I. Matthies, Dr. L. Altschmied, Dr. P. Schweizer).

Fig. 53: Schülerinnen beim Experimentieren in den Räumlichkeiten im Grünen Labor während der Schulaktionswoche (Foto: M. Kallas)./ Pupils while performing experiments during the school project's week in the facilities of the Green Laboratory (Photo: M. Kallas).

20. November 2007
Durchführung eines Projekttages für die 5. Klasse der Sehbehinderten- und Blindenschule Neukloster zum Thema „Rund um die Kartoffel" – Vielfalt, Erhaltung, Nutzung, 5 Personen (V. Miehe).

29. November 2007
Besuch von Mitgliedern des Verbandes Deutscher Mühlen, Bonn, 8 Personen, Vorstellung des Instituts und des Freisetzungsversuchs „Erhöhung des Korn-Proteingehalts von Winterweizen", Besichtigung der Freisetzungsversuchsfläche, Information über die Aufgaben der Genbank und Besichtigung des Samenkühllagers (R. Schnee, Dr. N. Weichert, P. Schreiber, Priv.-Doz. Dr. A. Börner).

5. Dezember 2007
Besuch des InWEnt-Trainingskurses „Veränderungsprozesse im Biodiversitätsmanagement" aus Bolivien, Brasilien, Ecuador, Kolumbien und Peru, 25 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Besichtigung des Samenkühllagers sowie des Herbariums und der Samensammlung, Besichtigung des Bereiches *In vitro*-Erhaltung und Cryo-Lagerung (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick, Dr. A. Senula, Dr. U. Lohwasser, K. Neumann, Dr. A. Weidner).

6. Dezember 2007
Besuch von Studenten der Hochschule Bremen, 40 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Vortrag zu den Arbeiten der Taxonomie am IPK, Besichtigung des Herbariums und der Samensammlung sowie des Samenkühllagers, Gewächshausbesichtigung (Priv.-Doz. Dr. A. Börner, Dr. F. Blattner, Dr. K. Pistrick, Dr. U. Lohwasser, J. Marlow).

13. Dezember 2007
Führungen durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank für Schüler des Käthe-Kollwitz-Gymnasiums Rostock, ca. 20 Personen (Dr. K.J. Dehmer).

20. Dezember 2007
Besuch von Studenten der Universität Stuttgart-Hohenheim, Institut für Pflanzenzüchtung, im Rahmen der Veranstaltung „Biodiversität und genetische Ressourcen", 16 Personen, Vorstellung des Instituts und der Arbeitsgruppe Experimentelle Taxonomie, Führung durch das Genomzentrum sowie die Arbeitsgruppen Taxonomie pflanzengenetischer Ressourcen, Ressourcengenetik und Reproduktion mit Samenkühllagerhaus und *In vitro*-Erhaltung und Cryo-Lagerung (Prof. A. Graner, Dr. F. Blattner, Dr. habil. P. Schweizer, Dr. K. Pistrick, Priv.-Doz. Dr. A. Börner, Dr. J. Keller).

Pressemitteilungen/ Press Releases

23. März 2007
Genbankarbeit am Leibniz-Institut in Gatersleben.

30. März 2007
Führungswechsel am Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) in Gatersleben.

21. Mai 2007
Kernbotschaften des IPK während des Mediengesprächs im Anschluss an die Demonstration „Rettet die Genbank Gatersleben" eines Aktionsbündnisses.

5. Juni 2007
Forschung hautnah erleben – Tag der offenen Tür am Biotechnologie-Standort Gatersleben.

26. Juni 2007
Wenn Pflanzen sich selbst klonen – Nutzen und Chancen der Apomixis-Forschung.

26. Juni 2007
Gentechnik und Genbank – Parlamentarier informieren sich vor Ort.

6. August 2007
Biotechnologie ist Chance und Zukunftsoption zugleich.

10. August 2007
Novelle des Gentechnikgesetzes in vorliegender Form hemmt Pflanzenforschung in Deutschland.

17. August 2007
BMBF fördert Erforschung des Gerstegenoms.

22. August 2007
Königlicher Besuch zu Gast auf dem Biotech-Campus in Gatersleben.

18. Oktober 2007
Rudolf-Mansfeld-Preis: Eignen sich europäische Maislandrassen für den Ökologischen Landbau?

Beiträge in der Presse und den Medien/ Contributions in Press and Media

(soweit erfasst/as for registered)

10. Januar 2007
Mitteldeutsche Zeitung, „Abgeordnete im Leibniz-Institut" (W. Mühlenberg).

11. Januar 2007
Mitteldeutsche Zeitung, „Gerste liegt unter Goldbeschuss – Gaterslebener Institut entwickelt automatisierten Test für Suche nach resistenten Genen bei Mehltaubefall" (Dr. P. Schweizer).

17. Januar 2007
Mitteldeutsche Zeitung, „Einzige Groß-Bank für Gene" (Prof. Dr. A. Graner).

1. Februar 2007
Mitteldeutsche Zeitung, „Strenge Auflagen für Versuch" (Dr. W. Weschke).

1. Februar 2007
Im Blickfeld (Monatsschrift), „Wir stellen bereit" (W. Mühlenberg).

2. Februar 2007
Mitteldeutsche Zeitung, „Zwischen Kunst und Wissenschaft" (Prof. Dr. U. Wobus).

6. Februar 2007
Mitteldeutsche Zeitung, „Kartoffelmuster tiefgefrostet" (Dr. J. Keller).

22. Februar 2007
dpa Frankfurt/M., Telefoninterview, „Medikamente und Impfstoffe vom Acker" (Dr. U. Conrad).

1. März 2007
Mitteldeutsche Zeitung, „Knoblauch wird jetzt auch international" (Dr. J. Keller).

15. März 2007
Mitteldeutsche Zeitung, „Ulrich Wobus wird Ehrenmitglied" (W. Mühlenberg).

15. März 2007
Mitteldeutsche Zeitung, „Genweizen kontra Genbank" (W. Mühlenberg).

19. März 2007
Mitteldeutsche Zeitung, „IPK profitiert von der EU-Förderung" (Prof. Dr. A. Graner, Prof. Dr. U. Wobus).

22. März 2007
Mitteldeutsche Zeitung, „Spezialbibliothek bald im Neubau" (B. Eise).

3. April 2007
mdr, Rundfunk, Interview „Genbank/Gentechnik" (Prof. Dr. A. Graner).

10. April 2007
dpa, Interview, „Genweizen erhitzt Gemüter – Bedroht er einmalige Pflanzensammlung?" (Prof. Dr. A. Graner).

12. April 2007
BILD, Magdeburg, „Video-Überwachung für Gen-Weizen" (Prof. Dr. U. Wobus).

16. April 2007
Mitteldeutsche Zeitung, Magdeburg, „Gentechniker greift Bundesminister an" (Prof. Dr. U. Wobus).

17. April 2007
Mitteldeutsche Zeitung, Aschersleben, „Salatmeer als Versuchsobjekt" (Priv.-Doz. Dr. A. Börner, M.-L. Graichen).

25. April 2007
MDR Wissenschaftsmagazin „Echt", Berlin, „Rettung aus der Vergangenheit – Wieso werden historische Kulturpflanzen plötzlich wieder wichtig für uns?" (Dr. U. Lohwasser, Dr. K. Pistrick).

10. Mai 2007
Leipziger Volkszeitung, Magdeburg, „Die Herren der Pflanzen" (Prof. Dr. A. Graner, Dr. J. Freitag).

15. Mai 2007
Newsletter NRW, Interview, „Forschen mit humanen embryonalen Stammzellen – aktuelle Entwicklungen" (Prof. Dr. Anna M. Wobus).

31. Mai 2007
ECO-Media TV, Hamburg, für ZDF-Sendung ‚Abenteuer Wissen', „Erhaltung der Vielfalt von Kulturpflanzen" (Priv.-Doz. Dr. A. Börner).

11. Juni 2007
Mitteldeutsche Zeitung, „Biowissenschaften für alle – Offene Türen im IPK und den am Biotech-Campus ansässigen Unternehmen" (Dr. J. Freitag, Prof. Dr. A. Graner, R. Czihal, J. Marlow).

13. Juni 2007
GenomXPress, „Bundesverdienstkreuz am Bande für einen renommierten Pflanzenforscher" (Dr. J. Freitag).

2. Juli 2007
CMA Centrale Marketing-Gesellschaft der deutschen Agrarwirtschaft mbH, Interview für Food, School & Life (Lehrermagazin), „Der grünen Gentechnik auf der Spur" (Dr. J. Freitag).

7. August 2007
ARD Tagesthemen, „Risiko- und Sicherheitsforschung" (Prof. Dr. A. Graner).

9. August 2007
Magdeburger Volksstimme, „IPK Gatersleben reagiert verhalten auf Gesetzentwurf" (Dr. J. Freitag).

23. August 2007
Mitteldeutsche Zeitung, „Königlicher Besuch in Gatersleben" (Prof. Dr. A. Graner).

25. September 2007
Mitteldeutsche Zeitung, „Von Gerste und von Genen" (Dr. N. Stein).

15. Oktober 2007
BRIGITTE WOMAN, „Sind Stammzellen der Jungbrunnen und das Wundermittel der Zukunft? – Zündstoff in der Petrischale" (Prof. Dr. Anna M. Wobus).

5. November 2007
Mitteldeutsche Zeitung, „Zentrum für das Institut“
(B. Eise).

8. November 2007
Argos Wirtschaftsmagazin für Mitteldeutschland, Leipzig, „Bundesland Sachsen-Anhalt – Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung Gatersleben“ (R. Schnee).

14. November 2007
Sächsische Zeitung, „Biotechnologie erobert den Osten“
(Prof. Dr. A. Graner).

26. November 2007
Mitteldeutsche Zeitung, „Informationen zu tropischen Pflanzen“
(Dr. K. Pistrick, J. Marlow).

28. November 2007
Mitteldeutsche Zeitung, „Mehr Platz und Ordnung für wissenschaftliche Bücher“
(Dr. T. Schuhmann, S. Winter).

Messen und Ausstellungen/ Fairs and Exhibitions

13. – 16. September 2007
Mitarbeiterinnen der Außenstelle Malchow präsentierten mit einem Informationsstand auf der 17. Fachausstellung für Landwirtschaft, Ernährung, Fischwirtschaft, Jagd, Forst und Gartenbau (MeLa) des Landes Mecklenburg-Vorpommern in Mühlengeez ihre Arbeit und die Aufgaben der Außenstelle in Malchow.

Fig. 54: Stand der Außenstelle Malchow bei der Mecklenburger Landwirtschaftsausstellung in Mühlengeez (Foto: E. Willner)./ The booth of the External Branch "North" at Malchow at the annual agricultural fair in Mühlengeez, Mecklenburg-Western Pomerania. (Photo: E. Willner).

9. – 11. Oktober 2007
Das IPK beteiligte sich im Rahmen des Gemeinschaftsstandes „Forschung für die Zukunft" mit zwei Posterbeiträgen zu den Themen „DNA-Sensoren zum Nachweis mykorrhizierter Pflanzen" (Prof. Dr. G. Kunze, Dr. K. Florschütz) und „Biosensor zum Nachweis östrogenwirksamer Substanzen in Wasser" (Dr. M. Körner, S. Uhlig, K. Simon, Dr. K. Florschütz, Prof. Dr. G. Kunze) an der BIOTECHNICA 2007 in Hannover.

Fig. 55: Dr. Kristina Tag (mi.) und Dr. Martina Körner (r.) aus der Arbeitsgruppe Hefegenetik im Gespräch mit einer Besucherin (l.) der BIOTECHNICA (Foto: F. Schröder)./ Dr. Kristina Tag (centre) and Dr. Martina Körner (r.), Yeast Genetics group, in a discussion with a visitor (l.) at the BIOTECHNICA, Hannover (Photo: F. Schröder).

Übersicht Drittmittelprojekte/ Overview of Additional Funding

Stand: 31.12.2007

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt-leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
ABTEILUNG GENBANK	***Bereich: Charakterisierung und Dokumentation***				
Arbeitsgruppe Genomdiversität					
Bioinformatik Centrum Gatersleben-Halle: Arbeitsgruppe Plant Data Warehouse	Prof. I. Große Dr. H. Knüpffer Dr. N. Stein Dr. U. Scholz	01.05.2002 31.10.2007	BMBF PDW 0312706A 161101	583.113,43	87.852,44 [3]
Verknüpfung von Genomforschung und genetischer Diversität: Assoziation zwischen DNA-Polymorphismus und Merkmalsvariationen bei Gerste und Roggen (Teilprojekt 1)	Dr. S. Stracke	01.08.2004 31.07.2007	BMBF GABI-Genoplante 2 0313098A 171102	166.921,39	63.493,54
GABI-MALT: Ein integrierter Ansatz zur Identifizierung von Kandidatengenen für das Merkmal Brauqualität bei Gerste	Prof. A. Graner Dr. M. Röder	01.08.2004 30.09.2008	BMBF 0313125A 171121	342.433,00	58.361,58 [3]
GABI-TILL: Aufbau einer zentralen Plattform zur Untersuchung von Leitgen-Funktionen in Feldfrüchten mit Hilfe der TILLING-Technologie	Dr. N. Stein	01.09.2004 31.12.2007	BMBF 0313123C 171122	459.010,00	129.812,57
GABI-TILL: Erweiterung und Anwendung der GABI-TILLING-Plattform zur Funktionsanalyse von Nutzpflanzengenen, Teilvorhaben B	Dr. N. Stein Dr. J. Kumlehn	01.09.2007 31.08.2010	BMBF 0315052B 181102	56.600,00	28.000,00 [3]
Aufbau einer genetisch verankerten physischen Karte des Gerstengenoms als Plattform für gezielte Genisolierung in den Triticeae Getreidespezies und als Grundlage für die Genomsequenzierung in Gerste (Teilprojekt A BARLEX)	Dr. N. Stein Dr. U. Scholz	01.07.2007 31.12.2010	BMBF GABI-BARLEX 0314000A 181121	3.979.503,00	62.000,00 [3]
EXBARDIV: Genomics-assisted analysis and exploitation of barley diversity (ERA-PG 061)	Prof. A. Graner	01.06.2007 31.05.2010	DFG GR 1317/5-1 201111	174.000,00	6.000,00
BARCODE: A platform for genomics-assisted dissection of barley morphology and development (ERA-PG 046)	Dr. N. Stein	01.09.2007 31.08.2010	DFG STE 1102/2-1 201112	490.500,00	15.000,00
German-Hungarian distributed project PlantResource to develop genetics for food production	Dr. N. Stein Prof. A. Graner Dr. P. Schweizer Dr. A. Börner	01.10.2005 30.09.2008	MK-LSA 3593A/04055T 301101	102.058,54	32.483,70 [3]

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Construction of a chromosome 3H specific BAC library for physical mapping in barley	Dr. N. Stein	01.01.2006 31.12.2007	DAAD D/05/11725 801111	3.756,00	917,00
Exploration of genetic resources collections at ICARDA for adaptation to climate change	Prof. A. Graner	01.01.2003 30.09.2007	1010133 921102	370.452,21	11.798,05
Establishment of an EMS mutagenesis protocol for *Nicotinia tabacum* L. with regards to the development of a TILLING population for functional genomics	Dr. N. Stein	10.12.2007 18.07.2008	1010165 921120	15.000,00	0,00
Zuwendung Arbeitsgruppe				**6.743.347,57**	**495.718,88**
Arbeitsgruppe Genbankdokumentation					
Bioinformatik Centrum Gatersleben-Halle: Arbeitsgruppe Plant Data Warehouse	Prof. I. Große Dr. H. Knüpffer Dr. N. Stein Dr. U. Scholz	01.05.2002 31.10.2007	BMBF PDW 0312706A 161101	583.113,43	87.852,43 [3]
Zuwendung Arbeitsgruppe				**583.113,43**	**87.852,43**
Arbeitsgruppe Plant Data Warehouse (BIC-GH-Gruppe)					
Bioinformatik Centrum Gatersleben-Halle: Arbeitsgruppe Plant Data Warehouse	Prof. I. Große Dr. H. Knüpffer Dr. N. Stein Dr. U. Scholz	01.05.2002 31.10.2007	BMBF PDW 0312706A 161101	583.113,43	87.852,43 [3]
GABI-Trilateral: Etablierung eines Netzwerkes samenspezifischer Genexpression und Analyse seiner Biodiversität (ARABIDO-SEED)	Prof. I. Große Dr. H. Bäumlein Dr. U. Conrad Dr. L. Altschmied	01.09.2004 31.08.2007	BMBF GABI-Trilateral 0313155 171103	51.987,89	10.908,51 [3]
Zuwendung Arbeitsgruppe				**635.101,32**	**98.760,94**
Summe Bereich Charakterisierung Dokumentation				**7.961.562,32**	**682.332,24**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Abteilung Genbank	***Bereich: Management und Evaluierung***				
Arbeitsgruppe Ressourcengenetik und Reproduktion					
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. A. Börner Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 181201	2.200,00	0,00 [3]
Gastaufenthalt Dr. Oxana Dobrovolskaya, Russland	Dr. A. Börner	01.06.2007 31.08.2007	DFG BO 1423/6-1 201204	6.160,00	6.160,00
Gastaufenthalt Dr. Svetlana Landjeva, Bulgarien	Dr. A. Börner	01.09.2007 30.11.2007	DFG BO 1423/7-1 201205	6.900,00	6.900,00
German-Hungarian distributed project PlantResource to develop genetics for food production	Dr. A. Börner Dr. N. Stein Prof. A. Graner Dr. P. Schweizer	01.10.2005 30.09.2008	MK-LSA 3593A/04055T 301201	101.224,09	32.750,22 [3]
Leafy Veg, AGRI GEN RES Leafy vegetables germplasm, stimulating use	Dr. A. Börner	01.01.2007 31.12.2010	EU-34,06 % 001 AGRI GEN RES 870/2004 711210 IPK-Anteil- 65,94 % 711210	45.981,00 89.019,00	0,00 12.868,00
7 Langzeitstipendiaten 2007: Pflanzengenetische Vielfalt und Ernährungssicherung Schwerpunkt: Sammlung, Erhaltung, Charakterisierung, Dokumentation und Evaluierung genetischer Ressourcen von Kulturpflanzen	Dr. A. Börner	16.04.2007 30.09.2007	InWEnt 901215	50.928,73	50.928,73
Forschungsstipendium Dr. I. Daniel, Nigeria Studying seed longevity of genebank collections	Dr. A. Börner	01.01.2007 31.05.2008	A.v. Humboldt-Stiftung 3-NRI/1121662 STP 901217	61.820,00	41.900,00
EWAC - The European Cereals Genetics Co-operative - Tagung	Dr. A. Börner	01.07.2007 31.12.2008	EWAC 901218	2.377,50	2.377,50
Collection, distribution, phenotyping and genotyping directed towards utilization of existing wheat genetics stocks to enhance tolerance/resistance of wheat cultivars to abiotic and biotic stresses	Dr. A. Börner	17.11.2005 31.12.2007	MEXICO 921201	5.562,69	1.264,89
Preparative isolation of sugar ester fractions from tobacco leaf surface exudates and exudate profiling of *Nicotiana* varieties	Dr. A. Börner	01.11.2007 30.05.2009	D1010165 921210	39.897,00	15.000,00
Zuwendung Arbeitsgruppe				**412.070,01**	**170.149,34**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung					
Datenerfassung zur genetischen Variabilität und Analytik von Arznei- und Gewürzpflanzen	Dr. J. Keller	01.10.2006 31.03.2008	BAZ/BMBF 22000306 101310	40.000,00	22.823,73
Liquid nitrogen influence on bulbs	Dr. J. Keller	09.08.2007 31.12.2007	DFG KE 581/2-1 201302	3.111,36	3.100,00
EURALLIVEG, AGRI GEN RES: Establishment of European Core Collection of vegetative alliums, covering garlic *(Allium sativum)* including molecular characterization of shallot *(Allium cepa* var. *aggregatum)*	Dr. J. Keller	01.04.2007 31.03.2011	EU 50 % 050 AGRI GEN RES 870/2004 711310 IPK Anteil - 50 % 711310	196.750,00 196.750,00	0,00 33.962,77
Zuwendung Arbeitsgruppe				**436.611,36**	**59.886,50**
Arbeitsgruppe Außenstelle „Nord“					
BioChancePlus-3: Der Kartoffelkrebs: Ein biotechnologischer Ansatz zur effizienten Nutzung natürlicher Resistenzfaktoren, Teilprojekt 4, KOSY	Dr. K. Dehmer	01.06.2007 28.02.2010	BMBF 0313966D 101800	91.280,00	16.000,00
Zuwendung Arbeitsgruppe				**91.280,00**	**16.000,00**
Summe Bereich Management und Evaluierung				**939.961,37**	**246.035,84**
Abteilung Genbank	***Bereich: Taxonomie und Evolution***				
Arbeitsgruppe Experimentelle Taxonomie					
Mechanisms of speciation in Southeast Asian antplants of the genus *Macaranga* (Euphorbiaceae) associated with *Crematogaster* ants	Dr. F. Blattner	01.03.2004 28.02.2007	DFG BL 462/2-2 202122	18.914,32	791,00
Speciation mechanisms underlying rapid radiations in South American and Central Asian species of *Hordeum* (Poaceae), Schwerpunktprogramm: Radiationen - Genese biologischer Diversität	Dr. F. Blattner	01.03.2006 28.02.2008	DFG BL 462/3-3 202124	105.900,00	40.555,84
Mechanisms of speciation in Southeast Asian ant-plants of the genus *Macaranga* (Euphorbiaceae) associated with *Crematogaster* ants, Schwerpunktprogramm: Radiationen - Genese biologischer Diversität	Dr. F. Blattner	01.03.2006 28.02.2008	DFG BL 462/5-3 202125	25.000,00	14.987,77
Forschungsreise zur Evaluierung und phylogenetischen und populationsbiologischen Untersuchungen westafrikanischer Kürbisgewächse (Cucurbitaceae)	Dr. F. Blattner	01.01.2007 31.12.2007	DFG 445 BEN-18/1/06 202127	5.462,00	5.462,00

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
The evolutionary history of *Hypericum* (Hypericaceae) with special emphasis on sect. *Hypericum* - Biogeography, character evolution, ecological shifts and age estimations	Dr. F. Blattner	01.07.2007 30.06.2010	DFG BL 462/6-1 202128	100.650,00	13.000,00
Forschungs- und Arbeitsaufenthalt - Dr. Violetta Kotseruba, Russland	Dr. F. Blattner	20.09.2007 19.11.2007	DAAD A/07/09344 802103	3.813,00	3.813,00
Zuwendung Arbeitsgruppe				**259.739,32**	**78.609,61**
Arbeitsgruppe Taxonomie pflanzengenetischer Ressourcen					
Pharmaceutical value of onions and related species (*Allium* L.) of Middle Asia and the Caucasus (PharmAll)	Dr. R. Fritsch Dr. K. Pistrick	01.01.2006 30.04.2008	Volkswagen Stiftung Az.: I/81 319 902302	48.400,00	29.383,38
Zuwendung Arbeitsgruppe				**48.400,00**	**29.383,38**
Summe Bereich Taxonomie und Evolution				**308.139,32**	**107.992,99**
Gesamtzuwendung Abt. Genbank				**9.209.663,02**	**1.036.361,07**
Abteilung Cytogenetik und Genomanalyse	***Bereich: Cytogenetik***				
Arbeitsgruppe Karyotypevolution					
Identification and functional characterization of protein components of the plant kinetochore complex	Prof. I. Schubert	01.01.2005 14.01.2007	DFG SCHU 951/9-3 203144	109.741,35	1.802,01
Dynamics of interphase chromosome territories and occurrence of homologous pairing of *Arabidopsis* chromosomes	Prof. I. Schubert	01.05.2006 30.09.2007	DFG SCHU 951/10-2 203156	54.055,17	41.070,75
Functional characterization of the plant centromeric histone variant CENH3 as a prerequisite to understand kinetochore formation	Prof. I. Schubert Dr. I. Lermontova	15.01.2007 14.01.2010	DFG SCHU 951/12-1 203157	180.000,00	57.000,00
Concerted evolution of histone methylation marks and other chromatin features	Dr. J. Fuchs Prof. I. Schubert Dr. A. Houben Dr. F. Mette	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 323101	149.425,00	43.264,42 [3]
Zuwendung Arbeitsgruppe				**493.221,52**	**143.137,18**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Chromosomenstruktur und -funktion					
Analysis of the relationship between heterosis and the epigenetic of DNA and histones in *Arabidopsis thaliana*	Dr. A. Houben Dr. F. Mette	13.06.2005 12.06.2007	DFG HO 1779/7-1 203153	29.019,72	6.361,08 [3]
Isolation von phosphorylierungs-abhängigen Histon H3-Interaktoren und Substratcharakterisierung von AtAurora-Kinasen in *Arabidopsis thaliana*	Dr. A. Houben	01.08.2005 14.01.2009	DFG HO 1779/8-1 203155	243.200,00	82.047,17
Analysis of the relationship between heterosis and the epigenetic of DNA and histones in *Arabidopsis thaliana*	Dr. A. Houben Dr. F. Mette	13.06.2007 12.06.2009	DFG HO 1779/7-2 203158	34.900,00	9.000,00 [3]
Analysis of uniparental elimination of chromosomes in wide crosses	Dr. A. Houben	16.05.2007 15.05.2010	DFG HO 1779/9-1 203159	126.002,00	13.000,00
Regulation der Chromosomendynamik in Pflanzen – Isolierung und Charak-terisierung von NIMA-ähnlichen Kinasen	Dr. A. Houben	01.10.2005 30.09.2008	MKLSA 3541A/1003T 303116	87.785,33	25.616,34
Chromosome condensation and histone phosphorylation	Dr. A. Houben	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 323102	149.425,00	44.528,61
Zuwendung Arbeitsgruppe				**670.332,05**	**180.553,20**
Arbeitsgruppe Apomixis					
3rd International Conference on Apomixis und 9th Gatersleben Research Conference, Gatersleben-Wernigerode 27.06.-02.07.2007	Dr. T. F. Sharbel	27.06.2007 02.07.207	DFG 4853/89/07 203401	11.412,15	11.412,15
3rd International Conference on Apomixis und 9th Gatersleben Research Conference, Gatersleben-Wernigerode 27.06.-02.07.2007	Dr. T. F. Sharbel	27.06.2007 02.07.207	DFG SH 337/2-1 203402	3.990,00	3.990,00
Apomixis evolution in St. John's wort (*Hypericum perforatum* L.)	Dr. T. F. Sharbel	01.06.2007 31.05.2010	DFG SH 337/1-1 203403	171.000,00	32.000,00
„IPK-Workshop" Apomixis: – a look towards the future – im Rahmen der Gatersleben Research Conference und anlässlich der EU-Ratspräsidentschaft Deutschlands, Wernigerode, 27.06.2007	Dr. T. F. Sharbel	01.01.2007 31.12.2007	MK-LSA 10MT 303410	9.423,08	9.423,08
Zuwendung Arbeitsgruppe				**195.825,23**	**56.825,23**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Genomplastizität					
GABI-OIL: Omics basierte Strategien zur Erhöhung des Ölgehaltes im Raps (Teilvorhaben G)	Dr. R. Schmidt	01.09.2007 31.08.2010	BMBF GABI-OIL 0315053G 183102	433.874,00	30.000,00
Zuwendung Arbeitsgruppe				**433.874,00**	**30.000,00**
Arbeitsgruppe Epigenetik					
Analysis of the relationship between heterosis and the epigenetic of DNA and histones in *Arabidopsis thaliana*	Dr. A. Houben Dr. F. Mette	13.06.2005 12.06.2007	DFG HO 1779/7-1 203153	29.019,73	6.361,08 [3]
Analysis of the relationship between heterosis and the epigenetic of DNA and histones in *Arabidopsis thaliana*	Dr. A. Houben Dr. F. Mette	13.06.2007 12.06.2009	DFG HO 1779/7-2 203158	34.900,00	9.000,00 [3]
Beitrag von Struktur und chromosomaler Lokalisation der Zielgene zur RNA-induzierten transkriptionellen Genaktivierung in *Arabidopsis thaliana*	Dr. F. Mette	01.01.2005 31.12.2008	SFB 648 UNI Halle 233101	405.366,51	118.893,54
Reisekosten zu 233101	Dr. F. Mette	01.01.2005 31.12.2008	SFB 648 Reisekosten 233102	5.528,02	1.886,46
Antagonisten der Geninaktivierung	Dr. F. Mette	01.10.2005 30.09.2007	MK LSA 3555A/1203T 303115	123.716,52	33.623,52
The impact of sequence organization and epigenetic modification on local chromatin arrangement	Dr. F. Mette Prof. I. Schubert Dr. A. Houben Dr. J. Fuchs	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 323103	149.425,00	47.468,88 [3]
Zuwendung Arbeitsgruppe				**747.955,78**	**217.233,48**
Arbeitsgruppe Mustererkennung (BIC-GH-Gruppe)					
3D Mikrodissektion biologischer Objekte und Analyse schock-gefrorener molekularer Komponenten	Dr. U. Seiffert Dr. A. Matros Dr. W. Weschke	01.07.2006 30.06.2009	BMBF 0313821A 103921	166.972,00	42.303,17 [3]
Bioinformatik Centrum Gatersleben-Halle: Erkennung räumlich-zeitlicher Entwicklungsmuster	Dr. U. Seiffert Dr. P. Schweizer Prof. U. Wobus	01.05.2002 31.10.2007	BMBF Muster 0312706A 163901	342.449,62	31.234,90 [3]

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Bioinformatik Centrum Gatersleben-Halle Management und Ausbildung	Dr. U. Seiffert	01.05.2002 30.04.2007	BMBF Management und Ausbildung 0312706A 165702	228.842,69	18.207,21
GABI-SEED II – Gerste als Modell- und Nutzpflanze: Genexpression-Netzwerke zur Bestimmung nutzungsrelevanter Merkmale des Getreidesamens	Dr. U. Seiffert	01.07.2004 30.06.2007	BMBF GABI-SEED II 0313115 173902	165.031,46	20.600,77
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Dr. U. Seiffert	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 183921	161.511,00	0,00
4D-Entwicklungsgradienten im Endosperm der Gerste: biologischer Nachweis, virtuelle Rekonstruktion und Identifizierung von Regulatorgenen	Dr. U. Seiffert Dr. W. Weschke Dr. L. Borisjuk	01.01.2006 14.11.2008	DFG WE 16008/2-1 203906	108.000,00	38.614,38 [3]
Zuwendung Arbeitsgruppe				**1.172.806,77**	**150.960,43**
Arbeitsgruppe *In vitro*-Differenzierung					
Entwicklung von Strategien zur Differenzierung von ES-Zellen in endodermale Vorläuferzellen und funktionelle hepatische Zellen (Verbundprojekt: Stammzell-basierte Leberregeneration)	Prof. A. M. Wobus	01.09.2005 31.08.2008	DLR/BMBF 01GN0527 103705	264.588,00	96.837,21
Schwerpunktprogramm „Embryonale und gewebespezifische Stammzellen: Regenerative Zellsysteme für einen Zell- und Gewebeersatz“	Prof. A. M. Wobus	01.09.2005 15.06.2008	DFG WO 503/3-3 203711	205.500,00	65.320,72
Schwerpunktprogramm „Embryonale und gewebespezifische Stammzellen: Regenerative Zellsysteme für einen Zell- und Gewebeersatz“	Prof. A. M. Wobus	01.04.2005 31.03.2007	DFG WO 503/4-3 203712	58.524,38	7.743,43
Functional Genomics in Engineered ES cells (FunGenES)	Prof. A. M. Wobus	01.03.2004 31.12.2007	EU LSHG-CT-2003-50394 713700	306.000,00	-27.246,62
Application and process optimization of human stem cells for myocardium repair (SC&CR)	Prof. A. M. Wobus	01.02.2004 31.01.2008	EU LSHB-CT-2004-502988 713701	191.618,00	-42.569,27
„TherCord: Development and preclinical testing of cord blood-derived cell therapy products“	Prof. A. M. Wobus	01.05.2006 30.04.2009	EU LSHB-CT-2005-018817 713702	200.000,00	120.504,07
Zuwendung Arbeitsgruppe				**1.226.230,38**	**220.589,54**
Summe Bereich Cytogenetik				**4.940.245,72**	**999.299,06**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Abteilung Cytogenetik und Genomanalyse	***Bereich: Genomanalyse***				
Arbeitsgruppe Transkriptomanalyse					
ERA-Net PlantGenomics – Verbundvorhaben: Sicherung einer nachhaltigen Produktion von Lebens- und Futtermitteln (CEREHEALTH, Teilvorhaben F)	Dr. P. Schweizer Dr. J. Kumlehn	01.05.2007 30.04.2010	BMBF 0313992F 103922	180.715,30	23.714,93 [3]
Bioinformatik Centrum Gatersleben-Halle: Erkennung räumlich-zeitlicher Entwicklungsmuster	Dr. U. Seiffert Dr. P. Schweizer Prof. U. Wobus	01.05.2002 31.10.2007	BMBF Muster 0312706A 163901	342.449,61	31.234,89 [3]
German-Hungarian distributed project PlantResource to develop genetics for food production	Dr. P. Schweizer Dr. N. Stein Prof. A. Graner Dr. A. Börner	01.10.2005 30.09.2008	MK-LSA 3593A/04055T 303903	92.688,57	31.617,06 [3]
Biowissenschaften: Strukturen und Mechanismen biologischer Informationsverarbeitung	Dr. P. Schweizer Dr. H.-P. Mock	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 323901	20.500,00	5.960,19 [3]
BioExploit: Exploitation of natural plant biodiversity for the pesticide-free production of food	Dr. P. Schweizer Dr. J. Kumlehn	01.10.2005 30.09.2010	EU FOOD-CT-2005- 513959 713920	330.762,00	105.592,74 [3]
PRO-GABI: Ein Netzwerk zur Identifizierung, Charakterisierung und Optimierung neuer monokotylspezifischer Promotoren für die Herstellung pilzresistenten Weizens	Dr. P. Schweizer Dr. J. Kumlehn	01.07.2004 31.12.2007	1010124 0313124 913909	213.066,96	48.115,09 [3]
GABI-NONHOST: A Consortium-Based Functional Genomics Initiative on Plant Nonhost Disease Resistance	Dr. P. Schweizer	01.01.2006 31.12.2007	1010124 913910	249.096,00	127.722,96
GABI-CANADA: Reduzierung des Gehaltes an *Fusarium*-Toxinen in Weizen mit einem genomischen Ansatz Teilprojekt A	Dr. P. Schweizer	01.10.2006 30.09.2009	BMBF-TU München 0313711A 913920	221.966,00	63.645,47
PRO-GABI: Ein Netzwerk zur Identifizierung, Charakterisierung und Optimierung neuer monokotylspezifischer Promotoren für die Herstellung pilzresistenten Weizens	Dr. P. Schweizer Dr. J. Kumlehn	01.07.2004 31.12.2007	1010124 0313124 916026	124.723,48	28.938,04 [3]
Zuwendung Arbeitsgruppe				**1.775.967,92**	**466.541,37**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Expressionskartierung					
Bioinformatik Centrum Gatersleben-Halle Metabolische und regulatorische Netzwerke	Dr. U. Seiffert Dr. L. Altschmied Dr. H.-P. Mock	01.05.2002 31.10.2007	BMBF Netzwerk 0312706A 165701	330.538,95	58.116,95 [3]
GABI-Trilateral: Etablierung eines Netzwerkes samenspezifischer Genexpression und Analyse seiner Biodiversität (ARABIDO-SEED)	Dr. L. Altschmied Dr. H. Bäumlein Dr. U. Conrad Prof. I. Große	01.09.2004 31.08.2007	BMBF GABI-Trilateral 0313155 175702	28.220,55	4.656,96 [3]
Zuwendung Arbeitsgruppe				**358.759,50**	**62.773,91**
Arbeitsgruppe Gen- und Genomkartierung					
Deutsch-russische Zusammenarbeit auf dem Gebiet der Agrarforschung: Studienaufenthalt Dr. Elena Salina zu Projekt 101 der Kooperationsvereinbarung 2006	Dr. M. Röder	06.11.2007 16.11.2007	BLE 521- 06.01.–01.10. Russland 103916	450,00	0,00
GABI-Malt: Ein integrierter Ansatz zur Identifizierung von Kandidatengenen für das Merkmal Brauqualität bei Gerste	Dr. M. Röder Prof. A. Graner	01.08.2004 30.09.2008	BMBF 0313125A 173903	365.841,00	95.045,91 [3]
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. M. Röder Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 183902	48.700,00	20.000,00 [3]
GABI-SEED II – Gerste als Modell- und Nutzpflanze Genexpression-Netzwerke zur Bestimmung nutzungsrelevanter Merkmale des Getreidesamens	Dr. M. Röder Prof. U. Wobus Dr. W. Weschke Dr. H.-P. Mock Dr. U. Seiffert Dr. H. Bäumlein	01.07.2004 30.06.2007	BMBF GABI-SEED II 0313115 173901	290.438,27	24.756,08 [3]
Fine mapping of a gene for weight in wheat – Dr. Elena Khlestkina, Russland	Dr. M. Röder	02.06.2007 01.09.2007	DFG RO 1055/6-1 203933	6.300,00	6.300,00
Assessment of genetic erosion and gene flow from cultivated sorghum (*Sorghum bicolor* (L.) Moench) to its wild progenitors: key research for biodiversity conservation and transgene risk assessment – Dr. Yifru Teklu, Äthiopien	Dr. M. Röder	01.09.2007 31.08.2008	A. v. Humboldt-Stiftung ATH 1123555 STP-2 903905	16.055,00	9.655,00
Study of sequence polymorphism and genetic diversity of key enzymes in the carbohydrate metabolism in polyploid wheats and their A and B genome progenitors using gene specific STS and SNP markers – Dr. Shailendra Sharma, Indien	Dr. M. Röder	01.08.2007 31.07.2008	A. v. Humboldt-Stiftung INI 1122058 STP-2 903906	9.600,00	4.000,00
Zuwendung Arbeitsgruppe				**737.384,27**	**159.756,99**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Bioinformatik					
Bioinformatik Centrum Gatersleben-Halle: Arbeitsgruppe Plant Data Warehouse	Prof. I. Große Dr. H. Knüpffer Dr. N. Stein Dr. U. Scholz	01.05.2002 31.10.2007	BMBF PDW 0312706A 161101	583.113,43	87.852,44 [3]
GABI-Trilateral: Vergleichende Genomforschung zur Regulation der Meristemaktivität bei Nachtschattengewächsen (Solanaceae)	Dr. U. Scholz	01.09.2004 31.12.2007	BMBF GABI - Trilateral 0313149A 175901	79.570,05	41.238,16
- (Genosome) Teilprojekt 1	Dr. U. Scholz	01.09.2004 31.12.2007	BMBF 176006	27.610,61	0,00
Aufbau einer genetisch verankerten physischen Karte des Gerstengenoms als Plattform für gezielte Genisolierung in den Triticeae Getreidespezies und als Grundlage für die Genomsequenzierung in Gerste (Teilprojekt A BARLEX)	Dr. U. Scholz Dr. N.Stein	01.07.2007 31.12.2010	BMBF GABI-BARLEX 0314000A 183960	387.331,00	58.000,00 [3]
Systems analysis of biopathways – Prof. Ming Chen, China	Dr. U. Scholz	01.08.2007 30.09.2007	DAAD A707/13035 803960	3.664,00	3.664,00
Entwicklung des Prototyps eines neuen Suchkonzeptes auf der Basis der Datenintegrationssoftware (BioEscorte)	Dr. M. Lange	01.08.2007 31.07.2008	1010124 BioEscorte 913960	71.400,00	35.700,00
Zuwendung Arbeitsgruppe				**1.125.078,48**	**226.454,60**
Summe Bereich Genomanalyse				**4.024.800,79**	**915.526,87**
Summe Abteilung Cytogenetik und Genomanalyse				**8.965.046,51**	**1.914.825,93**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Abteilung Molekulare Genetik					
Arbeitsgruppe Genwirkung					
3D Mikrodissektion biologischer Objekte und Analyse schock-gefrorener molekularer Komponenten	Dr. W. Weschke Dr. U. Seiffert Dr. A. Matros	01.07.2006 30.06.2009	BMBF 0313821A 105103	366.834,00	107.066,24 [3]
Bioinformatik Centrum Gatersleben-Halle: Erkennung räumlich-zeitlicher Entwicklungsmuster	Dr. U. Seiffert Dr. P. Schweizer Prof. U. Wobus	01.05.2002 31.10.2007	BMBF Muster 0312706A 163901	342.449,62	31.234,90 [3]
GABI-SEED II – Gerste als Modell- und Nutzpflanze: Genexpression-Netzwerke zur Bestimmung nutzungsrelevanter Merkmale des Getreidesamens	Prof. U. Wobus Dr. W. Weschke Dr. U. Seiffert Dr. M. Röder Dr. H.-P. Mock Dr. H. Bäumlein	01.07.2004 30.06.2007	BMBF GABI-SEED II 0313115 175101	532.125,43	68.127,67 [3]
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185102	74.400,00	55.000,00 [3]
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Prof. U. Wobus Dr. N. Sreenivasulu Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185104	24.700,00	12.000,00 [3]
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. W. Weschke Dr. N. Sreenivasulu Prof. U. Wobus Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185105	30.200,00	25.000,00 [3]
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Dr. L. Borisjuk	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 185106	211.620,00	0,00
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. H. Rolletschek Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185107	31.800,00	27.000,00 [3]

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Dr. W. Weschke Dr. H. Weber Dr. N. Sreenivasulu	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 185103	446.011,00	55.000,00 [3]
Die Rolle von plastidären Metabolittranslokatoren für Speicherstoffsynthese und Assimilatverteilung in Leguminosensamen	Dr. H. Weber	01.11.2004 14.01.2007	DFG WE 1641/6-2 205119	51.925,76	1.334,14
Sameneigene Photosynthese und ihre Rolle bei der Speicherung von Reservestoffen	Dr. H. Rolletschek Dr. L. Borisjuk	01.01.2005 28.02.2007	DFG RO 2411/2-1 205120	72.691,24	4.173,47
Schwerpunktprogramm: Dynamik und Regulation des pflanzlichen Membrantransports; „Die Rolle von Membrantransportprozessen in der Samenentwicklung und Samenreifung von Leguminosen und Gerste“	Dr. H. Weber Dr. W. Weschke	01.08.2005 31.07.2007	DFG WE 1641/5-3 205121	59.236,31	17.523,64
Rolle von Stickstoffmonoxid (NO) für die Regulation von Energie- und Speichermetabolismus in Samen	Dr. H. Rolletschek Dr. L. Borisjuk	01.01.2006 29.02.2008	DFG BO 1917/2-1 205122	81.500,00	51.980,98
4D-Entwicklungsgradienten im Endosperm der Gerste: biologischer Nachweis, virtuelle Rekonstruktion und Identifizierung von Regulatoren	Dr. W. Weschke Dr. L. Borisjuk Dr. U. Seiffert	01.01.2006 30.04.2010	DFG WE 16008/2-1 205123	188.000,00	87.161,32 [3]
Interaktion von ABC und Zuckersignaltransduktion in sich entwickelnden Erbsensamen	Dr. H. Weber Dr. I. Saalbach	01.03.2006 28.02.2008	DFG WE 1641/9-1 205124	125.900,00	64.298,38 [3]
Sameneigene Photosynthese und ihre Rolle bei der Speicherung von Reservestoffen	Dr. H. Rolletschek Dr. L. Borisjuk	01.03.2007 28.02.2008	DFG RO 2411/2-2 205125	37.000,00	33.000,00
Genomic studies of the tissue culture-derived finger millet line SE-7 showing the heritable phenotype “higher grain yield”	Dr. W. Weschke	03.05.2007 02.08.2007	DFG WE 1608/4-1 205126	11.300,00	11.300,00
Molecular genetics of heterosis of the plant’s earliest stage, the embryo, using the largeseeded faba bean as model	Dr. H. Weber	01.07.2007 30.06.2009	DFG WE 1641/10-3 205127	83.000,00	176,00
Entwicklung von genetisch neuen Winterweizen-Sorten mit erhöhtem Korn-Proteingehalt	Dr. W. Weschke Dr. H. Weber Dr. I. Saalbach	01.01.2007 30.06.2009	MK LSA 0045KL/08005T 305102	319.500,00	115.778,39 [3]
New strategies to improve grain legumes for food and feed	Dr. H. Weber	10.02.2004 09.02.2008	EU FOOD-CT-2004-506223 715100	160.565,00	24.555,38
Projektbezogener Personalaustausch mit Frankreich	Dr. H. Rolletschek	01.01.2007 31.12.2008	DAAD D/062822 805103	6.000,00	3.000,00
Comparative investigation of metabolic and physiological parameters of accumulation seeds	Dr. L. Borisjuk Dr. H. Rolletschek	01.03.2006 28.02.2007	1010157 782 925101	60.152,40	31.942,42
Comparative investigation of metabolic and physiological parameters of accumulation seeds	Dr. L. Borisjuk Dr. H. Rolletschek	01.05.2007 30.04.2008	1010157 b00160-1/2007 925102	81.500,00	40.750,00
Zuwendung Arbeitsgruppe				**3.398.410,76**	**867.402,93**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Genregulation					
Analyse gametophytischer Genexpression – Stipendiat D. Koszegi, Ungarn	Dr. H. Bäumlein Prof. U. Wobus Dr. W. Weschke Dr. U. Seiffert Dr. M. Röder Dr. H.-P. Mock	01.01.2005 30.06.2007	BMBF 0313115 175201	42.503,64	6.182,56 [3]
GABI-Trilateral: Etablierung eines Netzwerkes samenspezifischer Genexpression und Analyse seiner Biodiversität (ARABIDO-SEED)	Dr. H. Bäumlein	01.09.2004 31.08.2007	BMBF GABI-Trilateral 0313155 175202	96.730,76	15.049,04
GABI-POEM: Aufklärung initialer Mechanismen der Pollen-Embryogenese für die wissensbasierte Entwicklung von Methoden zur Herstellung reinerbiger Rekombinanten, Teilprojekt A	Dr. H. Bäumlein Dr. J. Kumlehn Dr. H.-P. Mock Dr. M. Melzer	01.09.2007 31.08.2010	BMBF GABI-POEM 0315047A 185201	252.477,60	11.000,00 [3]
Zuwendung Arbeitsgruppe				**391.712,00**	**32.231,60**
Arbeitsgruppe Phytoantikörper					
Internationale Zusammenarbeit in Bildung und Forschung mit Vietnam	Dr. U. Conrad	01.10.2007 30.09.2010	DLR-BMBF VNM 07/003 105802	27.106,00	5.504,00
GABI-Trilateral: Etablierung eines Netzwerkes samenspezifischer Genexpression und Analyse seiner Biodiversität (ARABIDO-SEED)	Dr. U. Conrad Dr. H. Bäumlein Dr. L. Altschmied Prof. I. Große	01.09.2004 31.08.2007	BMBF GABI-Trilateral 0313155 175801	47.600,62	12.753,03 [3]
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. U. Conrad Prof. U. Wobus Dr. W. Weschke Dr. N. Sreenivasulu Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185801	8.200,00	7.000,00 [3]
Genetic Engineering von Spinnenseidenproteinen und ihre Produktion in Pflanzen – ein neuer Weg zu maßgeschneiderten Schichtmaterialien –	Dr. U. Conrad	01.08.2007 31.12.2007	MK LSA 0051KL/0607T 305805	11.700,00	9.727,82
Biowissenschaften – Strukturen und Mechanismen biologischer Informationsverarbeitung	Dr. U. Conrad	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 325801	41.000,00	11.790,21
Recombinant pharmaceuticals from plants for human health Pharma-Planta	Dr. U. Conrad	01.02.2004 31.03.2008	EU LSHB-CT-2003-503565 715800	150.000,00	19.869,32
Kassenübertrag 2006			305802	0,00	8,35
Zuwendung Arbeitsgruppe				**285.606,62**	**66.652,73**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Netzwerkanalyse (BIC-GH-Gruppe) bis 30.10.2007 Arbeitsgruppe Pflanzenbioinformatik ab 1.11.2007					
Bioinformatik Centrum Gatersleben-Halle Metabolische und regulatorische Netzwerke	Prof. F. Schreiber Dr. L. Altschmied Dr. H.-P. Mock	01.05.2002 31.10.2007	BMBF Netzwerk 0312706A 165701	330.538,95	58.116,95 [3]
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Prof. F. Schreiber Dr. B. Junker Dr. W. Weschke Dr. L. Borisjuk Dr. H.-P. Mock Dr. J. Kumlehn	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 185702	202.240,00	20.000,00 [3]
Zuwendung Arbeitsgruppe				**532.778,95**	**78.116,95**
Arbeitsgruppe Dateninspektion					
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. M. Strickert Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. J. Kumlehn Dr. A. Börner	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 185901	3.200,00	0,00 [3]
Verarbeitung, Darstellung und Auswertung biologischer Daten mit neuen Methoden des maschinellen Lernens	Dr. M. Strickert	01.05.2007 31.12.2010	MK LSA XP3624HP/ 0606T 303904	688.750,00	59.053,99
Zuwendungen Arbeitsgruppe				**691.950,00**	**59.053,99**
Arbeitsgruppe Hybridweizen					
GABI-HYBWHEAT: Etablierung eines innovativen Systems zur Herstellung von Hybridweizen, Teilprojekt A	Dr. M. Gils	01.07.2007 30.06.2010	BMBF GABI- HYBWHEAT 0315043A 185101	984.307,00	130.000,00
Zuwendungen Arbeitsgruppe				**984.307,00**	**130.000,00**
Gesamtzuwendung Molekulare Genetik				**6.284.765,34**	**1.233.458,20**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Abteilung Molekulare Zellbiologie					
Arbeitsgruppe Molekulare Pflanzenphysiologie					
Molekularbiologische und biochemische Charakterisierung pflanzlicher Hexokinasen in Tabak	Dr. M. Hajirezaei	01.12.2006 30.11.2008	DFG HA 2996/2-1 206032	132.750,00	50.500,00
Zuwendungen Arbeitsgruppe				**132.750,00**	**50.500,00**
Arbeitsgruppe Angewandte Biochemie					
3D Mikrodissektion biologischer Objekte und Analyse schock-gefrorener molekularer Komponenten	Dr. A. Matros Dr. W. Weschke Dr. U. Seiffert	01.07.2006 30.06.2009	BMBF 0313821A 106009	135.646,00	42.971,41 [3]
Bioinformatik Centrum Gatersleben-Halle Metabolische und regulatorische Netzwerke	Dr. U. Seiffert Dr. L. Altschmied Dr. H.-P. Mock	01.05.2002 31.10.2007	BMBF Netzwerk 0312706A 165701	330.538,95	58.116,95 [3]
GABI-SEED II: Gerste als Modell- und Nutzpflanze: Genexpression-Netzwerke zur Bestimmung nutzungsrelevanter Merkmale des Getreidesamens	Dr. H.-P. Mock Dr. H. Bäumlein Prof. U. Wobus Dr. W. Weschke Dr. U. Seiffert Dr. M. Röder	01.07.2004 30.06.2007	BMBF GABI-SEED II 0313115 176001	258.549,71	55.237,06 [3]
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Dr. H.-P. Mock	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 186003	312.847,00	30.000,00
GABI-POEM: Aufklärung initialer Mechanismen der Pollen-Embryogenese für die wissensbasierte Entwicklung von Methoden zur Herstellung reinerbiger Rekombinanten, Teilprojekt A	Dr. H.-P. Mock Dr. J. Kumlehn Dr. H. Bäumlein Dr. M. Melzer	01.09.2007 31.08.2010	BMBF GABI-POEM 0315047A 186005	105.538,80	8.000,00 [3]
Biowissenschaften: Strukturen und Mechanismen biologischer Informationsverarbeitung	Dr. H.-P. Mock Dr. P. Schweizer	01.10.2005 31.12.2008	UNI Halle/MK LSA PAXB3599HP/ 0105T 326001	20.500,00	5.820,38 [3]
FLORA Flavonoids and related phenolics for healthy living using orally recommended antioxidants	Dr. H.-P. Mock	01.03.2005 28.02.2009	EU FOOD-CT-2005- 007130 716003	321.000,00	22.543,15
Phytosterole/Vorläufermoleküle von Phytosteroiden in Getreide, Teilprojekt 1	Dr. H.-P. Mock	01.03.2007 30.06.2008	2000041 TTR/05/00187 916017	73.830,00	49.220,00
Preparative isolation of sugar ester fractions from tobacco leaf surface exudates and exudate profiling of *Nicotiana* varieties	Dr. H.-P. Mock	01.11.2007 30.05.2009	1010165 926003	264.603,00	85.000,00
Zuwendung Arbeitsgruppe				**1.823.053,46**	**356.908,95**

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Arbeitsgruppe Strukturelle Zellbiologie					
Internationale Zusammenarbeit in Bildung und Forschung mit Indien	Dr. M. Melzer	01.01.2007 31.12.2007	BMBF/DLR IND 05/09 106011	10.644,00	10.461,00
GABI-POEM: Aufklärung initialer Mechanismen der Pollen-Embryogenese für die wissensbasierte Entwicklung von Methoden zur Herstellung reinerbiger Rekombinanten, Teilprojekt A	Dr. M. Melzer Dr. J. Kumlehn Dr. H. Bäumlein Dr. H.-P. Mock	01.09.2007 31.08.2010	BMBF GABI-POEM 0315047A 186006	105.538,80	7.200,00 [3]
Zuwendung Arbeitsgruppe				**116.182,80**	**17.661,00**
Arbeitsgruppe Pflanzliche Reproduktionsbiologie					
ERA-Net PlantGenomics - Verbundvorhaben: Sicherung einer nachhaltigen Produktion von Lebens- und Futtermitteln (CEREHEALTH, Teilvorhaben F)	Dr. J. Kumlehn Dr. P. Schweizer	01.05.2007 30.04.2010	BMBF 0313992F 106010	110.806,70	1.225,07 [3]
Verbundvorhaben: Optimierung der biologischen Sicherheit transgener Pflanzen. Teilprojekt 4: Selektionsmarkerfreie Getreidepflanzen durch androgenetische Segregation ungekoppelter T-DNAs	Dr. J. Kumlehn	01.04.2005 31.03.2008	BMBF 0313264M 126004	222.438,00	71.872,41
GABI-GRAIN: Entwicklung von Gerstenlinien mit gesteigertem Ertrag und verbesserter Kornqualität unter Trockenstress während der Kornfüllung, Teilprojekt A	Dr. J. Kumlehn Dr. N. Sreenivasulu Prof. U. Wobus Dr. W. Weschke Dr. U. Conrad Dr. H. Rolletschek Dr. M. Röder Dr. A. Börner Dr. M. Strickert	01.07.2007 30.06.2010	BMBF GABI-GRAIN 0315041A 186001	19.200,00	7.000,00 [3]
GABI-SysSEED, Verbundprojekt: Integrierte Modellierung des Primärstoffwechsels des sich entwickelnden Gersten-Endosperms unter dem Einfluss hormonaler Regulierung, Teilprojekt A	Dr. J. Kumlehn	01.07.2007 30.06.2010	BMBF GABI-SysSEED 0315044A 186002	99.534,00	15.000,00
GABI-POEM: Aufklärung initialer Mechanismen der Pollen-Embryogenese für die wissensbasierte Entwicklung von Methoden zur Herstellung reinerbiger Rekombinanten, Teilprojekt A	Dr. J. Kumlehn Dr. H. Bäumlein Dr. H.-P. Mock Dr. M. Melzer	01.09.2007 31.08.2010	BMBF GABI-POEM 0315047A 186004	406.136,80	26.300,00 [3]
GABI-TILL: Erweiterung und Anwendung der GABI-TILLING-Plattform zur Funktionsanalyse von Nutzpflanzengenen, Teilvorhaben B	Dr. J. Kumlehn Dr. N. Stein	01.09.2007 31.08.2010	BMBF 0315052B 186007	27.800,00	14.000,00 [3]
Establishment of cell-specifically inducible expression systems in transgenic barley and maize, Teilprojekt B3 Forschergruppe: Mechanisms of compatibility: Reprogramming of plant metabolism by fungal effector molecules	Dr. J. Kumlehn	01.04.2006 17.04.2008	DFG KU 2265/1-1 206030	182.000,00	91.611,48

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Interaktion von ABC und Zuckersignaltransduktion in sich entwickelnden Erbsensamen	Dr. H. Weber Dr. I. Saalbach	01.03.2006 28.02.2008	DFG WE 1641/9-1 206031	6.000,00	1.651,48 [3]
Entwicklung von genetisch neuen Winterweizen-Sorten mit erhöhtem Korn-Proteingehalt	Dr. I. Saalbach Dr. W. Weschke Dr. H. Weber	01.01.2007 30.06.2009	MK LSA 0045KL/08005T 306003	79.000,00	30.860,05 [3]
BioExploit: Exploitation of natural plant biodiversity for the pesticide-free production of food	Dr. J. Kumlehn Dr. P. Schweizer	01.10.2005 30.09.2010	EU FOOD-CT-2005-513959 716002	114.000,00	33.106,60 [3]
Phytosterole/Vorläufermoleküle von Phytosteroiden in Getreide, Teilprojekt 1	Dr. J. Kumlehn	01.03.2007 28.02.2008	2000041 TTR/05/00187 916016	84.530,00	84.530,00
PRO-GABI: Ein Netzwerk zur Identifizierung, Charakterisierung und Optimierung neuer monokotylspezifischer Promotoren für die Herstellung pilzresistenten Weizens	Dr. J. Kumlehn Dr. P. Schweizer Prof. U. Sonnewald	01.07.2004 31.12.2007	1010124 0313124 916025	466.234,31	123.853,72 [3]
Zuwendung Arbeitsgruppe				**1.817.679,81**	**501.010,81**

Arbeitsgruppe Hefegenetik					
Joint Research Project "Characterization of osmoresistance of *A. adeninivorans*"	Prof. G. Kunze	01.07.2002 31.12.2008	BMBF EGY/1K0A4A 106503	47.660,00	0,00
Entwicklung eines on-line Analysators zur Erfassung östrogener Wirkungen mittels Hefezellen-Dickschicht-Sensor; Entwicklung und Herstellung der mikrobiellen Komponenten	Prof. G. Kunze	01.09.2005 31.08.2007	BMBF-86,949 % KF0161801UL5 106504 IPK-Anteil-13,051% KF0161801UL5 106504	82.125,00 12.327,61	11.132,05 12.327,61
Mykorrhiziertes Vetivergras zur Kalihaldenbegrünung und als Quelle für nachwachsende Rohstoffe;	Prof. G. Kunze	01.04.2007 31.03.2010	AiF - 70 % KF0161802WZ6 106505 IPK-Anteil-30 % KF0161802WZ6 106505	121.614,00 52.120,00	23.104,00 18.316,91
Isolation, Funktions- und Transkriptionsanalyse von symbiose-relevanten Genen in *G. intradices* für die Entwicklung von verbesserten Wurzelkulturen - Internationale Zusammenarbeit mit Indien	Prof. G. Kunze	01.03.2007 31.12.2008	BMBF/DLR IND 06/036 106506	13.034,00	3.392,00
Host vector systems based on non-conventional yeasts – construction of transgenic strains with high recombinant anthocyanase activities - Gastaufenthalt Dr. Prasad, Indien	Prof. G. Kunze	30.07.2007 27.10.2007	DFG KU 967/7-1 206504	6.160,00	6.160,00
Etablierung eines auf Hefezellen basierenden Assays zur Erfassung östrogener Wirkungen im Rahmen der Umwelt-, Nahrungs- und Futtermittelanalytik	Prof. G. Kunze	01.12.2006 30.11.2009	MK LSA 3623A/0606T 306508	124.811,59	32.475,30

[3] Die Projektbearbeitung erfolgt durch mehrere Wissenschaftler aus verschiedenen Arbeitsgruppen und Abteilungen

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Wissenschaftliche Zusammenarbeit mit Neuseeland; Einsatz von mikrobiellen Biosensoren zur Messung von Schadstoffen	Prof. G. Kunze	01.01.2005 31.12.2008	DLR NZL 02/002 906506	5.156,00	1.722,00
Genexpression von Anthocyanasen in der nichtkonventionellen Hefe *Arxula adeninivorans*	Prof. G. Kunze	01.01.2006 31.12.2008	Dt. Bundesstiftung Umwelt AZ 20005/803 906509	4.200,00	270,47
scFv-Antikörper	Prof. G. Kunze	01.03.2006 29.02.2008	2000042 916504	91.549,20	59.598,52
TP1: Überexpression von Unibody in *Hansenula polymorpha* TP2: Überexpression von Unibody in *Arxula adeninivorans*	Prof. G. Kunze	01.11.2007 30.09.2008	2000027 916505	77.350,00	38.675,00
Verbundprojekt-Optimierung von genetisch modifizierten Hefen als Produzenten von Polymeren aus nachwachsenden Rohstoffen	Prof. G. Kunze	01.12.2004 01.01.2007	MW-LSA 75 % 6003211404/ 0404/00082 316502 1010145 25 % 316502	78.308,03 32.148,97	0,00 1.386,97
Zuwendung Arbeitsgruppe				**748.564,40**	**208.560,83**
Gesamtzuwendung Molekulare Zellbiologie				**4.638.230,47**	**1.134.641,59**

Wiss. Abteilung/Arbeitsgruppe Thema	Projekt- leiter	Beginn Ende	Drittm.geber Förderkennz. IPK Proj.-Nr.	Zuwendungen Gesamt EUR (SOLL)	Einnahmen 2007 EUR (IST)
Abteilung Verwaltung und Zentrale Dienste					
Entwicklung und Umsetzung eines Verwertungskonzeptes zur Verbesserung der schutzrechtlichen Sicherung und Professionalisierung der Verwertung von Forschungsergebnissen am Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung Gatersleben (IPK)	K. Menzel	01.11.2005 31.10.2008	BMBF/DLR 01SF0508 197900	194.880,00	64.960,00
Ausbau der Spezialbibliothek	Dr. T. Schuhmann	01.01.2004 31.12.2007	DFG LIS 2-553 89(1) 207603	30.679,04	7.676,67
Gesamtzuwendung VZD				**225.559,04**	**72.636,67**
Gesamtzuwendung im IPK				**29.323.264,38**	**5.391.923,46**
Zuwendungen für Partner					
GABI-Trilateral: Vergleichende Genomforschung zur Regulation der Meristemaktivität bei Nachtschattengewächsen (Solanaceae) - (Genosome) Teilprojekt 1	Dr. U. Scholz	01.09.2004 31.08.2007	BMBF GABI-Trilateral 0313149A 176006	114.629,34	28.768,00
Establishment of European Core Collection of vegetative alliums, covering garlic (*Allium sativum*) including molecular characterization, cryopreservation and virus elimination, and molecular characterization of shallot (*Allium cepa* var. *aggregatum*)	Dr. J. Keller	01.04.2007 31.03.2011	EU - 50 % 050 AGRI GEN RES 870/2004 RICP, Tschechien Univ. Basilicata, Italien Stichting DLO, Niederlande INRA, Frankreich Nordic Gene Bank, Schweden 711310	347.750,00	0,00
Pharmaceutical values of onions and related species *Allium* L. of Middle Asia and the Caucasus (PharmAll)	Dr. R. Fritsch	01.01.2006 30.04.2008	Volkswagen Stiftung Az.: I/81 319 902302	45.900,00	21.180,00
Collection, distribution, phenotyping and genotyping directed towards utilization of existing wheat genetics stocks to enhance tolerance/resistance of wheat cultivars to abiotic and biotic stresses	Dr. A. Börner	17.11.2005 31.12.2007	MEXICO IAS-CSIC Cordoba, Spanien ICG Novosibirsk, Russland 921201	4.279,00	0,00
Zuwendungen für Partner				**512.558,34**	**49.948,00**
Gesamtzuwendungen:				**29.835.822,72**	**5.441.871,46**

Gremien und Mitarbeiter/-innen in speziellen Funktionen/ Boards of the IPK and Employees in Special Functions

Gremien und Mitarbeiter/-innen in speziellen Funktionen

Der Stiftungsrat überwacht die Geschäftsführung des Direktoriums, überprüft die Wirtschaftsführung, genehmigt die Jahresrechnung und erteilt Entlastung für das jeweils abgelaufene Haushaltsjahr.

Mitglieder des Stiftungsrates im Jahr 2007:

MinDirig Dr. Joachim Welz, MK LSA, Magdeburg, (Vorsitz),
MinRat Dr. Jürgen Roemer-Mähler, BMBF, Bonn, (stellv. Vorsitz),
MinRat Thomas Reitmann, MK LSA, Magdeburg,
Martin Köhler, BMELV, Bonn,
Prof. Dr. Wulf Diepenbrock, Martin-Luther-Universität Halle-Wittenberg,
Prof. Dr. Wilfried Grecksch, Martin-Luther-Universität Halle-Wittenberg,
Prof. Dr. Eberhard Schäfer, Albert-Ludwigs-Universität Freiburg,
Prof. Dr. Joachim Kadereit, Johannes-Gutenberg-Universität Mainz.

Das Direktorium ist ein Kollegialorgan, zusammengesetzt aus den Leitern der wissenschaftlichen Abteilungen und dem Administrativen Leiter. Der Stiftungsrat bestellt einen der wissenschaftlichen Abteilungsleiter für drei Jahre zum Geschäftsführenden Direktor. Dieser bildet gemeinsam mit dem Administrativen Leiter die Geschäftsführung, die die Stiftung nach Maßgabe der Geschäftsordnung gerichtlich und außergerichtlich vertritt.

Das Direktorium im Jahr 2007:

Prof. Dr. Andreas Graner, Geschäftsführender Direktor und Leiter der Abteilung Genbank,
Bernd Eise, Administrativer Leiter und Leiter der Abteilung Verwaltung und Zentrale Dienste,
Prof. Dr. Ulrich Wobus, Leiter der Abteilung Molekulare Genetik,
Prof. Dr. Ingo Schubert, Leiter der Abteilung Cytogenetik und Genomanalyse,
Prof. Dr. Gotthard Kunze, komm. Leiter der Abteilung Molekulare Zellbiologie.

Der **Wissenschaftliche Beirat** berät den Stiftungsrat und das Direktorium in wissenschaftlichen und technischen Fragen. Er ist verantwortlich für die Bewertung der wissenschaftlich-technischen Arbeiten und fördert die Verbindung mit Einrichtungen des In- und Auslandes.

Mitglieder des Wissenschaftlichen Beirates im Jahr 2007:

Prof. Dr. Eberhard Schäfer, Albert-Ludwigs-Universität Freiburg, (Vorsitz),
Prof. Dr. Joachim Kadereit, Johannes-Gutenberg-Universität Mainz, (stellv. Vorsitz),
Dr. Reinhard von Broock, Fa. Lochow-Petkus, Bergen, (Vorsitz Genbankbeirat),
Prof. Dr. Thomas Dandekar, Julius-Maximilians-Universität Würzburg,
Prof. Dr. Ulf-Ingo Flügge, Universität zu Köln,
Prof. Dr. Ueli Großniklaus, Universität Zürich,
Prof. Dr. Barbara Hohn, Friedrich-Miescher-Institut, Basel,
Prof. Dr. Thomas Kühne, Bundesanstalt für Züchtungsforschung, Quedlinburg,
Dr. Ralf-Michael Schmidt, BASF Plant Science GmbH, Ludwigshafen,
Prof. Dr. Dieter Schweizer, Universität Wien.

Der Wissenschaftliche Beirat hat als Unterausschuss einen **Genbank-Beirat**, der den Stiftungsrat und das Direktorium in Abstimmung mit dem Wissenschaftlichen Beirat in allen Fragen der Genbankarbeit berät.

Mitglieder des Genbank-Beirates im Jahr 2007:

Dr. Reinhard von Broock, Fa. Lochow-Petkus, Bergen, (Vorsitz),
PD Dr. Christiane Gebhardt, Max-Planck-Institut für Züchtungsforschung Köln, (stellv. Vorsitz),
Dr. Jan Engels, Bioversity International, Rom,
Dir. und Prof. Lothar Frese, Bundesanstalt für Züchtungsforschung, Braunschweig,
Dr. Theo J. L. van Hintum, CGN Wageningen, Wageningen,
Prof. Dr. W. Eberhard Weber, Martin-Luther-Universität Halle-Wittenberg.

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Thomas Kruse (Vorsitzender),
Birgit Schäfer (1. Stellvertreterin),
Sibylle Pistrick, (2. Stellvertreterin),
Dagmar Böhmert,
Kathrin Gramel-Eikenroth,
Ute Riedel,
Evelyn Willner, Genbank-Außenstelle „Nord“, Malchow,
Dr. Hardy Rolletschek (Ersatzmitglied),
Frank Schröder (Ersatzmitglied).

Mitarbeiter/-innen des IPK in speziellen Funktionen im Jahr 2006:

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Thomas Lüttge (Qualitäts-Beauftragter für die Abteilung VZD),
Dr. Winfriede Weschke und Dr. Jochen Kumlehn (Beauftragte für Biologische Sicherheit),
Dr. Hans-Peter Mock (Beauftragter für Betäubungsmittel und Gefahrstoffe),
Prof. Dr. Andreas Graner (Beauftragter für Strahlenschutz)
Dr. Helmut Bäumlein (Ombudsmann),
Dr. Tankred Schuhmann (Beauftragter für Datenschutz),
Ellen Weiß (Gleichstellungsbeauftragte),
Hans-Jürgen Winkelmann (Fachkraft für Arbeitssicherheit),
Wolfgang Schmidt (Beauftragter für Abfallbeseitigung und Schwerbehindertenbeauftragter),
Peter Schreiber (Beauftragter für Havarie- und Katastrophenschutz),
Carmen Höpfner (Beauftragte für Lehrausbildung).

Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK)

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Stand: 31. Dezember 2007

Stiftungsrat
Vorsitzender:
MinDirig Dr. Joachim Welz
Stellv. Vorsitzender:
MinRat Dr. Jürgen Roemer-Mähler

Wissenschaftlicher Beirat
Vorsitzender:
Prof. Dr. Eberhard Schäfer

Direktorium
Prof. Dr. Andreas Graner [1)]
Geschäftsführender Direktor
Bernd Eise [1)]
Administrativer Leiter
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Prof. Dr. Ulrich Wobus
Prof. Dr. Gotthard Kunze (komm.)

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Geschäftsstelle
Roland Schnee

Personalrat
Vorsitzender: Thomas Kruse

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Prof. Dr. Andreas Graner

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- **Management und Evaluierung** — PD Dr. Andreas Börner
- **Taxonomie und Evolution** — Dr. Frank Blattner

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- **Genbank-dokumentation** — Dr. Helmut Knüpffer
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Abt. Cytogenetik und Genomanalyse
Prof. Dr. Ingo Schubert

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- **Genomanalyse** — Dr. habil. Patrick Schweizer

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- **Genomplastizität** — PD Dr. Renate Schmidt
- **Epigenetik** — Dr. Michael F. Mette
- **Mustererkennung** — Dr. Udo Seiffert
- ***In vitro*-Differenzierung** — Prof. Dr. Anna M. Wobus
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- **Expressionskartierung** — Dr. habil. Lothar Altschmied
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Prof. Dr. Ulrich Wobus

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- **Genregulation** — Dr. habil. Helmut Bäumlein
- **Phytoantikörper** — PD Dr. Udo Conrad
- **Pflanzenbioinformatik** — Prof. Dr. Falk Schreiber
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- **Hybridweizen** (BMBF-Projektgruppe) — Dr. Mario Gils

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Prof. Dr. Gotthard Kunze (komm.)

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- **Angewandte Biochemie** — PD Dr. Hans-Peter Mock
- **Strukturelle Zellbiologie** — Dr. Michael Melzer
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- **Hefegenetik** — Prof. Dr. Gotthard Kunze

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Bernd Eise

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- **Finanzwesen** — Martina Liewald
- **Technologietransfer und Recht** — Dr. Tankred Schuhmann
- **Materialwirtschaft und Allgemeine Dienste** — Ursula Deppner
- **Technik** — Willi Bertling
- **Versuchsfeld und Gärtnerei** — Katrin Menzel

Pflanzengenom-Ressourcen-Centrum (PGRC)	Koordinator: Dr. habil. Patrick Schweizer
Bioinformatik	Koordinator: Prof. Dr. Falk Schreiber

[1)] Geschäftsführung

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As of December 31, 2007

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MinDirig Dr Joachim Welz
Vice Chairman:
MinRat Dr Jürgen Roemer-Mähler

Scientific Advisory Board
Chairman:
Prof Eberhard Schäfer

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Prof Andreas Graner [1)]
Managing Director
Bernd Eise [1)]
Administrative Director
Prof Ingo Schubert
Prof Ulrich Wobus
Prof Gotthard Kunze (temp.)

Genebank Advisory Board
Chairman:
Dr Reinhard von Broock

Personnel Council
Chairman: Thomas Kruse

Managing Office
Roland Schnee

Dept. of Genebank
Head: Prof Andreas Graner

Programmes
- **Characterisation and Documentation** — Prof Andreas Graner
- **Management and Evaluation** — Dr Andreas Börner
- **Taxonomy and Evolution** — Dr Frank Blattner

Groups
- **Genome Diversity** — Prof Andreas Graner, Dr Nils Stein
- **Genebank Documentation** — Dr Helmut Knüpffer
- **Resources Genetics and Reproduction** — Dr Andreas Börner
- ***In vitro* Storage and Cryopreservation** — Dr Joachim Keller
- **External Branch "North"** — Dr Klaus Dehmer
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- **Quantitative Evolutionary Genetics** — Dr Karl Schmid
- **Taxonomy of Plant Genetic Resources** — Dr Frank Blattner (temp.)

Dept. of Cytogenetics and Genome Analysis
Head: Prof Ingo Schubert

Programmes
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- **Genome Analysis** — Dr Patrick Schweizer

Groups
- **Karyotype Evolution** — Prof Ingo Schubert
- **Chromosome Structure and Function** — Dr Andreas Houben
- **Apomixis** — Dr Timothy F. Sharbel
- **Genome Plasticity** — Dr Renate Schmidt
- **Epigenetics** — Dr Michael F Mette
- **Pattern Recognition** — Dr Udo Seiffert
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- **Transcriptome Analysis** — Dr Patrick Schweizer
- **Expression Mapping** — Dr Lothar Altschmied
- **Gene and Genome Mapping** — Dr Marion Röder
- **Bioinformatics and Information Technology** — Dr Uwe Scholz

Dept. of Molecular Genetics
Head: Prof Ulrich Wobus

Groups
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- **Gene Regulation** — Dr Helmut Bäumlein
- **Phytoantibodies** — Dr Udo Conrad
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- **Data Inspection** (Junior Research Group) — Dr Marc Strickert
- **Hybrid Wheat** (BMBF-funded Project Group) — Dr Mario Gils

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Head: Prof Gotthard Kunze (temp.)

Groups
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- **Applied Biochemistry** — Dr Hans-Peter Mock
- **Structural Cell Biology** — Dr Michael Melzer
- **Plant Reproductive Biology** — Dr Jochen Kumlehn
- **Yeast Genetics** — Prof Gotthard Kunze

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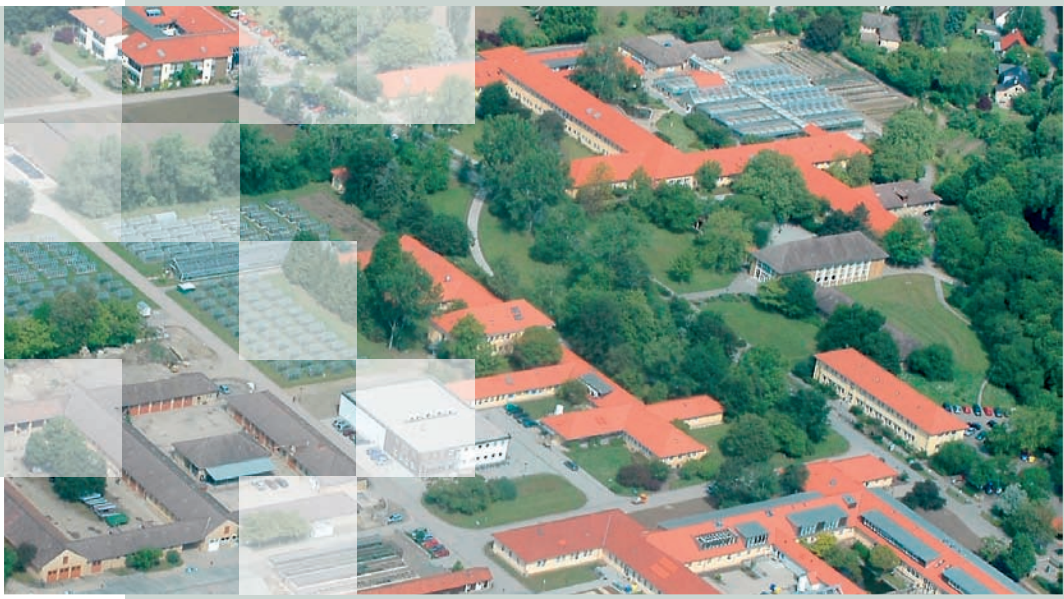
- **Finances** — Martina Liewald
- **Technology Transfer and Legal Matters** — Dr. Tankred Schuhmann
- **Materials, Management and General Services** — Ursula Deppner
- **Buildings and Equipment** — Willi Bertling
- **Experimental Fields and Nurseries** — Katrin Menzel

Plant Genome Resources Centre (PGRC)	Coordinator: Dr Patrick Schweizer
Bioinformatics	Coordinator: Prof Falk Schreiber

[1)] Management



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