LEIBNIZ INSTITUTE OF PLANT GENETICS AND CROP PLANT RESEARCH



RESEARCH REPORT 2022/2023



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

is a member of the Leibniz Association. It is organised as a non-profit foundation under public law. According to its statutes, the Institute conducts basic and application-oriented research on crop plants. The Institute resides at three locations, the headquarter in Saxony-Anhalt and two branch stations in Mecklenburg-Western Pomerania.



This research report presents the scientific achievements of IPK's research activities in 2022 and 2023 and demonstrates our researchers' sustained resilience and innovative strength despite increasing global threats. As the COVID-19 pandemic subsided, a sense of normalcy returned, reinvigorating personal interactions and lively discussions among staff members, which is imperative to develop new ideas and advance innovations. Soon after. however, another unexpected event challenged us and continues to leave deep marks on the research landscape: Russia's aggressive war against Ukraine. At a time when our world is facing climate change, resource limitations, loss of biodiversity and an ever-growing world population, this additional burden places a heavy load on us researchers, too. However, rising energy and food prices are nothing compared to the suffering of our colleagues and their families as a result of Russia's attack on Ukraine. We see science as a unifying and globally networking system and want our work to contribute to a better world.

The year 2023 also marked a cornerstone for our Institute's history as we celebrated our 80th anniversary while undergoing a year of leadership transitions, bringing new heads to our research departments, including the Federal *Ex situ* Genebank. These changes brought fresh perspectives together with a renewed commitment to prioritize high-quality research, marking the ambition to keep a world-leading position in crop research despite increasing economic constraints. Expanding and modernizing our technical and phenotyping infrastructures further demonstrated our commitment to valorise our genebank material by additional research data. We added the PhenoSphere to our fully-established research facilities and modernized our Satellite Collections North of our gene bank in Mecklenburg-Western Pomerania.

The use of CRISPR/Cas technologies has placed us at the centre of political debate and increased public interest, mainly due to the European Commission's proposal to amend legislation on genetic engineering of crops. We took this opportunity by engaging in interviews or discussion panels and explaining the scientific perspective to the public.

We also continued to improve the genetic profiling and characterisation of our plant collections by exploring the pan-genome of barley. Projects that combine science with societal impact addressed the engagement of research-interested citizens to bring almost forgotten crops into the scientific spotlight. In this regard, the INCREASE project has allowed us to step on new ground and gain experience in this area.

During the past two years, we could demonstrate our research advances in 332 peer-reviewed publications. Furthermore, major research grants demonstrate our scientists' continued excellence and dedication. Our collaboration with numerous national and international research institutions were continued or even intensified, in particular our partnership with the CEPLAS cluster of excellence in North Rhine-Westphalia. This underscores our wide engagement in scientific cooperation and our commitment to share knowledge. In 2022, we organised together with CEPLAS, an international summer school for young scientists, and in 2023, we founded the Alliance for Innovative Plant Science, TRANSCEND, at the Futurium in Berlin under the patronage of the Federal Minister of Education and Research, Bettina Stark-Watzinger.

We would like to thank all of the IPK's staff, partners and supporters for their unwavering support and commitment, which is crucial to the IPK's ability to fulfil its mission and contribute to some of the most pressing issues of our time. We invite you to explore the results of our research and to join the debate on the future of green biotechnology and the role of science in a rapidly changing world.

By providing insight into our scientific achievements, we hope this report will serve as a source of inspiration and dialogue. May it be read with interest and benefit.

We thank you for your interest and hope you will enjoy reading

Nicolaus von Wirén

Facts & Figures **2022/2023**



IPK media contributions

News	32	34
Press releases	13	14

External media contributions

Online 15 19	Print
TV 11 10	Radio96

Events	2 17
Participant numbers Events	<mark>512</mark> 2229
Institute tours	20 42
Institute visitors	445 879

	Funding (million euro)		2023
	Core funding	36.60	38.73
	Third-party funding	13.23	17.48
	Carryovers	3.91	4.02
	Total funding		60.22
	Third-party funding		
	EU	1.27	1.07
	BMBF		3.58
	BMEL	1.19	1.58
	BMWK	0.29	0.13
	DFG	1.23	2.05
	Leibniz	0.27	0.61
	Other	0.26	0.31
	Saxony-Anhalt	4.20	7.47
	Mecklenburg-Western Pomerania		(3.70)
	Private Sector	1.20	0.68
Million €	Total	13.23	17.48

Infrastructure

Greenhouse Area6	,470	m ²
Phyto Chamber	220	m ²
Field trials area	84	ha

PhenoSphere	
Rhizo Boxes	360
Growth Containers	.110

Federal *Ex situ* Genebank

Accessions	151,970 152,359
Genera	758 758
Species	

Genehank	
Ochebalik	
deliveries (2022 & 2023)	43,058
of which academic research	28,244
of which private breeding	10,208
thereof private persons and associations	4,606

The Institute in 2022 and 2023

The IPK combines scientific continuity with innovative technologies to develop novel concepts and approaches spanning a wide spectrum of fundamental and applied research. The numerous and exciting findings summarised in this research report are based on a research agenda that merges scientific excellence with societal relevance.

The IPK is based on four scientific departments, each providing particular expertise to cover five thematic areas of plant research. In addition to departmental research, Independent Research Groups serve as launching pads for young scientists to explore new topics and advance their careers. To further support early career development at the postdoctoral stage, Young Investigator Groups have been initiated in 2021. Here, young researchers who have secured their own project funding are mentored to develop their research programmes, increase their scientific visibility and thus gain independence. Being a significant milestone of the Institute's history, its 80th anniversary was celebrated on September 7th 2023. Over eight decades, the Institute, initially founded in Tuttenhof near Vienna and relocated to Gatersleben in October 1945, has significantly contributed to the conservation of and research into crop plant diversity. During the festive event, Andreas Graner, who joined the Institute in 1997 and served as the Managing Director since 2007, was given an official farewell, and the Board of Trustees appointed Nicolaus von Wirén to head the Institute as the new Managing Director from October 1st 2023 onwards.



Recent global challenges have highlighted the need for innovation and transformative change to address issues affecting food security and the environment. The IPK has responded to these challenges confidently, demonstrating its ability to adapt and thrive. The end of the coronavirus pandemic during the reporting period, has breathed new life to scientific exchange by reviving face-to-face meetings, workshops and conferences. The latter are deemed important, particularly for young scientists, in helping to establish their networks.

This report again highlights the exciting research activities at the IPK Leibniz Institute, bolstered through cooperation and partnerships with universities and research institutions in Germany and abroad. The following sections provide an overview of the most important developments at the institutional level and summarise the achievements of the individual research groups.

Organisational and Structural Developments

Compared to the previous reporting period, 2020/2021, there is a slight reduction, by about three per cent, in the number of staff from 467 (2021) to 460 (2023) employees. In 2022 and 2023, the Leibniz Institute of Plant Genetics and Crop Plant Research underwent several significant organisational and structural changes which reflect the continuous and dynamic advancement of the scientific agenda.

Ingmar Schmidt was appointed Administrative Director and Head of the Department of Administration and Central Services in March 2022. In this context, the "Technology Transfer and Legal Affairs" group was disbanded. The corresponding activities were re-assigned as a staff unit to the head of administration. In 2022, the independent research group "Metabolic Systems Interaction", led by Nadine Töpfer, was closed. Nadine Töpfer accepted a professorship at the University of Cologne to continue her scientific career. To strengthen the research activities on legume species, an independent research group, "Grain Legume Genomics", led by Murukarthick Jayakodi, was established in 2022. The group is funded for five years by a grant from the Leibniz Association. Also in 2022, the independent Heisenberg Group "Plant Architecture", led by Thorsten Schnurbusch, was merged into the Department of Breeding Research to sustainably strengthen research into the genetic architecture and molecular basis of yield formation in cereals. The research group, "Applied Biochemistry" in the Department of Physiology and Cell Biology, led by Hans-Peter Mock, was closed in 2022 due to his retirement.

In 2023, it was decided to launch two new Young Investigator Groups: The Young Investigator Group "In Silico Genebank Genomics" in the Genebank Department of **Amanda Souza Camara** and the Young Investigator Group "Agroecological Breeding" of **Samira El Hanafi** in the Breeding Research Department. In the Department of Physiology and Cell Biology a new research group on "Genetics and Physiology of Root Development" started in



Degrees of Students	2022	2023	Total
Bachelor	8	6	14
Master	20	11	31
PhD-Thesis	13	12	25
Total	41	29	70

Table 1: Graduates of the IPK Leibniz Institute in the years 2022 and 2023.



Presentations of IPK researchers	2022	2023	Total
Bachelor	203	257	460

Table 2: Lectures and presentations in the reporting years.

October 2023. It is headed by **Hannah Schneider**, who is on a joint appointment as professor for root research at the University of Göttingen. At the end of 2023, the Young Investigators Group "Sustainable Nutrient Management" at the same department, led by **Diana Heuermann**, was closed following her new appointment.

Appointments

Regarding appointments, in 2022, Fang Liu from the Breeding Research Department was appointed Assistant Professor at the Chinese Academy of Sciences in Wuhan Botanical Garden. In 2023, Ying Liu was appointed Associate Professor at the State Key Laboratory of Crop Genetics and Germplasm Enhancement at Nanjing University in China. In 2022, Silvia Bachmann-Pfabe from the Genebank Department was appointed W2 Professor of "Plant Nutrition and Soil Science" at the University of Applied Sciences in Neubrandenburg. Nadine Töpfer was appointed W2/W3 Professor for "Metabolic Reconstruction and Flux Analysis" at the University of Cologne. Hannah Schneider was appointed W2 Professor for "Root Science" at the University of Göttingen in October 2023. In October 2023, Nils Stein was appointed W3 Professor of "Crop Plant Genetics" at the Martin Luther University Halle and became Head of the Genebank Department. In October 2023, Ricardo Giehl was appointed co-head of the "Molecular Plant Nutrition" research group in the Department of Physiology and Cell Biology.

Prizes and Awards

The outstanding achievements of various scientists from different departments have been recognised with national and international awards. In 2022, **Martin Mascher** and **Nils Stein** received the "Gregor Mendel Innovation Award" for their exceptional achievements in analysing the genomes of wheat, barley and rye. In 2022, the Borlaug Global Rust Initiative's "Women in Triticum Early Career Award" was presented to **Samira El Hanafi**. In 2022, **Johannes Schneider** received the DLG "Wilhelm Rimpau

Award" for his outstanding master's thesis on the "Development of hybrid seed production and testing in crosses with plant genetic resources". In 2022, **Zhongtao Jia** was honoured with the "Marschner Young Scientist Award" at the 19th International Plant Nutrition Colloquium in Iguazu, Brazil, for his work on the hormonal and molecular regulation of root elongation under low nitrogen.

Training and young scientists

In addition to teaching at various universities and supervising the work of Bachelor-, Master- and PhD-students (see below), all PhD students at IPK are enrolled in a structured doctoral training programme, which is based on a Supervision Agreement signed by the PhD student and the Supervision Team. The curriculum consists of seminars, courses, and internships, and it serves to expand the students' theoretical and technical know-how. It also stresses the acquisition of soft skills. A PhD Student Board represents the interests of this group of young scientists. It organises the Plant Science Student conference, which is held annually in close collaboration with PhD students from the Leibniz Institute for Plant Biochemistry (IPB) in Halle.

IPK also supports the professional development of young postdocs. Thanks to the provision of a self-administered budget, various training opportunities and seminars are offered to help support career building. Every other year, the PostDoc Board organises a summer school. The PhD and PostDoc Board meet with the Board of Directors at least once a year to discuss the status quo and to further refine their programmes.

For IPK, promoting young talents also involves a parallel commitment to vocational training and further education. The Institute employed nine apprentices in 2022 and 2023 in vocational training in various professions. In addition, eight and eleven dual BSc students in "Biotechnology" enrolled at Anhalt University of Applied Sciences, Köthen, in 2022 and 2023, respectively, and two students in "Computer Science" at Otto-von-Guericke University Magdeburg completed their dual study programme at the Institute.

Gender Equality

IPK is implementing measures to improve gender equity and gender balance in science. The Institute strives to leverage the potential of female scientists. Ranking among the first institutions to receive a 'berufundfamilie' (profession and family) certificate, IPK aims to provide a professional environment that offers a nursing ground for excellent science and, at the same time, supports the needs of (mostly) young families. Because of the underrepresentation of female applicants for group leader positions, the Institute emphasises attracting female scientists in the recruiting phase. The overriding goal of gender equality work is to eliminate the underrepresentation of female scientists in leadership positions. To this end, a major focus was placed on personnel recruitment and career development.

Career development

In career development, a new structure, the establishment of so-called Young Investigator Groups, was developed. The main intention of the Young Investigator Groups is to support young scientists in the post-doc phase. The new funding format aims to increase talented researchers' scientific visibility and independence. The intermediate step of a Young Investigator Group, which lasts for a maximum of four years, is intended to increase the professional development and visibility of a group leader. Young Investigator Groups are based on extramural funding acquired by the group leader and are organisationally linked to a host department, which provides additional support and resources. Three such groups were active during the reporting period. One group, which was led by Diana Heuermann, was closed at the end of 2023 due to her career change. The second group continues to exist following the end of Mary-Anne Blaetke's parental leave.

Research Infrastructures

The Institute operates two major research infrastructures providing materials and scientific services. These are essential components for the implementation of the research agenda. Moreover, they provide biological resources and access to experimental facilities for external use nationally and internationally.

Federal Ex situ Genebank

The Federal *Ex situ* Genebank houses seeds, tubers, and plants, amounting to approximately 150,000 accessions covering about 3,000 botanical species. Ranking among the most extensive *Ex situ* facilities in the world, several 10,000 samples were distributed during the reporting period to users across the globe. To advance the utilisation of genetic resources for research and breeding, the services offered by the Genebank are upgraded and continuously updated by providing digitised information, including passport data, consolidated phenotypic information.

mation, and molecular data. In this way, the Federal Ex situ Genebank is being advanced into a biodigital resource center, which will successively increase its value as a research infrastructure. To facilitate genotype to phenotype mapping, the accession-based wheat and barley collections were extended by generating "precision collections" represented by "immortal" homozygous genotypes being genotyped. The genetic characterisation of collections is complemented at the phenotypic level by curating and evaluating legacy data and generating new information on agronomically relevant traits. A further pillar of the biodigital resource center is represented by the advancement of the IPK data warehouse and the web portals to facilitate speedy and informed access to information related to Plant Genetic Resources and to provide interfaces for data exchange with other related systems.

Digital Plant Phenotyping

The Institute houses many facilities for plant growth, amounting to 220 m² of controlled environment chambers, approximately 6,470 m² of greenhouse space and 84 ha of experimental field space. Phenotyping platforms installed in two greenhouses and one controlled environment chamber have enabled almost complete automation of whole plant phenotypic data acquisition. The worldwide unique PhenoSphere research facility enables highly automated and non-destructive digital phenotyping of plants under strictly controlled environmental conditions. It comprises a rhizotron system for studying root growth and architecture dynamics, and a container system for studying above-ground properties of plant stands in plots of 1 m². The rhizotron system, with 360 large rhizotrons, each measuring a rooted area of 60 x 90 cm², incorporates a high-resolution monochrome camera to capture roots and extract root traits through dedicated image analysis procedures. At the same time, top and side view RGB cameras record shoot growth and development. The container system is equipped with an automatically positionable multi-sensor camera system (PhenoCrane) to record a wide range of above-ground characteristics. It allows phenotyping in field-like scenarios with a wide range of air temperature, humidity and lighting settings that mimic the spectrum and intensity of sunlight, including rapid changes and diurnal cycles. Carbon dioxide levels can also be adjusted. The large volume containers (up to 110 containers of one cubic metre soil volume each) allow plant stands to grow and control irrigation and soil temperature with the same plant density as in the field. First demonstrated for maize, the system was proven to elicit plant growth and development progression very similar to that observed in the open field season that was than simulated in the PhenoSphere. Delayed due to COVID-19-related restrictions, the PhenoCrane multi-sensor platform was installed in 2021, which includes an RGB camera, a FluorCam 3D laser scanner and a hyperspectral camera (VNIR 350-900 nm). After extensive testing and optimising of measurement protocols in 2022, the facility became fully functional in 2023 and is now an integral part of the experimental operations of researchers at IPK and in collaboration with other partners.



Figure 1: Bruker AVANCE Neo 500 MHz NMR spectrometer funded by the European Regional Development Fund (ERDF).

The NMR plant imaging platform, funded by the European Regional Development Fund (ERDF), has been upgraded with a new vertical super-wide-bore NMR scanner (Bruker AVANCE Neo 500 MHz NMR). The installation was completed on time and marks an important milestone for non-invasive analysis of plant interiors. With this new scanner, the range for MRI application to various specimen sizes has increased by more than 100-fold, allowing for multi-seed measurements. Combined with Deep Learning algorithms, we can significantly increase the throughput of MRI-based seed phenotyping. This technology is used in DFG and BMBF projects, in collaboration with breeders, and for educational purposes. Additionally, the Bruker AVANCE 400 MHz NMR with cryo-system has been modified for high-resolution imaging and 13C-sucrose monitoring in living seeds to study the functional role of SWEET proteins and hypoxia in living seeds. A new methodology for tracer velocity measurements was also developed. The NMR platform includes state-of-the-art instrumentation, dedicated methodologies and specialists and now represents a new facet of the plant phenotyping network in Germany.

Microscopy, Analytics, and DNA-Sequencing

Light and electron microscopy are among the key technologies in plant research, and here at the IPK, we also link the different research disciplines. To maintain state-of-the-art technology in our portfolio, the microscopy equipment at the IPK was expanded with a Zeiss LSM 980 confocal laser scanning microscope with Airyscan 2 and a new Zeiss Elyra 7 with lattice SIM for super-resolution imaging microscope. These new additions, together with a Zeiss Lightsheet 7 microscope, provide an excellent platform for live cell imaging. The visualisation of dynamic cellular processes and the localisation of specific gene products in combination with ultrastructural analysis (i.e. scanningand transmission electron microscopy) enables the cell biological characterisation of a range of agronomically important features at the tissue, cellular and subcellular level. The new findings thus contribute directly to characterizing new plant properties contributing to yield stability and increased resilience in the face of climate change, enabling more sustainable agriculture.

State-of-the-art chromatography and mass spectroscopy are also available for the structural and functional analysis of nutrients and metabolites and for identifying proteins and peptides. A high-resolution ICP-MS instrument has been coupled with fluorescence-activated cell sorting to determine the nutrient composition in individual root cell populations.

High-throughput sequencing is performed at the IPK-central sequencing platform on all state-of-the-art systems. Short read sequencing-by-synthesis (SBS) is using the Illumina iSeq100 and NovaSeq6000 systems. While the iSeq100 system has a sequencing capacity of 1.2 Gb per run with up to 4 million sequencing reads, providing mainly the capacity for sequencing library QC, the NovaSeq6000 system offers high-throughput capacity with up to 8000 Gb raw sequencing data output per run and up to 20 billion sequencing reads with a maximum read length of 2 x 250 bp. SBS is applied to a diverse range of applications, including whole genome sequencing and resequencing, genotyping, transcriptome sequencing, methylome sequencing, small RNA sequencing, and 3D conformation capture (Hi-C) sequencing. These methods are essential for the comprehensive analysis of genetic information and support a wide range of research projects in genomics, epigenetics and functional genomics. Single-molecule sequencing is performed on two technology platforms with highly complementary value. Single-molecule sequencing for the generation of long reads, also known as single-molecule real-time sequencing (SMRT), has been performed at the IPK for several years, since June 2023, using the PACBIO Revio system (figure 4). This system offers 80-100 Gb sequencing capacity per SMRT cell. The technology allows for sequencing native genomic DNA fragments up to 22 kb with extremely high accuracy (99,95 % Q33, HiFi Circular Consensus Sequences). This sets a new standard for sequencing large and complex plant genomes. Applications include de novo genome sequencing for assemblies, 5mC methylation analysis and full-length transcript or isoform sequencing (Kinnex). In addition, a Prome-



Figure 2: Confocal Laser Scanning Microscopy (CLSM): Transversal stem section of barley with autofluorescence of chloroplasts (red) and cell walls (blue) of a vascular bundle. Light Sheet Fluorescence Microscopy (LSFM): Arabidopsis anther expressing histone H2 conjugated with RFP (in magenta) and nuclear pore protein NUP-136 conjugated with GFP (in green). Scanning Electron Microscopy (SEM): Developing barley spike with primordia of awn (in pink), glume (in green) and stamen (in orange). Super Resolution Microscopy (SRM) and Transmission Electron Microscopy (TEM): Dispersed chromatin arrangement without prominent chromocenters in interphase nuclei of Myristica fragrans. KNL1 immuno signals (in magenta), uniformly distributed within the DAPI-stained nucleus (global chromatin). N, nucleolus; Ne, nuclear envelope, Np, nuclear pore.



Figure 3: Impressions of IPK's two central research infrastructures, the Federal Ex situ Genebank and the IPK PhenoSphere.



Figure 4: The PacBio System. (A) PacBio Revio DNA sequencing device. (B) Preparation for a sequencing run. Workdeck layout is shown: (1) Sequencing plate with libraries and reagents, (2) pipette tip boxes, (3) Revio SMRT cell tray and (4) robot arm.



Figure 5: The ONT System. (A) PromethION 24 device composed of a computing (1) and DNA sequencing unit (2). (B) A flowcell inserted into the sequencer is shown. Samples and buffers are loaded using the inlet port (1). The sensor (2) is used for data recording, and the waste port (3) is required for the removal of reagents. The PromethION 24 can sequence up to 24 flowcells in parallel.

thION 24 instrument (Oxford Nanopore Technologies, ONT) is available for large-scale (60 – 200 Gb/flowcell, sequencing of up to 24 flowcells in parallel) direct DNA and RNA sequencing (figure 5). In contrast to traditional sequencing methods that use DNA polymerases, the ONT device sequences the DNA/RNA as it passes through nanopores. The changes in current profiles are recorded and translated into the base sequence. One exciting application of this technique is, for example, the generation of ultra-long sequences (>1 Mb), which makes it possible to close remaining gaps in the genomes and to produce continuous "Telomere-to-Telomere (T2T)" sequences of entire chromosomes. Additional planned areas of application include the sequencing of amplicons and plasmids and the detection of methylation patterns on a genomewide scale using the modified base calling function. These technologies are essential for the detailed analysis and understanding of plants' genetic diversity and functionality and contribute significantly to research and development in genomics and transcriptomics.

Information Technology and Digitalisation

Modern life sciences require the generation and analysis of large data sets from "omics" experiments, including many environmental parameters. Imaging technology is also becoming a key driver in the increasing digitisation of biological data. During the period under review, the computing power and data storage of the IPK has continued to grow. It currently holds one high-performance compute server (in total 60 CPU cores, 2 TB RAM), a Slurm cluster (1 control node, 1 submission node, 21 CPU compute nodes with 916 cores, 26 TB RAM and 4 GPU compute node with 276 cores, 4 TB RAM and 23 GPUs), network attached storage with 1.2 PB storage and 1.8 PB archive capacity. To ensure that data are available and freely accessible in a permanent and structured way to address biological questions, the Institute has been actively involved in initiatives such as "de.NBI" (German Network for Bioinformatics Infrastructure), "ELIXIR" (European Infrastructure Network for the Life Sciences), Data-Cite and the National Research Data Infrastructure (NFDI) initiative, the latter of which aims to ensure that scientific data remain FAIR - findable, accessible, interoperable and reusable. In this context, each accession in the Gene Bank has been assigned a unique digital identifier. In addition to the Gene Bank Information System, IPK hosts a number of other databases. The Barley Genomics BRIDGE portal, the PanBARLEX portal to investigate genes of the Barley Pangenome and the WiLDSI portal to explore the use of Digital Sequence Information - DSI are examples.

Publications

In the reporting period, 332 papers were published in peer-reviewed journals (177 in 2022 and 155 in 2023). Out of this, 64 scientific articles were published in journals with an impact factor greater than nine (figure 6), reflecting a continuous trend towards publication in high-impact journals. A complete list of the publications is given in the appendix of this report (page 108). Also, the tendency towards open-access publications in peer-reviewed journals was positive, with more than 80 per cent of publications freely available for researchers and all interested in our scientific results worldwide.

Research data are essential for scientific work and include measurements, surveys, audiovisual material and software. They can be published on their own or with scientific articles. Proper curation, standards and good scientific practice are key. Publishing data promotes global collaboration, verifies results and enables new research. Online repositories and data journals ensure data quality and long-term availability. For the first time, a separate PDF document lists selected data publications that follow the FAIR and CARE principles. FAIR ensures that data are accessible and reusable, while CARE emphasises ethical management. These principles guide IPK's responsible use of data. More details can be found in the separate PDF document "IPK Leibniz Institute Data Publications 2022/2023" on our website.

Scientific Library and Information Services

The scientific library is another infrastructure component of the IPK. It has a collection of about 82,700 media units related to the main research areas of the Institute.



Figure 6: Number and impetfactors of IPK publications in 2022 & 2023.

The main task of the library is to provide literature for the researchers on site, but the neighbouring biotech companies also use the service. The IPK's participation in the DEAL contracts with Wiley and SpringerNature is an important step in the open access process. This leads to an improved information supply for all participating institutions by extending reader access to the entire journal portfolio of the respective publishers. Authors are strongly encouraged to publish their research results in Open Access. The IPK supports the open science initiatives of the Leibniz Association. In 2023, 123 publications (2022: 143) were published in "Open Access". This is about 80 per cent of all peer-reviewed publications by IPK researchers. The trend towards 'open access' has been growing steadily for around ten years. The IPK is a member of the ORCID Germany consortium led by TIB Hannover. The "Open Researcher and Contributor ID" (ORCID) ensures a uniform, general, open standard of author identification. Due to active information and support services within the Institute, about 90 per cent of the researchers at IPK are registered at www.orcid.org.

Submitted data volume by study type (in TB)



Number of submitted studies



Figure 7: Example of IPK data publication using the example of submission of sequence data to EMBL repositories.

Funding

The IPK had 60.22 million euros in funding in 2022, including third-party grants and own income (2022: 53.74 million euros). This sum includes, on the one hand, grants within the framework of the Institute's core funding amounting to 38.73 million euros (2022: 36.6 million euros) and, on the other hand, self-financing funds carried over from the previous year amounting to 4.02 million euros (2022: 3.91 million euros) and transferable cash balances

totalling 4.02 million euros (2022: 3.91 million euros).

Regarding appropriation, personnel accounted for approximately 45 per cent (2022: 47 per cent) of total expenditures in 2023, and equipment accounted for 13 per cent (2022: 13 per cent). In 2023, investments in scientific equipment were covered by core funding and an investment into a new sequencing facility by the State of Saxony-Anhalt via the support of the European Regional Development Fund (ERDF). Institutional funds were primarily used to optimise the supply and distribution of energy on the campus. The development and structure of total expenditures from 2020 to 2023 are shown in table 3.

Third-party funding

In 2022 and 2023, third-party funding amounted to 13.23 million and 17.47 million Euros, respectively. The significant increase in third-party funding in 2023 is due to funding from the special Coronavirus Fund of the state of Saxony-Anhalt. This fund aims to increase the resilience of research institutions in the coming years. If this funding is discounted, the third-party funding in 2023 will amount to EUR 10.40 million. This is within the expected range of competitively acquired external funding for the Institute. The measures taken years ago to increase third-party funding have therefore, continued to bear fruit in 2022 and 2023, with competitive funding amounting to about 30 per cent of the IPK's core budget. Excellent basic research was made possible by acquiring extensive funding from the German Research Foundation (DFG) and the European Union. Of particular mention is the grant for the establishment of the independent research group "Grain Legume Genomics" supported as a Leibniz Junior Research Group (2022-2026) within the frame of the Leibniz Competition. Besides, the EU project AGENT and the EU-funded project "Legume Generation: Boosting innovation in breeding for the next generation of legume crops for Europe" are being coordinated by the Institute. An overview of the third-party-funded projects is given in the appendix of this report (page 125). The figures also demonstrate that the Institute is a sought-after partner for collaboration with other research institutions and the private sector, especially plant breeding. The majority of the income results from such cooperations. A major funding line was the German Plant Phenotyping Network – DPPN of the BMBF, in which one of three research infrastructure nodes have been established at IPK. Similarly, the AVATARS joint project is funded by the BMBF and coordinated by the IPK.

Research Cooperations and Collaborations

Cooperation with and teaching at nearby universities is an important draw for young scientists, links complementary research competencies, and develops the research landscape at the regional level. Based on joint appointments, the Institute entertains tight links with the Martin Luther University in Halle (MLU) (3x W3, 1x W2, 1x W1) and the University of Göttingen (1x W3, 1x W2). In addition, IPK scientists teach at numerous universities, totalling 72 and



Corporate expenditure	2022	2023
Staff costs	26,124,000.00	27,171,000.00
Operating expenses	14,895,000.00	14,314,000.00
Subtotal	41,019,000.00	41,485,000.00
Investments		
Equipment	6,130,000,00	7,226,000.00
Construction measures	1.089,000.00	806,000.00
Subtotal	7,219,000.00	8,032,000.00
Revenues	53,744,000.00	60,220,000.00

Table 3: Total expenditure and income of IPK Leibniz Institute in 2022 and 2023 by main cost category.

82 course hours per semester-week in 2022 and 2023, respectively. Scientists at the Institute were also involved in supervising students. In this context, 25 PhD students successfully defended their theses within the reporting period 2022/2023.

A highlight within the reporting period was the kick-off of TRANSCEND. The Plant Research Alliance for "Translational Plant Biodiversity Research for Sustainability -TRANSCEND" was initiated by the DFG-funded "Cluster of Excellence on Plant Sciences" (CEPLAS) in North Rhine-Westphalia and the "Leibniz Institute of Plant Genetics and Crop Plant Research "(IPK). The intention is to integrate expertise, research activities and capacities through TRANSCEND. The overall goal of this transregional cooperation is to contribute to generating the scientific knowledge to accelerate and increase the precision of breeding processes and to blaze the trail for establishing novel concepts in plant protection and plant nutrition with reduced impact on the environment, climate, resources and agro-ecosystems. To realise this vision, TRANSCEND intends to act as a turnstile for comprehensive and intensive cooperation beyond our institutional boundaries, involving a broad spectrum of other experts in plant, agricultural, ecological and environmental sciences. In addition, the dialogue with society and transfer of results from basic research into socio-economic exploitation will be put into focus. The kick-off on June 7th 2023, took place under the patronage of the Federal Ministry of Education and Research (BMBF) and with the participation of interested representatives from politics, science and society.

Leibniz Science Campuses and Leibniz Research Networks

The Institute has been actively shaping Leibniz's research campuses, alliances, and networks for many years. The "ScienceCampus Phosphorus Research Rostock" aims to address the challenges associated with phosphorus by utilising the combined expertise of five Leibniz Institutes and the University of Rostock. This interdisciplinary collaboration focuses on the comprehensive study of phosphorus, its chemical compounds and its role in agriculture, the environment and industrial processes. The initiative includes basic and applied research to develop new phosphorus-use technologies and transfer these innovations to industry. The "P-Campus" has been funded by the Leibniz Association for two periods from 2015 to March 31st 2024. The IPK has been a partner in the "ScienceCampus" since its inception.

The Leibniz ResearchCampus Halle – "Plant-Based Bioeconomy" was consolidated as the **"Science Campus Halle"** (WCH). The aim remains the networking and cooperation of regionally neighbouring Leibniz institutes and the Martin Luther University Halle-Wittenberg.

After two successful funding periods, the structure of this network is now being consolidated by the partners involved. A spin-off of this network initiative is the research project funded in Saxony-Anhalt on digitalisation in the plant sciences, entitled 'Model Region Central Germany - Digitalisation of plant value chains (DiP)'. Funded by the German Federal Ministry of Education and Research (BMBF), the project is part of the National Bioeconomy Strategy. The project aims to optimise the entire plant value chain through modern digitalisation technologies, including genome research, breeding, plant production, food production and material-chemical processing. A key objective is to make food, feed and bio-based raw materials climate-neutral, sustainable and resource-efficient. Research, development and innovation projects with a high research risk and a high degree of novelty and complexity are funded to support structural change in the coal mining region of Saxony-Anhalt and to contribute to economic development and prosperity.

Lighthouse projects include innovations in digitalisation, genome research, breeding and plant production, developing sustainable and climate-resilient cultivation systems for the Central German arid region and optimising value chains for special crops using data analysis, bioinformatics and biotechnology. The IPK is involved in several regional collaborative projects coordinated by the Martin Luther University Halle-Wittenberg.

A further bundling of competencies occurs at the level of Leibniz's research networks. The IPK is involved in two of these networks. The **Leibniz Research Network "Biodiversity,"** comprising 18 institutions across various scientific disciplines, aims to develop sustainable solutions for biodiversity conservation. In "10 Must Knows from Biodiversity Science 2022," 45 scientists present key insights into Earth's complex systems, focusing on ten crucial areas. The IPK led the section on agricultural transformation. The report aims to provide policy-makers with scientifically validated knowledge for better decision-making at all levels. It includes ten concrete recommendations (10 Must Dos) for the COP15 negotiations in 2022 and to support policy-making in Germany, the EU, and globally.

The Leibniz Research Network "Bioactive Compounds" brings together 17 institutions to consolidate research on biologically active molecules to address challenges such as incurable diseases, resistant bacteria and climate-induced yield losses. No single institute covers the full spectrum from discovery to application, so the network integrates institutes from four sections of the Leibniz Association. It aims to improve collaboration in drug development, crop protection and related fields by developing a communication platform for the exchange of expertise between participating institutes and external partners. In addition, based on its work on stem cells in cereals, the IPK is associated with the Leibniz Research Network "Stem Cells and Organoids", which was formed in 2021.

The Leibniz Strategy Forum on "Sustainable Agri-Food Systems", of which the IPK is a founding member, aims to resolve conflicts in agricultural and aquatic production systems using interdisciplinary expertise. It addresses soil and water eutrophication, biodiversity loss, and climate change. It seeks to integrate production systems and consider global interactions. The forum will develop strategies, holistic models, and solutions enabled by new technologies and digital transformation for sustainable biomass production. Over two years, members will work with stakeholders to develop a methodological framework and research approach for sustainable systems.

Work of the Boards

The Scientific Advisory Board advises the Board of Directors and and reports to the Board of Trustees on scientific and technical matters. In 2022, the Scientific Advisory Board reviewed the Molecular Genetics and Physiology and Cell Biology Departments as well as the Independent Research and the Young Investigator Groups. The latter two were as reviewed in 2023, along with the two departments Genebank and Breeding Research. The Board of Trustees met twice each in 2022 and 2023.

Scientific communication, conferences and events

Following the exclusively virtual formats during the coronavirus pandemic, face-to-face events and meetings were again organised during the reporting period. In both years, the Institute opened its doors to the public during the "Day of the Open House". The response and interest from visitors was overwhelming. Special events were organised for schoolchildren. During the "Future Days" event organised by the state of Saxony-Anhalt, pupils could learn about IPK's various fields of activity. In cooperation with the Woltersdorf Gymnasium in Ballenstedt, sixth-, tenth- and twelfth-grade pupils visited the Institute for special events as part of their biology classes. In addition, IPK researchers took over special teaching units at the Woltersdorf Gymnasium. The aim is to present science and research-related professions as future options and to arouse interest in vocational or university education in life sciences. An even younger audience was addressed in cooperation with a popular children's TV programme. In 2023, the motto was "Doors open for the mouse", and the Federal Ex situ Genebank presented its treasures. Above all, conferences and other science-related events stimulated the presentation of research results, scientific discussion and dialogue. Only a selection of events and meetings can be listed here. A more complete picture can be found on the Institute's website.

The EU project INCREASE conducted a citizen science project part on bean diversity and was continued in 2022 and 2023. After a successful start in 2021, several thousand people from across Europe participated as citizen scientists. The goal is to record important characteristics of 1,000 old bean varieties. Participants received seeds and documented growth and other traits via an app. The project included different levels of participation to cater to varying levels of expertise. Despite initial scepticism about data quality, the project proved promising as it collected extensive data and raised awareness of biodiversity. In July 2023, the IPK hosted a Citizen Science Day as part of the project. The aim was to promote agricultural biodiversity by evaluating the growth and drought tolerance of chickpeas and fava beans. The IPK invited 100 German participants to this citizen day to share their experiences and highlight the importance of citizen science for scientific research.

The CEPLAS-IPK Summer School took place in 2022 at Kloster Steinfeld, North Rhine-Westphalia, bringing together 53 doctoral students from 19 countries. The programme included workshops and lectures on topics such as global food security, resilience for scientists, publishing, and self-presentation. The event fostered scientific exchange and helped participants expand their professional networks. Organisers and participants emphasised the importance of direct interaction following the COVID-19 pandemic.

In May 2022, the IPK Leibniz Institute hosted a workshop of the "Controlled Environment Plant Phenotyping" working group of the International Plant Phenotyping Network (IPPN). Nearly 200 participants discussed the latest developments in plant phenotyping, including the concept of the "digital twin". The workshop featured lectures from international experts and tours of the IPK's phenotyping facilities. Thomas Altmann, the event organiser, highlighted advancements in the analysis and cultivation of crop plants.

From 22 to May 24th 2022, staff from 14 genebanks from developing countries were invited, in collaboration with Crop Trust, to a workshop in Gatersleben. The goal was to exchange information on the conservation and management of plant genetic resources. Participants were trained in various aspects of ex-situ conservation. The workshop offered extensive opportunities to learn about the IPK gene bank and to exchange ideas. The event took place as part of the BOLD project, which aims to strengthen global food security.

At the end of May 2022, and for the first time in Europe, the International Water Lentil Congress was hosted by the IPK Leibniz Institute. Ninety-four participants from 21 countries discussed the latest findings on water lentils, which are significant for human nutrition, energy production, and water purification. Ingo Schubert, the congress organiser, emphasised the potential of water lentils and their unique biological properties. The congress promoted scientific exchange and set new impulses for research and practical applications.

Engaging with journalists and making the IPK Leibniz Institute's research results accessible to the general public is vital to our public relations work. We recognise journalists' crucial role as important multipliers, amplifying the reach and impact of our research. For this reason, the IPK has organised events for journalists with partner institutions in 2022 and 2023 to further strengthen this important relationship. In 2022, 15 journalists from the Science Press Conference were invited by the IPK and the Crop Trust to the journalist college "Crop Diversity – Underpinning Climate-Resilient Agriculture" in Gatersleben. They visited important research infrastructures on the campus, such as the IPK PhenoSphere and the Federal *Ex situ* Genebank. They were informed about current research trends on sustainable, climate-resilient agriculture. Numerous IPK researchers were available for background discussions and interviews at both events. This resulted in several reports on the work of the IPK. But that's not all: the IPK was able to increase its visibility and further expand its media network.

In 2023, the focus of the journalist college was on "genetic engineering", which has been on everyone's lips since the EU Commission presented a new regulation of EU genetic engineering law. The IPK and the DFG-funded Cluster of Excellence CEPLAS took the broad discussion in politics, society and science as an opportunity to organise a journalists' college in Gatersleben. The 15 participants included editors from well-known national media such as SPIEGEL, Süddeutsche Zeitung and Tagesspiegel, representatives of regional media such as MDR and Mitteldeutsche Zeitung, and freelance science journalists. The participants were given guided tours and presentations on the scientific background of "new genomic techniques". The aim was then to shed light on the issue's ethical, political and legal aspects. Engaging in dialogue with the journalists and learning about their views and experiences in covering the issue was also important.

In 2022, a new medium for science communication was developed called "IPK stories". This multimedia tool combines text, sound, photos and videos. The objective is to draw attention to key areas of research that are popular and attractive to the interested public and multipliers such as teachers and journalists. Stories on key topics such as hybrid wheat, genome editing or the world's most advanced digital plant phenotyping infrastructure, the IPK PhenoSphere, are already available. New stories will be added continuously.

Highlights

24 - 25 May

The latest developments in plant phenotyping, such as the 'digital twin' concept, are discussed at an international workshop in Gatersleben.

29 May – 1 June

The International Conference on Duckweed Research and Applications is held for the first time in Europe. Nearly 100 participants discuss new findings on the smallest flowering plant, a new crop for Europe.

15 June

Every two years, the German Agricultural Society awards the Wilhelm Rimpau Prize for Young Scientists as part of its Field Days. Johannes Schneider, a young scientist from the IPK, is one of this year's winners. ()

2022

2 March

The two genebank sites in Malchow and Groß Lüsewitz are being modernised. A topping-out ceremony is held in Malchow in March.

8 March

An international team of researchers, including scientists from the Leibniz Institute IPK, has sequenced the genome of the field bean at the chromosome level in high quality. The results have been published in the scientific journal 'Nature'.

12 April

15 February

diversity.

16 March

After the kick-off in 2021, the

EU project INCREASE enters

the next round with its citizen

Swiss artist Christoph Hänsli

visited the IPK in July 2020.

The resulting paintings can

be seen in a gallery in Berlin.

science project on bean

The Hungarian Academy of Sciences makes Andreas Börner an honorary member. According to its statutes, this is possible for scientists working abroad who have achieved their field's highest international scientific level.

5 May

Pupils from the Wolterstorff Grammar School in Ballenstedt have visited Gatersleben for years for guided tours, lectures and discussions. The exchange is to become even closer in the future. A cooperation agreement is signed.

22 - 24 May

Crop Trust and IPK invite partners from 14 countries of the Global South to a workshop in Gatersleben.

7 June

18 May

An international team of

scientists from the Leibniz

sequenced a high-quality

Institute IPK, has successfully

reference genome of the culti-

vated oat and its closest rela-

tives from the genus Avena.

the journal Nature.

9 - 13 May

Their results are published in

The CEPLAS Summer School

time in cooperation with the

Leibniz Institute IPK, 53 PhD

students from 19 countries

meet at Steinfeld Abbey in

North Rhine-Westphalia.

is organised for the first

researchers, including

The Cluster of Excellence CEPLAS and the Leibniz Institute IPK established a new alliance for plant sciences TRANSCEND in Berlin. Federal Research Minister Bettina Stark-Watzinger (FDP) is the patron and welcomes the initiative.

10 June

Beautiful weather, numerous guided tours, experiments and information stands, and the first get-together after the coronavirus pandemic: the conditions for the Open Day could hardly have been better. Visitors flocked to the Gatersleben Research Campus.

21 June

The Genome Centre of the Leibniz Institute IPK houses a new, state-of-the-art sequencing machine from the US company Pacific Biosciences. According to the manufacturer, it is the first machine to be delivered to a research institution in Germany.

5 July

In Brussels, the EU Commission presents its legislative initiative to regulate so-called New Genomic Techniques (NGT) in plant research and breeding. The IPK explicitly welcomes the initiative in a statement.

18 June

The IPK Leibniz Institute opens its doors, and hundreds of visitors take the opportunity to visit the IPK PhenoSphere and the Genebank despite the extreme heat.

26 August

5 September

Martina Brockmeier took office as President of the Leibniz Association on 1 July 2022. During her visit to the IPK, she answered questions from staff and outlined the priorities of her term of office.

11 September

4 October

In an interdisciplinary approach involving plant breeders, geneticists, phytomedical scientists and bioinformaticians, an IPK research

team has identified new

Nature Genetics.

2 November

biological diversity for yield

components and yellow rust

resistance in old. non-native

varieties. Results published in

A team of researchers led by

the Leibniz Institute IPK has

barley using the Cas9 gene

resistance to important plant

modified a gene in winter

scissors to develop new

viruses. The results have

Biotechnology Journal'.

been published in the 'Plant

Researchers at the Leibniz Institute IPK have investigated how the behaviour of an individual wheat plant under restrictive light conditions influences the performance of the entire community. The results have been published in the Plant, Cell & Environment journal.

7 September

The IPK celebrates its 80th birthday. At the same time, Nicolaus von Wirén was inaugurated as Andreas Graner's successor managing director. A staff party on the campus follows the ceremony. An international team of researchers led by the Leibniz Institute IPK has uncovered a three-step sequence of molecular building blocks that control the growth of root hairs for nitrogen uptake. The results have been published in the journal Current Biology.

3 October

More than 50 children visit the Leibniz Institute IPK and the Genebank. The IPK is one of 712 institutions participating in the 'Open the doors with the mouse' campaign. The special 'Sendung mit der Maus' motto is 'Precious Treasures'.

08 – 09 November

Pulses are the focus of a new EU research project coordinated by the Leibniz Institute IPK. Kick-off meeting takes place in Gatersleben.

15 November

The MDR broadcasts the documentary 'Die Kornmacher' (the grain workers) about the IPK. After several months of shooting, the film is shown in the series 'Der Osten – Entdecke, wo Du lebst'.

17 November

The Gregor Mendel Foundation awards Nils Stein and Martin Mascher the Gregor Mendel Innovation Prize for their work in cereal genome research.

21 November

Using a synthetic screening platform, an international team of researchers led by the Leibniz Institute IPK has identified the missing steps of the tropane alkaloid biosynthesis pathway in Erythroxylum coca. The results have been published in the journal PNAS.

26 – 28 November

Since the EU Commission's proposal to revise European genetic engineering legislation, the topic of 'green genetic engineering' has been on everyone's lips. Reason enough for the IPK and the CEPLAS Cluster of Excellence to organise a Journalists' College on this topic.

29 November

Using the model plant Arabidopsis thaliana, a research team led by the Leibniz Institute IPK has shown how different coumarins alter iron uptake under acidic and alkaline conditions. The results have been published in the journal 'The Plant Cell'.

13 December

The PhenoSphere at the IPK is unique in the world. Reason enough to present the research infrastructure in a new multimedia story. 2023

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Department Genebank



Genomics of Genetic Resources (GGR) **Prof. Dr. Nils Stein**

Genebank Documentation (DOK) **Dr. Stephan Weise**

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Resources Genetics and Reproduction (RGR) **Prof. Dr. Andreas Börner**

Cryo- und Stress biology (CSB) PD Dr. Manuela Nagel

> Satellite Collections North (TEN) **Dr. Klaus J. Dehmer**

Experimental Taxonomy (ETX) **Dr. Frank Blattner**

Domestication Genomics (DG) **Dr. Martin Mascher**



Department Genebank



Head: Prof. Dr. Andreas Graner, Prof. Dr. Nils Stein (since 01.10.2023)

Mission

The conservation of plant genetic resources (PGR) in the Federal Ex situ Genebank is of very high societal and scientific importance, supporting our attempt to thwart the loss of crop-related agrobiodiversity in modern agriculture of the temperate climate zones. The resources provide the basis for innovative science in crop plants' evolution, domestication, and environmental adaptation. They can serve as the key to meet important or emerging crop improvement demands. For both, the management and conservation of PGR has to aim for the highest quality standards. Furthermore, the value of the PGR will be increased by matching them with comprehensive molecular, phenotypic and environmental data, which will foster knowledge-based utilization of PGR at research frontiers and for innovative approaches in modern plant breeding.

Conservation Management

The Federal *Ex situ* Genebank is one of the world's largest collections, both in terms of botanical diversity and the size of its collection. As of July 2023, the holdings comprise 152,359 accessions from 93 plant families representing 758 genera and 2,913 species.

The collection is maintained in Gatersleben and the two external sites, Malchow (oil and fodder crops) and Groß Lüsewitz (potato collections). For seed propagation, 5,193 accessions were cultivated

in the field or greenhouse during the reporting period (July 1, 2022 – June 30, 2023). For seed quality control, about 28,598 germination tests were carried out.

In addition to its living collections, the genebank accommodates a herbarium with 450,216 specimens, 110,361 reference samples of seeds and fruits and 57,989 cereal spikes. In the last two years, 43,058 samples were distributed to researchers, plant breeders or other interested stakeholders (Figure X). The distribution is based on the terms of the Standard Material Transfer Agreement (SMTA), ensuring that the relevant provisions of the International Treaty or the Nagoya Protocol are followed. Thus, since 1948, almost 1.2 million samples have been provided to users in Germany and abroad. Table 1 summarises the inventory.

In addition to the preservation of seed-borne accessions, the IPK operates one of the world's largest cryo-collections for vegetatively preserved plants. The collection comprises 2,461 accessions, including 2,047 potato as well as 157 mint and 253 *Allium* samples. The IPK collection of safety duplicates hosted at the Svalbard Global Seed Vault of the Crop Trust was increased to 66,994 accessions, representing around 44% of the total collection.

To support the coordinated conservation of genetic resources at the national and international level, the Genebank Department interacts closely with the Federal Ministry of Food and Agriculture (BMEL), the Alliance of Bioversity International and the International Center for Tropical Agriculture (Alli-



ance), and the Secretariat of the European Cooperative Programme for Plant Genetic Resources (ECPGR). The IPK Genebank Department has received the mandate from ECPGR to host and advance the European Search Catalogue for Plant Genetic Resources (EURISCO). Digital Object Identifiers (DOIs) have been assigned to all Federal *Ex situ* Genebank accessions to improve their tracking and documentation and enable linking with PGR-related data from other domains.

Research Highlights

Plant genetic resources are of increasing importance for research and application. Therefore, it has emerged as a research and management priority to enrich genebank material with dense digitized datasets. This can be achieved, i.e. by generating digital sequence information for entire or partial collections, an effort coined as *genebank genomics*, which will underpin the development of the genebank from a repository of PGR into an innovative research infrastructure. The scientific program of the Department delivers significant contributions to the two IPK Research Themes, "Valorisation of Plant Genetic Resources" and "Genome Diversity and Evolution".

The Department's research groups are assigned to three programs: Conservation Management and Evaluation, Characterisation and Documentation, Taxonomy and Evolution.

The research programme "Conservation Management and Evaluation" includes the continuous evaluation of selected agronomic traits. A further focus is the improvement of conservation management. Here, studies on the genetics of seed longevity were continued. Concerning vegetatively propagated species, we continually expand the cryo-collections of potato and *Allium*. The impact and role of endophytes during potato cryopreservation have become of interest. For garlic, extensive European cooperation is assessing the level of duplication in almost 2,000 accessions based on reduced representation sequencing, which will provide an important proxy for designing future garlic cryopreservation. *Lemna* is an emerging new species with promising application potential, and IPK has teamed up in international cooperation with an emphasis on testing the species' cryopreservation potential and properties.

The "Taxonomy and Evolution" research programme investigates phylogenetic classification and speciation within selected plant genera. The evolution of di- and tetraploid Hordeum bulbosum, the closest relative to domesticated barley (Hordeum vulgare), is a research focus, contributing to an IPK internal flagship project on the sequencing and assembly of the H. bulbosum genome. Furthermore, IPK is contributing in a leading role to the super pan-genome effort of sequencing all genomes of the diploid species in the genus Hordeum. The pan-genome of the crop species Hordeum vulgare has continued at even higher pace, facilitated through the extension of IPK's central sequencing platform comprising, since summer 2023, the latest single-molecule long-read sequencing instrument REVIO of the provider Pacific Biosystems. This activity was recently extended to study the barley pan-genome's epigenomic aspects.

The research programme "Characterisation and Documentation" focuses on describing genebank materials at various levels and the maintenance and further development of the Genebank Informa**Figure 1:** Distribution of 43,058 samples of plant genetics resources to different user groups.



Figure 2: The

European Search Catalogue for Plant Genetic Resources (EURISCO) provides information on more than 2 million accessions of crop plants and their wild relatives, conserved ex-situ by about 400 institutes. EURISCO is closely linked with local databases. These links allow a seamless exchange of data between different systems. This helps to maximise the accessibility and usefulness of stored genetic information and promotes research and conservation of genetic diversity.

tion System (GBIS). This is well complemented by the renewal of the mandate to the IPK Genebank for hosting and further developing the EURISCO catalogue and the coordination of the underlying network (Figure 2). This activity also made eminent contributions to the European H2020 project AGENT, establishing an active cooperation network between European genebanks. EURISCO also plays a central role in the Horizon Europe project PRO-GRACE, in which a concept for a research data infrastructure for PGR is being developed. Particular emphasis is placed on integrating passport data with phenotypic and molecular data to characterise the biological material.

The visible contributions of research groups of the Genebank Department to the field of Agricultural Genomics have led in the past to high-quality genomic resources for the cereal species barley, wheat and rye. These activities have been extended, and high-quality genome sequences have been produced by international collaboration with important crop species like oats (*Avena sativa*) and wild relatives of wheat. Additional high-quality genome assemblies were provided for wheat and barley. In 2022, a junior research group, funded by the Leibniz SAW competition and IPK core budget, has been initiated on broad bean (*Vicia faba*) genebank genomics and pan-genomics, and the group is associated with the Department Genebank.

A significant milestone in the field of genebank genomics, an activity that will trigger the development of the genebank into a biodigital resources centre, was reached in 2019 with the completion of the DNA fingerprinting of the entire barley collection, comprising more than 23,000 accessions. Since then, IPK has expanded this activity to a broad spectrum of collections. The entire wheat and broad bean collections are or will be soon genotyped by sequencing. Similar efforts are planned for other legume collections (pea, common bean) or have been partially achieved in international collaboration (pepper, eggplant, tomato, potato).

Outlook

Building on the expertise accumulated over eight decades, the Department stands for research-driven conservation of plant genetic resources collections. It warrants the sustainable preservation of one of the largest *ex-situ* collections of the world. It gives rise to innovations to improve its value as an infrastructure for research and crop plant improvement.

To further improve conservation management and better cover the research needs for forage plants and potatoes, the infrastructure advancement at the genebank sites in Groß Lüsewitz and Malchow had been initiated in 2021 and was accomplished by the end of 2023.

The technical progress in genome analysis and plant phenotyping will further accelerate the systematic characterisation of complete collections by DNA sequencing and trait analysis. It will allow for the comprehensive molecular characterisation of genebank collections. The availability of sequence information will benefit the conservation of genetic resources in manifold ways. In this context, we will continue on the path taken to further develop the genebank into a biodigital resources centre by linking the relevant information with conventional passport data.

By laying the foundation stone to establish the Federal *Ex situ* Genebank for Agricultural and Horticultural Crop Plants at IPK in 2003, the establishment of a quality management system according to ISO

Department Genebank

Species groups

Accessions

cereals and grasses	66213
wheat	28.318
barley	23.837
oat	4.864
rye	2.582
triticale	1.619
Aegilops	1.515
millets	842
maize	1.531
grasses	1.338

legumes	27.876
Phaseolus	9.011
field beans	3.046
soybeans	1.493
other beans	618
pea	5.393
chickpea	527
vetchling	515
vetches	1.845
lupines	2.738
lentils	462
clover	1.955
other legumes	273

Cucurbitaceae	2.666
pumpkins	1.054
melons	728
cucumbers	735
other Cucurbitaceae	149

vegetables	18.492
tomatoes	3.912
pepper	1.534
eggplants	113
beta beets	2.388
raphanus	768

5.470
1.293
953
254
215
1.148
2.181
2.564
675
494

flax	2.324
sunflower	677
dye plants	458
fibre plants	191
oil plants	548
other oil, fibre and dye plants	1.272

medicinal and spice plants	8.246
рорру	1.135
tobacco	590
other medicinal and spice plants	6.521
mutants	1.690
tomato mutants	743
soybean mutants	527
Antirrhinum mutants	420
Satellite Collections North	21.473
potatoes	6.348
oil and forage crops	15.125
rapeseed and feeding kale	2.645
grasses	11.145
red clover and alfalfa	1.335
Total	152.359

Table 1: Overview ofcollections from theGenebank by cropspecies

standards in 2007, and coordinating EURISCO since 2014, the Department has continued to set international standards for the conservation of genetic resources and cemented the value of the genebank as an internationally visible and widely used research infrastructure. By coordinating the H2020 project AGENT, IPK is leading innovation-driven research to build an actively cooperating genebank network to establish the possibility of using genomic prediction across genebank collections. The scientific focus of the Department on molecular genetics and genomics of the Triticeae has substantially contributed to implementing the IPK research programme. In the years to come, it will continue to help valorise plant genetic resources and further advance the research into genome diversity and evolution.



RESEARCH GROUP **GENOMICS OF GENETIC RESOURCES** (GGR)



Head: Prof. Dr. Nils Stein

Selected Publications

Kale*, S.M., A.W. Schulthess* et al.: A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. Plant Biotechnol. J. 20 (2022) 1730-1742.

Kamal, N. et al.: The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature 606 (2022) 113-119.

Navrátilová, P. et al.: Prospects of telomere-to-telomere assembly in barley: analysis of sequence gaps in the MorexV3 reference genome. Plant Biotechnol. J. 20 (2022) 1373-1386.

Schulthess*, A.W., S.M. Kale*, F. Liu* et al.: Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. Nat. Genet. 54 (2022) 1544-1552.

Jayakodi, M. et al.: The giant diploid faba genome unlocks variation in a global protein crop. Nature 615 (2023) 652-659.

* joint first authorship

Mission

Our research goal is to use state-of-the-art, high-throughput genomics to unlock the pangenomes of cereal crops and their wild relatives. This provides a new knowledge base for the discovery and the display of global genomic diversity of crop species like barley, wheat, and rye, including the respective collections of the Federal *Ex situ* Genebank. The established approach of genebank genomics, the systematic genotyping of entire genebank collections, and the integration with passport and characterisation and evaluation (C&E) data are being adopted in collaboration more broadly with crop species of IPK's Genebank. Furthermore, the concept has also been rolled out to other European genebanks to establish an active collaborative genebank network.

The improved (pan-)genomic resources in the cereals are being used for functional genomics to reveal the genetic control of soil- and insect-borne virus disease in barley, study genes involved in the regulation of barley morphology and architecture, as well as chloroplast differentiation and maturation. To aid the implementation of its research program and to provide services at an institute-wide level, the research group GGR operates and continuously extends and enhances a state-of-the-art next-generation DNA-sequencing platform.

Results

(Pan-)Genome Analysis

The research group takes a leading role in sequencing and re-sequencing the barley, wheat and rye genomes. The focus is the barley pangenome project, coordinated by IPK, including the research groups GGR and DG and BIT, and it involves broad international collaboration. Seven-ty-six genome assemblies were generated based on PACBIO HiFi sequencing, and the data is being prepared for publication. The barley genome is still recalcitrant for finished whole genome sequencing since large sequence repeat regions interfere with attempts of complete telomer-to-telomer sequencing (Navratilova *et al.* 2022). GGR contributes to establishing a *Hordeum* super-pangenome, an effort coordinated by Martin Mascher (DG), aiming to provide genome assemblies of all ~30 diploid species of the genus *Hordeum*. This activity also involves the *Hordeum bulbosum* IPK flagship project, coordinated by M. Mascher (DG) and bringing together research groups of the Genebank and Breeding Research departments (DG, ETX, GGR, BIT, CSF, ACB). Based on its expertise in genome sequencing, GGR actively contributes to the sequencing of other important crop species like wheat (Kale *et al.* 2022), oats (Kamal *et al.* 2022) and broad bean (Jayakodi *et al.* 2023).

Unlocking crop plant genetic resources

The research group has demonstrated the feasibility of genotyping entire crop collections of the IPK Genebank (Milner *et al.* 2019, Nat Genet) – a research area we and others have coined "genebank genomics" (Mascher *et al.* 2019, Nat Genet). Since then, part of the concept has been transferred to unlocking other important crop collections at IPK. In the BMBF-funded project Genebank2.0 (phase 1-3), coordinated by the QG group, all cultivated bread wheat accessions were genotyped by reduced-representation sequencing, and this effort is currently extended into wild wheat species and wheat of different ploidy. The value of such a project for the unlocking of genetic resources collections was well illustrated recently for the winter wheat collection (Schulthess *et al.* 2022). The effort in barley and wheat was taken by IPK now to the European level through coordination of the EU H2020 project AGENT, bringing together 18 genebank and genebank-informatics partners from all over Europe in a 5-year collaborative project with a total budget of 7 million EURO.



Figure. 1: The Horizon 2020 project AGENT, coordinated by GGR, aims at establishing an actively cooperating genebank network in EUROPE. Genotyped precision collections are being evaluated for biotic stress response under field conditions. Here the IPK spring barley precision collection observation plots are shown from an aerial view (picture by: C. Martin/IPK Leibniz Institute)

Embedding in IPK Research Themes

The research group contributes mainly to Research Themes 1, "Valorisation of Plant Genetic Resources", and 2 ", Genome Diversity and Evolution", of IPK's Research Strategy. Reference genome sequences and re-sequencing the two key crop species at IPK, wheat and barley, are essential for unlocking the genetic diversity represented in entire genebank collections. Genome sequencing and assembly innovations will facilitate future evolutionary studies in wild relatives or entire genera.

Outlook

The research group will continue its activity in structural genome and pan-genome analysis of barley, wheat, rye and wild relatives crop species. This will cover the areas of structural variation, pan-epi-genomics, developmental and tissue-specific 3D genome organisation, and the systematic characterisation of globally available genomic diversity. Direct access to IPK's Next Generation Sequencing (NGS) platform and its continued equipping with complementing innovative technology (PACBIO Revio, Illumina NovaSeq6000, ONT Promethion etc.) is providing excellent opportunities for this kind of research and for international collaboration and networking.

More information: www.ipk-gatersleben.de/en/genebank/genomics-of-genetic-resources/



Head: Dr. Stephan Weise

Selected Publications

Weise, S. et al.: Analysis of gaps in rapeseed (Brassica napus L.) collections in European genebanks. Front. Plant Sci. 14 (2023) 1244467.

Shaw, P.D. et al.: Database solutions for genebanks and germplasm collections. In: Ghamkhar, K., W. Williams & A.H.D. Brown (Eds.): Plant Genetic Resources for the 21st Century. The OMICS Era. New York: Apple Academic Press (2023) 285–309.

Kotni, P. et al.: EURISCO update 2023: the European Search Catalogue for Plant Genetic Resources, a pillar for documentation of genebank material. Nucleic Acids Res. 51 (2023) D1465-D1469.

Schulthess, A.W. et al.: Large-scale genotyping and phenotyping of a worldwide winter wheat genebank for its use in pre-breeding. Sci. Data 9 (2022) 784.

Schulthess*, A.W., S.M. Kale*, F. Liu* et al.: Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. Nat. Genet. 54 (2022) 1544-1552.

* joint first authorship

RESEARCH GROUP **GENEBANK DOCUMENTATION** (DOK)

Mission

The research group's activities cover a wide range of aspects of genetic resource documentation and genebank data handling. In particular, the research group develops and operates information systems for plant genetic resources (PGR). On the one hand, these support the workflows in the genebank. On the other hand, the aim is to better exploit plant genetic resources for various users in research and breeding. Integrating and curating data from different areas and sources and harmonising and exchanging data are thus essential tasks of the group.

Therefore, a priority is the further development and operation of the Genebank Information System (GBIS) with its core components GBIS/M (internal management system) and GBIS/I (online search and ordering system), as well as the European Search Catalogue for Plant Genetic Resources (EURISCO). These systems will ensure the long-term availability of comprehensive and high-quality PGR-related data. In this context, the research group also participates in the development of international information networks on PGR and biodiversity informatics.

In cooperation with other institute bioinformatics groups, the research group's activities are part of the strategy to transform the genebank into a biodigital resources centre.

Results

The Genebank Information System (GBIS) forms the institute's central infrastructure for supporting all processes related to the maintenance of genebank accessions. To ensure the performance and efficiency of the system in the long term, as with all IT systems, continuous further development of its various components is essential. In addition to technical adjustments, reacting regularly to new requirements is necessary. Related to this is the completion of a new tablet-based software, the PhenoApp, used to score accessions during seed multiplication at the genebank. Originally developed by JKI, it was recently extended to the specific needs of genebank work.

The coordination of EURISCO has been continued and further strengthened. The research group has been responsible for hosting and further developing EURISCO and coordinating the underlying network since 2014. EURISCO is operated on behalf of the European Cooperative Programme for Plant Genetic Resources (ECPGR) and provides a central hub for information on more than two million accessions maintained *ex situ* in over 410 collections in 43 countries. Close cooperation exists with the International Treaty and the Global Information System. The original 5-year hosting phase of EURISCO has already been extended for a second phase, and the ECPGR Steering Committee recently approved an extension for a further five years (2024-2028). In addition, the research group has received funding from 2022 to 2023 under a BLE-funded project to extend EURISCO to data on *in situ* conserved crop wild relatives.

In recent years, the research group has been involved in several Horizon 2020 projects. In the reporting period, the focus is on AGENT (2020-2025) and INCREASE (2020-2026). AGENT is a concerted action to activate genebanks, aiming to facilitate access to wheat and barley genetic resources for breeders and farmers through standardised protocols for data generation, documentation and delivery to users. The research group is mainly involved in two work packages that aim to develop guidelines and formats for data generation, exchange, and presentation and to develop the infrastructure for managing and analysing genotypic and phenotypic data on genetic resources. The INCREASE project, in turn, aims to advance the conservation of European plant genetic resources of four legume crops and to promote their use and valorisation. Amongst others, the conservation and evaluation of common bean genetic resources are being tested for the first time using a highly successful pan-European citizen science approach. The research group is responsible for the work package for developing the data infrastructure and the web portal and for integrating the data into a database, which forms the project's backbone.

Since the beginning of 2023, the working group has also been involved in the PRO-GRACE research project (2023-2025) under the Horizon Europe funding programme. PRO-GRACE aims



to develop a concept for a large European research data infrastructure for plant genetic resources. In this context, the working group is responsible for leading a work package on the inventory of PGR-related data and systems and information standards.

The continuous management, curation and analysis of genebank accession data (both historical and current) is one of the fundamental permanent tasks of the research group. This continuous improvement and supplementation of both passport and phenotypic data has significantly increased the quality and quantity of information available on the genebank accessions.

The research group is involved in the (further) development of international standards, e.g. for phenotypic data and *in situ* data.

Embedding in IPK Research Themes

GBIS, as a central infrastructure, supports the processes of all working groups involved in the conservation and processing of genebank accessions. During the reporting period, the working group processed and integrated accession-related data and made it available to various research projects. This will continue to be an important part of the strategy to transform the genebank into a biodigital resource centre. The research group is connected in many ways with other bioinformatics groups of the institute within the framework of Research Theme 1, "Valorisation of Plant Genetic Resources".

Outlook

The Genebank Documentation group will continue to operate and develop its well-established information systems, particularly GBIS and the recently extended EURISCO. It will also continue and intensify cooperation with national and international information networks on plant genetic resources and biodiversity.

The working group has been engaged in gap analyses for some time to contribute to the targeted identification of gaps in genebank collections. This has already resulted in a publication in 2023 and will continue (Figure 1).

In addition to the projects already underway, the working group is involved in the COUSIN consortium (Horizon Europe programme, five years). Starting in January 2024, COUSIN will develop and implement a roadmap for using crop wild relatives for breeding and farming. The working group will lead a work package to provide high-quality data.

Figure. 1: Result of ecological niche modelling of the rapeseed gene pool from Weise et al. (2023). The figure shows the predicted distribution areas of two species from the secondary gene pool, B. cretica and E. gallicum, under the climate change scenarios RCP 2.6 (optimistic) and RCP 8.5 (pessimistic) for the year 2070 as compared to current conditions. Gap analyses, in conjunction with ecological niche modelling, help to define priorities for targeted further development of genebank collections.

More information: www.ipk-gatersleben.de/en/research/genebank/genebank-documentation



RESEARCH GROUP **RESOURCES GENETICS AND REPRODUCTION** (RGR)



Head: Prof. Dr. Andreas Börner

Selected Publications

Schierenbeck, M. et al.: Association mapping unravels the genetics controlling seedling drought stress tolerance in winter wheat. Front. Plant Sci. 14 (2023) 1061845.

Rehman Arif, M.A. et al.: Genetic analyses of seed longevity in Capsicum annuum L. in cold storage conditions. Plants 12 (2023) 1321.

Nagel, M. et al.: Impacts of drought and elevated temperature on the seeds of malting barley. Front. Plant Sci. 13 (2022) 1049323.

Rehman Arif, M.A., I. Afzal & A. Börner: Genetic aspects and molecular causes of seed longevity in plants – a review. Plants 11 (2022) 598.

Rehman Arif, M.A. et al.: Genetic insight into the insect resistance in bread wheat exploiting the untapped natural diversity. Front. Genet. 13 (2022) 828905.

Mission

The research group is responsible for managing the genebank collection in Gatersleben, which entails the germplasm's long-term storage, multiplication and distribution comprising a wide spectrum of accessions representing most temperate crop species. The major research focus concerns seed longevity and a comprehensive phenotypic evaluation and genetic characterisation. Several bi-parental mapping populations and association mapping panels have been established in cereals to allow for the genetic analysis of various traits, focusing mainly on abiotic stress tolerance. In addition, material is used for various physiological and biochemical surveys in collaboration with partners within and outside IPK.

Results

The total number of accessions maintained at the Gatersleben site comprises 130,886 samples. Safety duplicates are available for 66,994 accessions (about 44% of the collection). They are kept at the Global Seed Vault, Svalbard, Norway. During the last 24 months, 28,598 germination tests have been performed. The annual distribution comprises 20,000 accessions, excluding the External Branch. About 8,000 accessions per season were grown for regeneration, evaluation, demonstration and research.

Studies on the genetics of seed longevity have been extended to *Capsicum*. 1,152 accessions stored in the genebank at -15/-18°C for over 40 years (from 1976 to 2017) were analysed for standard germination percentages after 5-40 years of storage. The data was used to determine the genetic causes of seed longevity, along with 23,462 single nucleotide polymorphism (SNP) markers covering all 12 *Capsicum* chromosomes. Using the association-mapping approach, we identified 224 marker-trait associations on all the *Capsicum* chromosomes (Figure 1). Several candidate genes were identified using the blast analysis of SNPs.

Research to improve the utilisation of genebank collections is focused on agronomic and abiotic stress traits of cereals (wheat, barley, rye). A genetic analysis (GWAS) aimed to identify QTLs/candidate genes influencing drought tolerance-related traits at the seedling stage using 261 diverse winter wheat panel accessions. Seeds from three consecutive years were exposed to polyethylene glycol 12% (PEG-6000) and a control treatment (distilled water). Association mapping analysis was applied based on 17,093 polymorphic SNPs. PEG treatment reduced shoot length (-36.3%) and root length (-11.3%) compared with control treatments, while the coleoptile length was increased by 11% under drought conditions, suggesting that it might be considered as an indicator of stress tolerance.

Seeds of the same panel (three consecutive crop seasons) were investigated for grain protein content (GPC) varying from 8.6 to 16.4% (11.3% on average). Significant natural phenotypic variation in GPC among genotypes and seasons was detected. GWAS analysis conducted with calculated best linear unbiased estimates (BLUEs) of phenotypic data and 90 K SNP array identified seven significant genomic regions harbouring GPC-associated markers on chromosomes 1D, 3A, 3B, 3D, 4B and 5A, of which those on 3A and 3B shared associated SNPs with at least one crop season. The verified SNP–GPC associations provide new promising genomic signals on 3A (SNPs: Excalibur_c13709_2568 and wsnp_Ku_c7811_13387117) and 3B (SNP: BS00062734_51) underlying protein improvement in wheat. Based on the linkage disequilibrium for significant SNPs, the most relevant candidate genes within a 4 Mbp window included genes encoding a subtilisin-like serine protease; amino acid transporters; transcription factors; proteins with post-translational regulatory functions; metabolic proteins involved in the starch, cellulose and fatty acid biosynthesis; protective and structural proteins, and proteins associated with metal ions transport or homeostasis.



Figure. 1: The plot of a genome-wide scan (GWAS analysis) of SNP markers associated with seed longevity over various storage periods in Capsicum accessions. The chromosomes are shown on the x-axis, the genome-wide scan -log10 (p values) is shown on the y-axis, and the significantly associated SNPs are highlighted in pink.

Embedding in IPK Research Themes

The research group is responsible for the management of the Gatersleben genebank collection. This includes the germplasm's long-term storage, multiplication, characterisation and distribution. The experimental work belongs to the IPK Research Theme 1, "Valorising of Plant Genetic Resources". In collaboration with other research groups within the Genebank department and other departments of the IPK, we use genebank accessions for phenotypic and genetic investigations.

Outlook

Studies on seed storability will be the main focus of the research. In addition to genetic analyses, seed material will be also used for various physiological and biochemical surveys. Furthermore, we plan to continue the biophysical investigations to model the relationship between seed viability, vigour, dormancy and longevity with delayed luminescence utilising artificial aged and long-term stored seeds. In cereals (wheat, barley, rye), bi-parental mapping populations and association mapping panels have been established. They will be used for further genetic analyses of agronomic traits, emphasising abiotic stress tolerance.

More information: www.ipk-gatersleben.de/en/research/genebank/resources-genetics-and-reproduction



RESEARCH GROUP **CRYO AND STRESS BIOLOGY** (CSB)



Mission

The Cryo and Stress Biology group is embedded in the Federal Ex situ Genebank and manages the long-term cryopreservation of clonally propagated potato (2,072 acc), Allium (253 acc) and mint (157 acc), representing one of the largest cryo-collections in the world. In addition, 236 in vitro accessions of mint, Brassica and Antirrhinum are maintained and distributed. The introduction of a triplicate system, the establishment of half-automated tanks at DSMZ and the parallel storage of data printed on film strips are increasing the security level of the cryo-collections. Research into molecular mechanisms, interaction with endophytic microorganisms and identification of duplicates based on GBS will support the cryopreservation work.

Results

Head: PD Dr. Manuela Nagel

Selected Publications

Kishchenko*, O., A. Stepanenko*, T. Straub* et al.: Ammonium uptake, mediated by ammonium transporters, mitigates manganese toxicity in Duckweed, Spirodela polyrhiza. Plants 12 (2023) 208.

Peterson, A. et al.: Cryopreservation of duckweed genetic diversity as model for long-term preservation of aquatic flowering plants. Plants 12 (2023) 3302.

Impe, D., D. Ballesteros & M. Nagel: Impact of drying and cooling rate on the survival of the desiccation-sensitive wheat pollen. Plant Cell Rep. 41 (2022) 447-461.

Nagel, M. et al.: Impacts of drought and elevated temperature on the seeds of malting barley. Front. Plant Sci. 13 (2022) 1049323.

Nagel, M. et al.: Global strategy for the conservation of potato. Global Crop Diversity Trust. Bonn, Germany (2022)

* joint first authorship

Impact of endophytes during potato cryopreservation (PotEND)

can influence plant performance. To understand the specific plant-endophyte relationship after cryopreservation, 2,017 cryopreserved potato lines were analysed, and RNA from 356 accessions with high and low regrowth potential was extracted. RNA was sequenced in collaboration with the AIT (Austria), and raw sequences were filtered and assembled to amplicon sequence variants (ASVs). The most abundant types in the high regrowth accessions were the bacteria order Propionibacterial (27%) and the bacteria order Micrococcales (28%) in the low regrowth lines. Beneficial and detrimental microorganisms are currently being cultured to inoculate selected genotypes for further analysis.

Endophytic microorganisms can switch between parasitism, commensalism and mutualism and

Cryopreservation of duckweed

Species from the duckweed family (Lemnaceae) are fast-growing aquatic plants that are important as feed for freshwater remediation and circular economy. Due to their clonal propagation, genetic resources are maintained in vitro. To develop a robust and rapid cryopreservation protocol for duckweed allowing long-term storage, duckweed fronds were sampled with a newly developed device, transferred to plant vitrification solution 3 and stored in liquid nitrogen. To evaluate the success of cryopreservation, fronds were rewarmed and then treated with pulsed illumination. In total, more than 20 accessions of the genera Spirodela, Landoltia, Lemna, and Wolffia were successfully recovered without any change in genome size (Figure 1A). Overall, the new protocol (Peterson et al. 2023) forms the basis for future research and routine cryopreservation of duckweed.

Conservation strategy for European garlic (Garli-CCS)

Most European garlic accessions are kept in field collections and require time-consuming and costly annual replanting. Therefore, an efficient conservation strategy is needed, including cryopreservation and improved usability of garlic accessions for breeders and producers. In the Garli-CCS project, 18 partners from 15 European countries have identified ~1,800 of the most important accessions and shipped dried leaves to IPK. The next steps will be to genotype the accessions with GBS and establish criteria for defining duplicates, e.g. based on the number of identical alleles. This will serve as a basis for rationalisation, prioritisation for cryopreservation and gap analysis.

Duckweed-based oral anti-viral vaccine for fish

The project aims to develop a duckweed-based platform for fish oral immunisation against Koi herpesvirus (KHV) by expressing the virus's major antigens in duckweed, which is a natural feed for fresh-water fish. To date, nine duckweed accessions have been tested, and the best level of GFP accumulation was obtained for Lemna turionifera 9434 and Landoltia punctata 7260



(Figure 1B). Genes coding envelope proteins ORF25, ORF81, ORF131, ORF136 and ORF149, and the capsid proteins ORF72 and ORF92 of KHV were codon-optimized for expression in duckweed and cloned into a deconstructed potato virus X-based vector. SDS-PAGE analysis of protein extracts from *Landoltia punctata* 7260 revealed significant enrichment of a recombinant protein with a molecular weight corresponding to ORF72, which was transiently expressed (Figure 1C). Currently, duckweed fronds accumulating ORF72 are further produced to test oral immunisation in fish.

Embedding in IPK Research Themes:

The research activities of members of the Cryo and Stress Biology group comprise the two IPK Research Themes 1, "Valorisation of Plant Genetic Resources" (conservation strategies for garlic and duckweed genetic resources), and 5, "Mechanisms of Resistance and Stress Tolerance" (investigations of complex stresses during cryopreservation). We actively collaborate with various IPK research groups (HET, MD, PBP, SZB, MPE, CSF) to coordinate material exchange, field multiplication and data management for securing and cryopreserving vegetatively propagated accessions (RGR, TEN, ETX, DOK).

Outlook

Cryopreservation is being applied to accessions of cultivated potato and *Allium* species and will be finalised over the next 15 to 20 years, dependent on the capacities and the collection size. In general, cryopreservation will become important for many genebanks. Hence, the Cryo and Stress Biology group has provided training for 16 genebanks and is actively contributing to developing standards and the organisation of training networks at the European (ECPGR) and international levels. In addition, the discussion on the conservation management of garlic genetic resources within ECPGR will support the decision-making process at IPK. Balancing genebank services, training workshops, and important research activities is challenging. We plan to continue research on the principles of cryopreservation, including the role of endophytes, specific genes, and transcription factors (e.g., *DREB/CBF, LEA* genes), RNA modifications, and DNA methylation changes during cryopreservation in various species. To realise these goals, two senior scientists funded by the Humboldt Foundation and one PhD student funded by the DFG have supported various topics and will actively contribute to further proposals.

Figure 1. Cryopreservation and application of duckweed genetic resources. A) Fronds of various duckweed accessions were successfully reactivated after PVS3 vitrification. Average regrowth was analysed one month after rewarming. B) Transient expression of GFP in La. punctata 7260 under white light (top) and 396 nm (bottom). C) SDS-Page analysis of purified by Ni2+-NTA chromatography-envelope protein ORF72 from KHV transiently expressed in duckweed.

More information: www.ipk-gatersleben.de/en/research/genebank/cryo-and-stress-biology



RESEARCH GROUP SATELLITE COLLECTIONS NORTH (TEN)



Head: Dr. Klaus J. Dehmer

Selected Publications

Hu, Y. et al.: Fate of P from organic and inorganic fertilizers assessed by complementary approaches. Nutr. Cycl. Agroecosyst. 124 (2022) 189–209.

Röckel*, F., T. Schreiber*, D. Schüler* et al.: PhenoApp: A mobile tool for plant phenotyping to record field and greenhouse observations [version 2; peer review: 2 approved]. F1000Research 11 (2022) 12.

Sampoux, J.P. & E. Willner: ImprovLoliumCol. Activity Report of the European Cooperative Programme for Plant Genetic Resources (ECPGR) (2022) 31 pp.

Hu, Y. et al.: Specific and intraspecific P efficiency of small-grain legumes as affected by long-term P management. Agronomy 13 (2023) 900.

Kirchgesser, J. et al.: Phenotypic variation of root-system architecture under high P and low P conditions in potato (Solanum tuberosum L.). BMC Plant Biol. 23 (2023) 68.

* joint first authorship

Mission

At IPK's sites at Gross Lüsewitz and Malchow on the island of Poel sites, the Satellite Collections North (TEN) maintain plant genetic resources (PGRs) of potatoes, oil and forage crops. We are responsible for the collection, preservation, characterisation, evaluation, documentation and distribution of more than 21,000 accessions.

Our collection-based research focuses on phenotypic and genotypic diversity, especially traits like nutrient efficiency in potatoes and forage legumes. Additionally, we study resistance/tolerance to diseases and the stimulation of germination in recalcitrant seeds via cold atmospheric pressure plasma treatment (CAP) to increase the accession-specific information available to our users.

Results

Phenotyping and genotyping in forage legumes, grasses and potatoes

Treatment of different accessions and seed lots of *Poa pratensis* and *Trifolium pratense* with CAP did not significantly increase germination rates. However, the germination speed was increased.

GBS genotyping of all 1,236 entries of IPK's *Medicago* collection indicated no clear separation of the two crop species *M. sativa* and *M. x varia*, while their progenitor species *M. falcata* also showed some affiliation to this complex (Figure 1A). Regarding overall phylogeny, the cultivated material of section *Medicago* was separated from the other sections (Figure 1B). In respect to within-accession response to phosphorus (P) supply, screening 200 diverse alfalfa entries revealed a high variation for biomass formation. In a three-year field trial, 60 accessions underwent up to four cuts per year, confirming a trade-off between forage quality and yield for each cut.

When alfalfa and red clover accessions were evaluated for their ability to utilise phosphorus (P) from recycled fertilisers in two-pot experiments and a two-year field trial, an equivalence to inorganic P fertilisers was shown. No intraspecific differences in P uptake were found. Interspecifically, red clover showed higher P uptakes in the first field year and alfalfa in the second field year.

Finalising P use efficiency studies in 200 mainly starch potatoes, the frequency distributions of the phenotypic traits exhibited heterogeneous patterns, suggesting a complex genetic control and different factors influencing the observed phenotypic variation. Membership function value for P stress tolerance (MFVP) as a comprehensive index identified genotypes with the highest MFVP as the most tolerant genotypes under P stress, confirmed by a heatmap (hierarchical clustering) based on standardised phenotypic traits' data. GBS-based PCAs showed no clear geographical clusters and a certain degree of separation based on utilisation (starch vs table).

Hydroponics-based screenings of 225 table potato accessions for nitrogen (N) and P efficiency revealed a large variation in both traits. Regarding N, a good correlation to field results could be shown.

Collection management and enhanced evaluations

The collections at Gross Lüsewitz contain 6,348 accessions from 140 tuber-bearing *Solanum* species. At Malchow 15,125 oil and fodder crop entries from 18 genera and 132 species are maintained.

In 2022 and 2023, material from 3,446 accessions was provided to 160 users. Germination rates were determined for 10,581 seed lots, and 15,034 or 83% of the seed propagated accessions are saved at the Svalbard Global Seed Vault. 2,072 potato accessions are cryopreserved at Gatersleben (cooperation with CSB Group).


Figure 1: GBS-based principal component analysis of (left panel) accessions of the cultivated Medicago species M. sativa and M. x varia plus their supposed progenitor species M. falcata; (right panel) the entire IPK Medicago germplasm collection (sections according to Small, 2011)

1,467 accessions were regenerated. At Malchow, C&E data were collected for 1,249 entries. Potato accessions were evaluated for *Globodera pallida* (22 accessions/110 genotypes), potato wart resistance (134 accessions), and tuber dormancy (188 accessions).

Embedding in IPK Research Themes

Focusing on potatoes, oil, and fodder crops, TEN research fits perfectly into IPK Research Theme 1, "Valorisation of Plant Genetic Resources" and broadens knowledge on the accessions studied. To add to the overall goal of a biodigital Resource Centre, TEN endeavours to phenotype and genotype its accessions as comprehensively as possible by constantly enhancing the information available on their germplasm and contributing C&E data to GBIS and EURISCO.

Outlook

For an enhanced PGR valorisation, we will further phenotype our entries for nutrient efficiency and drought tolerance – traits of increased future relevance. A comprehensive pheno- and genotypic screen of all clonal material will pay special attention to potatoes. *In vitro* and seed management will continuously improve with CAP treatments increasing early seedling vigour. Combined with our ISO 9001 quality management, this will ensure that high-quality material being delivered to our users. Safeguarding sustainable conservation management, the TEN infrastructure was substantially modernised in 2023. This will underpin our efforts in high-quality PGR conservation and support any attempts towards intensified application oriented research.

More information: www.ipk-gatersleben.de/en/research/genebank/satellite-collections-north



Head: Dr. Frank R. Blattner

Selected Publications

Karami-Moalem, S. et al.: Transcriptome differential display of a drought-tolerant early flowering spineless mutant of safflower (Carthamus tinctorius) and identification of candidate genes. Crop Sci. 63 (2023) 2329-2346.

Raca, I. et al.: Disentangling Crocus series Verni and its polyploids. Biology 12 (2023) 303.

Böhnert, T. et al.: Plant migration under long-lasting hyperaridity – phylogenomics unravels recent biogeographic history in one of the oldest deserts on Earth. New Phytol. 234 (2022) 1863-1875.

García, N. et al.: Atacamallium minutiflorum (Amaryllidaceae, Allioideae), new genus and species from the coastal desert of northern Chile. Taxon 71 (2022) 552-562.

Seidl, A. et al.: Genotyping-by-sequencing reveals range expansion of Adonis vernalis (Ranunculaceae) from Southeastern Europe into the zonal Euro-Siberian steppe. Sci. Rep. 12 (2022) 19074.

RESEARCH GROUP **EXPERIMENTAL TAXONOMY** (ETX)

Mission

The research group focuses on the phylogenetic classification and evolution of crops and their wild relatives and is an important part of Research Theme 2, "Genome Diversity and Evolution", of the IPK research strategy. We use experimental studies to link molecular markers and phylogenetic data with ecological, cytogenetic and morphological traits and to analyse plant–environment interdependency on and below the species level in an evolutionary framework. The other important part of the group's work regards curatorial management of the taxonomic collections and arriving at suitable nomenclatural treatments of crops and their wild relatives.

Results

In *Hordeum*, we clarified the evolution of *Hordeum bulbosum*, the closest relative of *H. vulgare* (Figure 1). Based on collections of the diploid populations thriving in the Mediterranean together with Genebank materials for western Asian tetraploids, we conducted phylogeographic analyses and sequenced multiple di- and tetraploid cytotypes for haplotype-ordered reference-quality genomes. The species originated most probably in today's southernmost Italy/adjacent North Africa, spreading to the Adriatic Sea's eastern coast and through Sicily into the western Mediterranean. The tetraploid cytotype originated multiple times and/or was introgressed locally from diploids. This research was part of an IPK flagship project conducted with the research groups Domestication Genomics, Genomics of Genetic Resources and Chromosome Structure and Function.

Within the international pan-Hordeum project consortium, we contribute the materials for genome sequencing of all diploid and some important polyploid species and work on a comparative transcriptome atlas to infer transcriptional differences among the *Hordeum* species.

Within a DFG-funded project, we were able to uncover the evolution of saffron (*Crocus sativus*) as a segmental tripolyploid that originated within *C. cartwrightianus*, a crocus species from southern Greece and the Aegean Islands. Analyses of metabolites (together with the research group Applied Biochemistry) and transcriptomes showed that the wild populations in Attica are most similar to cultivated saffron regarding carotenoid content and gene expression. Surprisingly, saffron has no additional metabolites absent in the wild populations but contains fewer carotenoids occurring in higher amounts. We interpret the large number of accessory secondary compounds found in the wild progenitor populations as intermediate stages that in saffron were completely converted into the typical saffron carotenoids like, e.g., safranal and picrocrocin through higher and more specific metabolic enzyme activities.

Crocuses exhibit exceptionally diverse chromosome numbers and karyotypes, even within closely related species. For spring crocuses (series *Verni*) we are currently trying to reconstruct karyotype evolution by combining cytogenetics with genome size measurements and phylogenomic data. Initial results indicate fusions of chromosomes, resulting in a decrease in chromosome numbers over time and multiple rearrangements of chromosome arms within species. By genome sequencing, we want to infer specific traits of *Crocus* genomes that induce karyotype volatility and do crossing experiments to estimate the influence of karyotype differences on fertility (DFG funded).

The Eurasian steppe belt is the largest area on Earth with steppe vegetation. To understand the evolution of this vegetation unit in space and time, we analysed multiple key steppe species with groups in Osnabruck, Vienna, and Barnaul. We use population genomic analyses to infer migration routes, cold- vs. warm-period refugia, ages of the taxa and colonisation directions. Our results indicate that steppe vegetation was recruited from very diverse vegetation units that came in contact with the expanding steppe belt. Thus, typical Eurasian steppe species have closest relatives in the Mediterranean, Irano-Turania highlands, Balkans, or the mountains belonging to the Alpine orogenesis in Europe. Partly, these species go back to progenitors pre-adapted to the



ecological conditions of the steppe, while a smaller amount evolved in situ within the already established steppe habitats. Important refugial areas for steppe plants during Pleistocene glacial cycles were detected, particularly in the north of the Black Sea in the west and the Altai Mountains in the east (DFG funded).

The herbarium of the IPK currently holds a collection of about 450,000 specimens, with additional 109,000 samples in the seed and fruit collection and 56,000 in the spike collections. New specimens added to the collection consist mostly of reference materials of Genebank accessions and for individuals with published sequence data, but also the important type specimens for newly described *Allium* and *Crocus* taxa were included. Thus, the herbarium is integral for documenting biodiversity-related research within the IPK. Specimens of crops and wild plants of the IPK herbarium have been digitised and are accessible online via the "Virtual Herbaria" portal of the Vienna-based database system JACQ. The digitisation of herbarium vouchers is ongoing.

Embedding in IPK Research Themes

Our work is mostly connected to Research Theme 2, "Genome Diversity and Evolution." Here, we contribute to the IPK flagship project on the evolution of *Hordeum bulbosum*, the pan-Hordeum project, and the ERC project on the phylogenomics of the genus *Hordeum* and cooperate closely with the cytogenetics groups regarding karyotype evolution.

Outlook

We contribute with our experience in phylogeographic analysis in a DFG Collaborative Research Centre of the universities of Aachen, Bonn, Cologne and Heidelberg dealing with organismic evolution at the dry limit, up to now mostly conducted in the Atacama Desert (DFG-SFB 1211) and newly also extended to Namibia. We will expand our work on karyotype evolution to other groups of crocuses and genera within (initially) monocots which show highly dynamic karyotypes to understand the general genomic mechanisms involved in volatile karyotypes. **Figure 1:** Phylogeographic analysis of intraspecific relationships among extant diploid Hordeum bulbosum populations. The phylogenetic tree is plotted on a distribution map of the populations in the central and western Mediterranean Basin. Numbered nodes of the tree indicate subsequent splits of ancestral populations. This GBS-based analysis used barley (H. vulgare), the closest relative of H. bulbosum, as an outgroup



RESEARCH GROUP **DOMESTICATION GENOMICS** (DG)



Head: Dr. Martin Mascher

Selected Publications

Schulthess*, A.W., S.M. Kale*, F. Liu* et al.: Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. Nat. Genet. 54 (2022) 1544-1552.

Kale*, S.M., A.W. Schulthess* et al.: A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. Plant Biotechnol. J. 20 (2022) 1730-1742.

Guo, Y. et al.: Six-rowed wild-growing barleys are hybrids of diverse origins. Plant J. 111 (2022) 849-858.

Schreiber, M. et al.: Recombination landscape divergence between populations is marked by larger low-recombining regions in domesticated rye. Mol. Biol. Evol. 39 (2022) msac131.

Kubalová, I. et al.: Helical coiling of metaphase chromatids. Nucleic Acids Res. 51 (2023) 2641–2654.

* joint first authorship

Mission

The research group Domestication Genomics studies how domestication and adaptation have shaped genetic diversity in crops and their wild relatives. Our study objects are temperate cereals such as barley, wheat, rye, and oats. Our research goals are: (i) to clarify the relationship between crops and their progenitors and wild relatives; (ii) to trace the demographic trajectories of cereal crops as they moved from their Near Eastern centre of origin into Europe; (iii) to understand the molecular consequences of domestication on patterns of nucleotide diversity, gene expression and gene regulation. We apply methods of population genetics, genome informatics and gene expression analysis. Along the way, we develop (pan-)genomic infrastructures for cereal crops and their wild relatives (Figure 1).

Results

We have capitalised on our prior work in genebank genomics and pan-genomics of wheat and barley. This work was done closely with the research groups GGR, RGR, BR and BIT and national and international collaborators. Molecular passport data were generated by genotyping-by-sequencing for the entire winter wheat collection comprising 7651 accessions. A resistance gene atlas was compiled for a representative core set of 907 hundred accessions, including modern cultivars and old landraces. Insights gleaned from these data include (i) the high prevalence of resistance-conferring crop-wild introgressions in European wheat elite varieties, (ii) the definition of donor germplasm for pre-breeding based on genomic prediction, (iii) the mapping of a locus conferring resistance against yellow rust on wheat chromosome 6A.

The pangenome infrastructure of barley was expanded. It comprises genome sequence assemblies of 76 genotypes, 53 domesticated, and 23 wild barleys (*H. spontaneum*). Twenty of these assemblies were annotated with transcriptome data. This sequence resource helped us (i) to compare pangenome complexity in wild and cultivated forms and (ii) to study the evolution of structurally complex loci controlling disease resistance, inflorescence architecture, and malting quality.

We have advanced genebank genomics in wheat and barley. Our barley genome variation database has grown from the 22,000 samples genotyped in the BRIDGE project (2015-9) to 36,000 records. Among them are accessions of ICARDA, the national genebank of Japan and wild barleys of the B1K collection from Israel. In addition, several European genebanks contributed GBS data in the frame of the EU-funded AGENT project. Analogous efforts are carried out in wheat. These data allow us to find duplicated accessions and define "bridging" collections that underpin across-genebank genomic prediction.

We have constructed a pangenome of *Hordeum bulbosum*. This species is closest among ~33 *Hordeum* species to *H. vulgare*, including domesticated barley and its immediate wild progenitor *H. vulgare* subsp. *spontaneum*. We expanded our TRITEX sequence assembly pipeline to construct chromosome-scale haplotype-resolved sequence assemblies of heterozygous genomes with the help of accurate long-read sequencing and chromosome conformation capture sequencing (Hi-C) data. We used this newly acquired ability to assemble the genome sequences of four diploid and six tetraploid *H. bulbosum* clones, yielding a total of 32 haplotypes. Using these data, we investigated the relationships between diploid and tetraploid cytotypes. This research was supported by an IPK flagship project (2020-2022).

As with genome assembly, Hi-C data also plays an important role in modelling the higher-order structure of mitotic barley chromosomes as a helical coil. Work in this research area was done with the CSF group at IPK and collaborators from the Institute of Experimental Botany in Olomouc, Czech Republic. The biophysical framework developed in that effort has been expanded to holocen-



tric species studied by the CSF group. Amanda Souza Camara, the biophysicist who worked on the German-Czech project MITOCHROM, has now acquired DFG funds independently to support her temporary PI position (own position, 2022-2025).

Embedding in IPK Research Themes

The research group contributes mainly to Research Themes 1, "Valorisation of Plant Genetic Resources", and 2 ", Genome Diversity and Evolution", of IPK's Research Strategy.

Outlook

We will continue to study the population genomics of wild and domesticated barley and wheat using sequence assemblies and resequencing data. A PhD student is currently analysing the historical relationships between barley populations and the strengths of bottlenecks as barley moved out of the Fertile Crescent. As part of this endeavour, we established the hybrid origin of feral six-rowed barleys. A DFG Near-East cooperation project with Thorsten Schnurbusch and Zvi Peleg (Hebrew University of Jerusalem) further supports research into barley crop-wild hybrids.

In addition to wheat, barley and their direct wild progenitors, we also study the genomes of more distant wild relatives and other cereal crops such as oat and rye. Research into barley wild relatives is supported by an ERC Starting Grant. We have launched the Pan-Hordeum consortium to construct a genus-wide pangenome of the genus *Hordeum*. To do so, we will assemble, annotate and analyse the genome sequences of all diploid and selected tetraploid species in the genus. As of October 2023, we have assembled 25 *Hordeum* genome sequences. Gene annotation using transcriptome data is underway.

Martin Mascher is the coordinator of PanOat, a pan-genome project of oat (*Avena sativa*). PanOat's goals are (i) to study genome evolution in this genus comprising diploid, tetraploid and hexaploid taxa, and (ii) to provide a genomic research infrastructure of oat on a par with barley. As of October 2023, 32 *Avena* genomes have been assembled and annotated. Moreover, resequencing data, gene expression, and epigenetic data are being analysed. In the future, we want to assemble the genomes of all ~30 *Avena* species to underpin genus-wide pan-genomics in the genus analogous to what is done in *Hordeum*.

Figure 1: How to set up a

pangenome project. (a) A representative core set is selected for the crop and its wild progenitor. Secondary and tertiary gene pool accessions are added to build the pangenome for higher taxonomic units. (b) Reference-quality genomes (represented in coloured hexagons) are generated for a small set of accessions and aligned to each other to catalogue the full complete of sequence variation in a species. (c) The detected variants are genotyped in a wider germplasm panel using short-read sequencing. (d) Combining assemblies and resequencing data underpins genetic analyses such as GWAS and population genetic inquiries into pan-genome complexity. Functional gene expression and epigenomics data will supplement pangenomes to assist hypothesis generation. All information is provided to the research community in a user-friendly web interface. Image source: Schreiber et al. 2021 (https://doi.org/10.1093/ dnares/dsaa030).

More information: www.ipk-gatersleben.de/en/research/genebank/domestication-genomics

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Quantitative Genetics (QD) Prof. Dr. Jochen C. Reif

Bioinformatics and Information Technology (BIT) **Dr. Uwe Scholz**

Chromosome Structure and Function (CSF) **Prof. Dr. Andreas Houben**

Kinetochore Biology (KB) **Dr. Inna Lermontova**

Biotrophy and Immunity (BIM) **Dr. Dimitar Douchkov**

Research Group Plant Architecture (PBP) **Prof. Dr. Thorsten Schnurbusch**

Senior Guest Group (Emeritus Group): Karyotype Evolution (KTE) **Prof. Dr. Ingo Schubert**

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Department Breeding Research



Head: Prof. Dr. Jochen Reif

Breeding progress through the redistribution and fixation of genetic variation is based on the organisation, regulation and distribution of genetic information at the chromosomal level. The Department of Breeding Research investigates the regulation and evolution of cell division processes, and chromosomal regions are analysed. The knowledge gained in this way is used to develop efficient breeding tools, focusing on designing efficient haploid inducer lines.

In recent years, omics-based techniques have significantly increased the quantity and quality of research data. In the Department of Breeding Research, innovative approaches are investigated for storing and analysing these data to make it fully usable for pre-breeding and breeding. In addition, methods are developed for predicting performance and studying the genetic architecture of agriculturally relevant traits. The developed statistical toolbox is applied to dissect complex traits. Underlying candidate genes for seed or grain size, yield and resistance are identified, validated and subsequently characterised. The overarching aim of this work is to increase the efficiency of pre-breeding and breeding.

Research activities within the Breeding Research Department take place in the Quantitative Genetics (QG), Bioinformatics and Information Technology (BIT), Chromosome Structure and Function (CSF), Kinetochore Biology (KB), Biotrophy and Immunity (BIM) and Plant Architecture (PBP) research groups. The following scientific achievements are considered as highlights in 2022/2023:

Chromosome Biology

High-temperature increases centromeremediated genome elimination frequency and enhances haploid induction in *Arabidopsis*

Plant breeding can be accelerated by applying haploid induction technology, followed by whole-genome duplication, which enables the development of lines with complete homozygosity in a single step. In the traditional breeding method, seven to nine generations of inbreeding are required to achieve the desired level of homozygosity.

In a collaboration between the research groups Kinetochore Biology, Chromosome Structure and Function, Meiosis, and Domestication Genomics, an efficient haploid induction technology based on manipulating the kinetochore proteins was reported. (Ahmadli et al., 2023)

It was demonstrated that the mutant of the CENH3 assembly factor, Kinetochore Null2 (KNL2), induced haploids when pollinated by the wild-type. We discovered that short-term temperature stress of the knl2 mutant increased the efficiency of haploid induction 10-fold (Figure 1). Furthermore, a cenh3-4 mutant functioned as a haploid inducer in response to short-term heat stress, even though it did not induce haploids under standard conditions. We also demonstrated that a point mutation in the CENPC-k motif of KNL2 is sufficient to generate haploid-inducing lines, suggesting that haploid-inducing lines in crops can be identified in a naturally occurring or genetic induced mutant population, avoiding the generic modification (GM) approach at any stage. Thus, we identified KNL2 as a new target gene for generating haploid-inducer lines and showed that exposure of centromeric protein mutants to high temperatures strongly increase their haploid induction efficiency. The knowledge gained will be applied to generate haploids in various crop species.

Genome Analyses

The study by Huang et al. (2023) unveils a previously unrecognized mechanism whereby the circadian clock in the vasculature of the barley inflorescence controls plastid differentiation and nutrient signal-



Figure 1: A model of haploid induction by uniparental chromosome elimination in crosses of the knl2 mutant with the wild-type under standard and heat-stress conditions. (A) The phenotype of the haploid gl-1 plant and a histogram of its ploidy analysis by flow cytometry (FC) (1) in comparison with the diploid knl2xgl1-1 hybrid (2). (B) Under standard growth conditions, the combination of small centromeres of the haploid inducer (knl2 mutant) with wild-type centromeres in the hybrid zygote leads to centromere competition, followed by complete or partial elimination of the genome and formation of CENH3 haploid (1%) and aneuploid (0.5%) progeny of the wild-type. (C) Short-term exposure of the haploid inducer (knl2) to heat stress can further reduce cenH3 level, cause significant mitotic and meiotic abnormalities and thus result in increased haploids up to 10% when the inducer is crossed with wild-type plants.

Department Breeding Research

Figure 2: Uncovering the yield breeding value of plant genetic resources (PGR) for pre-breeding through 'Elite×PGR' hybrids. (A) Disease susceptibility masks the PGR contribution to yield, but these limitations are overcome in 'Elite×PGR' (F1) hybrids. (B) Parenting effects of 36 elite cultivars on the yield per se performance (Mg/ha) across multiple field experiments of 198 PGR tested in 361 'Elite×PGR' hybrid backgrounds. (C) Yield per se performance across multiple field experiments for 15 modern check cultivars and 7 and 166 F3:4 advanced bridging.



ling, thereby sustaining heterotrophic floral meristem growth and reproductive success. Moreover, the findings demonstrate that the circadian clock is required for a timely switch from the floral primordia initiation state to the growth state. The study further shows that the number of initiated floral primordia is largely determined by flowering time genes, but the fates of the distal floral primordia are controlled by at least three independent quantitative trait loci. So, what are the molecular underpinnings of the barley yield potential? Authors identify for the first time a vascular-expressed CCT Motif Family gene (HvCMF4) required for spikelet primordia growth and successful pollination. They show that HvCMF4 specifically functions after the initiation of spikelet primordia through the wiring of the circadian clock from the inflorescence vasculature to control the greening of the neighbouring tissue and, thus, autotrophic energy production. This grain number determination mechanism has not been described before and appears unique to the Triticeae species, which features early inflorescence greening during spikelet initiation.

GiPS: Genomics-informed parent selection uncovers the breeding value of wheat genetic resources

The great efforts to preserve existing diversity in Genebanks are justified by the potential role of plant genetic resources (PGRs) in improving crops - a concept whose practical realisation has fallen short of expectations. The Genebank 2.0 & 3.0 project, in which seven IPK working groups have been involved, has identified new biodiversity for yield and resistance to yellow rust infection from old and non-native varieties to make them available for crop production. Over more than six years, the IPK Leibniz Institute's extensive collection of old wheat varieties was tested in the laboratory and field trials for their yield performance and resistance to yellow rust infection using innovative approaches. The yield potential was determined (Figure 2) by crossing old varieties with adapted elite varieties. Only then did the yield potential of the old varieties become visible, and it was possible to develop high-performance bridging lines for wheat breeding from promising old varieties by crossing them with current varieties.

Furthermore, the study's results enabled a major step towards an agriculture that uses less or no pesticides. Comprehensive sequencing of old and new varieties, in combination with valuable field data, made it possible to identify potential new gene variants for resistance to yellow rust infection. With the new genome regions discovered in some old exotic varieties that are not native to this country, the wheat resistance portfolio can be diversified.

Outlook

The department's research work and the knowledge gained are pursued with the aim of developing innovative approaches to unlocking the genetic diversity of crops in breeding. To this end, research in the three areas of chromosome biology, genome analysis, and breeding informatics will be continued.

In the field of chromosome biology, our goal is to better understand the mechanisms of chromosome segregation so that we can specifically influence them. This includes, for example, the induction of haploids to increase efficiency in the production of double-haploid lines. In addition, the internationally leading role in research on the segregation of B chromosomes is to be further expanded. Understanding the genetic architecture of important agronomic traits is key to implementing knowledge-based plant breeding. The department will intensify its research to understand important agronomic traits. In addition to the work on biotic stress, a new focus on understanding the interaction between plants within and across crops will be developed. The aim is to increase the resilience of crop production by boosting genetic diversity.

The potential of Big Data for plant breeding and genetics will be further explored in the area of breeding informatics. In this context, one focus of the work is on developing powerful prediction models from artificial intelligence that benefit from the availability of Big Data. In doing so, the department can draw on extensive data from public-private partnerships and extensive historical data from genetic resources. This enables the department to significantly contribute to the institute-wide research theme for valorising plant genetic resources.



RESEARCH GROUP **QUANTITATIVE GENETICS** (QG)



Head: Prof. Dr. Jochen C. Reif

Selected Publications

Berkner, M.O. et al.: Choosing the right tool: Leveraging of plant genetic resources in wheat (Triticum aestivum L.) benefits from selection of a suitable genomic prediction model. Theor. Appl. Genet. 135 (2022) 4391-4407.

Gogna, A. et al.: Gabi wheat a panel of European elite lines as central stock for wheat genetic research. Sci. Data 9 (2022) 538.

Hinterberger, V. et al.: High-throughput imaging of powdery mildew resistance of the winter wheat collection hosted at the German Federal ex situ Genebank for Agricultural and Horticultural Crops. GigaScience 12 (2023) giad007.

Rembe, M. et al.: The potential of genome-wide prediction to support parental selection, evaluated with data from a commercial barley breeding program. Plants 11 (2022) 2564.

Schulthess*, A.W., S.M. Kale*, F. Liu* et al.: Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. Nat. Genet. 54 (2022) 1544-1552. * joint first authorship

Mission

The Quantitative Genetics research group focuses on developing, implementing and evaluating "omics"-based breeding strategies to increase selection gain in (pre-)breeding programs. Our research goals are (1) to redesign the use of genetic resources for breeding, (2) to improve predictive breeding approaches, and (3) to expand the toolbox of statistical genomics. The model crop is wheat, but research activities include other plants such as barley, soybean, or Arabidopsis thaliana.

Results

New genetic variation from old and exotic varieties for environmentally friendly wheat cultivation. Genebanks worldwide make an important contribution to the conservation of biological diversity. In the Federal Ex situ Genebank at the IPK Leibniz Institute alone, more than 150,000 old varieties are preserved. In addition to negative traits, old and exotic varieties possess many valuable gene variants that have been lost in modern varieties but may be crucial for plant production in the future. But how can this hidden treasure of valuable biodiversity be tapped for agriculture? In the interdisciplinary Genebank 2.0 & 3.0 project, a genomics-informed pre-breeding strategy was implemented for wheat improvement that does not discriminate against non-adapted germplasm. Dense genetic profiles were collected and analysed for a trait-tailored IPK winter wheat collection sample and evaluated for grain yield and resistance to yellow rust in bespoke core sets. Breeders already profit from wild introgressions, but plant genetic resources still offer useful yet unused diversity. Potential donors of resistance sources not yet deployed in breeding were detected, while the pre-breeding contribution of plant genetic resources to yield was estimated through 'Elite x plant genetic resources' F1 crosses. Genomic prediction within and across genebanks identified the best parents for crosses with elite cultivars whose advanced progenies can outyield current wheat varieties in multiple field trials.

Data-driven breeding of resilient wheat varieties. The increasing complexity of genotype-environment interactions due to climate change challenges genomic predictions, especially in diverse and contrasting environments. Incorporating Big Data methods is essential to effectively predict the performance of genotypes in harsh environments and utilise the extensive and diverse data from breeding programs. Curated phenotypic and genomic Big Data were used to predict grain yield, as determined in public post-registrational trials using Genomic Best Linear Unbiased Predictions (GBLUP). The transition from using a single training dataset to Big Data significantly improved the accuracy of wheat grain yield prediction (Figure 1), highlighting the significant advantage of using Big Data even with traditional prediction methods. In addition, Big Data was used for a benchmarking study between the traditional GBLUP and dynamic Convolutional Neural Networks (CNN), a versatile Artificial Intelligence approach. CNNs were not superior to GBLUP approaches but benefited more from an increase in the training population, indicating their potential utility in aggregating more and more data.

Benchmarking analysis of fast algorithms for genome-wide association studies. Genomewide association studies (GWAS) are a key tool for identifying genetic variants associated with complex traits in diverse populations. In the last 1.5 decades, many fast GWAS algorithms based on a state-of-the-art linear mixed model have been published to cope with the rapidly growing data size. A comprehensive benchmarking analysis of commonly used GWAS algorithms focusing on additive genetic effects was performed, and the mathematical approaches implemented in the different algorithms were summarised in a unified way. The analysis of 3 extensive experimental data sets with 12 selected algorithms showed inconsistent results in identifying quantitative trait loci (QTL). The performance of these algorithms evaluated in ~10,000 simulated data sets with different population sizes, heritability and genetic architecture showed the impact of these parameters on the performance of QTL identification and the false positive rate of the different



algorithms. Based on these results, a general guideline for algorithm selection was developed for the research community. Furthermore, we developed a one-dimensional screen for epistatic hubs and tested it in large-scale wheat data. Our results indicate that some QTLs contribute to the expression of phenotypic variance mainly via interactions with many other loci (Figure 2), confirming findings in *Arabidopsis thaliana*.

Embedding in IPK Research Themes

The Quantitative Genetics research group activities contribute mainly to the Research Theme 1, "Strategies for the Valorisation of Plant Genetic Resources."

Outlook

The goal is to continue research on (pre-)breeding methodology and theoretical and applied quantitative genetics in wheat. The ongoing focus is on (1) breeding methodology in self-propagating species, (2) trait-adapted utilisation strategies of genetic wheat resources for breeding, and (3) expanding the toolbox of statistical genomics. A future focus will be on using artificial intelligence algorithms in conjunction with breeding-relevant Big Data. In addition, the research work is being expanded to include methods for pre-breeding peas.

Figure 2: (A) Manhattan plot of one-dimensional genome-wide association mapping scan for heterotic QTLs for grain yield in a large winter wheat population. (B) Digenetic epistatic interaction effect of detected heterotic QTLs with the genetic background.





Head: Dr. Uwe Scholz

Selected Publications

König, P. et al.: DivBrowse—interactive visualization and exploratory data analysis of variant call matrices. GigaScience 12 (2023) giand025.

Arend, D. et al.: From data to knowledge – big data needs stewardship, a plant phenomics perspective. Plant J. 111 (2022) 335-347.

Beier, S. et al.: Recommendations for the formatting of Variant Call Format (VCF) files to make plant genotyping data FAIR [version 2; peer review: 2 approved]. F1000Research 11 (2022) 231.

Röckel*, F., T. Schreiber*, D. Schüler* et al.: PhenoApp: A mobile tool for plant phenotyping to record field and greenhouse observations [version 2; peer review: 2 approved]. F1000Research 11 (2022) 12.

Schulthess*, A.W., S.M. Kale*, F. Liu* et al.: Genomics-informed prebreeding unlocks the diversity in genebanks for wheat improvement. Nat. Genet. 54 (2022) 1544-1552.

* joint first authorship

RESEARCH GROUP **BIOINFORMATICS AND INFORMATION TECHNOLOGY** (BIT)

Mission

The Bioinformatics and Information Technology research group addresses data management and serves different phases of the data life cycle. Within the National Research Data Infrastructure (NFDI), the group is active and leading in establishing the FAIRagro and NFDI4Biodiversity consortia. As part of the German Network for Bioinformatics Infrastructure (de.NBI), BIT coordinates the plant bioinformatics unit and contributes to German ELIXIR activities by offering services and training activities for plant scientists. Furthermore, the group takes on the important responsibility of supporting the operation of all central IT services. Since 2011, the group has been leading the implementation of an IPK laboratory information management system (LIMS).

Results

Together with international partners from the ELIXIR plant community, guidelines were developed to describe genotypes, sequences and genotyping data according to FAIR criteria in general and then deposited in a defined order in public repositories (see https://faircookbook.elixir-europe.org/content/recipes/reusability/miappe.html). One special data domain in this field is variation data or so-called genomic diversity data. The commonly used file format is Variant Call Format (VCF). We published recommendations for the formatting of metadata in such VCF files. The flexibility of this format specification can be used as a generic interchange format across domains. These works are essential for documenting various downstream analyses of the plant genetic resources (PGR) stored in the IPK Genebank and for recording key performance indicators of using the PGRs in the future.

Additionally, we developed and published the reusable web-based software DivBrowse (Figure 1) for interactive visualisation and exploratory analysis of genomic diversity data stored in VCF files (see https://faircookbook.elixir-europe.org/content/recipes/reusability/miappe.html). It offers also gene annotation data and features like interactive calculation of variant frequencies and principal component analysis.

Furthermore, the data publication infrastructure Plant Genomics & Phenomics Research Data Repository (e!DAL-PGP) has developed successfully and is actively used (end of October 2023: 294 DOIs, accesses from more than 290,000 unique IP addresses with a total download volume of 2.4 Petabyte). e!DAL-PGP provides FAIR access to datasets used in several research articles. A detailed overview of usage can be found at this website: https://doi.ipk-gatersleben.de/report.

To enable the exploration and quantification of the use and provision of nucleotide sequence data as one kind of Digital Sequence Information (DSI) in the scientific literature, we developed together with our collaborators the WILDSI portal (https://wildsi.ipk-gatersleben.de). The underlying data set results from an automatic pipeline that extracts and links sequence records from the European Nucleotide Archive (EMBL-ENA) to citations in open-access publications aggregated in Europe PubMed Central repository.

Together with collaboration partners, we provided access to datasets of the new version of the barley pan-genome. This includes genome assemblies in pseudomolecule quality and the associated gene models, including nucleotide and protein sequences of more than 70 different barley genotypes. All data sets are downloadable in the Shared Data section of the IPK Galaxy Web instance (see "Shared Data" on https://galaxy-web.ipk-gatersleben.de).

Furthermore, the BIT group is also leading a pilot project called "BreedFides" to develop a comprehensive and sustainable concept for a data trustee-supported infrastructure (https://breedfides.de/ language/en/). This project is also in tight cooperation with industry partners and is based on a use case to open the data space of various trials and value checks for wheat breeding data. In the future, this will allow a trustful exchange between breeding companies and scientific partners and will be adaptable to the wider agronomy domain. This will open previously closed data spaces and help get new insights to improve breeding research.



Finally, data management processes were further developed in various projects such as AVATARS, AGENT, Genbank3.0 and SHAPE-P3.

Embedding in IPK Research Themes

The group contributes to the IPK Research Themes 1 and 2, "Valorisation of Plant Genetic Resources" and "Genomic Diversity and Evolution". BIT is also involved in the other three Research Themes through cooperation with many IPK groups. With its experiences in FAIR-compliant research data management, the group has been able to contribute to collaborative projects and substantially contribute to the IPK's participation in the establishment of the National Research Data Infrastructure NFDI.

Outlook

Considering the FAIR criteria, the goal is to advance the development of the Federal *Ex situ* Genebank at the IPK into a biodigital resource centre. Specifically, the following points are to be worked on:

- development of an integrated material management
- supporting the transformation of data into community-agreed standards (e.g. phenotyping data as MIAPPE-compliant ISA-Tab)
- semi-automated registration of genotypes in the EMBL-BioSamples database with subsequent automated submission of sequencing results to EMBL-ENA (European Nucleotide Archive) and of variation data to EMBL-EVA (European Variation Archive), taking into account appropriate authorisations as well as data protection settings

Active participation in networks like the National Research Data Infrastructure (NFDI), the German Network for Bioinformatics Infrastructure (de.NBI), and the European Infrastructure for Biological Information in the Life Sciences (ELIXIR) will be further expanded.

Figure 1: Overviews of the DivBrowse tool: A) Main graphical user interface with the visualisation of allele calls on sample and variant level B) Example of the windowed summary statistics along the genome for each single barley chromosome C) Interactive scatterplot for visualisation of the result of a principal component analysis D) Hierarchically-clustered heatmap of the euclidean distances between samples based on alleles of a specific gene.

More information: www.ipk-gatersleben.de/en/research/breeding-research/bioinformatics-and-information-technology



RESEARCH GROUP CHROMOSOME STRUCTURE AND FUNCTION (CSF)



Head: Prof. Dr. Andreas Houben

Selected Publications

Boudichevskaia, A. et al.: Rye B chromosomes differently influence the expression of A chromosome-encoded genes depending on the host species. Chromosome Res. 30 (2022) 335-349.

Demidov, D. et al.: Haploid induction by nanobody targeted ubiquitin-proteasome-based degradation of EYFP-tagged CENH3 in Arabidopsis thaliana. J. Exp. Bot. 73 (2022) 7243–7254.

Ebrahimzadegan, R. et al.: Meiotic segregation and post-meiotic drive of the Festuca pratensis B chromosome. Chromosome Res. 31 (2023) 26.

Kubalová, I. et al.: Helical coiling of metaphase chromatids. Nucleic Acids Res. 51 (2023) 2641–2654.

Kuo, Y.-T. et al.: Holocentromeres can consist of merely a few megabase-sized satellite arrays. Nat. Commun. 14 (2023) 3502.

Mission

The research group deciphers the regulation, organisation, segregation and evolution of mitotic, meiotic and interphase chromosomes to unravel basic mechanisms of chromosome biology in model, wild and crop species. The knowledge gained will be used to accelerate and optimise crop plant breeding processes and develop novel chromosome analysis and manipulation tools. Different DNA-, RNA- and protein-based methods combined with bioinformatics and optical and transgenic tools are employed to reach the goals.

Results

Centromere diversity: holo-centromeres can consist of only a few megabase-sized satellite arrays

The centromere is the chromosome region where the microtubules attach during cell division. In contrast to monocentric chromosomes with one distinct centromere, holocentric species usually distribute hundreds of centromere units along the entire chromatid. We assembled the chromosome-scale reference genome and analysed the holo-centromere and (epi)genome organisation of the lilioid *Chionographis japonica* / Melanthiaceae (Figure 1). Remarkably, each of its holocentric chromatids consists of only 7 to 11 evenly-spaced megabase-sized CENH3-positive, minisatellite-containing units. Using polymer simulations, we modelled the formation of prometaphase line-like holo-centromeres from interphase centromere clusters. Our findings broaden the knowledge about centromere diversity, showing that holocentricity is not restricted to species with numerous and small centromere units (Kuo et al. 2023).

Targeted CENH3 protein degradation results in haploids

The generation of haploid plants accelerates the crop breeding process. We tested whether targeted *in vivo* degradation of the CENH3 protein can be harnessed to generate haploids in *Arabidopsis thaliana*. We showed that a recombinant anti-GFP nanobody fused to either heterologous F-box or SPOP/BTB ligase proteins can recognise maternally derived EYFP-tagged CENH3 *in planta* and make it accessible for the ubiquitin-proteasome pathway. Outcrossing of the gCENH3-EYFP complemented cenh3.1 mother with plants expressing the GFP-nanobody-targeted E3-ubiquitin ligase resulted in haploids, whereas in reciprocal crosses, no haploid induction occurred. Thus, the uniparental degradation of EYFP-fused gCENH3 during early embryogenesis decreases its level at centromeres and subsequently weakens the centromeres. Consequently, maternal chromosomes undergo elimination, resulting in haploids (Demidov et al. 2022).

Meiotic segregation and post-meiotic drive of the *Festuca pratensis* B chromosome

In many species, B chromosome (Bs) transmission does not follow the Mendelian laws of equal segregation and independent assortment. This deviation results in B transmission rates higher than 0.5, a process known as 'chromosome drive'. We studied the behaviour of the B chromosome of *Festuca pratensis* during all meiotic and mitotic stages of microsporogenesis. Mostly, the Bs of *F. pratensis* segregate during meiosis like standard A chromosomes. The drive of the B happens during the first pollen mitosis, by which the B preferentially migrates to the generative nucleus. During second pollen mitosis, the B divides equally between the two sperms. Despite some differences in the frequency of drive between individuals with different numbers of Bs, at least 82% drive was observed. Flow cytometry-based quantification of B-containing sperm nuclei supports the FISH data (Ebrahimzadegan et al. 2023).



Embedding in IPK Research Themes

The projects of the research group CSF are part of the IPK Research Themes 2 and 3, "Genome Diversity and Evolution" and "Mechanisms of Plant Reproduction".

Outlook

- Novel types of male and female haploid inducers will be generated to enable the CENH3-degradation-based approach to generate haploid wild-type plants at high frequency.
- Candidate genes regulating the rye B chromosome drive and the tissue-specific elimination of *Ae. speltodies* Bs will be identified and evaluated.
- The mono-to-holo-centromere transition will be investigated by characterising the centromere types of closely related species within the Melantiaceae family.
- Novel applications of the CRISPR-FISH method will be developed.
- The consequences of CRISPR/Cas9-engineered chromosome translocations on the epigenome and transcriptome will be determined.
- After deciphering that the chromatids of barley metaphase chromosomes are formed by helically coilded chromatid threads called chromonemata (Kubalova et al. 2023), we plan now to analyse the lower chromatin organisation within the chromonema by applying oligo-FISH and super-resolution microscopy.

Figure 1: Megabase-sized satellite arrays form holo-centromeres. (a) Chromosome-level

scaffolds of C. japonica. The centromere repeats Chio1 (red) mapping shows ~ 100 centromere units in the genome assembly. (b) Distribution of genes, high-copy centromeric Chio satellite repeats, and transposable elements (TEs), as well as the enrichment of CENH3. euchromatin-mark H3K4me2, and heterochromatin-mark H3K9me2 ChIPsea along chromosome 2. (c) Condensed metaphase chromosomes show line-like CENH3 signals on the poleward surface of each chromatid, at interphase CENH3 signals cluster in chromocenters. CENH3 distribution along a single chromosome and nuclei are depicted as schemata. Scale bars: 5 µm.

More information: www.ipk-gatersleben.de/en/research/breeding-research/chromosome-structure-and-function



RESEARCH GROUP **KINETOCHORE BIOLOGY** (KB)



Head: Dr. Inna Lermontova

Selected Publications

Ahmadli*, U., M. Kalidass* et al.: High temperature increases centromere-mediated genome elimination frequency and enhances haploid induction in Arabidopsis. Plant Commun. 4 (2023) 100507.

Demidov, D. et al.: Haploid induction by nanobody targeted ubiquitin-proteasome-based degradation of EYFP-tagged CENH3 in Arabidopsis thaliana. J. Exp. Bot. 73 (2022) 7243–7254.

Moebes, M. et al.: Optimization of quantitative reverse transcription PCR method for analysis of weakly expressed genes in crops based on rapeseed. Front. Plant Sci. 13 (2022) 954976.

Schubert, V., Weißleder, A. & I. Lermontova: Simultaneous EYFP-CENH3/H2B-DsRed expression is impaired differentially in meristematic and differentiated nuclei of Arabidopsis double transformants. Cytogenet. Genome Res. 163 (2023) 74–80.

Zuo*, S., R. Yadala* et al.: Recurrent plant-specific duplications of KNL2 and its conserved function as a kinetochore assembly factor. Mol. Biol. Evol. 39 (2022) msac123.

* joint first authorship

Mission

The research group Kinetochore Biology is interested in studying the organisation, establishment, and maintenance of the kinetochore complex in plants.

Our primary research goals are:

- 1. To unveil the molecular mechanisms governing kinetochore assembly and function.
- 2. To develop an efficient haploid induction approach based on manipulating kinetochore proteins.
- 3. To investigate the impact of environmental factors on the kinetochore assembly and haploid induction efficiency.

Results

A fundamental aspect of the cell cycle is the equal distribution of replicated chromosomes between two daughter cells. An essential role in the cell cycle plays the kinetochore, a complex protein structure that assembles at specialised chromosomal domains called centromeres. The kinetochore controls the attachment of centromeric chromatin to the spindle apparatus and the correct segregation of chromosomes during cell division.

The centromere-specific histone H3-variant CENH3 is essential for kinetochore formation and centromere function. Its deposition at centromeres depends on CENH3 assembly factors, chaperones, transcription of the centromeric repeats, and the epigenetic status of centromeric chromatin.

The *KNL2* gene in plants underwent three independent ancient duplications. Please use this text as a subheading. To gain insight into the origin and diversification of the *KNL2* gene, we reconstructed its evolutionary history in the plant kingdom (Zuo *et al.*, 2022). Our results indicate that the *KNL2* gene in plants underwent three independent ancient duplications in ferns, grasses, and eudicots. Additionally, we demonstrated that *KNL2* genes could be divided into two clades: *aKNL2* and *βKNL2* in eudicots and *γKNL2* and *δKNL2* in grasses, respectively. The confirmed centromeric localisation of *β*KNL2 and mutant analysis indicates that it is involved in the loading of new CENH3 (Figure 1A, B) and cell cycle (Figure 1D, F) regulation (Figure 1C). The heterozygous *βknl2* plants had a high rate of seed abortion (Figure 1D), and the germinated homozygous mutants did not develop beyond the seedling stage (Figure 1E).

High temperature increases the haploid induction frequency in Arabidopsis

Double haploid production is the most efficient way to create true breeding lines in a single generation. We reported that a mutant of $\alpha KNL2$ can be used as a haploid inducer when pollinated by the wild-type (Ahmadli *et al.*, 2023). We discovered that short-term temperature stress of the $\alpha knl2$ mutant increased the efficiency of haploid induction by tenfold. We also demonstrated that a single point mutation in the CENPC-k motif of $\alpha KNL2$ is sufficient to generate haploid-inducing lines, implying that haploid-inducing lines in crops can be identified in naturally occurring or chemically induced mutant populations, avoiding the genetic modification (GM) approach.

In collaboration with the CSF group, we showed that targeted in-vivo degradation of the CENH3 protein can be used to produce haploids with a frequency of up to 7.6% in *Arabidopsis thaliana* (Demidov *et al.*, 2022).

Generation of double haploids in rapeseed and radish

In a project supported by KWS and in collaboration with the CSF group, we focused on transferring KNL2- and CENH3-based haploid induction methods to the rapeseed. To understand the mechanism of haploid induction in rapeseed, we optimised several techniques, including ploidy



Figure 1: Identification and primary analysis of $\beta knl2$ mutants. (A) Schematic representation of the T-DNA insertion position in the genomic fragment and protein. (B) Super-resolution microscopy images showing nuclei of WT (Col-0) and *βknl2* null mutants immune-stained with anti-CENH3 antibodies in meristematic cells (top) and differentiated cells (bottom). (C) Representative ploidy analysis histogram of WT seedlings as control (left panel) and abnormal seedlings of *βknl2* null mutants (right panel). (D) Representative siliques with red arrowheads showing abnormal whitish glossy-seed phenotype from heterozygous β knl2-1 and β knl2-2 plants. (E) Two weeks old in vitro germinated seedlings from Col-0, *βknl2-1*, and $\beta knl2-2$ heterozygous (+/-) and homozygous mutants (-/-). (F) Nuclear magnetic resonance (NMR) spectrometry of siliques of heterozygous *βknl2-1* and βknl2-2 mutants compared to WT (Col-0) and a ßknl2-2 mutant complemented with a BKNL2 genomic fragment (collaboration with AAN group).

measurement in microtiter plates, pollen immunostaining, and transcriptional RT-qPCR analysis of low-expressed epigenetic genes exemplified by KNL2 (Moebes *et al.*, 2022). The project, supported by Enza Zaaden, aims to transfer the *KNL2*-based haploid induction method to radish.

Embedding in IPK Research Themes

The projects of the Kinetochore Biology group fall under the IPK Research Themes 2, "Genome Diversity and Evolution" and 3, "Mechanisms of Plant Reproduction".

Outlook

The Kinetochore Biology group intends to continue focusing on the detailed functional characterisation of known kinetochore proteins and the identification and functional characterisation of new components of the kinetochore complex in *Arabidopsis* and crop plants. Furthermore, we will explore the molecular basis of centromeric transcription and post-translational modifications of kinetochore proteins. The knowledge gained will allow us to better understand the mechanism of kinetochore assembly and function in mitosis and meiosis and provide us with the ability to influence these processes to obtain efficient haploid inducers in different crop species. In addition to rapeseed and radish, we plan to apply the KNL2-based haploid induction approach to lupin. We will also study the effects of various abiotic stress conditions on kinetochore assembly, chromatin structure, and haploid induction efficiency. Furthermore, our goal is to establish new collaborations with international and national partners.

More information: www.ipk-gatersleben.de/en/research/breeding-research/kinetochore-biology





Interim Head: Dr. Dimitar Douchkov

Selected Publications

Bapela, T. et al.: Breeding wheat for powdery mildew resistance: genetic resources and methodologies – a review. Agronomy 13 (2023) 1173.

Dracatos, P.M., S. Lück & D.K. Douchkov: Diversifying resistance mechanisms in cereal crops using microphenomics. Plant Phenomics 5 (2023) 0023.

Hinterberger, V. et al.: High-throughput imaging of powdery mildew resistance of the winter wheat collection hosted at the German Federal ex situ Genebank for Agricultural and Horticultural Crops. GigaScience 12 (2023) giad007.

Kloppe, T. et al.: Two pathogen loci determine Blumeria graminis f. sp. tritici virulence to wheat resistance gene Pm1a. New Phytol. 238 (2023) 1546-1561.

Hinterberger, V. et al.: Mining for new sources of resistance to powdery mildew in genetic resources of winter wheat. Front. Plant Sci. 13 (2022) 836723.

RESEARCH GROUP **BIOTROPHY AND IMMUNITY** (BIM)

Mission

At the intersection of plant pathology and genetics, our group is dedicated to unravelling the complexities of plant immune responses, particularly focusing on basal and broad-spectrum disease resistance. Leveraging the established model pathosystems of wheat and barley powdery mildews, we research the genetic context of plant-pathogen interactions across diverse genetic backgrounds. Central to our research is the innovative Microphenomics technology pioneered by our team at IPK-Leibniz Institute. We aim to decode the genetic and genomic elements of the plant resistome, encompassing resistance genes, signalling cascades, regulatory mechanisms, antimicrobial compound production, structural defences, and other integral aspects of plant immunity. Our goal is to harness this knowledge to develop sustainable plant protection strategies.

Results

Discovery of novel Mlo-like gene and putative pathogen-specificity of the different Mlo gene family clades

In a recent large-scale wheat stripe rust resistance phenotyping study conducted under the Gene-Bank 2.0 & 3.0 projects framework, we identified a strongly associated resistance locus on chromosome 2B. This locus, subsequently identified as a novel Mlo-like gene, was characterised by a single gene annotation. Detailed sequencing of various alleles and homeo-alleles of this gene revealed a unique 7-amino acid deletion near the C-terminus of the encoded protein. Notably, genotypes harbouring this deletion exhibited heightened resistance to stripe rust. Further investigations were extended to several TILLING lines of Cadenza and Kronos with mutations in the Mlo8 gene. Many of these lines demonstrated enhanced resistance, leading us to postulate the discovery of the first stripe rust-associated Mlo gene. While confirmatory studies are ongoing, this finding represents a crucial step in understanding rust resistance mechanisms.

Concurrently, collaborators in the SHAPE project reported the identification of a third resistance-related Mlo-like gene in barley. This discovery is particularly noteworthy given that, until recently, Mlo1 was the sole Mlo gene associated with disease resistance, specifically known for its robust and long-lasting resistance to powdery mildew. However, the new findings expand this paradigm, indicating that different Mlo-like genes can confer resistance to other pathogens, specifically stripe rust and leaf rust. These genes are phylogenetically distinct, belonging to separate clades within the Mlo-like gene family. This emerging evidence prompts a critical inquiry into the pathogen specificity of Mlo-like genes. If these observations are validated, they could significantly advance our understanding of Mlo-like gene functions and their role in plant immunity. Such knowledge could fundamentally alter our approach to developing disease-resistant crop varieties.

A conceptual framework for breeding nonhost resistance

In our recent research, we focused on Nonhost Resistance (NHR), a phenomenon known as the most potent, broad-spectrum, and durable form of plant defence against a wide array of pathogens. NHR characterises an ideal defence mechanism, exhibiting a singular phenotype of complete resistance, which presents significant challenges for scientific study. The lack of phenotypic variation in NHR hinders genetic analysis and complicates traditional breeding approaches. However, recent advancements, including contributions from our laboratory, have revealed that NHR does indeed exhibit phenotypic variability, though at a microscopic level. This discovery, while fundamental, introduces new challenges, particularly the labour-intensive nature of microscopic examination of large numbers of plants, typical in screening processes. Our breakthrough came with the implementation of the high-throughput microphenomics system. Utilising this technology, we uncovered the hidden variability of NHR in different grass species. The application of microphenomics allowed us to employ standard genetic analysis techniques such as Genome-Wide Association Studies



(GWAS). Through this approach, we identified several loci associated with NHR in barley. Some of these loci encompassed genes previously known to be involved in NHR, while others were novel findings.

This advancement in understanding the subtle variations in NHR marks a significant step in plant pathogen resistance research. It enhances our comprehension of NHR's mechanisms and opens new avenues for breeding nonhost disease-resistant crops through genetic analysis.

Embedding in IPK Research Themes

The work of the research group Biotrophy and Immunity contributes mainly to Research Theme 5, "Mechanisms of Resistance and Stress Tolerance," and Research Theme 1 "Valorisation of Plant Genetic Resources".

Outlook

As we look to the future, our research is aimed at promising opportunities. The possibility of breeding for nonhost resistance (NHR) is now a concrete goal within our reach, thanks to the availability of sophisticated tools and methodologies. Our immediate and long-term objectives include:

Exploration of the secondary and tertiary gene pools: A key focus will be to explore and introduce NHR traits from the secondary and tertiary gene pools of wheat and barley. This approach holds the potential for uncovering novel resistance genes and mechanisms that could revolutionise crop breeding strategies.

Furthermore, leveraging advanced phenomics and genomics tools, we aim to deepen our understanding of the plant resistome. This involves the methodical study of the inherent genetic mechanisms that control plant resistance in different species.

Moreover, we aim to become a leader in high-throughput microphenomics. Our ultimate goal is establishing our lab as a leading center for high-throughput microphenomics, specifically focusing on fungal diseases. This specialised focus will enable us to make significant contributions to plant pathology.

In summary, our outlook is centred on harnessing cutting-edge technologies and innovative research strategies to push the boundaries of our understanding of plant resistance, ultimately contributing to sustainable and resilient agricultural practices.

Figure 1: Discovery of novel Mlolike gene (TaMlo8) and putative pathogen-specificity of the different Mlo gene family clades. The TaMlo8 gene is located in chromosome 2B of wheat, in a locus associated with stripe rust resistance (left figure). Recently, colleagues from the SHAPE project discovered a third Mlo-like gene associated with leaf rust resistance in barley. The genes are relatively distant, located in different clades of the Mlo-like gene family.

 $\textit{More information: } www.ipk-gatersleben.de/en/research/breeding-research/biotrophy-and-immunity } \\$



Head: Prof. Dr. Thorsten Schnurbusch

Selected Publications

Shanmugaraj, N. et al.: Multilayered regulation of developmentally programmed pre-anthesis tip degeneration of the barley inflorescence. Plant Cell 35 (2023) 3973–4001.

Huang, Y. et al.: A molecular framework for grain number determination in barley. Sci. Adv. 9 (2023) eadd0324.

Golan, G., R. Abbai & T. Schnurbusch: Exploring the tradeoff between individual fitness and community performance of wheat crops using simulated canopy shade. Plant Cell Environ. 46 (2023) 3144-3157.

Koppolu, R., S. Chen & T. Schnurbusch: Evolution of inflorescence branch modifications in cereal crops. Curr. Opin. Plant Biol. 65 (2022) 102168.

Kamal, R. et al.: Spikelet abortion in six-rowed barley is mainly influenced by final spikelet number with potential spikelet number acting as a suppressor trait. J. Exp. Bot. 73 (2022) 2005–2020.

RESEARCH GROUP **PLANT ARCHITECTURE** (PBP)

Mission

Our understanding of the molecular genetics of spike or spikelet development is very limited in small-grain cereals. Functional knowledge of genes that regulate key developmental traits such as inflorescence branching, spikelet initiation, or abortion is almost completely lacking in most cereal crops. We are utilising natural and induced spike variants from wheat and barley spikes to clarify the genetic makeup of genes underlying developmental phenotypes for reduced and increased grain number per spike.

Results

Towards a better understanding of the genetic and molecular determinants of spikelet survival in cereal crops

One promising avenue for improving the grain yield of cereal crops, including wheat (*Triticum spp.*) and barley (*Hordeum vulgare L.*), involves reducing spikelet mortality. Spikelets, the grainbearing units of cereal spike-type inflorescences, usually form in excess and subsequently degenerate during development; increased spikelet survival is linked to increased numbers of grains per spike. Therefore, reducing spikelet mortality is an intriguing approach to improve grain yield.

In cereal crops such as barley, pre-anthesis tip degeneration (PTD) starts with growth arrest of the inflorescence meristem dome, followed basipetally by the degeneration of the floral primordia and the central axis. Due to its quantitative nature and environmental sensitivity, inflorescence PTD constitutes a complex, multi-layered trait affecting final grain number. Our group's previous results indicated that spikelet survival in barley is highly genetically controlled and predictable under standardised growth conditions, consistent with a developmentally programmed mechanism. Within the **ERC-funded LUSH SPIKE** project, we elucidated the molecular underpinnings of spike PTD; we combined metabolomic, transcriptomic, and genetic approaches to show that barley spike PTD is accompanied by sugar depletion, amino acid degradation, and abscisic acid responses involving transcriptional regulators of senescence, defence, and light signalling (Figure 1A). Based on transcriptome analyses, we identified barley *GRASSY TILLERS1* (HvGT1), encoding an HD-ZIP transcription factor, as an important modulator of spike PTD (Figure 1B).

Moreover, we found that floral primordia initiations in barley are molecularly decoupled from their maturation into grains. While initiation is dominated by flowering-time genes, floral growth is specified by light signalling, chloroplast, and vascular developmental programs orchestrated by barley CCT MOTIF FAMILY 4 (HvCMF4), which is expressed in the inflorescence vasculature. Consequently, mutations in HvCMF4 increase primordia death and pollination failure, mainly through reducing rachis greening and limiting plastidial energy supply to developing heterotrophic floral tissues. Based on our findings, we thus propose a molecular framework that leads to barley spike PTD, the manipulation of which may increase yield potential in barley and other related cereals (Figure1).

Exploring the tradelight for the second seco

The genetic heritage of wheat (*Triticum spp.*) crops has been shaped by millions of years of pre-domestication natural selection, often driven by individual competition. However, genetic improvements in yield potential are thought to involve selection towards reduced competitiveness, thus enhancing adaptation to the crop environment. We investigated potential trade-offs between individual plant fitness and community performance using a population of introgression lines carrying chromosome segments of wild emmer (non-domesticated) in the background of an elite durum cultivar. We focused on light as a primary factor affecting plant–plant interactions and assessed morphological and biomass phenotypes of single plants grown in mixtures under sunlight and a simulated canopy shade and the relevance of these phenotypes for the mono-



culture community in the field. We found that responses to canopy shade resemble responses to high density and contribute to both the individual and the community. Stepwise regressions suggested grain number per spike and its persistence under shade are essential for productive communities, advocating their use as a breeding target during early generation selection. Overall, multiple phenotypes attained under shade could better explain community performance. Our novel, applicable, high-throughput set-up provides new prospects for studying and selecting single-plant phenotypes in a canopy-like environment. Thus, we will apply this new approach to discover loci, genes and alleles related to improved community performance, allometric growth and enhanced grain numbers using bi-parental mapping populations and chromosome introgression lines of wheat and possibly barley.

Embedding in IPK Research Themes

Work within the research group Plant Architecture relates predominantly to the Research Theme 4, "Growth & Metabolism".

Outlook

Our ongoing work, collaborations, and activities may provide sufficient opportunities for us to continue our seminal studies in spike and spikelet growth and development in wheat and barley. Future challenges will be to generate reporter or sensor lines (stable transformants) for sophisticated phenotypic, microscopic, and cellular analyses of developmental phenotypes. Besides, we will continue our path towards developing agroecological genetics approaches with the view of deeper insights into allometric growth responses and biomass allocation in a crop canopy context.

Figure 1: Proposed model of spike PTD in barley (From

Shanmuqarai et al. 2023). A) Apical spikelets in the barley inflorescence undergo death, involving processes related to senescence, ABA biosynthesis, and increased ROS, chlorophyll, and protein catabolism. B) HvGT1, identified as one of the putative modulators of spike PTD, acts as a growth repressor that negatively affects the development of apical spikelets. Its loss-of-function (orange "X" symbol) promotes apical growth with delayed degeneration and enhanced differentiation of apical spikelets, thereby increasing the final spikelet number. ABA, abscisic acid; ROS, reactive oxygen species, GT1, GRASSY TILLERS1; NAC, (NAM [no apical meristem], ATAF1/2, CUC [cup-shaped cotyledon]); IM, Inflorescence meristem.

More information: www.ipk-gatersleben.de/en/research/breeding-research/plant-architecture



SENIOR GUEST GROUP (EMERITUS GROUP): **KARYOTYPE EVOLUTION** (KTE)



Head: Prof. Dr. Ingo Schubert

Selected Publications

Stepanenko, A. et al.: The ribosomal DNA loci of the ancient monocot Pistia stratiotes L. (Araceae) contain different variants of the 35S and 5S ribosomal RNA gene units. Front. Plant Sci. 13 (2022) 819750.

Hoang*, P.T.N., J. Fuchs* et al.: Chromosome numbers and genome sizes of all 36 duckweed species (Lemnaceae). Plants 11 (2022) 2674.

Bog, M. et al.: Strategies for intraspecific genotyping of duckweed: comparison of five orthogonal methods applied to the giant duckweed Spirodela polyrhiza. Plants 11 (2022) 3033.

Jayakodi, M. et al.: The giant diploid faba genome unlocks variation in a global protein crop. Nature 615 (2023) 652-659.

Peterson, A. et al.: Cryopreservation of duckweed genetic diversity as model for long-term preservation of aquatic flowering plants. Plants 12 (2023) 3302.

* joint first authorship

Mission

Traditionally, we focus on the evolution of genomes and karyotypes of related plant groups with varying genome sizes and chromosome numbers. We study the reasons and consequences of genome size variability by testing for whole genome duplications, chromosome rearrangements, and potential interspecific hybridisation, e.g., among the five duckweed genera. We quantify the outcome of DNA double-strand break (DSB) repair at the sequence and chromosome level to elucidate its impact on evolutionary stability versus dynamics of small versus large genomes.

Results

Evolutionary cytogenomic studies on duckweed and related genomes: rDNA loci of the ancient monocot species *Pistia stratiotes* were determined, localised and sequence-characterised (Stepanenko et al. 2022). Genome size and chromosome number were determined or surveyed from the literature for one or more accessions of all 36 species of the five duckweed genera (Hoang et al., 2022). The surprising intraspecific variability of genome size and chromosome number has been studied by various approaches for species of the duckweed genus *Lemna* (Bog et al. 2022) and revealed several unsuspected interspecific hybrids and ploidy variants, confirmed by genomic *in situ* hybridisation with DNA of the presumed parental species (Figure 1). These data also explain the difficulty of determining species based on (overlapping) morphological traits. A collaborative manuscript (Ernst et al.) is submitted. Since May 2022, a Ukrainian refugee, Dr. Anton Stepanenko, has been integrated into the group and works on the molecular diversity of duckweed genomes, supported by a Leopoldina fellowship.

DSB repair modes and genome evolution: We contributed to interpreting the genome evolution of the large diploid Vicia faba genome (Murukarthick et al., 2023). We are still searching for a master's student to work on DSB repair mechanism(s) in hexaploid wheat (*versus* diploid barley) in collaboration with the groups of Dr. J. Kumlehn (Plant Reproductive Biology) and Prof. T. Schnurbusch (Plant Architecture).

Embedding in IPK Research Themes

The cytogenomic work of our project group fits well into IPK's Research Theme 2: "Genome Diversity and Evolution".

Outlook

Our expertise could contribute i) to further elucidation of genome and karyotype evolution within the emerging crop plant family of duckweeds, ii) to international collaboration on duckweed diversity, iii) to resolve pathways and consequences of erroneous DSB repair, particularly in polyploid plant genomes, and iv) to study genomic diversity of the large diploid genome of *Vicia faba* (13 Gbp/1C).



Figure 1: GISH with genomic DNA of Lemna minor (red) and Le. turionifera (green) confirmed that the clone 8627 represents a triploid hybrid (Le. x japonica) with 42 Le. minor and 21 Le. turionifera chromosomes; yellow dots mark individual chromosomes (images: PNT Hoang).

More information: www.ipk-gatersleben,de/en/breeding-research/senior-guest-group-karyotype-evolution-kte-emeritus-group



Department Molecular Genetics



Heterosis (HET) **Prof. Dr. Thomas Altmann**

Automated Plant Phenotyping (APP) **Dr. Kerstin Neumann**

Image Analysis (BA) **Dr. Evgeny Gladilin**

Metabolic Diversity (MD) **Dr. John D'Auria**

Seed Development (SE) **Dr. Jozefus H. M. Schippers**

Assimilate Allocation and NMR (AAN) **PD Dr. Ljudmilla Borisjuk**

Network Analysis and Modelling (NAM) **Dr. Jedrzej Jakub Szymanski**

Young Investigators Group "Integrated Mechanistic Models" (IMM) **Dr. Mary-Ann Blätke**



Department Molecular Genetics



Head: Dr. Thomas Altmann

Mission

Sustainable production of food and feed, as well as renewable raw materials and energy sources of adequate quantity and quality, present great challenges in a world facing continuous population growth and severe environmental changes. Therefore, the major aim of the Molecular Genetics (MOG) department is to gain detailed information on the molecular processes that determine plant performance. The investigations focus on the dynamics of vegetative growth and metabolism, as well as the development and filling of seeds. The major research goals are molecular-genetic identification and characterisation of determining factors, elucidating the affected molecular processes, and developing genetic solutions for crop improvement.

Research Status

The research program of the Molecular Genetics department aims to elucidate molecular processes that govern the expression of plant performance traits and use the acquired knowledge to devise and test genetic and epigenetic strategies for targeted improvement of the crop performance potential. The focus is on the investigation and modulation of plant performance manifested in biomass accumulation and seed production capacity. Following the philosophy that "nothing in (plant) biology makes sense, except in the light of space and time and condition", the main research approaches involve the cultivation of suitable plant populations under appropriately controlled conditions simulating field-like dynamic environments, non-invasive phenotyping involving optical or NMR-based techniques, temporally and spatial resolved molecular/biochemical 'omics' analyses, and computational systems analyses and modelling. Relevant factors and regulators identified in this way will be modified using biotechnological approaches or natural variants to improve the performance capacity of crop plants.

Contributing predominantly to IPK's Research Themes 4, Growth and Metabolism, and 5, Mechanisms of Resistance and Stress Tolerance, MOG addresses the central strategic IPK goals to uncover fundamental processes of plant adaptation and performance and to help tailoring crop plants to improve traits and sustainability. Using its core competences, MOG supports the IPK-wide research expertise and infrastructure by the coordination of IPK's Plant Phenotyping Platform management and use, and of the Bioinformatics Area of `Systems Analyses and Modelling'.

With seven permanently installed Research Groups and a Young Investigator's Group (Integrated Mechanistic Models – IMM), which combine complementary expertise, the MOG department is fully enabled to address its goals and to carry out its major tasks. The formerly associated independent RG on Metabolic Systems Interactions (MSI) was closed upon the appointment of its leader as Professor of Metabolic Reconstruction and Flux Modelling at the University of Cologne and integration into the Cluster of Excellence on Plant Sciences (CEPLAS).

The scientific expertise and the technical competencies of the eight research groups of the MOG department provide the basis to pursue three tightly interlinked research areas:

- Growth Dynamics during vegetative development and under dynamically changing, field-like conditions.
- Seed Biology addresses developmental and metabolic processes in seeds that control and regulate cell, tissue, and organ formation, as well as seed filling and maturation and
- Systems Genetics to elucidate molecular-genetic mechanisms (including heterosis) and to elaborate improvement strategies through dynamic multi-omic QTL detection, functional network analysis, and modelling of regulatory and metabolic processes.



Figure 1: The IPK PhenoSphere plant phenotyping platforms. The Container-based cultivation system with the PhenoCrane (a) multi-trait phenotyping installation, designed to impose contemporary and future weather scenarios in a fully controlled manner and elicit corresponding field-like performance responses of investigated crop plants. The Rhizotron system (b) is used for integrated high-resolution root and shoot imaging.

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Figure 2: Close-up views of thefully air-conditioned containers where the plants are grown in conditions similar to those in the field (c, d).





Research Highlights

Major highlights of the MOG research work

performed in 2022 and 2023 relate to important scientific advances addressing plant performance-related processes, improvements and use of phenotyping facilities, and the development of novel research tools:

Scientific research highlights include the insight that even mildly contrasting conditions such as constant vs. fluctuating illumination, which deliver the same amount of daily perceived photons per unit area, reveal vastly different sets of QTL governing the expression of growth-related traits in Arabidopsis. An integrated analysis of extensive multi-omics data, GWAS, QTL co-localisations, and systems analyses identified and prioritised well-supported candidate genes for metabolic variation, early vegetative growth, and biomass accumulation in a spring-type rapeseed breeding population.

Four superior genotypes for drought tolerance during vegetative development were identified in a collection of 60 chickpea genotypes maximised for genetic diversity. To further decipher drought tolerance and gain a better understanding of the underlying mechanisms, phenotypic details were evaluated of near isogenic lines of elite wheat varieties with introgressed QTLs of wild emmer.

Detailed transcriptome analysis of syncytium subdomains at the onset of its cellularisation revealed gene regulatory networks that govern the development of endosperm transfer cells and the aleurone of the barley endosperm. A mechanistic view on sugar transport within a barley grain mediated by SWEETs was elaborated, and a dual capacity of the HvSWEET11b protein in transporting sugars and cytokinins was discovered, disclosing an efficient means of coordinating the grain's development and filling. Acclimation to hypoxia was analysed in developing maize kernels and roots using an integrated approach. It was revealed that mitochondrial adaptation is essential for central endosperm, whereas assimilate transfer via basal endosperm avoids hypoxic limitation. Stem cell functionality could be preserved under hypoxic stress in roots by overexpression of phytoglobins.

The steps of tropane alkaloid biosynthesis in Erythroxylaceae were elucidated and verified through reconstruction of the biosynthetic pathway in yeast. Furthermore, the BAHD acyltransferase gene family in plants and the expanding roles of the members were characterised.

New developed statistical models that connect genetic variation with environmental parameters and metabolic profiles led to the identification of an enzyme (KCS4) that regulates levels of polyunsaturated fatty acids and unsaturated triacylglycerols and which is suggested to be involved in adaptation to light availability and growth seasons.

Research infrastructure advances

were achieved by reaching two major milestones in IPK's non-invasive plant phenotyping platforms: (1) Through detailed comparisons of maize growth over four consecutive years in the field, in glasshouse cultivation and two seasons with different climate

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Figure 3: High magnetic field 9.4T and 11.T MRI "Wide-Bore" (left) and "Super-Wide-Bore" (right) equipment established at the IPK enables a wide range of non-invasive investigations on a variety of plant organs (such as seeds shown in the centre) or even whole plants.

regimes in the PhenoSphere, it was demonstrated that field-like plant growth rates and developmental progression can be achieved in the container system of this fully controlled environment simulation facility. (2) The unique 11.7T Super Wide Bore NMR device was successfully installed to measure large plant samples (including agriculturally important sink organs such as fruits, roots and tubers).

Research tool development

resulted in the creation of DeepShoot, a novel image analysis program that provides a user-friendly, fully automated and efficient solution for the segmentation and extraction of shoot phenotypic data of plants such as Arabidopsis, maize, barley, and wheat analysed by the use of the high-throughput platforms of IPK or similar installations elsewhere.

Outlook

The MOG department is dedicated to making key conceptual and tangible contributions to the future long-term goal of enabling genome sequence variation-based prediction of crop plant performance in certain environmental scenarios. This will depend on biological knowledge of the molecular mechanisms that govern important performance-related regulatory and metabolic processes in plants and the involved genes to estimate the consequences of sequence variation. Thus, major priority will be given to gaining the necessary knowledge base through integrating spatially and temporally resolved phenotype and molecular omics analyses under specifically designed environmental conditions and by combining them with genetic mapping (systems mapping), network analyses, and process modelling. Integral is the experimental testing and validation of the predictions from mathematical modelling and machine learning / artificial intelligence approaches on performance characteristics of certain sets of defined genotypes exposed to relevant and informative environmental regimes. To enable this, MOG will (i) further support the use of IPK's innovative HTP plant phenotyping facilities, such as the Rhizotron and the Container/PhenoCrane systems in the PhenoSphere and the NMR/MRI facility for plant organ or whole plant analyses. Furthermore, (ii) it will pursue central joint projects establishing mechanistic links between genomic sequence variation, environmental factors, and phenotypic expression of plant performance-related traits. A prominent example is the AVATARS project, which strives for The Virtual Seed by using Augmented Reality and Advanced Virtuality (AR / AV) for interactive data visualization and exploration and assessing genetic and environmental factors affecting seed quality (germination ability).



RESEARCH GROUP **HETEROSIS** (HET)



Head: Prof. Dr. Thomas Altmann

Selected Publications

Hashemi-Petroudi, S.H. et al.: Initial description of the genome of Aeluropus littoralis, a halophile grass. Front. Plant Sci. 13 (2022) 906462.

Heuermann, M.C. et al.: Natural plant growth and development achieved in the IPK PhenoSphere by dynamic environment simulation. Nat. Commun. 14 (2023) 5783.

Meyer, R.C. et al.: Dynamic growth QTL action in diverse light environments – characterization of light regime-specific and stable QTL in Arabidopsis. J. Exp. Bot. 74 (2023) 5341–5362.

Shi, R. et al.: Integrated phenotyping of root and shoot growth dynamics in maize reveals specific interaction patterns in inbreds and hybrids and in response to drought. Front. Plant Sci. 14 (2023) 1233553.

Wang, H. et al.: INTERMEDIUM-C mediates the shade-induced bud growth arrest in barley. J. Exp. Bot. 73 (2022) 1963–1977.

Mission

The research group Heterosis (HET) studies plant performance, primarily in maize, rapeseed and barley crops, and in the model *Arabidopsis*. Major aims are identifying and characterising (epi) genetic factors that influence and control vegetative plant growth performance and heterosis in relevant dynamic environmental conditions and elucidating the affected molecular and physiological mechanisms. Systems biology approaches are combined with high-throughput, non-invasive phenotyping techniques applied to plants cultivated in sophisticated controlled environment facilities to detect pertinent genes, emphasising loci contributing to growth progression and biomass heterosis in dynamic environments.

Results

Detailed comparisons of maize growth data over four consecutive years in IPK fields, one in the glasshouse and two under different weather regimes in the IPK PhenoSphere Container System, showed that the PhenoSphere field-like environments can be simulated in terms of the evoked plant growth rates and the progression of developmental stages, resulting in field-typical plant growth performance (Heuermann *et al.*, 2023). A single (field) season simulation proved superior to the glasshouse and an averaged season over three years: The simulated weather regime of the single-season triggered plant growth and development progression very similar to that observed in the field. These results affirm the outstanding experimental opportunities to investigate molecular/genetic processes determining plant performance in diverse weather scenarios simulating natural fluctuations provided by this unique research infrastructure.

In 2022-2023, substantial progress was made in the identification of genes/QTL controlling vegetative plant growth and the affected molecular/physiological processes: Assessing vegetative growth in 382 Arabidopsis accessions cultivated under constant or fluctuating light intensities, using high-throughput phenotyping and genome-wide association studies (GWAS) showed that the complements of genetic factors affecting plant growth are largely specific for particular environmental scenarios. Eighteen protein-coding genes and one miRNA gene were identified as potential candidate genes at 10 QTL regions consistently found under both light regimes (Meyer et al., 2023). Combining extensive multi-omics data, GWAS, QTL co-localisations, and system-genetic analyses in a diverse rapeseed population with 477 spring-type lines allowed to pinpoint 15 well-supported candidate genes for metabolic variation, early vegetative growth and biomass accumulation, despite the extended regions of linkage disequilibrium typically present in canola breeding populations (Knoch et al., 2023). Detailed analyses of INTERMEDIUM-C (INT-C) mutants in barley showed that INT-C is expressed in tiller buds, required for bud growth arrest in response to shade, and targets genes belonging to auxin and gibberellin biosynthesis and signalling pathways (Wang et al., 2022). Important contributions were made to the validation of effects of novel exotic Early Flowering 3 alleles on barely development (Zahn et al., 2023), to the de novo assembly and initial description of the genome of the halophile grass Aeluropus littoralis (Hashemi-Petroudi et al., 2022), and to the analyses of salt stress-responses of important gene families (Arab et al., 2023; Hashemipetroudi et al., 2022, 2023).

Jointly with the APP and Image Analysis (BA) groups, important advances of IPK's plant phenotyping infrastructure were achieved, such as enabling simultaneous root and shoot growth assessment (Shi *et al.*, 2023) and the analysis of Arabidopsis, maize, and wheat plant appearance in different rotational side- and top-views via DeepShoot (Narisetti *et al.*, 2022).

Embedding in IPK Research Themes

HET predominantly addressed the *Systems Genetics* research area of the Molecular Genetics (*MOG*) department, focusing on vegetative development. Via the large transdisciplinary research



Figure 1: Fully controlled simulation of field-like environments in the IPK PhenoSphere, the experimental research field of molecular plant research for the future.

When the single (field) season of 2016 was simulated, plant growth and development progression were very similar to those observed in the field that year, unlike cultivation in the glasshouse or upon simulation of an averaged season over three years (Heuermann et al., 2023). Plant heights and growth speeds over time were observed in seven field and indoor environments. (a) The PhenoSphere as seen from the outside. View into compartment 1 of the PhenoSphere early (b) and late (c) in the growth period. (d) The field 2016 at the IPK field site.

field 2016

field 2017

field 2018

field 2019 glasshouse

120

PhenoSphere avo henoSphere 2016 sim

140

Plant height is plotted as a best-fit logistic growth curve representing the growth trend of the maize population in each environment versus days after sowing (DAS). The growth speed is given as the first derivative of the fitted curve representing the change in plant height in per cent per DAS for each environment. Colours used: field 2016 as Sky

Blue (#66CCEE), field 2017 as Forest Green (#228833), field 2018 as Silver (#BBBBBB), field 2019 as San Marino (#4477AA), glasshouse as Turmeric (#CCBB44), PhenoSphere avg as Froly (#EE6677), and Pheno-Sphere 2016 sim as Royal Heath (#AA3377).

project AVATARS, HET also contributed to the MOG research area Seed Biology. The projects are embedded in the IPK Research Themes 4, "Growth and Metabolism", 5, "Mechanisms of Resistance and Stress Tolerance", and 1 "Valorisation of Plant Genetic Resources"; HET co-ordinates jointly with APP the IPK-wide plant phenotyping efforts and the corresponding research infrastructure enhancement, maintenance and use.

60

80

Days after sowing (DAS)

100

40

Outlook

4

3

N

0

0

20

Investigating Arabidopsis, maize, rapeseed, and barley, the HET RG will (i) identify and characterise genetic loci that determine the extent of biomass production and seed yield and quality under relevant dynamic environmental conditions and also integrate spatial dynamics at the organ level (shoot in interaction with the root) (ii) analyse epigenetic effects on growth, biomass heterosis and stress resilience, (iii) perform time-resolved systems analyses of growth dynamics in inbreds and hybrids, (iv) conduct systems mapping of hybrid-performance related processes in dynamic environments, (v) evaluate genetic, physiological and morphological predictors of yield / hybrid-performance parameters. HET leads the MOG department-wide AVATARS project devoted to the elucidation of molecular processes determining seed quality, which are affected by strong genotype x environment interactions in rapeseed, and to develop novel ways of Big Data exploration using virtual reality (VR) approaches.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/heterosis



RESEARCH GROUP AUTOMATED **PLANT PHENOTYPING** (APP)



Mission

Optimising crop performance is a main task in ensuring future crop yields under the two major challenges: growing world population and ongoing climate change. The APP manages key plant phenotyping facilities at IPK (whole plant phenotyping platforms in climatised glass houses, a phytochamber, and the PhenoSphere). The APP research focus is on employing plant phenomics to gain an understanding of plant growth and performance under optimal and abiotic stress conditions, such as drought and heat. By combining relevant mapping panels and genome-wide information, the genetic architecture of complex traits with temporal dynamics, such as biomass formation or drought tolerance, is elucidated in cereals and legumes.

Head: Dr. Kerstin Neumann

Selected Publications

Bellucci, E. et al.: Selection and adaptive introgression guided the complex evolutionary history of the European common bean. Nat. Commun. 14 (2023) 1908.

Heuermann, M.C. et al.: Natural plant growth and development achieved in the IPK PhenoSphere by dynamic environment simulation. Nat. Commun. 14 (2023) 5783.

Lauterberg, M. et al.: Engaging precision phenotyping to scrutinize vegetative drought tolerance and recovery in chickpea plant genetic resources. Plants 12 (2023) 2866.

Lauterberg, M. et al.: Precision phenotyping across the life cycle to validate and decipher drought-adaptive QTLs of wild emmer wheat (Triticum turgidum ssp. dicoccoides) introduced into elite wheat varieties. Front. Plant Sci. 13 (2022) 965287.

Narisetti, N. et al.: Deep learning based greenhouse image segmentation and shoot phenotyping (DeepShoot). Front. Plant Sci. 13 (2022) 906410.

Results

A critical point in indoor greenhouse pot-based phenotyping is connection to field conditions. In a research collaboration with the Hebrew University and the Julius Kühn Institute (JKI), we could replicate the yield advantage under drought conditions of QTL identified in field studies in one of our HTP systems. The two QTLs originating from wild emmer were introgressed into Israelian wheat cultivars, and near-isogenic lines (NILs) were generated. In the first experiment covering the whole life cycle of wheat on a pot-based phenotyping platform, we applied a drought and temperature scenario mimicking Israelian field conditions as best as possible. Drought slowly started in the tillering stage and kept at a mild level until after flowering, then drought intensified. We confirmed the field results of a higher grain yield and shed more light on the processes leading to the higher grain yield (Lauterberg et al., 2022). The 7A QTL resulted in a slower reaction of biomass growth to drought, a higher water use efficiency (WUE) under drought, and better photosynthetic performance, particularly under drought. It caused a "stay green effect" during ripening under drought. Overall, plants of the NIL had higher biomass from the late tillering stage onwards and were growing taller, independent of the treatment (Fig. 1). The second QTL on 2B was reaching higher grain yield under drought mainly by increased tillering and thereby higher yield despite decreased TKW.

The spring drought setup from cereals was adapted to chickpeas. In the frame of INCREASE, a core panel of 200 plant genetic resource lines of both desi and kabuli seed types was screened on the HTP platform. Biomass and plant height were strongly reduced, while stress signs in the form of colour ratios were increased in line with reduced photosynthesis (Lauterberg et al., 2023). The data set is currently being explored for GWAS and the collected metabolomic data (in collaboration with the MD group). We will next shed new light on the response to combined heat and drought with a Humboldt grant starting in 2024.

Additionally, APP was working in the frame of the Brace project with the well-known HEB-25 panel (a subpanel of 400 lines used for yield trials in the consortium). We aimed to explore the drought response at the same phenology stage (BBCH 31) and, therefore, started the drought individually based on the growth stage. The first results show a high data quality and a strong effect of drought with a huge phenotypic diversity in the panel.

Last, we have successfully conducted one experiment on coffee and cacao plants with the rhizopot setup of the large HTP system in the frame of the EU project BOLERO. The large image data set is currently being analysed with the BA group.

APP also manages the IPK phenomics facilities (with the research group HET). The Pheno-Sphere is in full operating mode, and the APP supported the conduct of five containers and eight rhizotron system experiments. In the pilot phase of DPPN Access, four collaborative projects were conducted in 2023. Further, several high-throughput phenotyping training courses, workshops, and short-term scientific missions were realised in the EU twinning project STARGATE frame.



Figure 1: Curves of biomass, plant height and the average colour value during the whole life cycle (DAS = days after sowing) for plants of the parent BarNir and the corresponding NIL carrying the wild emmer QTL on 7A in well-watered and drought treatment.

Embedding in IPK Research Themes

The APP research focus is deeply embedded into IPK Research Themes: "Growth and Metabolism" (4), "Mechanisms of Resistance and Stress Tolerance" (5), and the "Valorisation of Plant Genetic Resources" (1). Barley, wheat, and chickpea Plant Genetic Resources (PGR) are characterised by their growth characteristics and abiotic stress tolerance in combination with omics approaches to reveal the underlying mechanisms. Within the INCREASE project, we are involved in valorising legume PGR.

Outlook

The chickpea work is complemented by a Humboldt grant, where the combined response to heat and drought is explored. Next, we address the challenge of phenology with the research groups BA and NAM in the DFG HetCrop project. Within BOLERO, the root plasticity of coffee and cacao, including wild species, is evaluated. The network of collaborators is strengthened by the DPPN Access and Stargate project and by the role of K. Neumann as the new chair of the EWG Phenotyping of the Wheat Initiative. Our wheat image data integration into a global wheat data set (lead Andreas Hund) has been decided. In collaboration with the Humboldt University Berlin, our wheat phenomic data are integrated into a publication with field phenotyping data.

A proposal led by Martin Luther University Halle-Wittenberg plans further research into cereal single-plant growth vs. plant stands. INCREASE's citizen science experiment has a huge outreach to the public, and future funding is sought beyond the project's duration. In the One Planet fellow-ship, we explore options for future collaboration with partners from Benin.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/automated-plant-phenotyping



RESEARCH GROUP IMAGE ANALYSIS (BA)



Head: Dr. Evgeny Gladilin

Selected Publications

Narisetti, N. et al.: Deep learning based greenhouse image segmentation and shoot phenotyping (DeepShoot). Front. Plant Sci. 13 (2022) 906410.

Henke, M. & E. Gladilin: Virtual laser scanning approach to assessing the impact of geometric inaccuracy on 3D plant traits. Remote Sens. 14 (2022) 4727.

Narisetti, N. et al.: Awn image analysis and phenotyping using BarbNet. Plant Phenomics 5 (2023) 0081.

Maria Antony, A.N., N. Narisetti & E. Gladilin: FDM data driven U-Net as a 2D Laplace PINN solver. Sci. Rep. 13 (2023) 9116.

Liu, A. et al.: Investigation of the impact of supplemental reflective films to improve micro-light climate within tomato plant canopy in solar greenhouses. Front. Plant Sci. 13 (2022) 966596.

Mission

The research group image analysis (BA) focuses on developing algorithms and integrative software tools for quantitatively analysing multimodal and multidimensional image data from different macroscopic and microscopic imaging systems and high-throughput phenotyping facilities. The research goals of the group include the development of methods for image enhancement, segmentation, registration, classification, quantitative characterisation (phenotyping) and computational modelling of relevant plant structures, e.g., shoots, roots, leaves, awns, seeds, cells, etc., as well as efficient implementation of algorithmic pipelines and user-interfaces for automated and semi-automated image processing.

Results

In 2022-2023, the research activities of the Image Analysis group focused on (i) extension of machine and deep learning (DL) solutions for fully automated plant image analysis [1]; (ii) development of novel approaches to image- and model-based assessment of physiological plant properties [2,4]; as well as (iii) 3D modelling and analysis of plant structures, in particular, B. napus seeds within the scope of the BMBF Avatars project see Figure 1. Based on previously developed methods and tools for conventional plant image processing, segmentation and co-registration, the Image Analysis group generated a large amount (1000x) of ground truth image data, which was subsequently used for training of deep learning segmentation models tailored to different plant types, views, modalities and phenotypic facilities including two major IPK (Rhizotron and conveyor-based) high-throughput plant phenotyping platforms. The first successful tests of the DL-based methods were performed on diverse shoot and root datasets, including a large variety of different plant types, demonstrating almost real-time algorithmic performance of image segmentation. In addition to conventional traits of plant geometry and optical appearance (such as shape, size, and colour), the Image Analysis group works on methods for image- and model-based assessment of physiological plant properties. In [2], an approach to 3D model-based assessment of plant-light intersection was presented; see Figure 1(b). Within the scope of in-house cooperation with the GGR group, a DL model for automated segmentation of awn barbs was developed and applied to the automated assessment of phenotypic properties and classification of four different wheat genotypes [3], Figure 1(c). Within the scope of the BMBF-funded Avatars project, the Image Analysis groups develop methods for automated analysis of hyperspectral and MRI images. An algorithmic pipeline was applied for spatial alignment and 3D statistical modelling of B. napus seeds and seed organs from the MRI image data provided by the AAN group, Figure 1 (d). The Image Analysis group participates and contributes to several third-party-funded projects, including BMBF AVATRS, BMBF SmartRoot, EU STARGATE, and EU Bolero.

Embedding in IPK Research Themes

The research group BA contributes to Research Theme 4, "Growth and Metabolism", and closely cooperates with the IPK research groups HET, APP, AAN, MPE, and BIT on quantitative plant image analysis and phenotyping. Furthermore, the RG BA contributes to analysing microscopic image data acquired by CSF and GGR. Furthermore, the group contributes to Research Theme 5, "Mechanism of Resistance and Stress Tolerance".


Figure 1: Figure 1. An overview of image analysis applications: (a) Screenshot of a GUI tool for fully automated analysis of greenhouse-grown plant shoots [1]; (b) Simulation of plant-light interaction using a ray-tracing approach [2]; (c) Example of fully automated segmentation of awn barbs using a pre-trained deep learning model [3]; (d) Statistical shape models of three genetic lines and four developmental stages of B. napus seeds computed from MRI image data provided by the AAN group.

Outlook

Future plans of the BA group include further development of conventional and novel machine and deep learning methods for plant image segmentation, registration, classification, and automated phenotyping. The BA group will extend its research activities to investigate automated data augmentation methods and novel efficient approaches to physiological plant modelling and hidden parameter estimation. Given the large interest in quantifying particular plant parts (i.e., single leaves, spikes, parts of the root system architecture, etc.), dedicated activities are planned to detect and quantify small image structures in macroscopic and microscopic images. A particular challenge for the BA group consists of balancing state-of-the-art research activities and a growing amount of technical tasks, including maintenance and adaptation of algorithmic frameworks and software tools to new/unseen data and altering experimental setups.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/image-analysis



RESEARCH GROUP **METABOLIC DIVERSITY** (MD)



Head: Dr. John D'Auria

Selected Publications

Chavez*, B.G., P. Srinivasan* et al.: Elucidation of tropane alkaloid biosynthesis in Erythroxylum coca using a microbial pathway discovery platform. Proc. Natl. Acad. Sci. U.S.A. 119 (2022) e2215372119.

Moghe, G. et al.: BAHD Company: The ever-expanding roles of the BAHD acyltransferase gene family in plants. Annu. Rev. Plant Biol. 74 (2023) 165-194.

Leite Dias, S. et al.: A new fluorescence detection method for tryptophan- and tyrosine-derived allelopathic compounds in barley and lupin. Plants 12 (2023) 1930.

Rizzo, P. et al.: Plant synthetic biology: from inspiration to augmentation. Curr. Opin. Biotechnol. 79 (2023) 102857.

Wang, Y.-J. et al.: Genomic and structural basis for evolution of tropane alkaloid biosynthesis. Proc. Natl. Acad. Sci. U.S.A. 120 (2023) e2302448120.

* joint first authorship

Mission

The Metabolic Diversity (MD) group established in 2019 aims to use advanced biochemistry, chemistry, and genetics methods to explore how important crops produce and use plant-based metabolites. The group investigates the reasons behind the diversity and variation of plant compounds across all taxonomic levels. The group also analyses how these factors affect cultivated plants' growth, health, seed quality, and yield. Additionally, the group employs synthetic biology and biochemical engineering to gain further insight into these dynamics. Altogether, the MD group's work contributes to developing new hypotheses about how genetics and metabolism interact in plants.

Results

The MD group has several main research topics that fit its objectives of studying plant metabolites. These are: (i) Identifying metabolites and their biosynthetic pathways in Poaceae plants that are involved in various stress responses (ii) Setting up genetic and biochemical resources for studying napthodianthrone production in different plant families such as Hypericaceae and Polygonaceae (iii) Finding out all the biochemical steps for making tropane alkaloids in Erythroxylaceae plants and showing them using synthetic biology platforms.

Synthetic biology is an important tool for the MD group's future work. It allows the manipulation of genes and enzymes in different organisms, using powerful techniques to find important plant traits for agriculture. A significant milestone recently achieved is the reconstruction of the pathway leading to the tryptophan-based alkaloid gramine from barley and producing the allelopathic compound in yeasts and other plants. Our future goals include using these systems to study the ecology of the biotic and abiotic interactions mediated by gramine. We have successfully employed synthetic biology in yeast to find and characterise the unknown parts of tropane alkaloid biosynthesis.

The MD group also continues to work on the genetics of hypericin production and apomixis in *Hypericum perforatum* (St. John's wort) and related plants. We have prepared and submitted several grant applications this year about transcript profiling of Hypericum. We have also expanded our collaboration with members of the Institute for Plant Biochemistry (IPB) and other top researchers in hypericin biosynthesis from the University of Hannover. We continue our research and development for SpaceEx, a project for visualising mRNA transcripts on tissue sections, which has advanced to the optimisation stage and already has yielded valuable results.

The MD group collaborates within the institute, such as the 'Obi von Knobi' project, which aims to understand the dynamic effects of organic farming on the yield and metabolic quality of garlic and other allium species. Further collaborations include the fava bean 'REPLACE' project, the rye 'Stabilstroh' project, and projects looking into barley, wheat, tomato and cowpea drought and heat tolerance metabolism. Within Germany, the MD group is pursuing grants and projects about enzyme diversity in lipids and secondary metabolites with members of the Max-Plank Institute for Molecular Plant Physiology and the Pharmacy School at the University of Braunschweig. The MD group also successfully connected with six European partners participating in the EPPN2020 transnational access program. These ongoing focus on assessing metabolite changes occurring in multiple agronomically important species due to either abiotic (drought) or biotic (fungal infection) stress treatments. Exchange students from transition countries are currently being trained to analyse data from field experiments performed in their home institutions.

Embedding in IPK Research Themes

The work performed by Metabolic Diversity group members squarely falls under the aegis of Research Theme 4, "Growth and Metabolism". The group's main interests are understanding the



Buckwheat Collection

Fava Bean Collection (REPLACE)

interplay of environmental and genetic factors and how they affect the metabolic outcomes of crop plants and, by extension, their growth characteristics. While most of our work corresponds with this theme, we are also associated with Research Theme 5, "Mechanisms of Resistance and Stress Tolerance".

Outlook

The future priorities for the Metabolic Diversity group continue to focus on generating high-quality metabolomic data regarding economically important crop plant species. Specifically, next year, the focus will continue on internal collaborations within the IPK dealing with barley, buckwheat, garlic, rapeseed, and maise. The group will perform exploratory experiments to develop a program to understand important genes involved in hemp fibre and seed oil quality. Additionally, the group will continue working with medicinal plant species that are also important crops for Europe. We intend to expand the group's cohort of graduate students via external funding and opportunities such as the IMPRS program (Max Planck Society) with particular emphasis on chemical analytics and chemical ecology.

Figure 1: A representative example of the plant and metabolites being studies by members of the Metabolic Diversity Group. Measurements are predominantly made either by GC-TOF or LC-TOF instrumentation. The MD group utilises the vast Genebank diversity collections available at the IPK for metabolite pathway analysis.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/metabolic-diversity



RESEARCH GROUP **SEED DEVELOPMENT** (SE)



Head: Dr. Jozefus Schippers

Selected Publications

Zhao, L. et al.: The Arabidopsis thaliana onset of leaf death 12 mutation in the lectin receptor kinase P2K2 results in an autoimmune phenotype. BMC Plant Biol. 23 (2023) 294.

Hartwig, T. et al.: Hybrid allele-specific ChIP-seq analysis identifies variation in brassinosteroid-responsive transcription factor binding linked to traits in maise. Genome Biol. 24 (2023) 108.

Hertig, C.W. et al.: Dissection of developmental programs and regulatory modules directing endosperm transfer cell and aleurone identity in the syncytial endosperm of barley. Plants 12 (2023) 1594.

Eysholdt-Derzsó*, E., T. Renziehausen*, S. Frings*, S. Frohn* et al.: Endoplasmic reticulum-bound ANAC013 factor is cleaved by RHOMBOID-LIKE 2 during the initial response to hypoxia in Arabidopsis thaliana. Proc. Natl. Acad. Sci. U.S.A. 120 (2023) e2221308120. * joint first authorship

Geisslitz, S. et al.: Breeding from 1891 to 2010 did not increase the content of amylase/trypsin-inhibitors in wheat (Triticum aestivum). npj Sci. Food 7 (2023) 43.

Mission

The alternation of generations in flowering plants results in the formation of seeds, which contain the next generation (embryo) and a start-up package (endosperm). Cereal grains are essential for humans' dietary needs, animal feeding, and industrial processing. Current climate change and the increased extreme weather events represent a major challenge for agricultural practice and productivity.

The Seed Development (SE) group aims at understanding the molecular mechanisms controlling plant development and stress adaptation. The main goal is to perform molecular functional genomics studies in cereals to characterise relevant processes and provide means to tailor crops for future needs.

Results

The SE group contributes actively to our understanding of grain development, the exploration of novel molecular pathways and the development and implementation of novel methods for functional genomics in crops.

The research of the SE group can be divided into several topics that align with its objective to obtain a molecular understanding of plant development and stress adaptation. These topics are (i) Molecular and genetic regulation of endosperm and endosperm transfer (ETC) cell development in barley, (ii) Implications and regulation of reactive oxygen species (ROS) homeostasis for plant development and stress signalling, (iii) Sink-source relationships during senescence and grain filling. Next to that, we have developed two main methodology platforms: laser capture microdissection (LCM) coupled to RNA-seq and DNA-affinity Purification Sequencing (DAP-SEQ) to enable the elucidation of molecular and genetic pathways.

The study of endosperm development focuses on elucidating gene-regulatory networks (GRNs) to obtain a molecular understanding of seed formation in a spatial and temporal resolution. An important goal was the implementation of DAP-seq in barley, wheat, sugar beet and maise. This has resulted in elucidating the GRNs of transcription factors regulating barley endosperm development, sugar beet size, maise drought tolerance and spike development in barley and wheat. Our current goals are to validate the GRNs through genetic models and use the obtained knowledge for targeted approaches.

In addition, the SE group continues its molecular research on two-component signalling (TCS) pathways: stress signalling pathways (hypoxia and drought) and ROS signalling. We have uncovered in mosses an essential role of superoxide dismutase for male gametogenesis. We will test this knowledge in the future in cereals, as heat waves harm plant fertility and their reproductive success.

Next, we are keenly interested in studying sink-source interactions during whole plant senescence and grain development. Our recent work uncovered a link between proteasome homeostasis and the onset of leaf senescence. The degradation of proteins and transport of amino acids will be a focus point for the future.

The SE group is well-embedded within the MOG department through the AVATARS project. In addition, we have active collaborations within the IPK on elucidating GRNs using DAP-seq and transcript analysis using the LCM platform. Furthermore, we collaborate actively with researchers in Germany and outside, aligning with the group's main aims. In recent years, we have hosted multiple BSc and MSc students, and the group has been represented numerous times at national and international conferences.



Figure 1: Type-B response regulator (RR) activity is specific for the ETC region of barley grains. Strong GFP activity (green) was monitored between 4 and 7 days after flowering (DAF); expression is enhanced by the synthetic auxin NAA. Barley plants were transformed with the TCSn::GFP reporter construct; the TCSn promoter contains variations of the ARR type-B motifs from Arabidopsis. GFP activity in T3 Grains from two independent lines (E4 + E7) was analysed by confocal microscopy; the specificity of signals was confirmed by the lambda signature.

Embedding in IPK Research Themes

The work performed in the SE group mainly contributes to the following IPK Research Themes: "Mechanisms of Plant Reproduction" (3), "Growth and Metabolism" (4) and "Mechanisms of Resistance and Stress Tolerance" (5).

Outlook

The SE group aims to provide new insights into plant development and stress adaptation by performing state-of-the-art molecular and genetic studies in diverse plant species. Specifically, we will extend our studies and intensify our collaborations on barley, maise and sugar beet. The group is highly open to collaborations with other researchers regarding our established platforms and the pursuit of collaborative research funding. The main challenge for the group is to maintain an excellent research level.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/seed-development



RESEARCH GROUP **ASSIMILATE ALLOCATION AND NMR** (AAN)



Head: PD Dr. Ljudmilla Borisjuk

Selected Publications

Radchuk, V. et al.: SWEET11b transports both sugar and cytokinin in developing barley grains. Plant Cell 35 (2023) 2186-2207.

Langer, M. et al.: Causes and consequences of endogenous hypoxia on growth and metabolism of developing maize kernels. Plant Physiol. 192 (2023) 1268-1288.

Borisjuk, L. et al.: Seeing plants as never before. New Phytol. 238 (2023) 1775-1794.

Mayer, S. et al.: Quantitative monitoring of paramagnetic contrast agents and their allocation in plant tissues via DCE-MRI. Plant Methods 18 (2022) 47.

Teh, J.T. et al.: NTRC regulates CP12 to activate Calvin-Benson cycle during cold acclimation. Proc. Natl. Acad. Sci. U.S.A. 120 (2023) e2306338120.

Mission

Our research aims to better understand the relationships between assimilate supply, metabolism and seed architecture, thereby uncovering mechanisms for improved traits in major crops. We apply topographical in vivo approaches to analyse assimilate uptake and transport towards and within the developing seeds, and the conversion of assimilates into storage products in traditional crops and model plants. Our approaches rely on non-invasive procedures such as magnetic resonance imaging (MRI) and near-infrared micro-spectroscopy combined with mass spectrometry and molecular tools. Our method developments are at the forefront of MRI approaches on plants.

Results

The spatial analysis of assimilate allocation to improve seed filling is an important long-term goal of our research group. We have elucidated the role of SWEETs ("Sugars Will Eventually be Exported Transporter") during grain filling and proposed the mechanistic model of sugar import into developing barley grain. Only three (HvSWEET4, HvSWEE11b and HvSWEET15a) of 23 SWEET genes showed the highest expression in grains. When expressed in Xenopus oocytes, HvSWEET4 displayed high glucose transport activity, HvSWEET15a facilitated sucrose transport, and HvSWEET11b transported both sugars (sucrose, glucose) and cytokinins efficiently. Barley plants lacking functional HvSWEET11b could not produce viable grains. Even a moderate reduction in HvSWEET11b transcripts affected sugar and cytokinin allocation from maternal seed tissues towards the endosperm, ultimately reducing seed size. The dual function of HvSWEET11b in transporting sugars and cytokinins in the developing grains plays a crucial role in efficiently coordinating grain development and filling (Radchuk et al., 2023, Plant Cell).

Metabolic acclimation to spatial (internal and external) conditions defines the efficiency of plant performance. We analysed acclimation to hypoxia in developing maize kernels and roots. It was found that the metabolism of the central endosperm occurs under endogenous hypoxia. In contrast, the transfer layer of the basal endosperm received a superior oxygen supply, avoiding any hypoxic limitation to the assimilate uptake of the kernel. Mitochondrial adaptations to hypoxia were of primary importance that influenced the grain development (Langer et al. Plant Physiology, 2023). Various reciprocal responses in gene expression and metabolite levels revealed several pathways and regulatory circuits regulated by local oxygen availability (including auxin and cyclic nucleotide metabolism, starch, ascorbate and ethylene synthesis). The multi-omics driven analysis of maize stem cells that control root growth showed that overexpression of phytoglobins (ZmPgb1.1) could preserve stem cell functionality under hypoxic stress, thereby improving plant performance (Mira et al. Plant Physiology, 2023).

Studying dynamic processes in living organisms is one of the most promising research areas, which necessitates the development of new approaches and technological solutions. We expanded our non-invasive NMR-imaging platform by establishing a unique super-wide bore 11.4T NMR scanner (granted by "Europäischer Fonds für regionale Entwicklung") and adapted it for measurements on large plant specimens (including main storage organs like fruits, taproots, tubers). This represents a significant milestone for future research. We designed a new approach for plant Dynamic Contrast-Enhanced Magnetic Resonance Imaging (pDCE-MRI) to enable the dynamic in vivo analysis of transport processes in plants. The new approach has been tested in situ on a cereal crop (Hordeum vulgare). It allows us to identify vascular regions and estimate their involvement in allocating tracers (paramagnetic compounds). pDCE-MRI opens a perspective for further development of tracer-aided MRI experiments in plant biology (Mayer et al., 2022, Plant Methods). Technological improvements are not restricted to MRI and have successfully contributed to various fields of plant biology (Borisjuk et al., 2023, New Phytol; The et al., 2023, PNAS;).



Embedding in IPK Research Themes

Our work is integrated into the IPK Research Themes 4, "Growth and Metabolism" and 5, "Mechanisms of Resistance and Stress Tolerance". New method developments enabled contributions to Research Themes 1, "Valorisation of Plant Genetic Resources", and 2, "Genome Diversity and Evolution" (studies on the role of SWEETS). To provide services on an institute-wide level, our research group is developing technological platforms such as MRI, FTIR, and MS.

Outlook

Our scientific focus remains on the study of assimilate allocation and seed biology in major cereal, oil and protein crops. A significant challenge is to refine the non-invasive visualization of sucrose allocation in maize and rice grains and introduce MRI for species of Beta, Coffea and Rosa. We continue advancing our MRI platform with complementary applications and new methods to enable non-invasive *in vivo* imaging of plant growth and metabolism. This, combined with Deep Learning approaches, is aimed at overcoming the current limitations of the application of MRI in plant research and breeding. Besides MRI, FTIR and MS-analytic will also provide excellent networking opportunities and international collaboration opportunities for our research group.

Figure 1: MRI-based non-invasive investigation of barley and

maize. (A) The effect of knocking down HvSWEET11b on sucrose allocation. The distribution of 13C-labeled sucrose in developing grains set by WT and SWEET11b-knockdown transgenic lines; sucrose concentration is colour-coded; tissues present in the grain are identified in the insert shown on the left. (B) MRI-based analysis of developing maize kernels. The upper row shows lipid maps, indicating the presence of lipids at the endosperm surface and in the embryo; arrows indicate the lack of lipidous layers at the basal endosperm region. The lower row shows a 3D model (left) and two water distribution maps (middle/ right panel) acquired at 15 and 30 days after pollination; please note steep hydration gradients inside the endosperm. (C) Visualisation of gadolinium (used as contrast agent, CA) distribution and transport in barley stems using pDCE-MRI; 3D-insert shows CA accumulation in stem's vasculature; middle panel shows CA distribution in virtual stem cross-section in comparison to sucrose distribution (measured by FTIR imaging; right panel). Abbreviations: ac, apoplastic cavity; em embryo; es/en, endosperm; Is, lateral spikelet; pc, pedicel; pe, pericarp; np, nucellar projection; vb, vascular bundle. (Graphic design by S. Ortleb and L. Kalms.)

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/assimilate-allocation-and-nmr





Head: Dr. Jędrzej Jakub Szymański

Selected Publications

Arend, D. et al.: From data to knowledge – big data needs stewardship, a plant phenomics perspective. Plant J. 111 (2022) 335-347.

Luzarowska, U. et al.: Hello darkness, my old friend: 3-KETOA-CYL-COENZYME A SYNTHASE4 is a branch point in the regulation of triacylglycerol synthesis in Arabidopsis thaliana. Plant Cell 35 (2023) 1984-2005.

Panda, S. et al.: Steroidal alkaloids defense metabolism and plant growth are modulated by the joint action of gibberellin and jasmonate signaling. New Phytol. 233 (2022) 1220-1237.

Treves, H. et al.: Carbon flux through photosynthesis and central carbon metabolism show distinct patterns between algae, C3 and C4 plants. Nat. Plants 8 (2022) 78–91.

Zheng, S. et al.: Metabolic diversity in a collection of wild and cultivated Brassica rapa subspecies. Front. Mol. Biosci. 9 (2022) 953189.

RESEARCH GROUP **NETWORK ANALYSIS AND MODELLING** (NAM)

Mission

We are interested in novel machine learning and graph theory applications in crop biology in the Network Analysis and Modelling group. Our primary objective is to uncover molecular mechanisms that translate genetic sequence variation into observable phenotypes, such as improved yield, accumulation of specific biochemical compounds, or increased pathogen resistance. Additionally, we offer statistical expertise, machine learning solutions, and data visualisation tools that enable integrating and interpreting data generated by the Molecular Genetics department.

Results

Our methodology is centred on developing and applying new computational techniques to multimodal data collected for crops, including genomic data, gene expression, metabolic profiles, phenomic parameters, and environmental factors. We collaborate closely with experimental groups to analyse data and design experiments. In a recent study on the lipid composition of Arabidopsis thaliana ecotypes, we developed statistical models that connect genetic variation with environmental parameters and metabolic profiles. This work led to the identification and characterisation of 3-KETOACYL-COENZYME A SYNTHASE 4 (KCS4), an enzyme that modulates carbon metabolism by regulating polyunsaturated fatty acids and unsaturated triacylglycerols during extended periods of darkness. Distinct haplotypes of KCS4 were prevalent in populations from varying climates, suggesting a connection between KCS4 function and adaptation to light availability and growth seasons (Luzarowska et al., 2023). In collaboration with the Max Planck Institute of Molecular Plant Physiology in Potsdam, we examined the dynamics of carbon flux through photosynthesis and central metabolism in plants and algae that exhibit diverse photosynthetic characteristics and carbon assimilation mechanisms (Treves et al. 2022), uncovering environmental adaptations at the metabolic flux level. In another study, we analysed the domestication and selection processes that have shaped flavour and aroma traits in 100 cultivars of Brassica rapa (Zheng et al. 2022), revealing numerous novel compounds in cabbage and its relatives, as well as metabolic features subject to selection pressure during the domestication and breeding of Brassica rapa. Moreover, we are engaged in developing strategies for managing and analysing crop data, ranging from high-throughput phenotyping "big data" approaches (Arend et al. 2022) to the integration and harmonization of various omics data for the identification of gene candidates and regulatory interactions within molecular networks (Panda et al. 2022).

The research group NAM is part of the Cluster of Excellence on Plant Sciences (CEPLAS) and maintains a close partnership with the Bioinformatics department at the Forschungszentrum Jülich. We collaborate with the Leibniz Institute of Plant Biochemistry (IPB) Halle and Leibniz Institute of Vegetable and Ornamental Crops (IGZ) Großbeeren as part of the Leibniz Collaborative Excellence project. We also collaborate closely with the Weizmann Institute of Science (Israel) to uncover gene functions in the specialised metabolism of tomatoes. Furthermore, we have established multiple collaborations within CEPLAS focusing on deep learning-based sequence analysis and gene regulation inference, involving partners such as Max Planck Institute for Plant Breeding Research in Cologne, the University of Cologne, and the Forschungszentrum Jülich.

Embedding in IPK Research Themes

The research group NAM interacts with interested parties from all departments concerning transcriptomics and statistical data analysis without considering the particular research focus. NAM's research focuses on large-scale omics analyses and questions raised in the research groups HET, SE, and AAN. Our focus is on Research Theme 4, "Growth and Metabolism". The recent progress of the research group in deep learning-based sequence analysis has tightened its links with the IPK Research Theme 2, "Genome Diversity and Evolution".



Figure 1: Multi-omics data generation, modelling and machine learning approaches to unravel complex biological processes in plant research and interactions in variable environments. These are becoming essential tools in modern plant science, revolutionising the analysis and prediction of biological processes, revealing complex interactions and thus improving research and breeding programmes.

Outlook

In the coming years, we will focus on developing deep-learning methods for the functional annotation of genetic variations and their integration into breeding programs. We are currently training algorithms that associate gene regulatory sequences with DNA binding and gene expression patterns, aiming to efficiently identify polymorphisms that drive genotype-specific gene regulation. Additionally, we are venturing into the Digital Twin concept, drawing parallels between biological systems and game design. This initiative is materialised in the "PlantEd Game Project," which uses plant molecular networks as the basis for a real-time strategy game, allowing AI agents to manage these networks in fluctuating environments. The latest PlantEd version, installation instructions, and a gameplay tutorial are available on our GitHub: https://github.com/NAMlab/ PlantEd. Our foremost challenge in the near future is to advance these machine-learning tools and validate their practical utility in breeding and crop management strategies.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/network-analysis-and-modelling where the second sec



YOUNG INVESTIGATOR GROUP INTEGRATED MECHANISTIC MODELS (IMM)



Head: Dr. Mary-Ann Blätke

Mission

The young investigator's group IMM, established in 2021, is dedicated to advancing crop breeding through computational biology. IMM aims to unravel the molecular mechanisms underlying plant growth, development, and metabolic regulation by employing integrative approaches to analyse multimodal data. This research lays the foundation for developing integrative data- and mechanism-based models, enabling predictions of plant performance in different environments and genetic settings. These models and their explainability contribute to trust-based decision-making in breeding programs, ultimately yielding resilient, climatically adapted, and resistant crops.

Results

Since its establishment in 2021, IMM has been primarily focused on deriving a multi-organ whole seed model for the metabolic network of B. napus seed metabolism within the AVATARS project (work had to be halted due to maternal and parental leave from September 2021 to June 2023). This model integrates organ-specific time-resolved multimodal data sets from the project partners to gain insights into the metabolic changes during seed development. Leveraging the relatedness of A. thaliana and B. napus as members of the Brassicaceae family, we construct the metabolic network based on the curated AraCore model and the reconstruction of lipid metabolism from databases such as AraLip, PlantCyc, KEGG, and PlantSeed. By associating flux balance-derived metabolic phenotypes with seed traits, such as seed vigour and germination ability, we aim to predict these traits under genetic and environmental variations. The construction of the metabolic network adheres to community standards, including compliance with MIRIAM guidelines, promoting reproducible science and encouraging its reuse within the plant science community. Integrating the updated AraCore model and the lipid metabolism-specific network forms the basis of the reconstructed metabolic network for B. napus seed metabolism. We identify the likely flux-carrying enzymes or transport proteins in the A. thaliana and B. napus genomes for comparisons with earlier publications.

In terms of publications, we have summarised the "Gatersleben Research Conference 2019 on Applied Bioinformatics for Crops" and highlighted recent advances in the field through a Research Topic in Frontiers in Plant Sciences [Blätke et al. 2021 (doi: 10.3389/978-2-88966-620-1), Blätke et al. 2021 (10.3389/fpls.2021.640394)], emphasising the significance of bioinformatics and computational biology in improving crops. Additionally, a review titled "Advances in Flux Balance Analysis by Integrating Machine Learning and Mechanism-based Models" was published in the Computational and Structural Biotechnology Journal [Sahu et al. 2021, (doi: 10.1016/j.csbj.2021.08.004)]. Previous work on the multimodal analysis of tomato fruit development carried out as part of the NAM research group headed by Jedrzej Jakub Szymanski, is still in preparation for submission.

IMM's participation in the organising committee of the German Conference on Bioinformatics for 2021 online and 2022 on-site events expands our professional network and enhances our visibility in the national and international bioinformatics community. We secured DFG funding (GZ: BL 1848/1-1) for the German Conference on Bioinformatics 2021 as an important international scientific event.



Embedding in IPK Research Themes

As part of the BMBF-funded AVATARS project, the research covered is mainly related to IPK Research Theme 4, "Growth and Metabolism". Within AVATARS, research questions are addressed collaboratively with the research groups HET, SE, AAN and BA. Research Themes 2, "Genome Diversity and Evolution" and 5, "Mechanisms of Resistance and Stress Tolerance", are addressed in past and ongoing research.

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IMM aims to establish an internationally acknowledged research profile and to increase its national and international visibility by revolutionising crop breeding through computational approaches. This vision entails the development of virtual breeding hubs based on digital crop twins, leveraging integrated scholarly knowledge, descriptive models (e.g. molecular networks, kinetic models), and data-driven models to create executable predictive knowledge graphs. Al – deep learning and natural language processing – has to be a central part of the envisioned hubs. Therefore, IMM aims to explore:

- Uses of AI to analyse multimodal datasets (including multi-temporal, -spatial, -omic data)
- Synergies of AI and descriptive models
- Dynamic and executable knowledge graphs

Figure 1: Workflow to create an integrative metabolic whole seed model for B. napus seed development as part of the AVATARS project.

More information: www.ipk-gatersleben.de/en/research/molecular-genetics/integrated-mechanistic-models-young-investigators-group





Department Physiology and Cell Biology

Molecular Plant Nutrition (MPE) Dr. Ricardo Giehl & Prof. Dr. Nicolaus von Wirén

Young Investigator Group Sustainable Nutrient Management (NNM) **Dr. Diana Heuermann**

Genetics and Physiology of Root Development (GPW) **Prof. Dr. Hannah Schneider**

Plant Reproductive Biology (PRB) **Dr. Jochen Kumlehn**

Structural Cell Biology (SZB) **Dr. Michael Melzer**



Department Physiology and Cell Biology



Head: Prof. Dr. Nicolaus von Wirén

Mission

Research in the department focuses on plant transport and metabolic and developmental processes, which are relevant for their agronomic performance and stress tolerance or their adaptation to agricultural and biotechnological production systems. Establishing and steadily improving analytical and technical platforms with related competencies in physiology, biochemistry, cell biology, and biotechnology achieve these fundamental and application-oriented research goals. With a focus on pathogen resistance, resource efficiency or improved quality traits, departmental research addresses core topics of the German National Sustainability Strategy and the Federal High-Tech Strategy, as well as several UN sustainability goals.

Research Status

Departmental research is firmly committed to the generation of crop cultivars with beneficial traits also by the use and development of genome editing technologies. The PRB group used as show-case durum wheat that under some growth conditions can accumulate very high levels of cadmium in the grains. This is largely due to a Heavy Metal ATPase3-B1 (HMA3-B1) gene variant that represents a tandem duplication of 17 nucleobases that abolishes its function. The intact allele of this transporter gene is active in the root and ensures that the cadmium taken up is sequestered in vacuoles and cannot enter the shoot and grain. The defective hma3 allele is thought to have prevailed through early breeders' selection under conditions of limited zinc availability because HMA3 transports besides cadmium also zinc. Since most arable soils are not Zn deficient, we sought to restore the functional HMA3 allele in current durum wheat cultivars using genome editing to reduce cadmium levels in the grain. Therefore, homology-mediated end joining of Cas9-cleaved DNA was employed, which goes beyond conventional genome editing approaches based on DNA repair via nonhomologous end-joining. Functional validation of a designed Cas9/gRNA construct in wheat protoplasts revealed precise restoration of the previously knocked-out allele in more than 50% of the mutated sequences. Stably transformed durum lines carrying the same 17-nucleobase duplication have been generated, and their cadmium content in the grains is currently being determined.



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Research Highlights

Using doubled haploid (DH) lines is one of the most effective biotechnological measures in modern plant breeding. One of the options for producing DH lines is to employ haploidy-inducing lines as paternal parents. Among the progeny resulting from such crosses, maternal haploids can be found that have lost the paternal genome during early embryogenesis. The PRB group generated primary barley mutants carrying Cas9-triggered mutations in PHOSPHOLIPASE A1 (PLA1), which produced about 6% haploid progeny upon pollination of wild-type plants. The haploidy-inducing capacity of homozygous pla1 M2 mutants was then validated by pollination of various barleys, which likewise resulted in useful efficiencies across all accessions tested.

While testing genome-edited crops in the field is still prohibited by the gene technology law (Gentechnikgesetz), the department successfully established approaches improving the investigation of crop root systems in the field. Using an automated soil corer to take soil samples down to 1 m depth, the vertical distribution of root biomass formation can be determined species-specific, even in mixed stands of different plant species. This approach allowed us to determine the contribution of catch crop roots to nitrogen and phosphorus carry-over to the following crop and environmental conditions that increase the importance of the roots for nutrient transfer (Heuermann et al. 2022, Eur. J. Agron.). Mapping element distribution along different root cell layers is fundamental to fully understand how roots partition nutrients and toxic elements with aboveground parts. In a cross-departmental approach, we developed a method that combines fluorescence-activated cell sorting (FACS) with high-resolution ICP-MS (HR-ICP-MS) to determine the concentration of up to 11 mineral elements in four main root cell populations (Fig. 1). This approach enabled us to assess element concentrations in different cell types, and to explore the consequences of perturbed xylem loading and complex nutrient interactions at cell type-specific level. This new method detected manganese enrichment in hair-forming epidermal cells as a response to limited iron availability. We demonstrated that manganese loading into vacuoles can efficiently retain this metal in roots when confined to root hairs but not to endodermal cells, suggesting the existence of cell type-specific constraints for efficient metal sequestration in roots. With the new approach, it will be possible to uncover novel mechanisms involved with ion distribution and transport pathways at high spatial resolution (Giehl et al., 2023, Nat. Commun.).

Flooding events are expected to become more frequent due to climate change, leading to losses of crop productivity. By investigating metabolic and transcriptomic profiles of roots and leaves of water-

Figure 1: Cell

type-specific mapping of ion distribution in roots. (A) Schematic representation of the developed FACS-ICP-MS method. Root protoplasts are isolated from cell type-specific reporter lines by cell wall digestion. Protoplast populations are separated by FACS, and multiple mineral elements in sorted cells are determined with HR-ICP-MS. (B) Concentrations of the indicated elements in four root cell types. Concentrations per unit tissue water (mM) were calculated according to the average volume of each sorted cell type. Bars represent means ± SD at element-specific scales, and average values are indicated.

Department Physiology and Cell Biology

logged wheat plants, we identified local responses to oxygen depletion confined to roots while alterations in carbohydrate metabolism and amino acid metabolism were associated with whole-plant (systemic) responses. Waterlogging decreased root-to-shoot translocation of nutrients, hormones and amino acids and strongly increased alanine concentration in the xylem sap. Alanine supplementation of excised leaves increased glucose concentration when the leaves were derived from waterlogged plants. Our results suggest that alanine plays an important role not only as an amino-nitrogen donor but also as a vehicle for carbon skeletons that can produce glucose de novo in response to altered energy demands triggered by waterlogging (Cid et al., J. Exp. Bot., Cid et al., 2023, J. Exp. Bot).

Pre-anthesis tip degeneration is a common feature of apical meristems in cereal crops. It starts with growth arrest of the inflorescence meristem dome, followed by degeneration of floral primordia. To elucidate the molecular underpinnings of apical meristem degradation in barley, Thorsten Schnurbusch initiated a concerted approach that included four PZB groups. Metabolomic, transcriptomic, and genetic approaches showed that meristem degradation is accompanied by sugar depletion, amino acid degradation, and hormone responses involving transcriptional regulators of senescence, defence, and light signalling. Based on the identification of an HD-ZIP transcription factor and a gene-editing approach, a knockout mutant of this transcription factor improved apical spikelet formation, suggesting a possible strategy to increase grain number in cereals (Shanmugaraj et al. 2023, Plant Cell).

Future Priorities

Of major priority in departmental research is the advancement and application of novel methods of site-directed genome engineering, which go beyond current targeted mutagenesis approaches by facilitating the generation of precisely intended modifications of the genomic DNA sequence. These approaches will be employed, for instance, to modify the function of genes that enhance abiotic and biotic stress tolerance, nutrient efficiency and plant architecture in cereals. In cooperation with groups of the other departments, promising variants of such genes have been identified by QTL mapping of relevant traits in barley and other cereals or by re-sequencing known genes in lines with contrasting phenotypes. In addition, knowledge about trait-modifying allelic variants of Arabidopsis genes are currently used in translational approaches for precise genome editing in barley.

With the successful recruitment of a new professor and establishment of her research group "Genetics and Physiology of Root Development", the department is strengthening its research profile in root-related research topics. The new professor-ship builds a bridge to the Faculty of Agricultural Sciences at the University of Göttingen. Currently, the new group is integrated in cooperative research projects and engages in the exploration of new root traits and the development of new methods in root phenotyping using the infrastructure that has been set up in the IPK-PhenoSphere.

Department Physiology and Cell Biology



RESEARCH GROUP **MOLECULAR PLANT NUTRITION** (MPE)



Head: Dr. Ricardo Giehl & Prof. Dr. Nicolaus von Wirén

Mission

The Molecular Plant Nutrition group investigates the transport and metabolism of mineral nutrients, their impact on phytohormone regulation, and their role in physiological and morphological responses to stress or agricultural production conditions. The research includes nutrient sensing mechanisms, especially those involved with the adjustment of root developmental processes to local nutrient availabilities or systemic plant signals. We further investigate nutrient efficiency and enrichment mechanisms in seeds and the nutrient-dependent regulation of abiotic stress responses.

Results

Selected Publications

Liu, Y. et al.: PDX1.1-dependent biosynthesis of vitamin B6 protects roots from ammonium-induced oxidative stress. Mol. Plant 15 (2022) 820-839.

Beier, S. et al.: Silicon mitigates potassium deficiency by enhanced remobilization and modulated potassium transporter regulation. Environ. Exp. Bot. 198 (2022) 104849.

Jia, Z., R.F.H. Giehl & N. von Wirén: Nutrient-hormone relations: Driving root plasticity in plants. Mol. Plant 15 (2022) 86-103.

Giehl, R.F.H. et al.: Cell type-specific mapping of ion distribution in Arabidopsis thaliana roots. Nat. Commun. 14 (2023) 3351.

Jia, Z. et al.: A spatially concerted epidermal auxin signaling framework steers the root hair foraging response under low nitrogen. Curr. Biol. 33 (2023) 3926-3941. Plants adjust to nitrogen (N) limitation by reshaping their root systems. A low-cost strategy to significantly increase the nutrient-acquiring surface of roots is the stimulation of root hair development. We found that N deficiency strongly increases root hair elongation in *Arabidopsis thaliana*, a response crucial for plant fitness under mild N deficiency. By combining transcriptomics, molecular genetics and cell biology approaches, we identified a spatially defined signalling framework that promotes low N-induced root hair elongation (Fig. 1A). The mechanism involves the recruitment of specific molecular players of auxin biosynthesis, transport and signalling that eventually activate the epidermal transcriptional module RHD6-LRL3 to stimulate root hair elongation (Jia et al., 2023, Curr. Biol.).

High ammonium concentrations, as found in ammonium-enriched fertilizer bands in agricultural crop production, can inhibit root growth. We found that ammonium uptake induces the accumulation of reactive oxygen species (ROS) along the stele of the elongation and differentiation zone in root tips (Fig. 1B). By screening ammonium sensitivity in T-DNA insertion lines of ammonium-responsive genes, we identified *PDX1.1*, which catalyzes de novo biosynthesis of vitamin B6. Disruption of *PDX1.1* increases root sensitivity to ammonium, while *PDX1.1* overexpression largely prevents ammonium-induced root growth inhibition. We further demonstrated that PDX1.1-dependent biosynthesis of non-phosphorylated forms of vitamin B6 suppresses hydrogen peroxide accumulation and counteracts ammonium-induced oxidative stress in root tips. The uncovered mechanism can be exploited to improve root tolerance to ammonium toxicity and improve root contact with N fertilizers (Liu et al., 2022, Mol. Plant).

The beneficial nutrient silicon (Si) is known to alleviate growth suppression and deficiency symptoms of several nutrient disorders, but little is known about the underlying regulatory processes. When investigating the impact of Si on potassium (K) deficiency responses in barley, we found that Si nutrition improved growth and metabolite homeostasis and partly reverted the K deficiency transcriptome signature in leaves but not in roots. In the short term, Si supply to K-starved roots induced the expression of the vacuolar K exporter *KCO1* and increased root-to-shoot trans-



location rates of the K analogue rubidium. In the long run, the more efficient remobilization of root K pools restored K-dependent metabolic processes in shoots for the sake of continued assimilate provision to roots. Thus, our study identified a sequence of physiological processes by which Si partially alleviates K deficiency and indicated that Si interferes with systemic K deficiency signal-ling in roots to alter the regulation of K transporters (Beier et al., 2022, Environ. Exp. Bot.).

Embedding in IPK Research Themes

With discoveries on plant responses and adaptations to nutrient deficiencies, the group's research is central to Research Theme 5, "Mechanisms of Resistance and Stress Tolerance". By performing mapping approaches on barley root and seed traits in inter-departmental collaborations, the group also contributes to IPK Research Themes 1, Valorization of Plant Genetic Resources" and 4, "Growth and Metabolism".

Within IPK and beyond, the group offers access to its technical platforms, which consist of UPLC-MS/MS (phytohormones), HR-ICP-MS (mineral elements), IR-MS (stable isotopes), and IC/LC-MS (primary metabolites and specific metabolite groups).

Outlook

Improved nutrient use efficiency is key for sustainable crop production. Thus, the group will continue its research on the identification and functional characterisation of mechanisms underlying nutrient allocation and nutrient-responsive root development and physiology but will further intensify the focus on barley. By combining root phenotyping in the rhizotron platform installed in the IPK-PhenoSphere with nutrient and tracer analyses, we aim to identify novel allelic variants determining optimal root growth in response to limiting or locally available nitrogen fertilizers as well as root traits best associated with improved nitrogen capture. Building on natural variation identified in Arabidopsis or barley genes, we are also targeting specific molecular processes with advanced genome editing technologies (CRISPR-Cas technology) to improve barley root growth under nutrient-limiting conditions. Figure 1: Spatially coordinated root developmental responses to limited N or high ammonium availability. (A) Low N increases root hair elongation by activating a spatially coordinated auxin signalling cascade that enters the root hair developmental program at the RHD6-LRL3 module. (B) Spatial accumulation of reactive oxygen species (ROS) in roots exposed to nitrate (NO3-) or increasing concentrations of ammonium (NH4+). Excess ROS in ammonium-exposed roots inhibits meristem size and cell elongation (arrowheads) and can be partially overcome by PDX1.1-mediated vitamin B6 biosynthesis.

More information: www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/molecular-plant-nutrition



YOUNG INVESTIGATOR GROUP SUSTAINABLE NUTRIENT MANAGEMENT (NNM)



Head: Dr. Diana Heuermann

Selected Publications

Groß, J. et al.: Influence of small-scale spatial variability of soil properties on yield formation of winter wheat. Plant Soil 493 (2023) 79-97.

Heuermann, D. et al.: Distinct metabolite classes in root exudates are indicative for field- or hydroponically-grown cover crops. Front. Plant Sci. 14 (2023) 1122285.

Gentsch, N. et al.: Soil nitrogen and water management by winter-killed catch crops. SOIL 8 (2022) 269-281.

Heuermann, D. et al.: Catch crop mixtures have higher potential for nutrient carry-over than pure stands under changing environments. Eur. J. Agron. 136 (2022) 126504.

Mission

The work of the perspective group NNM aims to improve the utilization and cycling of nutrients in agricultural crop rotations by the use of catch crops. We focus on characterising morphological and physiological root traits of different catch crop species and their effect on target crops. Specifically, we address the following questions:

- (i) What is the role of the vertical distribution of root biomass, of morphological root traits and metabolites released by roots on the nutrient uptake capacity of individual catch crop species and their mixtures?
- (ii) Which properties of catch crops increase their potential to reduce nutrient losses from agricultural soils?
- (iii) To what extent can catch crops alter the root morphology and the nutrient uptake by the target crop?

Results

Catch crops have a major function in accumulating nutrients in their biomass for subsequent transfer to the following target crop. However, individual catch crop species differ in their nutrient uptake capacities, while catch crop mixtures allow combining favourable aspects of different species. Our field trials showed that a mixture of four catch crop species accumulated more or at least as much nutrients as the best-performing pure stand across different locations and years, indicating that a mixture is more durable and robust in nutrient transfer when environmental conditions vary (Heuermann et al. 2022, Eur. J. Agr.).

Reasons for different nutrient uptake capacities lie e.g. in species-specific root properties, for example the root system and the quantity and composition of root exudates. Both are highly diverse among catch crop species. In the context of high phosphorus accumulation, phacelia roots exuded a significantly higher amount of organic acids than three other catch crop species, which is favourable for the solubilization of phosphate from sparingly available sources (Heuermann et al. 2023, Front. Plant Sci.). In addition, among eight investigated species phacelia showed the highest activity of acid phosphatase in its root exudates and the highest density of root hairs – both important features for phosphorus acquisition (Bouaoui, G.: Identification of physiological and morphological characteristics for phosphorus accumulation in different catch crop species. Mohammed VI Polytechnic University (Morocco), 2023. M.Sc. thesis in NNM group).

A further root exudate-mediated effect of catch crops is the capacity to inhibit the soil nitrification process via the release of biological nitrification inhibitors. Especially during winter periods with high precipitation, it is considered beneficial to reduce the formation of nitrate, which is highly prone to leaching. This can be achieved by inhibiting ammonium oxidation. In a field screening, we found the two Brassica species white mustard and oil radish as most efficient in inhibiting soil nitrification in autumn cultivation (Simon, A: Einfluss von Zwischenfrüchten auf die Nitrifikationsprozesse im Boden. Anhalt University of Applied Sciences, 2022. B.Sc. thesis in NNM group).

An interesting metabolite-based effect of catch crops has been observed on the root system distribution of a following maize crop when we analysed maize root biomass using qPCR- based quantification of root biomass along the vertical soil profile. Only clover stimulated the rooting depth of maize that was grown directly after the catch crop. By contrast, mustard, phacelia and oat, which developed much deeper root systems than clover, resulted in suppressed root elongation of maize. Interestingly, in dual mixtures with clover, the inhibiting effect of phacelia and oat was not apparent anymore. The effect appears to be mediated by root exudates as proven in a hydroponic growth assay. Moreover, after a rough fractionation based on polarity, the promoting or inhibiting effect of clover or mustard exudates, respectively, could be allocated to specific frac-



Maize growth on catch crop root exudate fractions in a bioassay



Figure 1: Shoot and root biomass of maize in a hydroponic growth assay with nutrient solution containing root extract fractions from mustard, clover or no exudates (control). Bars show means -s.d.; n=6. When denoted by an asterisk, means of mustard or clover were different from the respective control fraction at the 5 % significance level; unpaired t-Test. Extraction agent abbreviations: MTBE = Methyl-ter-butyl-ether, EA = Ethyl acetate, But = Butanol.

tions that were used as extraction solvents (Methyl-ter-butyl-ether fraction for clover; butanol fraction for mustard; Fig. 1). This opens the path for a bioassay-guided identification of metabolites with root-growth promoting or inhibiting function.

Embedding in IPK Research Themes

Fractionation

from catch crops

The NNM group addresses specifically topics of the IPK research theme 5 by investigating the importance of morphological and physiological root traits for nutrient acquisition by different catch crops in pure stands and mixtures, by analysing nutrient transfer to the subsequent crops in crop rotations, and by identifying root-released metabolites from catch crops that influence the root growth of the subsequent crop and the soil N cycle. These investigations are critical to understand and improve plant-soil interactions and lay basis for sustainable agricultural practice.

Outlook

In December 2023, the group was closed as the group leader moved on to a new position elsewhere. Ongoing work will be finished until mid-2024 by group technicians, and current collaborative projects will be taken over by Prof. Dr. N. von Wirén and Dr. R. Giehl (MPE group).

More information:

www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/sustainable-nutrient-management-young-investigators-group



GENETICS AND PHYSIOLOGY OF ROOT DEVELOPMENT (GPW)



Head: Prof. Dr. Hannah Schneider

Selected Publications

Huang, G. et al.: Ethylene inhibits rice root elongation in compacted soil via ABA- and auxin-mediated mechanisms. Proc. Natl. Acad. Sci. U.S.A 119 (2022) e2201072119.

*Lopez-Valdivia, I. et al.: Gradual domestication of root traits in the earliest maize from Tehuacan. Proc. Natl. Acad. Sci. U.S.A 119 (2022) e2110245119.

*Schneider, H.M.: Characterization, costs, cues and future perspectives of phenotypic plasticity. Ann. Bot. 130 (2022) 131-148.

*Schneider, H.M. et al.: Transcription factor bHLH121 regulates root cortical aerenchyma formation in maize. Proc. Natl. Acad. Sci. U.S.A. 120 (2023) e2219668120.

*Schneider, H.M. et al.: Root angle in maize influences nitrogen capture and is regulated by calcineurin B-like protein (CBL)-interacting serine/threonine-protein kinase 15 (ZmCIPK15). Plant Cell Environ. 45 (2022) 837-853.

*These publications are based on work that has been carried out when Prof. Dr. Hannah Schneider was at The Pennsylvania State University, USA and the Wageningen University and Research, The Netherlands.

Mission

The Genetics and Physiology of Root Development (GPW) group was established at the end of 2023 and investigates the genetic and physiological basis of plant root adaptations to drought and low soil fertility. Natural variation for root anatomical and architectural phenotypes can have significant effects on soil resource acquisition by modifying the placement of roots in soil domains where limiting resources are most available, improving the metabolic efficiency of soil exploration, altering the radial and axial transport of resources, influencing rhizodeposition, and impacting interactions with soil biota including mycorrhizal fungi, pathogens, and the rhizosphere microbiome. The group focuses on understanding the genetic and physiological basis of plant root adaptations to edaphic stress.

Results

Since the establishment of the research group in October 2023 several research projects are currently ongoing. Three major topics are currently covered by the group: (1) identification of the physiological function of root architectural and anatomical traits for soil resource capture, (2) discovery of genes underlying root phenotypes, and (3) development of modern tools and approaches in root phenotyping. Manuscripts with results from collaborations focused on characterising the physiology and genetic control of root anatomical and rhizosphere traits have been sent to peer review. Given the fact that the group is in its establishment phase, particularly emphasis has been put on recruiting personnel including students and postdocs. In spring 2024, two postdocs will start in the group on projects involving the genetic architecture and physiological function of anatomical traits.

Requests for funding from the DFG are currently written and other collaborative project proposals are currently in development. The group has established and maintains new collaborations with researchers at the IPK, in Germany and abroad. Embedded in the Department of Physiology and Cell Biology, GPW will provide vital links to ongoing research in root biology and plant nutrition (MPE) with research on structural changes at the cellular and subcellular level using microscopy facilities (SZB) and with genome editing (PRB), in which collaborations can help validate the function of important genes for stress tolerance. In addition, this group links closely with Faculty of Agricultural Sciences at the Georg August Universität of Göttingen with a Root Science Professorship where collaborations are being established in the Department of Crop Genetics and Plant Nutrition.

Embedding in IPK Research Themes

We aim to understand and genetic and physiological basis of the formation of important root traits to improve plant performance and growth, particularly in edaphic stress. For example, we are working to functionally validate novel genes for root anatomical and architectural traits that enhance soil exploration and yield under suboptimal nutrient conditions. With discoveries in the function and genetic control of root characteristics, GPW is embedded in IPK Research Theme 5 'Mechanisms of Resistance and Stress Tolerance' and Research Theme 4 'Growth and Metabolism.'



Figure 1: The research group GPW focuses on studying the genetics and physiology of root development through three main activities: identifying the function of root traits for water and nutrient acquisition and stress tolerance, discovering genes controlling root traits, and developing tools and approaches in root phenotyping.

Outlook

A main priority for the newly formed research group GPW will be the establishment of an internationally recognised research profile and the gain of visibility in Germany and abroad. This will be driven by the development of root phenotyping approaches combined with genetic and physiological studies in the laboratory, greenhouse, and field in collaboration with colleagues at the IPK, within Germany, and abroad. Particular emphasis will be placed on the topics of root phenotypic plasticity, root responses to multiple, simultaneous or successive stresses, and multiple interacting root traits in crop plants such as barley, maize, and wheat.

More information: www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/genetics-and-physiology-of-root-development



RESEARCH GROUP **PLANT REPRODUCTIVE BIOLOGY** (PRB)



Head: Dr. Jochen Kumlehn

Selected Publications

Gerasimova, S.V. et al.: WAX INDUCER 1 regulates β-diketone biosynthesis by mediating expression of the Cer-cqu gene cluster in barley. Int. J. Mol. Sci. 24 (2023) 6762.

Hoffie, R.E. et al.: Novel resistance to the Bymovirus BaMMV established by targeted mutagenesis of the PDIL5-1 susceptibility gene in barley. Plant Biotechnol. J. 21 (2023) 331-341.

Hölzl, G. et al.: Ablation of glucosinolate accumulation in the oil crop Camelina sativa by targeted mutagenesis of genes encoding the transporters GTR1 and GTR2 and regulators of biosynthesis MYB28 and MYB29. Plant Biotechnol. J. 21 (2023) 189-201.

Huang, Y. et al.: A molecular framework for grain number determination in barley. Sci. Adv. 9 (2023) eadd0324.

Dinh, H.X. et al.: The barley leaf rust resistance gene Rph3 encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of Puccinia hordei. Nat. Commun. 13 (2022) 2386.

Mission

The Plant Reproductive Biology research group has a strong focus on the establishment of enabling technologies such as plant genetic engineering and the generation of true-breeding plants originating from haploid cells. Through the development of biotechnological methods, the group aims to facilitate both basic research and translational approaches to improving crop plant performance. In this context, special attention is devoted to biological mechanisms relevant to plant reproduction, domestication, plant-pathogen interaction, and the formation of yield components.

Results

In landraces and wild relatives of cultivated barley, alleles of the susceptibility factor *PROTEIN DISULFIDE ISOMERASE-LIKE 5-1 (PDIL5-1)* were identified to confer resistance to all relevant bymovirus strains. Whereas introgression by crossing to the European winter barley breeding pool proved tedious, time-consuming and associated with unwanted linkage drag, we took a CRISPR-associated (Cas) endonuclease approach involving two barley cultivars. Homozygous barley mutants were produced, and some of those carrying novel *PDIL5-1* alleles were manually infected with Barley Mild Mosaic Virus. All translational frame-shift mutations and certain in-frame mutations conferred resistance to this virus. Under glasshouse conditions, virus-resistant mutants showed no significant adverse effects in growth and yield, which aligns with the observation that some landraces also harbour knockout alleles of *PDIL5-1* (Hoffie et al., 2023).

The EUCARYOTIC TRANSLATION INITIATION FACTOR 4E is another barley susceptibility factor recruited by bymoviruses. Targeted single nucleotide exchanges were achieved at two positions in the *HvEIF4E* gene by base editing resting on a Cas9 nickase-cytidine deaminase gene fusion. This resulted in nine novel alleles in addition to a precise recreation of a resistance-associated mutation known from historical material. These mutants represent promising germplasm for expanding the resistance portfolio against the yellow mosaic virus disease.

The resistance of plants to abiotic and biotic stressors depends mainly on the wax formations deposited on the epidermis. In a joint study in 2021 with the Institute of Cytology and Genetics in Novosibirsk, we knocked out the *WAX INDUCER 1* gene of barley by employing gene-specifically addressed Cas9 endonuclease, which led to a significant reduction in the formation of epicuticular waxes on the leaf sheath and to a corresponding glossy phenotype. A transcriptome analysis performed with these *win1* mutants revealed a strong regulatory influence of WIN1 on the genes of the known *Cer-cqu* cluster located on chromosome 2H. The ultimate result of this study was the expansion of the *Cer-cqu* cluster to include nearby co-regulated genes as well as the identification of HvWIN1 as a master mediator of the biosynthesis of β -diketones and alkylresorcinol, whereby the developmental and organ-specific regulation of the *Cer-cqu* gene cluster plays a decisive role (Gerasimova et al. 2023).

Camelina (*Camelina sativa*) is an oilseed plant that is comparatively tolerant to various adverse conditions, such as drought and nutrient-poor soils. In addition, its seeds' unique fatty acid profile renders camelina particularly suitable for providing food and health products. In cooperation with colleagues from the University of Bonn, we knocked out the *MYB28* and *MYB29* transcription factors that are positive regulators of the biosynthesis of aliphatic glucosinolates. As a result, we were the first to generate lines of a Brassicaceae crop with no detectable glucosinolate content in their seeds, thereby setting the grounds to produce plant oil of unprecedented quality (Hölzl et al., 2023).

A	1356 bp Deletion, hap-XXVIII	Non-synonymous S hap-XVIII	SNP,	
в	Pre-Sto frames	op SNPs or shifts		HvPDIL5-1res
Ta 5'	rget Motif 1: TM 2: UTR ATG	1 † TM 3 + 4: Exon 3		//vPD/L5-1sus
С	Mutant line	Induced Mutation	D	
	Target Motif 1		Arrest Control of Cont	
	GPTM1_P12	2 bp Deletion	i de alt	
	GPTM1 P16	1 bp Deletion		
	Target Motif 2			
	lgri_4_P1	2 bp Deletion		
	lgri_6_P2	22 bp Deletion		
	lgri_7_P1	4 bp Insertion		
	GPTM2_P11	1 bp Insertion		
	GPTM2_P22	21 bp Deletion		
	Target Motif 4			DIAN
	GPTM4_P5	Base substitutions A254T + T236A		
	GPTM4_P14	2 bp Deletion		
	GPTM4_P21	1 bp Insertion	- BaMMV	+ BaMMV

Embedding in IPK Research Themes

By establishing and providing cutting-edge genetic engineering and further biotechnological methods, the PRB group takes on a major integrating function for cross-departmental research and is involved in all five strategic IPK Research Themes. PRB head Jochen Kumlehn coordinates the Research Theme 3, "Mechanisms of Plant Reproduction".

Outlook

Our future efforts to improve the precision in genome editing approaches will focus on homology-mediated end joining of Cas endonuclease-processed DNA. To extend the IPK's genome editing platform, we will establish Cas9 from *Staphylococcus aureus* and Cas12a variants, which both have particularly beneficial features. For the same reason, we envisage further reducing the dependency of genetic engineering on the genotype by pursuing various approaches. Traits addressed by genome editing comprise nutrient use efficiency and durable resistance to multiple rusts. We recently embarked on a project to establish components of apomictic development in barley. Moreover, the group will continue its efforts to establish advanced biotechnologies for scientifically important model species such as St. John's wort (*Hypericum perforatum*), buckwheat (*Fagopyrum esculentum*), Boechera as well as for the hitherto under-utilized pseudo-cereal quinoa (*Chenopodium quinoa*).

virus-resistant barley by genome editing. (A) By screening the barley diversity in the IPK's genebank, several haplotypes of the known susceptibility gene HvPDIL5-1 were discovered that render barley resistant against infections with Barley Mild Mosaic Virus (BaMMV) and Barley Yellow Mosaic Virus. (B) The gene regions mutated in these resistant accessions were addressed in susceptible barley cultivars by customized guide RNAs and Cas9 endonuclease. (C) Various PDIL5-1 mutants were generated, most of which carried frame-shift mutations entailing functional knockouts. Listed are events from which homozygous M2 lines were obtained. All tested lines proved resistant to manual infection with BaMMV in the glasshouse. (D) Resistant lines grown in the glasshouse did not show adverse effects on yield components investigated. res: resistant allele, sus: susceptible allele, TM: target motif, GP: cv. Golden Promise; BaMMV: Barley Mild Mosaic Virus

Figure 1: Generation of

More information: www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/plant-reproductive-biology



RESEARCH GROUP **STRUCTURAL CELL BIOLOGY** (SZB)



Head: Dr. Michael Melzer

Selected Publications

Huang, Y. et al.: A molecular framework for grain number determination in barley. Sci. Adv. 9 (2023) eadd0324.

Kuo, Y.-T. et al.: Holocentromeres can consist of merely a few megabase-sized satellite arrays. Nat. Commun. 14 (2023) 3502.

Daszkowska-Golec, A. et al.: Multi-omics insights into the positive role of strigolactone perception in barley drought response. BMC Plant Biol. 23 (2023) 445.

Liu, Y. et al.: PDX1.1-dependent biosynthesis of vitamin B6 protects roots from ammonium-induced oxidative stress. Mol. Plant 15 (2022) 820-839.

Saado, I. et al.: Effector-mediated relocalization of a maize lipoxygenase protein triggers susceptibility to Ustilago maydis. Plant Cell 34 (2022) 2785–2805.

Mission

As central facility for light and electron microscopy, the RG SZB provides a platform that covers application, maintenance and guided use of equipment and the development of new protocols for preparation and subsequent structural analysis of plant tissues. In the framework of own research projects, internal and external cooperations, the group mainly investigates plant organ and organelle morphology, cellular ultrastructure and the spatial distribution of enzymes and molecules as analysed by light, electron or fluorescence microscopy. With a focus on vascular structures, lodging resistance and drought stress, the group contributes to the characterisation and improvement of agronomically relevant traits in crops or biotechnological procedures.

Results

Vascular patterning is of great importance for plant form and function, yet there are few studies on the vascular anatomy of cereal plants and of inflorescences in particular, although these are of great importance for yield formation. Using barley as an example, we have started to clarify the relationship between the vascular dynamics within the spike rachis and spike size. Using serial internode sections from several barley lines with different spike sizes, we analysed internode diameter, vascular area and number of veins along the mature barley rachis. Our investigation revealed that the rachis vasculature is the result of a two-step process involving an initial lay-out followed by size adjustment according to floret fertility and spike size. Transport capacity appears mainly regulated by vein size. The functional processes of long distance transport and local supply to spikelets are spatially separated while a vascular continuity between rachis and spikelets appears not essential (Fig 1).

Together with the RG PRB and the University of Silesia, Poland, we continued the investigation of the role of strigolactones (SLs) in barley in response to drought stress. The analysis of transcriptome, proteome, phytohormones and physiological responses revealed that drought sensitivity of the TILLING mutant *hvd14* is related to weaker induction of ABA-responsive genes, lower jasmonic acid content, higher abundance of reactive oxygen species, and lower wax biosynthesis and deposition than in wild-type plants. In addition, we identified a set of transcription factors that lost upregulation in the mutant. Currently, various SL mutants that were generated by RNA-guided Cas9 endonuclease technology and are defective in biosynthesis or signal transduction are being analysed.

In cooperation with the RG MPE and the University Rosario, CONICET (Argentina), we have shown by immunolocalization and electron microscopy that targeting of the bacterial flavodoxin to chloroplasts of mesophyll but not bundle sheath maize cells confers increased drought tolerance. By identifying the type of intervention required to improve stress tolerance in plants ectopically expressing flavodoxin, we provide a more effective rationale for engineering crops for better growth and yield in stressful environments. In addition, the combination of tissue-specific expression with alternative electron shuttles, such as flavodoxin, provides a novel research tool to investigate the complex relationship between environmental stress and C4 photosynthesis.

An ongoing challenge is the establishment of high pressure freezing as high-end method for sample preparation of plant tissues. In the past 2 years, we were able to decisively optimize protocols for cryofixation of plant tissue thanks to our new Compact 03 HPF system. In particular, the successful cryofixation of leaf material is crucial for future high-end immunolocalization and ultrastructure studies (Fig. 2).



Figure 1: Spike morphology of barley, cv. Golden Promise. (a) Mature spike and central view of the rachis after removal of spikelets. (b) Schematic view of the rachis showing the two opposite rows of median veins and the alternate arrangement of nodes on either side of the rachis. Serial internode sectioning enables the analysis of vascular changes when passing a node (A to B = internodal) and between two nodes (C to D = intranodal). (c) Transverse internode sections reveal three types of vascular bundles. (d) Schematic view of internode shape in grey. (e) Schematic view of size and distribution of main vascular bundles. M, median; L, lateral; OL, outer lateral; P, peduncle. Bar = 1000 µm (a), 200 µm (c, d, e). (T. Rutten, M. Melzer).



Figure 2: High Pressure Freezing of plant tissues for ultrastructural analysis. (a) Mesophyll chloroplast of maize leaf, (b) barley pollen with canobacteria as filler for high pressure freezing, (c) epidermis cell wall of a wheat leaf, (d) anther cell of Arabidopsis thaliana. CB, cyanobacteria; Ch, chloroplast; CS, cytoplasmic strand; CW, cell wall; D, dictyosome; ER, endoplasmatic reticulum; M, mitochondrion; ML, middle lamella; N, nucleus; P, plastid; Px, peroxisome; S, starch; V, vacuole (M. Melzer, T. Rutten).

Embedding in IPK Research Themes

Investigations on the role of strigolactones in barley in response to drought, studies on lodging resistance and vascular organisation in crops contribute to research focus 4 (Growth & Metabolism) and 5 (Mechanisms of Resistance and Stress Tolerance).

As the central facility for microscopy, the RG SZB is also involved in a large number of internal and external collaborations that cover a wide range of research topics. The work of the group is thus linked to all IPK Research Themes..

Outlook

In order to determine structural and morphological traits of lodging in crop plants, pre-selected contrasting accessions of wheat and barley are currently undergoing detailed histological examination. In this context, a mapping population of 200 barley accessions from the IPK Genebank is currently analysed.

By extensive cell biological investigations and the generation of single-nuclei gene expression data (in cooperation with CEPLAS) we aim at defining gene regulatory networks that underpin differential leaf anatomy in C3 species and C3-C4 intermediates of the Brassicaceae. The cooperation will help leveraging synergies between IPK and CEPLAS and hence strengthen the strategic partnership between IPK and CEPLAS.

More information: www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/structural-cell-biology



Independent Research Groups

Meiosis (ME) Dr. Stefan Heckmann

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Applied Chromosome Biology (ACB) **Prof. Dr. Hua Jiang**

Grain legume genomics (GLG) **Dr. Murukarthick Jayakodi**





INDEPENDENT RESEARCH GROUP **MEIOSIS** (ME)



Head: Dr. Stefan Heckmann

Selected Publications

Schreiber, M. et al.: Recombination landscape divergence between populations is marked by larger low-recombining regions in domesticated rye. Mol. Biol. Evol. 39 (2022) msac131.

Ahmadli*, U., M. Kalidass* et al.: High temperature increases centromere-mediated genome elimination frequency and enhances haploid induction in Arabidopsis. Plant Commun. 4 (2023) 100507.

Feng, C. et al.: TurboID-based proteomic profiling of meiotic chromosome axes in Arabidopsis thaliana. Nat. Plants 9 (2023) 616–630.

Steckenborn*, S., M. Cuacos* et al.: The meiotic topoisomerase VI B subunit (MTOPVIB) is essential for meiotic DNA double-strand break formation in barley (Hordeum vulgare L.). Plant Reprod. 36 (2023) 1-15.

Tamilselvan-Nattar-Amutha, S. et al.: Barley stripe mosaic virus-mediated somatic and heritable gene editing in barley (Hordeum vulgare L.). Front. Plant Sci. 14 (2023) 1201446.

* joint first authorship

Mission

The independent research group Meiosis, currently majorly funded by the European Research Council (ERC) in the frame of the ERC Starting Grant MEIOBARMIX, focuses on the process of meiosis in plants. During meiosis, genetic variation arises through homologous recombination (HR), harnessed during breeding. However, in many plants, HR events are limited in number and enriched at chromosome ends. This skewed distribution is particularly found in cereals such as barley, whereby a large portion of the genetic material remains untapped during breeding. Hence, altering meiotic HR outcome (frequency and distribution) is attractive to overcome this plant recombination bottleneck.

Results

The molecular cytogenetic activities of the team can be broken down into three key research areas, together aiming to manipulate plant meiotic recombination landscapes: i) understanding of the mechanisms underlying meiotic HR control, including chromosome axis and synaptonemal complex (SC) regulation, ii) development of novel tools and strategies to assess and modify meiotic HR outcome, and iii) application of acquired knowledge in barley to modify its recombination landscape. The key results of our team in the three subareas are as follows:

To dissect the meiotic chromosome axis's role in crossover (CO) formation, we performed proteomic profiling of the meiotic chromosome axis in Arabidopsis using axis proteins fused to TurboID (TbID) coupled with mass spectrometry. Among 39 identified candidates, most known axis-related and novel proteins were found. After mutant screening, we identified (at least) four novel candidates with a meiotic mutant phenotype. Among them, one was found to be part of the SC. In its absence, SC formation is disrupted, chiasma formation is reduced, and CO levels are increased. The exact meiotic role of other candidates is under investigation. We also generated plants expressing the only known (ZYP1) and the novel identified SC protein fused to TbID to dissect the composition of the SC.

We established heteroallelic marker systems based on plant phenotypes to dissect meiotic HR events at a given genomic locus. Embarking on these systems, we are exploring whether, either by tethering the endogenous DSB-complex or by expressing different endonucleases specifically in meiotic cells, targeted meiotic DSBs can be induced and what is their repair outcome. To rapidly assess (meiotic) gene function in barley, we established barley stripe mosaic virus-induced genome editing (BSMVIGE), enabling heritable editing at target sites without the need of stable genetic transformation. Given the impact of the axis and the SC on the recombination landscape, we have isolated various axis and SC mutants via BSMVIGE in barley. Crystal digital PCR-based single pollen nucleus genotyping has been utilised to measure CO rates in pro- and anti-CO factor mutants and spikes of different ages or grown under different conditions, showing recombination rate plasticity.

In barley, we functionally dissected genes known in Arabidopsis to be required for DSB (DSB induction complex) or CO formation (pro-CO factors) and to actively inhibit CO formation (anti-CO factors). In the case of *mtopVIB* (member of the DSB induction complex), meiotic DSB and CO formation were completely abolished. While depletion of the anti-CO factor RECQ4 results in a *hyperrecombination* phenotype, depletion of the anti-CO factor FIGL1 results in reduced levels of class I CO but increased levels of class II CO. Moreover, HEI10 is critical for class I CO formation (pro-CO factor). Based on BSMVIGE, we have isolated barley mutants defective for different steps of the meiotic programme, which are currently under investigation.



Figure 1: Selected research activities of team ME. Left: TurboID-mediated biotinylation of meiotic chromosome axes in Arabidopsis thaliana. Right: A novel SC protein identified reflects spatiotemporal asymmetry in meiotic progression in barley.

Embedding in IPK Research Themes

Our research on meiosis is tightly linked to the activities of the Department of Breeding Research, particularly in chromosome biology. We contribute with our research on meiotic chromosome behaviour and recombination control underpinning plant fertility to the IPK Research Theme 3, "Mechanisms of Plant Reproduction."

Outlook

The future main topics of our team will be to 1) dissect the impact of candidate genes and biotic and abiotic factors on the barley recombination landscape 2) elucidate the precise role of the identified candidates in the meiotic chromosome axis and recombination and TbID-based isolation of novel components of the SC 3) develop and apply tools for targeted induction of meiotic recombination 4) dissect local HR frequency and identify factors involved and 5) apply and further develop of novel tools (e.g. pollen nucleus genotyping, BSMV-based microscopy) to study and modify meiotic recombination.

More information: www.ipk-gatersleben.de/en/research/independent-research-groups/meiose



INDEPENDENT RESEARCH GROUP **APPLIED CHROMOSOME BIOLOGY** (ACB)



Head: Prof. Dr. Hua Jiang

Selected Publications

Yi, J. et al.: Meiocyte size is a determining factor for unreduced gamete formation in Arabidopsis thaliana. New Phytol. 237 (2023) 1179-1187.

Piskorz, E.W. et al.: Double-haploid induction generates extensive differential DNA methylation in Arabidopsis. J. Exp. Bot. 74 (2023) 835–847.

Wang, N. et al.: The plant nuclear lamina disassembles to regulate genome folding in stress conditions. Nat. Plants 9 (2023) 1081–1093.

Xu, L., J. Cheng & H. Jiang: Mutation of histone H3 serine 28 to alanine influences H3K27me3-mediated gene silencing in Arabidopsis. Plant Physiol. 190 (2022) 2417–2429.

Cheng, J. et al.: H3K9 demethylases IBM1 and JMJ27 are required for male meiosis in Arabidopsis thaliana. New Phytol. 235 (2022) 2252-2269.

Mission

The independent research group Applied Chromosome Biology focuses on investigating the genetic and epigenetic regulation of reproductive development. Our primary focus is to better understand the molecular mechanisms that control fertility, a critical aspect of crop breeding. In addition, the impact of rising temperatures on reproduction is a major concern, as it is associated with a decline in global crop yields. Consequently, there is an urgent need for new knowledge and approaches to improve reproductive thermotolerance. This is essential to ensure sustainable fertility and optimal crop yield in the face of climate change.

Results

Research activities aim to a) Identify the role of epigenetic regulation in reproduction, b) Understand how cytoplasmic compartments maintain ploidy stability during meiosis, and c) identify novel regulators required for enhanced reproductive thermotolerance. Embarking on genetics, epigenetics, biochemistry, and cytogenetics, key results of our team include:

a) Identifying the role of H3K9 demethylation in reproduction. Dimethylation of histone H3 lysine 9 (H3K9me2) is a crucial modification for genome stability, yet its role in plant development is largely unknown. We show that H3K9 demethylases IBM1 and JMJ27 cooperatively regulate crossover formation and chromosome segregation in male meiosis by removing H3K9me2. In addition, IBM1 and JMJ27 interact with the Precocious Dissociation of Sisters 5 (PDS5) cohesin complex cofactors to regulate male meiosis and gene expression independently of H3K9 demethylation. These findings uncover a novel role of H3K9me2 removal in meiosis and a new function of H3K9 demethylases and cohesin cofactors in meiotic transcriptional regulation.

b) Exploring how cytoplasmic compartments separate spindles during male meiosis. We investigated the mechanisms of unreduced gamete formation in male meiosis, a process important for polyploidization. Specifically, we have found the role of the organelle band, meiocyte size, and vesicle trafficking in unreduced gamete formation.

c) Identifying epigenetic alterations in polyploids and doubled haploids. We showed that in Arabidopsis, different tetraploid ecotypes presented different flowering times. Accordingly, the level of a repressive epigenetic mark, trimethylation of histone H3 at lysine 27 (H3K27me3), was differentially altered after genome doubling between different ecotypes, potentially leading to different flowering times. Moreover, we also explored the epigenetic effect of ploidy changes in doubled-haploidisation. Our results showed that DH induction leads to abundant regions with differential DNA methylation associated with altered gene expression.

Embedding in IPK Research Themes

Our research on reproduction and fertility is closely linked to the research of the department Breeding Research, particularly in the area of chromosome biology. We contribute with our research efforts on genetic and epigenetic fertility regulation to the IPK Research Theme 3, "Mechanisms of Plant Reproduction".

Outlook

In December 2023, the group was closed as the group leader received a DFG-Heisenberg fellowship and moved on to a new position elsewhere.



Figure 1: Selected research activities of team ACB: Fertility (A, B) and meiosis in WT and ibm1 jmj27 (C) (Cheng et al., 2023).

More information: www.ipk-gatersleben.de/en/research/former-research-groups/2024/angewandte-chromosomenbiologie



INDEPENDENT RESEARCH GROUP **GRAIN LEGUME GENOMICS** (GLG)



Head: Dr. Murukarthick Jayakodi

Selected Publications

Jayakodi, M. et al.: The giant diploid faba genome unlocks variation in a global protein crop. Nature 615 (2023) 652-659.

Zhang, H. et al.: Advancing grain legumes domestication and evolution studies with genomics. Plant Cell Physiol. 63 (2022) 1540–1553.

Wang, Y. et al.: High-resolution mapping of Barley mild mosaic virus resistance gene rym15. Front. Plant Sci. 13 (2022) 908170.

Kamal, N. et al.: The barley and wheat pan-genomes. In: Edwards, D. (Ed.): Plant bioinformatics: methods and protocols. (Series: Methods in molecular biology, Vol. 2443) New York, NY: Humana (2022) 147-159.

Sudha, M. et al: Dynamic transcriptome profiling of mungbean genotypes unveil the genes respond to the infection of mungbean yellow mosaic virus. Pathogens 11 (2022) 190.

Mission

The independent research group Grain Legume Genomics (GLG) was established in 2022. Our group aims to activate plant genetic resources to develop a genomic breeder's toolkit for faba bean (*Vicia faba* L.). Specifically, we want to collect molecular passport data for thousands of faba bean accessions, generate chromosome-scale reference sequences for at least twelve diverse genotypes, and build a pan-genome infrastructure. In addition, for a panel of hundreds of diverse lines, we will collect deep resequencing data and obtain metabolic profiles to identify genomic regions associated with nutritional quality as future targets for genomics-assisted crop improvement.

Results

Faba bean (Vicia faba L.), belonging to the tribe Fabeae, is a widely grown grain legume supplying dietary protein for humans and livestock. Originating in Southwest Asia, the faba bean is one of the founder crops of modern agriculture and is rich in carbohydrates, fibre, and micronutrients. The wild progenitor of the faba bean is still unknown, but archaeological records date back to its subsistence in el-Wad (Mount Carmel, Israel) about 14,000 years ago. V. faba has long appeared as a model to study plant cytogenetic phenomena due to the advantage of six giant chromosome pairs of 1.3 to 3.3 Gb (2n=2x=12). Furthermore, the faba bean is the largest diploid crop genome that serves as a true model to understand the fundamental route of genome size expansion in angiosperms, which exhibit a quite broad range of genome size variations. The great ability of faba bean to fix atmospheric nitrogen, adapt to diverse agro-climatic conditions, support farmland biodiversity and increase cereal crop yield in crop-rotation systems offers unprecedented opportunities to build a sustainable farming system for food and nutrition with fewer environmental footprints in temperate regions. As part of international consortia, we assembled the giant diploid faba bean genome (~ 13 Gb) as a first step. Especially chromosome 1 is a size of \sim 3.4 Gb, which is bigger than the entire human genome. Our faba bean genome assembly is one of the major technical milestones in plant genomics. Our study was published very recently in Nature (PMID: 36890232). Subsequently, we maximised the genome assembly quality with a bio-nano optical map, which enabled us to increase the contiguity of scaffolds and implement the pan-genomics study in faba bean. Further, assessing genetic diversity is a primary step in implementing a pan-genome study. However, the lack of cost-effective genotyping limits the characterisation of large germplasm collections, understanding genetic diversity across populations, and implementing breeder tools like genomic selection. Genotyping-by-sequencing (GBS) offers high-resolution genotyping for model and non-model plant species. Species with complex genomic architecture, like faba bean, require optimisation of GBS with proper restriction enzyme (RE) to realise the full potential of GBS. Recently, our research evaluated GBS with various REs and found the appropriate combination for faba bean genotyping. With our optimised GBS protocol, we fingerprint 2,648 accessions representing global diversity to accelerate faba bean breeding and research. Collectively, our efforts will unearth hidden precious plant resources for future crop improvement in sustainable production systems.

Embedding in IPK Research Themes

Our research is embedded in IPK Research Theme 1, "Valorisation of Plant Genetic Resources and 2, "Genome Diversity and Evolution". Particularly, our ongoing project on faba bean is embedded in IPK's mid-term strategy of transforming its genebank into a biodigital resources centre, which necessitates the extension of the genebank genomics toolkit to crop species other than IPK's traditional forte, the cereals wheat and barley.



Figure 1: (a) Intrachromosomal contact matrix of assembled chromosomes. The red colour intensity indicates the normalized Omni-C Hi-C links between 1-Mb windows on each chromosome. The antidiagonal pattern in chromosome 1 represents the Rabl configuration. (b) Distribution of major families of satellite repeats (FabTR-83 in green, FabTR-64 in red, FabTR-53 in magenta and Fokl in yellow). (c) Distribution of major families of satellite repeats on metaphase chromosomes visualized by multicolour fluorescent in situ hybridization. (d) Distribution of genomic components, including recombination (cM per Mb), gene density, LTR retrotransposons of Gypsy and Copia, full-length LTR-retrotransposon (fl-LTR) insertions, satellite repeats and DNA methylation (CH, CHG and CHH context) on chromosome 1. The red dashed line represents the centromere position. This figure is taken from the original publication PMID: 36890232; DOI: 10.1038/s41586-023-05791-5, licensed under a Creative Commons Attribution 4.0 International License.

Outlook

We will develop a global diversity space for faba beans using our GBS sequencing. This will allow us to select a set of 500 diverse genotypes to study important biochemical traits such as vicine and convicine and amino acids. Furthermore, we are establishing a pangenome consortium ("PanFaba") with multinational partners for faba bean. As this consortium's main partner, we have selected 12 representative genotypes covering faba bean diversity space. Besides, we expand our research activities into bitter vetch (*Vicia ervilia*) genomics with our Israeli partner.

More information: www.ipk-gatersleben.de/en/research/former-research-groups/2024/koernerleguminosen-genomik

Publications

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Abo-Elyousr, K.A.M., **A.M.I. Mourad**, P.S. Baenziger, A.H.A. Shehata, P.E. Eckstein, A.D. Beattie & **A. Sallam**: Identification of putative SNP markers associated with resistance to Egyptian loose smut race(s) in spring barley. Genes 13 (2022) 1075.

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Dreyer, B.H.: Superoxide dismutase 1 is a multifunctional protein that can act as transcriptional regulator in Arabidopsis. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2023) 145 pp.

Forster, M.A.: The role of root plasticity and cytokinins on the adaptation of barley plants to localized nitrogen supply. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2023) 76 pp. Garbaden, C.: Funktionale Validierung von Non-Host-Resistenz-Kandidatengenen der Gerste mittels transient-induzierter Gen-Silencing. (Bachelor Thesis) Hochschule Anhalt, Fachbereich Angewandte Biowissenschaften und Prozesstechnik, Köthen (2023) 72 pp.

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Hecht, H.: Identification of Fe-specific novel genes using transcriptome analysis in stem base of petunia cuttings. (Bachelor Thesis) Hochschule Anhalt, Fachbereich Angewandte Biowissenschaften und Prozesstechnik, Köthen (2023) pp.

Heliel, O.F.H.: Functional evaluation of *RAMO-SA2* cis-regulatory regions from different grass species for shaping inflorescence architecture in barley. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. (2023) 168 pp.

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Huch, C.: Charakterisierung des Einflusses der Stickstoffernährung und von Zwischenfrüchten mit hoher nitrifikationshemmender Wirkung auf den Nitrifikationsprozess im Boden und auf die Stickstoffeffizienz von zwei Sommerweizengenotypen. (Bachelor Thesis) Ernst-Abbe-Hochschule, Fachbereich Medizintechnik und Biotechnologie, Jena (2023) 47 pp.

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Kurra, V.: Impact of resistance genes on cereal dwarf virus key epidemiological parameters in barley. (Master Thesis) Georg-August-Universität Göttingen, Fakultät für Agrarwissenschaften, Göttingen (2023) 45 pp.

Nagesh, K.: Characterization of NAC6 transcription factor in barley during development and stress. (Master Thesis) Universität Hohenheim, Stuttgart (2023) 51 pp.

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Schönau, L.: Analyse der CENH3 Expression in verschiedenen Sorten von *B. napus*. (Bachelor Thesis) Ernst-Abbe-Hochschule Jena, Fachbereich Medizintechnik und Biotechnologie, Studiengang Biotechnologie, Jena (2023) 41 pp.

Shanmugaraj, N.: Spatiotemporal multi-omics analyses of the barley (*Hordeum vulgare* L.) inflorescence reveal a multilayered regulation of developmentally programmed pre-anthesis tip degeneration. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. (2023) 193 pp.

Słomińska-Durdasiak, K.M.: Host-induced gene silencing as resistance strategy against pathogens. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. (2023) 135 pp. **Steckenborn Coria, S.**: Towards the induction of site-directed meiotic recombination. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. (2023) 106 pp.

Topali, G.: Untersuchung des Kandidatengens AT5G04280 bezüglich eines möglichen Beitrags zu frühen Wachstumsunterschieden in *Arabidopsis thaliana*. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2023) 43 pp.

Vásquez Valerio, F.: Gene regulatory networks in barley: Analysis of transcription factor binding sites. (Bachelor Thesis) Instituto Tecnológico de Costa Rica, Costa Rica (2023) 35 pp.

Vogt, A.: *In silico* and *in vivo* analysis of the *Arabidopsis thaliana* protein AtFutsch to aid the investigation of the *Secale cereale* protein NCR28 and its role in rye B-chromosome drive. (Master Thesis) Ruprecht-Karls-Universität Heidelberg, Fakultät Biowissenschaften, Heidelberg (2023) 107 pp.

Wang, H.: Differential regulation of the proteasome by internal and external factors during plant development. (PhD Thesis) RWTH Aachen, Aachen (2023) 136 pp.

Wegner, U.: Spezifische ω -Transaminasen zur Herstellung von enantiomerenreinen β - und γ -Aminosäuren. (PhD Thesis) Universität Greifswald, Mathematisch-Naturwissenschaftliche Fakultät, Greifswald (2023) 142 pp.

Xu, L.: Insights into the role of an Arabidopsis nuclear matrix binding protein AHL22 in chromatin regulation and hypocotyl growth. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. (2023) 98 pp.

Patents 2022

Wilde, P., V. Korzun, J. Menzel, **R. Zhou**, **N. Stein** & B. Hackauf: Restorer Pflanze. (Industrieanmeldung durch KWS SAAT SE & CO KGAA) Offenlegung: 29.06.2017, IPK-Nr.: 2014/04, W02017109012A1; Erteilung in EP als EP3393234B1 am 15.12.2021 und in USA als US11312967B2 am 26.04.2022. (2022).

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Third party projects

Third-party funded projects acquired and ongoing in the 2022/2023 reporting period.

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
EpiC-p-epBAR: Das Pan-Epigenom der Gerste	Stein, N.	BMBF	01/07/22	30/06/25	657.135
Fortress-Wheat: Bioökonomie International 2021: Untersuchung und Aufklärung neuer genetischer Variation in der Interaktion zwischen Weizen und Rostkrankheiten für einen pestizidreduzierten Weizenanbau-TP2	Mascher, M.	BMBF	01/10/22	30/09/25	40.462
Physics4Seeds: Effekte einer Plasmabehandlung auf Keimfähigkeit von Rotklee und Rispengras	Dehmer, K.J.	BMBF	01/07/20	31/10/22	141.814
Fortress-Wheat: Bioökonomie International 2021: Untersuchung und Aufklärung neuer genetischer Variation in der Interaktion zwischen Weizen und Rostkrankheiten für einen pestizidreduzierten Weizenanbau-TP1	Reif, J.	BMBF	01/10/22	30/09/25	232.092
Euroduckweed: Etablierung eines Europäischen Zentrums für Was- serlinsenforschung in Kiew	Schubert,I.	BMBF	01/12/21	31/05/23	34.750
EpiChrom: EpiC-Epigenetik, Epigenetische Konsequenzen von Chro- mosomrestrukturierungen – TP B	Houben, A.	BMBF	01/07/22	30/06/25	338.612
TomKin: Produktion haploider Tomaten mit Hilfe der Manipulation des Kinetochors	Lermontova, I.	BMBF	01/05/20	31/12/22	15.954
BreedFides: Verbundprojekt: Entwicklung eines nachhaltigen Daten- ökosystems für die Pflanzenzüchtung – BreedFides; Teilvorhaben: Förderierte Dateninfrastruktur für eine Datentreuhänderschaft und deren Tests anhand von Use Cases	Lange, M.	BMBF	01/01/22	31/12/24	362.721
DROMAMED: PRIMA-Verbundprojekt: Nutzung von mediterranen genetischen Ressourcen von Mais zur Verbesserung der Stress- toleranz; Teilv.: Präzisionsphänotypisierung von Maislienien aus mediterranen Populationen für Trocken- und Hitzestress-bezoge- nen Mer	Altmann, T.	BMBF	01/06/21	30/11/24	249.936
DPPN-Access: Förderung der Nutzung von Anlagen und Technolo- gien zur Pflanzenphänotypisierung	Altmann, T.	BMBF	01/01/22	31/12/23	154.000
KABA-2021: Innovative Technologien für die verbesserte Züchtung und Vermehrung von Kaffee- und Bananenpflanzen in Kuba	Rolletschek, H.	BMBF	01/07/21	30/06/24	62.954
INPUT: KMU-innovativ-23: INPUT – Entwicklung eines Schnell-Test- Systems zur Steuerung des Produktionsfaktoren-Inputs während der Erzeugung doppelt haploider Weizenlinien, Teilprojekt B	Mock, HP.	BMBF	01/05/19	31/07/22	256.390
Seedmaker: Aufklärung epigenetischer Mechanismen der Endo- spermbildung für die Entwicklung apomiktischer Kulturpflanzen	Kumlehn	BMBF	01/07/22	30/06/25	440.172
BonaRes (Modul A, Phase 3): CATCHY – Zwischenfrüchte als agronomische Maßnahme für nachhaltige Bodenfruchtbarkeit und Ertragssicherheit, SP 2	Wirén, N.	BMBF	01/04/21	31/03/24	458.609
Verbundprojekt: The Fabulous Fabrication Community- fabUNITY; Teilvorhaben PLANTlab, Mint Cluster	Freitag, J.	BMBF	01/01/21	31/12/23	26.500
WiLDSi-VorweRts: Wissensbasierte Lösungsansätze für Digitale Sequenzinformation – Wissenschaftliche Lösungsansätze für digitale Sequenzinformation: Vorbereitung weitere Ratschläge	Freitag, J.	BMBF	01/08/21	31/12/23	134.197
PrimedPlant-2: Priming als eine Strategie zur Verbesserung der Resistenz von Kulturpflanzen und ein mögliches Züchtungsziel	Douchkov, D.	BMBF	01/02/20	31/03/23	210.155

PrimedPlant-3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Priming für eine verstärkte Abwehr als eine Strategie zur Optimie- rung der Resistenz und ein mögliches Zuchtziel (PrimedPlant-3) – Teilprojekt A	Douchkov, D.	BMBF	01/04/23	31/03/26	497.715
IdeMoDeResBar-II: Pflanzenzüchtungsforschung-P2-Verbundvor- haben-Identifikation, Modifikation und Nutzung von Resistenzen gegen bedeutende Pathogene der Gerste, Teilprojekt C	Kumlehn Dr. J.	BMBF	01/02/20	31/01/23	402.606
de.NBI-Spring School 2023, 1317. März 2023	Scholz, U.	BMBF	01/01/23	31/12/23	17.148
P4ST:WIR! Physics for Food	Dehmer, K.J.; Neumann, K.	BMBF	01/01/23	31/12/24	284.507
Genebank2.0-P2: Pflanzenzüchtungsforschung-P2-Verbundvorha- ben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Stein, N.; Ma- scher, M.; Reif, J.; Douchkov, D.;Scholz, U.wirèn, N.	BMBF	01/11/19	31/10/22	1.797.671
SHAPE-P2: BMBF "Pflanzenzüchtungsforschung für die Bioöko- nomie": Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom – Erforschung der strukturellen Genomdiversi- tät für die Gerstezüchtung	Stein, N.; Mascher, M.; Reif, J.; Scholz	BMBF	01/02/20	31/01/23	1.349.848
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorha- ben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Stein, N.; Schnur- busch, T.; Mascher, M.; Reif, J.; Douch- kov, D.; Scholz, U.	BMBF	01/11/22	31/10/25	2.013.287
SHAPE-P3: Pflanzenzüchtungsvorhaben-P3-Verbundvorha- ben:Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom – Erforschung der strukturellen Genomdiversi- tät für die Gerstenzüchtung (SHAPE3) – Teilprojekt A	Stein, N.; Mascher, M.; Reif, J.; Scholz	BMBF	01/02/23	31/01/26	2.247.538
IPD-DSI: Unterstützung der internationalen Prozesse sowie der Diskussionen zum Thema DSI unter Einbeziehung von Positionen der Forschung	Freitag, J.; Scholz, U.	BFN	20/05/21	31/01/22	18.435
Spitfire/Cornet: Screening of <i>Pisum sativum</i> (pea) accessions for pea necrotic yellow dwarf virus resistance	Lohwasser, U.	BMWK	01/11/21	31/08/24	241.258
DH-radish: Erzeugung von Rettich/ Radieschen DH-Inducerlinien	Lermontova, I.	BMWK	01/11/20	31/10/23	119.871
HORTENSIEN: Entwicklung hochgradig phyllodulcinhaltiger Tee- hortensien (Hydrangea ssp.) zur großindustriellen Nutzung in der Lebensmittel- und Getränkeindustrie; Biochemische und physiologi- sche Untersuchungen zur Erhöhung des Phyllodulcingehaltes	Hajirezaei, M.	BMWK	01/10/19	30/09/22	187.363
Züchtung innovativer Gartenbohnensorten durch Assoziationska- nierung; Identifizierung neuer Marker für Bakteriose-Resistenzen, Hülsen-Qualitätsparameter und Durchwurzelungstiefe bei der Gartenbohne und Nutzbarmachung der genetischen Diversität	Lohwasser, U.; Ma- scher, M.; Otto. L.	BMWK	01/04/19	31/10/22	185.989
InnoLuteus: Verbundvorhaben: Innovative Züchtungsstrategien zur Verbesserung der Anbauwürdigkeit der Gelben Lupine (Lupinus Iuteus) in Deutschland; Teilvorhaben 2: Merkmalserfassung von IPK Genbankakzessionen	Lohwasser, U.	BMEL	01/04/19	31/03/22	181.994
LINSEL: Selektion geeigneter Sortentypen von Linsen (Lens culina- ris) für nachhaltige Anbausysteme	Lohwasser, U.	BMEL	15/02/19	14/06/22	35.798
PreLuteus: Entwicklung von ertragreichen und resistenten Prebree- ding Linien bei der Gelben Lupine in Deutschland; Teilvorhaben 2: Prüfung der Trockenstresstoleranz	Lohwasser, U.	BMEL	01/10/22	30/09/25	86.896
CiLaKlima: "Screening genetischer Ressourcen von Kichererbse (Ci- cer arietinum) und Saat-Platterbse (Lathyrus sativus): Anpassung an den Klimawandel in Deutschland mit alternativen Leguminosen für die menschliche Ernährung (CiLaKlima)"	Lohwasser, U.	BMEL	01/12/22	30/11/25	122.637
SIMULTAN: Sicherung von Multifunktionalität in der Grobfutterpro- duktion durch Artenreichtum im intensiven Grasland	Lohwasser, U.	BMEL	01/04/23	31/05/26	210.016
WiLGeR: Evaluierung genetischer Ressourcen zur züchterischen Verbesserung von Winterlinsen für den Mischfruchtanbau (Winter Lens Genetic Resources)	Lohwasser, U.	BMEL	01/09/23	31/12/26	82.710

FUGE: Monitoring der Fusariumarten und Entwicklung genomischer Werkzeuge zur effektiveren Züchtung von Saathafer	Mascher, M.	BMEL	15/12/20	14/06/24	168.907
DETECT: Machbarkeitsstudie zu Nachweis- und Identizierungsver- fahren für genomeditierte Panzen und panzliche Produkte-Teilvor- haben DETECT	Mascher, M.	BMEL	01/01/21	30/11/23	82.425
P-Stärke: Züchterische Verbesserung der Phosphor-Aneignungs- effizienz von Stärkekartoffeln und eine ressourcenschonende Roh- stoffproduktion; Teilvorhaben 1	Dehmer, K.J.	BMEL	01/03/19	31/10/22	197.517
Effikar: Selektion und Züchtung nährstoffeffizienter Phytophthora- resistenter Kartoffelzuchtstämme für einen nachhaltigen ökologi- schen Landbau	Dehmer, K.J.	BMEL	01/11/19	29/02/24	342.272
LuzNutz: Erhöhung der Anbauwürdigkeit von Luzerne (<i>Medicago</i> sativa L.) als Futterpflanze – Neue Impulse für die Königin der Futterpflanzen	Dehmer, K.J.	BMEL	01/02/21	31/01/24	297.057
KIBREED: Verbundprojekt Züchtung von Standortangepassten Sor- ten mittels Algorithmen der Künstlichen Intelligenz-Teilprojekt A	Reif, J.	BMEL	01/06/21	31/05/24	369.334
Brand-Resist: Verbesserung der Steinbrand- und Zwergsteinbrand- resistenz in Brotweizen durch systematische Nutzung genetischer Variation (Brand-Resist)	Reif, J.	BMEL	15/09/23	31/08/28	82.478
RustHealth: Genetische Analyse und Modellierung der Weizen-Rost- interaktion zur Entwicklung stabiler, mehrfachresistenter Weizen- sorten (RustHealth) – Teilprojekt C	Reif, J.	BMEL	01/09/23	31/08/26	206.515
Sterilkam2: Entwicklung der Elternkomponenten für die Erzeugung einer sterilen Kamillesorte – Projektphase 2	Otto, L.	BMEL	01/02/19	31/10/22	508.923
STRESS-STOPP: Verbundprojekt: Steigerung der Trockenstressad- aptation in Raps: Ertragsstabilität und Stresstoleranz als Selektions- targets für Optimierung via physiologischer Phänotypisierung-TP C	Altmann, T.	BMEL	15/08/23	14/08/26	230.744
DETECT: Machbarkeitsstudie zu Nachweis- und Identizierungsver- fahren für genomeditierte Panzen und panzliche Produkte – Teilvor- haben DETECT	Kumlehn J.	BMEL	01/01/21	30/11/23	451.340
FASTFLOW: Verbundprojekt: Generationsbeschleunigung bei Win- terweizen durch vernalisationsunabhängige Induktion der Ähren- bildung – TP 1	Kumlehn J.	BMEL	01/04/20	31/03/24	577.710
Sus-Agri-CC: InnovativeBiodünger zur Ertragssteigerung von Ge- treide und Gartenbaukulturen unter dem globalen Klimawandel: Aufdem Weg zur Nachhaltigkeit von landwirtschaftlichen Systemen gegen den Klimawandel inariden Zonen	Hajirezaei, M.	BMEL	01/06/21	31/05/24	170.146
QUIZ: Züchtung von Quinoa für den Anbau in Deutschland	Kumlehn J.	BMEL	01/03/23	28/02/26	204.299
SMARTROOT: Wurzelarchitektur- und Wurzelplastizitätsmerkmale für stickstoffeffiziente und trockenstressresiliente Gerstensorten	Wirén, N.	BMEL	01/04/23	31/03/26	432.039
DERUST: Entwicklung dauerhafter und rassenunspezifischer Ge- treideresistenz gegen Rostkrankheiten und Mehltau (DERUST) – Teilprojekt A	Kumlehn J.	BMEL	01/04/23	31/03/26	399.335
NEATWHEAT: Verbesserung physiologischer und morphologischer N-Effizienzmerkmale in Winterweizen für eine nachhaltige Pflanzen- produktion	Wirén, N.	BMEL	01/10/23	30/09/26	317.433
FDCA: Verbundvorhaben: Entwicklung maßgeschneiderter Bio- katalysatoren für die Herstellung von 2,5-Furandicarbonsäure auf Basis von Zuckern aus Lignocellulose; Teilvorhaben 2: Herstellung rekombinanter Hefestammefiir die Synthese von FDCA und	Wirén, N.	BMEL	01/04/23	31/03/26	325.872
HYFLOR: Verbundprojekt: Erforschung der Genetik der Blühbiologie bei Weizen zur effektiven Erzeugung von Hybridweizen, TP 1	Schnurbusch, T.; Reif, J.	BMEL	01/10/19	30/09/24	1.131.610
BigData: Nutzung von Big Data in Weizen zur Präzisionszüchtung	Reif, J.; Scholz, U.b65	BMEL	01/02/20	31/01/25	760.938

Amobila: Verbundvorhaben: Arzneipflanzenanbau als Instrument einer modernen, ertragsorientierten und zugleich biodiversitäts- fördernden Landwirtschaft; Teilvorhaben3: Ertragsrelevanz von Be- stäubern, Bestäubungswegen und-distanzen an der Echten Kamille	Otto, L.	BMEL	01/03/23	28/02/26	180.475
SINO-Chinesisch-Deutsches Mobilittätsprgramm: Unlocking genetic basis of cultivated barley to adapt district environments by popula- tion genomics	Mascher, M.	Chinesisch- Deutsches Zentrum für Wirtschaft, DFG	01/11/22	31/10/25	88.962
SINO, Chinesisch-Deutsches Mobilitätsprogramm: The mechanism of chromatin de-condensation in the companion vegetative nucleus during male germline maturation in Arabidopsis	Jiang, H.	Chinesisch- Deutsches Zentrum für Wirtschaft, DFG	01/01/21	31/12/23	88.956
Projektbezogener Personenaustausch Ägypten 2021-2023 Assoc. Prof. Dr. Ahmed Sallam	Börner, A.	DAAD	01/09/22	31/12/22	2.688
"A detailed genetic approach to improve abiotic stress tolerance in wheat", Projektbezogener Personenaustausch Ägypten 2021 – 2023	Börner, A.	DAAD	01/01/22	31/12/23	2.960
Forschungskostenzuschuss zur Unterstützung des Forschungsvor- habens von Herrn Dr. G. Li	Reif, J.	DAAD	15/09/21	14/09/23	4.800
Projektbezogener Personenaustausch Brasilien 2022, Evolution and structure of holocentric chromosomes in plants	Houben, A.	DAAD	01/01/22	31/12/22	10.454
Projektbezogener Personenaustausch Tschechien 2022-2024	Houben, A.	DAAD	01/01/22	31/12/23	1.953
Primeln: Aufklärung der Funktion und Evolution des Heterostylie- Supergens bei Primeln	Himmelbach, A.	DFG	01/01/20	31/12/22	22.696
Genetische Grundlagen der Grannen- und Stigmabehaarung in Gerste- oder, warum braucht Kulturgerste raue Grannen?	Stein, N.	DFG	01/12/19	31/12/23	221.650
Evolution und Funktion des Heterostylie-Supergens bei Amsinckia (Boragi-naceae)	Himmelbach, A.	DFG	01/10/21	30/09/24	47.600
POTEND: "KartoffelEndophyten-Interaktion und die Reaktion auf Stress (POTEND Stress)"	Nagel, M.	DFG	01/06/22	31/05/25	308.750
CSCS-HvWOXs: Stammzellsysteme bei Getreide (CSCS): Etablie- rung, Aufrechterhaltung und Beendigung	Schnurbusch, T.	DFG	01/07/22	30/06/26	311.500
WILD SIX ROW: Adaptive Introgressionen in Hybridschwärmen zwischen Wild- und Kulturgerste in Israel	Schnurbusch, T.	DFG	01/03/22	28/02/25	6.100
Weizenblütchen: Der Blüherfolg eines Blütenstandes hängt von seinem Rückgrat ab – erste Einblicke in das Wachstum und die Ent- wicklung der Rachis und ihre Auswirkungen auf die Fruchtbarkeit der Weizenblüten und die Kornzahl	Schnurbusch, T.	DFG	01/01/23	31/12/25	238.550
WILD SIX ROW: Adaptive Introgressionen in Hybridschwärmen zwischen Wild- und Kulturgerste in Israel	Mascher, M.	DFG	01/03/22	28/02/25	216.250
"Modellierung der Mechanismen der mitotischen Chromosomen- kondensation mithilfe von Polymersimulationen"	Camara, A.s.	DFG	01/08/22	31/07/25	333.450
ISRAEL: WILD SIX ROW	Mascher, M.	DFG	01/03/22	28/02/25	89.100
Safrangenom – "Identische Genome, doch verschiedene Eigen- schaften: Der Safrankrokus als Modell für die Epigenetik von Quali- tätsmerkmalen und Umweltanpassungen"	Blattner, F.	DFG	01/07/20	30/06/23	10.650
Analyse der komplexen Karyotypevolution in Korkussen	Harpke, D.	DFG	01/04/22	31/03/25	343.203
Aufklärung der funktionellen Rolle von A. <i>thaliana</i> KNL2 zur epige- netischen Regulation der Kinetochore-Ausbildung der Pflanzen	Lermontova, I.	DFG	01/04/19	30/09/23	202.682
Analyse von Cluster-Holocentromeren – eine neuartige Zentromer Variante der Lililaes Chionographis	Houben, A.	DFG	01/09/20	31/08/23	208.065
DroRep : Ultrastruktur-Untersuchungen zur DNA-Replikation in Drosophila Polytän-Chromosomen mit Hilfe von Super-auflösender Mikroskopie	Schubert, V.	DFG	01/04/20	31/05/23	14.945

Aufklärung des Mechanismus der nicht reduzierten Gametenbil- dung bei Arabidopsis thaliana	Jiang, H.	DFG	01/07/21	30/06/24	222.528
CRISPR-FISH: Entwicklung eines CRISPR-Imaging-Toolsets zur Ab- bildung von DNA und RNA in strukturell konserviertem Chromatin, das für Superauflösungsmikroskopie und Elektronenmikroskopie geeignet ist, und seine Anwendung zur Untersuchung der	Houben, A.	DFG	01/06/21	31/05/24	210.550
Das Protein-Protein-Interaktionsnetzwerk von KNL2 in Pflanzen	Lermontova, I.	DFG	15/06/21	30/06/24	216.650
Histon:Identifizierung der Rolle der H3K9-Demethylierung in der Meiose von Arabidopsis"	Jiang, H.	DFG	01/05/22	31/01/24	107.349
Identifizierung und funktionelle Charakterisierung von Genen betei- ligt am Prozess der wurzelspezifischen Eliminierung von B-Chromo- somen in Aefilops speltoides	Houben, A.	DFG	01/06/22	31/05/25	214.950
B-Chromosome: Chromosomendrive von Roggen B Chromosomen – Analyse der molekularen Grundlagen"	Houben, A.	DFG	01/06/23	31/05/26	216.150
Analyse von Cluster-Holocentromeren – ein neuartige Zentromer Variante der Lililaes Chionographis – Die Evolution von Mono- zu Holozentromeren	Houben, A.	DFG	01/03/23	28/02/25	250.500
Zentromerische Transkripte und ihre Funktion für die Entstehung des zentromerischen Chromatins und den Aufbau des Kinetochors	Lermontova, I.	DFG	01/04/23	31/03/26	225.350
Licorice-Iran: Genetische Verbesserung und Erhaltung der geneti- schen Ressourcen von Süßholz (<i>Glycyrrhita glabra</i>)	Otto, L.	DFG	01/06/23	31/08/24	27.450
Barley: "Entschlüsselung der wichtigsten Regulatoren der Ährchen- determinierung bei Gerste"	Koppolu, R.	DFG	01/05/23	30/04/26	382.550
NFDI4BioDiversity – A Consortium for the National Research Data Infrastructure (NFDI)	Scholz, U.	DFG	01/01/21	30/09/25	533.689
Maiskornentwicklung: Untersuchungen zur Maiskornentwicklung und Relevanz von Sauerstoffmangel im Endosperm	Rolletschek, H.	DFG	01/02/19	30/04/22	193.842
SWEETs: Aufklärung der Zuckerallokation in den Samen von Gerste und Reis	Borisjuk, L.	DFG	01/07/19	31/01/22	231.902
GCB2022: Deutsche Konferenz für Bioinformatik 2021, Halle/Saale, 06.09.2022-08.09.2022	Blätke, A.m.	DFG	01/06/21	30/09/22	24.400
MRI-KI:Kombination von NMR-Imaging (MRI) mit Künstlicher Intelli- genz (KI) für neuartige Anwendungen in der Samenbiologie	Borisjuk, L.	DFG	01/01/22	31/12/22	7.564
Identifizierung und funktionelle Charakterisierung von Genen betei- ligt am Prozess der wurzelspezifischen Eliminierung von B-Chromo- somen in Aefilops speltoides	Thiel, J.	DFG	01/12/22	30/11/25	11.000
BRACE: Reaktion und Adaption der Gerste auf sich wandelnde Umweltbedingungen, SusCrop, ERA-NET	Neumann, K.	DFG	01/06/22	31/05/25	49.800
HETCROP: Vorhersagegestützte Normalisierung der Entwicklungs- heterochronie bei parallelen molekularen und phänomischen Studien in Pflanzen	Neumann, K.	DFG	01/10/23	30/09/26	232.400
Erscheinung und Funktion von CuZnSOD-Proteinen während der Evolution früher Landpflanzen im Rahmen des Schwerpunkt- programms SPP 2237 MAdLand – Molekulare Adaptation an das Land: Evolutionere Anpassung der Pflanzen an Veränderung	Schippers, J.	DFG	01/09/20	29/02/24	221.290
Identifizierung und funktionelle Charakterisierung von Genen betei- ligt am Prozess der wurzelspezifischen Eliminierung von B-Chromo- somen in Aefilops speltoides	Szymanski, J.j.	DFG	01/06/22	31/05/25	9.800
ARF: Funktionelle Charakterisierung Eisen-abhängiger Mechanis- men. die die Bildung von Adventivwurzeln in Petunienstecklingen fördern	Hajirezaei, M.	DFG	01/01/20	31/12/22	384.569
INSIGHT: Untersuchungen der Rolle von Strigolactonen in Gerste als Antwort auf Trockenheit	Melzer, M.	DFG	01/02/20	29/02/24	225.100
CYBDOM: Proteins HYP1 beim Phosphormangel-abhängigen Primärwurzelwachstum	Wirén, N.	DFG	01/03/20	31/03/24	228.050

WURZELLÄNGE: Verlängerte Wurzeln zur effizienten Erschließung von Stickstoffquellen durch Veränderung der Brassinosteroid- und Auxinbioynthese und Signaltransduktion	Wirén, N.	DFG	01/12/20	31/05/24	344.400
CATCH-BNI: Erhöhte Stickstoffnutzungseffizienz in der Landwirt- schaft durch Zwischenfrüchte als Produzenten natürlicher Nitri- fikationsinhibitoren	Wirén, N.	DFG	01/04/21	31/12/24	276.050
HvMTP1;2: Erschließung und Nutzung der genetischen Variation des Metalltransporters HvMTP1;2 in Halmknoten zur verbesserten Organentwicklung, Verlagerung von Spurenelementen und Bioforti- fikation in Gerste"	Wirén, N.	DFG	01/09/22	31/08/25	442.150
AmmoniumTransport: Molekulare Regulation der wechselseitigen Interaktion zwischen Ammonium- und Nitrataufnahme in Pflanzen- wurzeln	Wirén, N.	DFG	01/08/23	30/07/25	267.058
OAK:Open Access Publikationen	Winter, S.	DFG	01/02/22	31/01/25	99.100
FAIRAgro: FAIRe Dateninfrastruktur für die Agrarsystemforschung	Reif, J.	DFG	01/03/23	29/02/28	1.183.554
ELIXIR-2017: Collaboration agreement with the node/ Commissio- ned Services Contract 06/ DE-IPK-2017-Integration	Scholz, U.	ELIXIR Hub	01/01/20	27/05/22	44.640
ELIXIR Hub-2021: Collaboration agreement with the node/ Com- missioned Services Contract DE-IPK-2021-Communityled	Arend, D.	ELIXIR Hub	08/07/21	31/12/23	14.625
Generation of radish DH inducer Lines	Lermontova, I.	Enza Zaden Research& Development	01/11/20	31/10/23	18.007
AGENT: Activated GEnebank NeTwork	Stein, N.; Weise, S.; Mascher, M.; Reif, J.; Scholz, U.; Opper- mann, M.; Lange, M.	EU	01/05/20	30/04/25	966.250
CROPDIVA: Climate Resilient Orphan croPs for increased DIVersity in Agriculture	Börner, A.	EU	01/09/21	31/08/25	53.000
PRO-GRACE: Promoting a Plant Genetic Resource Community for Europe	Weise, S.	EU	01/01/23	30/06/25	195.000
MEIOBARMIX: Meiosis in barley: Mixing it up (ERC)	Heckmann, S.	EU	01/02/21	31/01/26	1.497.875
AgroServ: Integrated SERvices supporting a sustainable AGROeco- logical translation, EMBL	Arend, D.	EU	01/09/22	31/08/27	30.833
STARGATE: Sensors and daTA tRaininG towards highperformance Agri-food sysTEms	Neumann, K.	EU	01/01/21	31/12/23	143.619
BOLERO: Breeding for coffee and cocoa root resilience in low input farming systems based on improved rootstocks	Neumann, K.	EU	01/10/22	30/09/26	273.084
CHROMADAPT-The role of chromatin in the long-term adaptation of plants to abiotic stress (TP im ERC)	Kumlehn J.	EU	01/05/17	30/04/22	70.510
INCREASE: Intelligent Collections of Food Legumes Genetic Re- sources for European Agrofood Systems	Neumann, K.; Opper- mann, M.; Lange, M.	EU	01/05/20	30/04/26	1.100.038
TRANSFER: Edaphic adaptation in barley wild relatives and its transfer to the domesticate (ERC)	Mascher, M.; Börner, A.; Wirèn, N.	EU	01/02/21	31/01/26	1.499.928
Legume Generation: Boosting innovation in breeding for the next generation of legume crops for Europe	Otto, L.; Lohwasser, U.	EU	01/09/23	29/02/28	886.991
CAPITALISE – COMBINING APPROACHES FOR PHOTOSYNTHETIC IMPROVEMENT TO ALLOW INCREASED USTAINABILITY IN EURO- PEAN AGRICULTURE	Altmann, T.; Lange, M.	EU	01/04/20	30/11/24	693.398
Erbringung wissenschaftlicher Dienstleistungen im Rahmen des Deutschen Netzwerks für Bioinformatik-Infrastrukturen (de.NBI) TTR_01/2022	Scholz, U.	FIRMA	18/03/22	31/12/27	455.000
Beet-ROS: Regulating sugar beet size through the modulation of cell proliferation and expansion by reactive oxygen species	Schippers, J.	FIRMA	01/02/20	31/12/23	310.000
BayKlimaFit: Genetik der Mykorrhiza vermittelten Stressresistenz in Mais	Neumann, K.	FIRMA	01/11/22	31/12/24	29.412

TRORA: Trockentoleranter Raps: Verbesserung der Trockentoleranz von Raps durch ektopische Expression von ABA-Rezeptorgenen	Kumlehn	FIRMA	01/03/23	28/02/25	10.084
dwarf rye: root trait characterisation in dwarf type rye	Giehl, R.	FIRMA	01/04/23	31/05/24	16.025
Uncovering the biochemical and molecular processes causing growth promotion of plants when exposed to plasma-activated water	Wirén, N.	FIRMA	01/09/23	31/08/26	351.563
Hopfengarn: Aufarbeitung von Hopfenfaser-Rohprodukten durch biotechnologische Spaltung von Lignin mit Kupferperoxidasen	Wirén, N.	FIRMA	01/10/22	31/08/24	200.800
A 100 year Seed Longevity Experiment in the Svalbard Global Seed Vault	Nagel, M.	FIRMA	12/03/21	11/03/31	26.464
Garlic_CCS: European Cooperative Programme for Plant Genetic Resources – Phase XI	Nagel, M.	FIRMA	18/08/23	31/08/25	30.000
Implementation of the ECPGR European Evaluation network (EVA) on wheat/barley and vegetable crops (carrot, lettuce and pepper), GenR 2019-2	Weise, S.	FIRMA	01/06/20	30/09/22	137.856
A1539-Extension of EURISCO for Wild Relatives (CWR) in situ data and preparation of pilot countries' data sets	Weise, S.	FIRMA	01/10/22	31/12/23	54.237
Hy-Gain, Capturing Heterosis for Smallholders Ph. IIOPP1209850	Houben, A.	FIRMA	19/03/20	31/07/23	499.505
Transcriptome profiling of phloem tissues in Soybean	Thiel, J.	FIRMA	29/06/21	31/12/22	61.000
Chitin Interactions in plant disease mitigation and analysis of Erythroxylum species	D Auria, J.	FIRMA	01/06/22	01/06/27	9.129
KAUST: Deciphering the quantitative regulation of host specificity in the barley in the barley-rust pathosystem	Kumlehn Dr. J.	FIRMA	01/03/22	30/06/24	91.200
Generation of rapeseed haploid inducer lines	Lermontova, I.; Houben, A.	FIRMA	01/11/19	30/04/23	525.000
ALIVE: Untersuchungen zur Introgression von QTL-Allelen mit hoher Ährchen-bzw. Blütchenfertilität in Gerste zur Verbesserung der Er- tragsbildung in Getreide"	Schnurbusch, T.	INVESTITIONS- BANK Sachsen- Anhalt	01/07/19	31/12/22	507.960
Erweiterung der NMR-Plattform des IPK um ein Super Wide Bore NMR-Gerät	Borisjuk, L.	INVESTITIONS- BANK Sachsen- Anhalt	01/12/19	31/07/22	2.183.894
HyperSpEED-Hypericum multi Spezies Exploration der Extrakt-Di- versität als Beitrag zur Verbesserung der Lebensqualität im Alter	Rizzo, P.	INVESTITIONS- BANK Sachsen- Anhalt	05/06/20	30/09/22	373.730
INDUCEPROT: Induced Accumulation of Recombinant Proteins in Barley Endosperm	Hensel, G.	INVESTITIONS- BANK Sachsen- Anhalt	01/03/19	30/06/22	175.806
Thüringer Linsensorten: Etablierung einer regionalen Saatgutpro- duktion der Kyffhäuserlinse und der Dornburger Speiselinse	Lohwasser, U.	Land Thüringen	01/07/23	31/12/24	13.881
Anschubfianzierung der strategischen Forschungserweiterung bei IPK Gatersleben, Teilesammlungen Nord	Schmidt, I.	Landesförder- institut Mecklen- burg-Vorpom- mern (LFI MV)	01/01/23	31/12/23	366.000
Anschubfianzierung der strategischen Forschungserweiterung bei IPK Gatersleben, Teilesammlungen Nord	Schmidt, I.	Landesförder- institut Mecklen- burg-Vorpom- mern (LFI MV)	01/01/23	31/12/23	350.000
REPLACE: a genomic breeder's toolkit for faba bean	Jayakodi, M.	Leibniz- Gemeinschaft	01/02/22	31/01/26	995.160
Leibniz-WissenschaftsCampus (LWC) Phosphorforschung Rost- ock;TP II.3: efficiency of forage legumes and their capacity to utilize P from recycling products	Dehmer, K.J.	Leibniz- Gemeinschaft	01/11/19	31/01/23	75.900
MedRhizo: Erfassung der Kulturpflanzen-Wurzelarchitektur in Me- dium Size-Rhizotronen	Dehmer, K.J.	Leibniz- Gemeinschaft	01/01/23	30/11/23	8.000

KETCHUP: Klimate Enhanced Tomato breeding Capturing Heat-re- silience Using integrative Phenotyping	Szymanski, J.j.	Leibniz- Gemeinschaft	01/04/20	31/12/23	382.572
VolCorn: Volatilome of a Cereal Crop-Microbiota System under Drought and Flooding	Hajirezaei, M.	Leibniz- Gemeinschaft	01/04/19	31/12/22	192.915
SAW AID-CROP: Amorphous silica in soils and plants Improves Drought stress tolerance of crops	Wirén, N.	Leibniz- Gemeinschaft	01/03/22	28/02/26	312.904
Matching-Fonds: Galyna Chebotar 15.06.22-14.09.22	Deike, S.	Leibniz- Gemeinschaft	01/06/22	31/08/22	8.500
MATCHING-FONDS: OKSANA PONOMARENKO	Deike, S.	Leibniz- Gemeinschaft	01/06/22	31/08/22	9.750
MATCHING-FONDS: laroslav Plutenko	Deike, S.	Leibniz- Gemeinschaft	21/05/22	31/08/22	3.600
Matching-Fonds: Larisa Korkota	Deike, S.	Leibniz- Gemeinschaft	07/08/22	22/10/22	7.450
Matching-Fonds: Rosa Shpirka	Deike, S.	Leibniz- Gemeinschaft	07/08/22	22/10/22	7.450
Matching-Fonds: Marharyta Hoi	Deike, S.	Leibniz- Gemeinschaft	20/06/22	31/10/22	6.500
Matching-Fonds: Olha Yalikova	Deike, S.	Leibniz- Gemeinschaft	20/06/22	31/10/22	6.500
Matching-Fonds: Larisa Korkota	Deike, S.	Leibniz- Gemeinschaft	01/09/23	15/09/23	1.650
Matching-Fonds: Roza Shpirka	Deike, S.	Leibniz- Gemeinschaft	01/09/23	15/09/23	1.650
Matching-Fonds: Olha Yalikova	Deike, S.	Leibniz- Gemeinschaft	01/09/23	25/09/23	2.750
Matching-Fonds: Iaroslav Plutenko	Deike, S.	Leibniz- Gemeinschaft	01/09/23	15/10/23	8.750
Genexpressionsatlas: Ein Genexpressionsatlas für die wilden Verwandten der Kulturgerste	Mascher, M.	MWU	01/07/22	31/12/24	310.000
In Silico: Einrichtung einer Nachwuchsforschergruppe "Insilico Genbank-Proteomik"	Camara, A.s.	MWU	01/06/23	31/12/25	180.000
UpMix, Freisetzung von Leistung und Nachhaltigkeit durch Genotypen und Pflanzenmischungen	Reif, J.	MWU	01/06/23	31/12/25	250.000
Barley: Veränderung der meiotischen Rekombinations- landschaft in der Gerste (<i>Hordeum vulgare</i>)	Heckmann, S.	MWU	01/01/23	31/12/25	302.200
GRDC-OAT: Oat genomics resources for breeders and pre-breeders	Mascher, M.	Murdoch University	01/11/20	31/12/22	85.000
Sequence analysis of a new Hypericum genome	Rizzo, P.	POLYFLY S.L., Spanien	01/03/23	29/02/24	4.500
Wricke-Preis zur Förderung der Kulturpflanzenforschung	Mascher, M.	SONSTIGE	01/04/20	31/03/25	30.000
exchange on conservation and characterisation/ regeneration techniques of PGRFA for their enhanced utilization incl. CWR	Lohwasser, U.	Sortenförde- rungsgesell- schaft – SFG mbH	01/06/23	30/06/23	1.769
Humboldt-Forschungsstipendium für Postdoktoranden an Dr. Matias Schierenbeck	Börner, A.	STIFTUNG	01/03/21	29/02/24	28.800
Forschungskostenzuschuss für Dr. Amira Mourad	Börner, A.	STIFTUNG	01/07/21	31/08/24	33.200
Galyna Chebotar: "Genome-wide association study of seed longevity and the relationship to (semi-) dwarfing alleles in barley"	Börner, A.	STIFTUNG	01/09/22	31/08/23	34.827
Forschungsaufenthalt Prof. Dr. Abdel-Fattah Badr 01.07 30.09.2023	Börner, A.	STIFTUNG	01/07/23	30/09/23	13.710
Forschungsaufenthalt Mayada Mahdy Ibrahim 01.0730.09.2023	Börner, A.	STIFTUNG	01/07/23	30/09/23	4.585

Anton Peterson: Reliable cryopreservation of duckweed"	Nagel, M.	STIFTUNG	01/07/22	31/08/22	4.759
Olena Kishchenko: Duckweed-based oral antiviral vaccine for fish"	Nagel, M.	STIFTUNG	01/07/22	31/08/22	4.959
Forschungsstipendium für Dr. Olena Kishchenko des Philipp Schwartz-Fellowships (AvH)	Nagel, M.	STIFTUNG	01/09/22	29/02/24	87.360
Forschungsstipendium für Anton Peterson des Philipp Schwartz- Fellowships (AvH)	Nagel, M.	STIFTUNG	01/09/22	29/02/24	85.680
Humboldt-Forschungsstipendium für Postdoktoranden an Herrn Dr. Raz Avni	Mascher, M.	STIFTUNG	01/03/21	29/02/24	32.900
laroslav Plutenko: "Combining nuclear magnetic resonance imaging (MRI) with Artificial Intelligence (AI) for next level applications in seed biology"	Borisjuk, L.	STIFTUNG	01/09/22	31/08/23	20.400
High-throughput non-invasive root and shoot phenotyping training	Neumann, K.	STIFTUNG	01/03/23	31/03/24	29.693
USDA, PLANT BREEDING PARTNERSHIP: Continuing to develop and validate the tools for Hybrid Wheat, Uni Nebraska	Reif, J.	University of Nebraska	01/06/20	30/04/23	27.822
Pollination trials in oilseed crops (<i>Brassica napus</i>)	Willner, E.	POLYFLY S.L. Almeria, Spain	01/04/23	05/03/24	8.400
Improving abiotic stress tolrerance in wheat	Börner, A.	Assiut University, Ägypten	20/07/22	19/07/24	4.303
Erhaltung der Diversität des Apenninenschwingels	Willner, E.	Beat Boller, Zürich	15/10/20	31/03/24	9.377
Cucurbitlocal: Exploitation of Cucurbita local germplasm for sustai- nable agriculture	Lohwasser, U.	Bioversity International	26/04/21	15/01/23	6.000

BMBF – Federal Ministry of Education and Research

BFN – Federal Agency for Nature Conservation BMWK – Federal Ministry for Economic Affairs and Climate Action

BMEL – Federal Ministry of Food and Agriculture

MWU - Ministry of Science, Energy, Climate Protection and Environment of Saxony-Anhalt

DFG – German Research Foundation

DAAD – German Academic Exchange Service

EU – European Union

Gatersleben Lectures 2022/2023

Gatersleben Lectures 2022

09. February 2022 **"A tale of two teosintes: the hybrid origin of maize"** Prof. Dr. Jeffrey Ross-Ibara, University of California, Davis, USA

22. March 2022

"Origin and evolution of auxin response" Prof. Dr. Dolf Weijers, Wageningen University, The Netherlands

20. April 2022

"Biodiversity and Ecosystem Services: Insights from IPBES and IPCC Intergovernmental Processes"

Prof. Dr. Josef Settele, Helmholtz-Centre for Environmental Research (UFZ), Halle

24. May 2022

"The Art and Design of Harmony in Arbuscular Mycorrhizal Symbiosis of Cereals"

Prof. Dr. Uta Paszkowski, University of Cambridge, United Kingdom

07. June 2022

"Studies in Near Eastern plant domestication; the minority view" Prof. Dr. Shahal Abbo, Hebrew University of Jerusalem, Israel

12. July 2022

"From molecular to evolutionary analysis: genomics-based dissection of the wheat – powdery mildew interaction"

Prof. Dr. Beat Keller, University of Zurich, Switzerland

20. September 2022

"The Dynamics of Root Development" Prof. Dr. Philipp Benfey, Duke University, Durham, USA

25. October 2022

"Breeding wheat for the world: opportunities & challenges" Prof. Dr. Alison Bentley, CIMMYT, Mexico

13. December 2022

"Fascinating World of Plant Volatiles: Beyond the Traditional View" Prof. Dr. Natalia Doudareva, Purdue University, College of Agriculture, Lafayette, USA

Gatersleben Lectures 2023

28. February 2023

"Applying Evolutionary Theory to Improve Plant Production"

Prof. Dr. Jacob Weiner, University of Copenhagen, Frederiksberg, Denmark

21. March 2023

"How does macroevolution work? The speciation is driven by the creation and preservation of system information during a crisis"

Prof. Dr. Henry H.-Q. Heng, Wayne State University, School of Medicine, Detroit, USA

25. April 2023

"Inflorescence development in response to abiotic stress in barley" Prof. Dr. Maria von Korff Schmising, Heinrich-Heine-Universität

9. May 2023

"How stressful was plant terrestrialization? Contribution of transcription factors and redox processes to land plant adaptation" Prof. Dr. Sabine Zachgo, University of Osnabrueck

11. July 2023 **"The plant egg cell"** Prof. Dr. Thomas Dresselhaus, University of Regensburg, Germany

26. September 2023

"Feed the future: Integration of next generation technologies to wheat breeding"

Prof. Dr. Curtis Pozniak, University of Saskatchewan, College of Agriculture and Bioresources, Saskatchewan, Canada

14. November 2023

"Life with more than one genome"

Prof. Dr. Yves van de Peer, VIB-UGent Center for Plant Systems Biology, Bioinformatics and Evolutionary Genomics, Zwijnaarde, Belgium

Genetic Seminars 2022

21.04.2022

"Regeneration in planarian flatworms [the plants of the animal kingdom]" Dr. Jochen Rink

Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany

05.05.2022

"Feeling the Vrn: Adapting cereal development to changing climates" Dr. Laura Dixon, University of Leeds, UK

07.06.2022

"Regulation of flavonoid metabolism during eggplant fruit ripening: a story of unusual pigmentation" Dr. Sayantan Panda, Weizmann Institute

of Science, Rehovot, Israel

20.06.2022

"Phenotypic plasticity in plant defense within and across generations: From molecular mechanisms to evolutionary consequences"

Dr. Meret Huber, University of Münster, Germany

23.06.2022 "Tracing the development

of wheat spikes through time" Dr. Anna Backhaus, John Innes Centre

(JIC), Norwich, UK

28.06.22

"Investigations into the origins of the highly nutritious Andean pseudocereal quinoa (Chenopodium quinoa)"

Rick Jellen and Jeff Maughan, Brigham Young University, Provo, USA

27.06.2022

"Uniparental genome elimination induced genome instability: a case study on the origin of a high organogenic and perennial mutant in Arabidopsis thaliana"

Dr. Ravi Maruthachalam, Indian Institute of Science Education and Research (IISER) Thiruvananthapuram, India

29.06.2022

Fascinating biology of the wild sorghum b chromosome

Karafiátová Miroslava, Institute of Experiemental Botany of the Czech Academy of Sciences, Olomouc, Czech Republic

01.08.2022

"Identification of gene and developing SNP markers associated with fragrance for increasing fragrance in Thai fragrant rice landraces"

Assist. Prof. Dr. Tonapha Pusadee, Chiang Mai University, Thailand

05.08.2022

"Nano-visualization study of barley chromosome by helium ion microscope (HIM), SEM, and high voltage transmission electron microscope (HVTEM)."

Prof. Dr. Nobuko Ohmido, Kobe University, Japan

07.09.2022

"The greening ashore: How plants changed the climate before we did" Dr. Mona Schreiber, University of Marburg, Germany

10.10.2022 "Dissecting Sexual and Asexual reproduction in plants"

Charles Underwood, Max Planck Institute for Plant Breeding Research (MPI-Z), Cologne, Germany

14.10.2022

"Chromosome elimination during hybrid embryogenesis of Poaceae: wheat/oat × Pennisetum wide hybridization" Dr. Takayoshi Ishii,

Tottori University, Japan

02.11.2022

"The crop saffron crocus – its emergence as a triploid clone, updates on its genome, and why we care about it"

Dr. Tony Heitkam, Technische Universität Dresden, Germany

23.11.2022

"The Ph1/ZIP4 story: stabilisation of wheat as a polyploid and its impact on breeding."

Dr. Azahara C. Martín, John Innes Centre (JIC), Norwich, United Kingdom

14.12.2022

"Induced genetic variation: Precision breeding utilizing conventional breeding technologies, An innovative, accelerated trait development process, enables consumer accepted precision breeding, utilizing non-GM technologies"

Agnieszka Nielsen, Carlsberg business unit Traitomic, Denmark

19.12.2022

"The evolution of an ancient and

"special" B chromosome of birds" Alexander Suh, University of East Anglia, U.K. and Uppsala University, Sweden

Genetic Seminars 2023

06.02.2023

"Horizontal transfer, meiotic drive, and mitotic losses could explain the origin and the presence/absence polymorphism of fungal accessory chromosomes"

Michael Habig, Judith Müller, Christian-Albrechts-Universität, Kiel, Germany

08.03.2023

"Breeding modernization and implementation of genomic selection in rice breeding"

Dr. Parthiban Prakash, International Rice Research Institute (IRRI), Philippines

24.04.2023

"Albrecht Kossel und die Nukleinbasen: Ein Nobelpreisträger aus Mecklenburg" Edith und Joachim Framm, Wismar, Germany

10.05.2023

"From Genome Mapping of Traits to Genome Designing of Crops"

Prof. Dr. Shifeng Cheng, Agricultural Genomics Institute at Shenzhen (AGIS), Chinese Academy of Agricultural Sciences, China

27.04.2023

"Pairing classical techniques and statistical genetics to characterise rust resistance genes"

Dr. Laura Ziems, University of Sydney, Australia

03.05.2023

"Multi-dimensional genome competition in plant hybrids"

Dr. David Kopecky, Institute of Experimental Botany, Olomouc, Czech Republic

12.05.2023

"Form Follows Function – Formation of the Arabidopsis 3D Genome Structure" Dr. Vinzenz Handrick, Leibniz Institute für Plant Biochemistry, Halle, Germany

17.05.2023

"A faba bean pan-genome for advancing sustainable protein security"

Dr. Alan H. Schulman, University of Helsinki, Finnland

19.06.2023

"Unlocking host resistances against soil-borne bymoviruses"

Prof. Dr. Ping Yang, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, China

23.06.2023

"Does barley exhibit resistance to Fusarium graminearum?"

Gary J. Muehlbauer, University of Minnesota, USA

26.06.2023

"Improving the adaptation of Australia's youngest major crop – canola (raps)"

Matthew Nelson, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Perth, Australia

01.08.2023

"Sweet sorghum genomics and molecular breeding"

Prof. Dr. Hai-Chun Jing, Institute of Botany, Chinese Academy of Sciences, Beijing, China

04.09.2023

"Chemical emasculation in plants using trifluoromethanesulfonamide (TFMSA)"

Dr. Takayoshi Ishii, Tottori University, Japan **"Oryzawheat, wheat plants possessing**

wheat-rice hybrid mitochondria" Dr. Takashi Okamoto, Tokyo Metropolitan University, Japan

19.09.2023

"The quiet life of a structural biologist...and then came AlphaFold2" Professor Richard Garratt, University of São Paulo (USP), Brazil

28.09.2023

"Turning blue in the green lineage: evolution of oxygen sensing and adaptation to hypoxia" Francesco Licausi, University

of Oxford, UK

29.09.2023

"Atypical disease resistance genes across the genome of wheat"

Evans Lagudah, Commonwealth Scientific and Industrial Research Organisation (CSIRO), University of Sydney, Australia

13.11.2023

"Land Use and Nutrition: plant pangenomes and gene expression regulation"

Agnieszka Golicz, Justus Liebig University Gießen, Germany

08.12.2023

"Macroevolutionary dynamics of genome size driving trait flexibility and diversification in angiosperms" Frau Dr. Sreetama Bhadra, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany

Vavilov Seminars 2022

28.06.2022 "Pflanzen im Harz und seinem Vorland – eine Kleinausgabe der mitteleuropäischen Flora"

Dr. Hans-Ulrich Kison, Harz National Park, Germany

19.10.2022

"The molecular regulations of root stem cell homeostasis" Prof. Dr. Yvonne Stahl, Heinrich-Heine University, Düsseldorf, Germany

Vavilov Seminars 2023

01.02.2023

"100 Years: Development of the Tyrolean gene-bank"

DI Dr. Christian Partl, Amt der Tiroler Landesregierung Abteilung Landwirtschaftliches Schulwesen und Landwirtschaftsrecht, Innsbruck, Österreich

01.02.2023

"The collection of alpine landraces in South Tyrol (Italy)"

Dr. Manuel Pramsohler & Dr. Giovanni Peratoner, Laimburg Research Centre, Italy

15.02.2023

"Flexibility matters – How protein disorder shapes organismal tolerance to water loss"

Dr. Anja Thalhammer, Universität Potsdam, Germany

31.05.2023

"Within and beyond the stringent response – RSH and (p)ppGpp in seed development, longevity and germination"

Dr. Justyna Boniecka, Nicolaus Copernicu University, Toruń, Poland

07.06.2023

"Securing the USDA-ARS National Plant Germplasm System as the climate changes"

Dr. Gayle Volk, U.S. Department of Agriculture USDA, Fort Collins, USA

21.06.2023

"The International Potato Center – Maintenance and cryobanking of potato and Andean Root and Tuber Crops"

Rainer Vollmer, Internation Potato Center (CIP), Lima, Peru

25.09.2023

"From Fingerprinting to a Pangenome – the use of Genetic Sequence Data from a clonal Genebank"

Dr. David Ellis, International Potato Center (CIP), Lima, Peru

29.11.2023

"Plant Genetic Resources for Food and Sustainable Agriculture"

Prof. K.C. Bansal, Indian Council of Agricultural Research (ICAR), Krishi Bhavan, India

13.12.2023

"How seeds adapt their germination time without impacting their stress-reactiveness?" Dr. Guillaume Née, University

Münster, Germany

Waterman Seminars 2022

30.05.2022

"Al methods to predict value chain potentials for genetic resources" Luigi de Gaudenzi, Senckenberg Biodiversity and Climate Research Center, Frankfurt am Main, Germany 12.06.2022 "Exploitation of genomic resources to advance forage breeding programs" Yutang Chen, Eidgenössische Technische Hochschule (ETH) Zurich, Switzerland

Waterman Seminars 2023

02.10.2023

"The mobility of ancient selfish genetic elements shaped the evolution of the plant mitochondrial splicing apparatus" Simon Zumkeller, Heinrich-Heine University, Düsseldorf, Germany

12.10.2023

"GridScore - The open-source plant phenotyping app" Sebastian Raubach, James Hutton Institute, Scotland

06.11.2023

"Leveraging Comparative Genomics for Crop Improvement" Dr. John T. Lovell, DOE Joint Genome Institute & Hudson Alpha Institute for

Cell Biology Seminars

Biotechnology, USA

26.04.2022

"Plant and mammalian synthetic biology: from optogenetics to synthetic pathway reconstruction" Prof. Dr. Zubriggen, Heinrich-Heine University, Düsseldorf, Germany

11.10.2022

"From Gene Editing to Chromosome and Tissue Engineering" Prof. Dr. Holger Puchta, Karlsruher Institut für Technologie (KIT), Germany

24.10.2022

"To shed light on life in the dark: Interactions between rice and beneficial endophytes" Prof. Dr. Barbara Reinhold-Hurek,

University Bremen, Germany

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 Automated Plant

 Automated Plant

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