



GERMAN PLANT BREEDING CONFERENCE 2024

Abstract Book

March
19 – 21,
2024

#GPZ2024



Hochschule
Geisenheim
University





DEAR COLLEAGUES,

We warmly welcome you to the German Plant Breeding Conference 2024 at Hochschule Geisenheim University, the main conference of the German Society of Plant Breeding (GPZ). With over 800 members, the GPZ stands as one of the main societies for plant breeding in Europe, providing a crucial exchange platform for breeding researchers through its biennial main conference.

Our research at Hochschule Geisenheim University is both practice- and theory-oriented, focusing primarily on viticultural and horticultural crops and their diverse production and processing areas. This month marks the launch of our new Department of Plant Breeding, a consolidation of the former departments of grapevine breeding and molecular plant sciences, significantly supported by the LOEWE program of the state of Hesse. The aim of our plant breeding group in Geisenheim is to develop and implement cutting-edge tools and approaches that can help to accelerate the crop genetic improvement process. Our key research areas include genomics, phenotyping, quantitative genetics and biotechnology with a specific focus on viticultural and horticultural crop species.

Therefore, we are honoured and excited to host this important conference that brings together international plant breeding experts from public and private organisations. Under the theme "Accelerating Crop Genetic Gain", this year's GPZ conference focusses on the latest innovations in plant breeding research that can help to accelerate crop genetic gain and deliver urgently needed breeding solutions for future agriculture.

We are delighted by the overwhelming interest in this year's conference. With nearly 300 registrations, the conference has been booked out several weeks ago. We are excited about our confirmed six keynotes from world-leading researchers, incl. Mark Cooper (University of Queensland, AU), Agnieszka Golicz (JLU Giessen, DE), Hans Daetwyler (Bayer CropsScience, NL), Daniela Bustots-Korts (Universidad Austral de Chile, CL), Dorcus Gemenet (CGIAR, KE) and Holger Puchta (Karlsruhe Institute of Technology, DE). In addition, the scientific committee has selected 29 conference talks and 110 scientific posters from over 170 abstract submissions, showcasing the latest advances in genomics, predictive breeding, quantitative



genetics, resistance & tolerance breeding, crop modelling, and precision breeding. We are particularly delighted to see a significant number of presentations from early career researchers this year.

Believing in the pivotal role of young scientists and breeders in the future of plant breeding, we recently concluded the "Next Generation Breeders" Workshop for early-career breeding researchers from March 17-18, 2024. During this year's main GPZ conference, the "Young GPZ" will be formed, featuring elected early career representatives who will contribute to the GPZ board.

Our sincere gratitude extends to all sponsors and supporters, notably our Platinum sponsors Crop Trust and Bayer, our Gold sponsors KWS and BASF, the LOEWE program of the state of Hesse, and 15 additional Silver and Bronze sponsors. Their generous support has enabled us to create an engaging program, featuring scientific presentations and social events, all while striving to keep registration fees as affordable as possible, especially for early-career researchers.

Wishing you an inspiring conference filled with fruitful discussions and memorable experiences. We hope that you enjoy your time at Hochschule Geisenheim University in the beautiful Rheingau.

Warm regards on behalf of the organising committee,
Kai Voss-Fels

Professor & Head of Department of Plant Breeding
Hochschule Geisenheim University
Germany

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The full Abstract Book including all poster abstracts can be downloaded here.



http://epaper.hs-gm.de/Abstract_Book_GPZ_2024_Geisenheim.pdf

PROGRAM

Platinum Sponsors:



19/03/2024

11:00 – 12:30 Registration, Poster setup
12:30 – 13:00 Welcome

SESSION 1 “MANAGING AND MINING CROP DIVERSITY USING GENOMIC TOOLS”; CHAIR: MARIA VON KORFF SCHMISING

13:00 – 13:40 **KEYNOTE: AGNIESZKA GOLICZ, JUSTUS LIEBIG UNIVERSITY GIESSEN, GERMANY – MODERN GENOMIC TECHNOLOGIES TO ACCELERATE CROP GENETIC GAIN**

13:40 – 14:00 **Christina Waesch***, Martin-Luther University Halle-Wittenberg, Germany – Pollen and anther morphological variation was shaped by domestication in rye (*Secale cereale* L.)

14:00 – 14:20 **Anne-Kathrin Pfrieme***, Julius Kühn-Institut, Germany – Unlocking the potential of wheat genetic resources: Fine mapping and validation of unexploited leaf and stripe rust resistances

14:20 – 14:40 **Sarah Schiessl-Weidenweber**, Justus-Liebig Universität Gießen, Germany – Meiosis genes variation in the triangle of U

14:40 – 15:00 **Akanksha Singh**, University of Cologne, Germany – Recent landraces from novel environments can serve as reservoirs of genetic diversity in grain amaranth

15:00 – 15:45 Coffee break

SESSION 2 “INNOVATIVE MODELLING STRATEGIES FOR FUTURE CROP IMPROVEMENT”, CHAIR: TSU-WEI CHEN

15:45 – 16:25 **KEYNOTE: DANIELA BUSTOS-KORTS, INSTITUTE FOR PLANT PRODUCTION AND PROTECTION, UNIVERSIDAD AUSTRAL DE CHILE, VALDIVIA, CHILE – CHALLENGES AND OPPORTUNITIES ARISING FROM GXE AT DIFFERENT SCALES**

- 16:25 – 16:45 **Tien-Cheng Wang***, Humboldt University Berlin, Germany – Location determines yield performance consistency in winter wheat (*Triticum aestivum* L.): case study from multi-environment trials and simulation results
- 16:45 – 17:05 **Lukas Roth***, Institute of agricultural sciences, Switzerland – High-throughput field phenotyping to facilitate the prediction of crop performance for new environments and new genotypes in breeding
- 17:05 – 17:25 **Marta Malinowska**, Aarhus University, Denmark – Root traits as a key driver in accelerating and streamlining perennial ryegrass improvement
- 17:30 - 18:15 Founding meeting of „Young GPZ“.
- 18:15 - 19:00 General Assembly of the German Society of Plant Breeding
- 19:00 – 21:00 Happy Poster Session with Flying Dinner
- 21:00 – 23:30 Networking in the “Geisenheim Breeders’ Lounge”

20/03/2024

- 08:00 – 08:30 Coffee / Registration

SESSION 3 “ACCELERATING CROP BREEDING FOR IMPROVED CLIMATE RESILIENCE AND SUSTAINABILITY”, CHAIRS: LEE HICKEY & ANDREAS STAHL

- 08:30 – 09:10 **KEYNOTE: DORCUS GEMENET, INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER (CIMMYT), KENYA – FOOD AND NUTRITION SECURITY IN THE GLOBAL SOUTH: CROP IMPROVEMENT INTERVENTIONS BY CGIAR AND PARTNERS**
- 09:10 – 09:30 **Thomas Miedaner**, University of Hohenheim, Germany – Dwarfing genes in wheat, triticale and rye hinder genetic gain in *Fusarium* head blight resistance
- 09:30 – 09:50 **Alan Humphries**, South Australian Research and Development Institute, Australia – Introgressing crop wild diversity to improve alfalfa drought tolerance for Kazakhstan and Kyrgyzstan
- 09:50 – 10:10 **Lilian A. Okiro***, Egerton University, Kenya – Evaluation of genetic diversity and genome-wide association studies of resistance to bacterial wilt disease in potato
- 10:10 – 10:40 Coffee break
- 10:40 – 11:00 **Miguel Sanchez-Garcia**, International Centre for Agricultural Research in the Dry Areas (ICARDA), Morocco – New strategies of the Global Barley Breeding Program of the CGIAR to accelerate genetic gains under Climate Change
- 11:00 – 11:20 **Dennis E. Tippe***, Tanzania Agricultural Research Institute (TARI), Tanzania, – Biodiversity for Opportunities, Livelihoods and Development (BOLD): Harnessing crop diversity to mitigate the effects of changing climate - Finger Millet component
- 11:20 – 11:40 **Annika Schildberg***, Institut für Pflanzenzüchtung, Universität Kiel, Germany, – Unraveling the function of the cyst nematode resistance gene Hs4 in different genomic backgrounds
- 11:40 – 12:00 **Hannah Robinson**, University of Queensland, Australia, – Breeding for stable disease resistance: a commercial wheat breeding case study using genomic prediction
- 12:00 – 14:00 Happy Poster Session with Flying Lunch

SESSION 4 “DESIGNING FUTURE CROPS USING MODERN BREEDING TECHNOLOGIES”, CHAIRS: MORGANE ROTH & DANIELA HOLTGRÄWE

- 14:00 – 14:40 **KEYNOTE: HANS DAETWYLER, BAYER CROP SCIENCE, VEGETABLES BY BAYER R&D, SWITZERLAND – TRANSFORMING VEGETABLE BREEDING**
- 14:40 – 15:00 **Tianyu Lan***, Heinrich-Heine University Düsseldorf, Germany – Adapting to the heat: stress response and reproductive success in barley
- 15:00 – 15:20 **Michaela Jung***, Agroscope, Switzerland – Genomic prediction of apple traits integrating environmental covariables and non-additive effects
- 15:20 – 15:40 **Etienne R. Patin***, INRAE EGFV, France – Genetic variability of drought responses and root traits in wild *Vitis* species with an interest to be used as grapevine rootstocks
- 15:40 – 16:00 **Gesa Helmsorig***, Heinrich-Heine-University Düsseldorf, Germany – Early maturity ? (eam?) is a modulator of photoperiod sensitivity in barley
- 16:00 – 16:30 Coffee break
- 16:30 – 17:10 **KEYNOTE: HOLGER PUCHTA, JOSEPH GOTTLIEB KÖLREUTER INSTITUTE FOR PLANT SCIENCES, KARLSRUHE, GERMANY – USING CRISPR/CAS FOR PLANT BREEDING: FROM GENE EDITING TO CHROMOSOME ENGINEERING**
- 17:10 – 17:30 **Nina Trubanová***, University College Dublin, Republic of Ireland – Genome specific association study (GSAS) for exploration of intravarietal variability in hemp (*Cannabis sativa*)
- 17:30 – 17:50 **Shanice Van Haeften***, The University of Queensland, Australia – Unravelling the Genetics of Mungbean Canopy Dynamics Using UAV-Derived Prediction Models
- 17:50 – 18:10 **Max Schmidt***, Hochschule Geisenheim University, Geisenheim – Exploring the (epi)genetic diversity in grapevine
- from 19:30 Conference Dinner at “Mein Bahnhof”, Am Rottland 1, 65385 Rüdesheim am Rhein

21/03/2024

- 08:00 – 08:30 Coffee / Registration

SESSION 5 “PREDICTING A PATH FOR FUTURE CROP IMPROVEMENT”, CHAIRS: ROD SNOWDON & KAI VOSS-FELS

- 08:30 – 09:10 **KEYNOTE: MARK COOPER, UNIVERSITY OF QUEENSLAND, AUSTRALIA – RETHINKING THE “BREEDER’S EQUATION”: EMERGING OPEN QUESTIONS**
- 09:10 – 09:30 **Hanna Marie Schilbert***, Bielefeld University, Germany – From Bitter to Better: Optimizing the Taste of Rapeseed Protein for Human Consumption by applied Genome Research
- 09:30 – 09:50 **Johanna Åstrand***, Lantmännen, Sweden – Genetic gain in spring barley and genomic prediction strategies for efficient breeding of yield in different row types
- 09:50 – 10:10 **Po-Ya Wu***, Julius Kühn-Institute, Germany – Optimal implementation of genomic selection in clone breeding programs—Exemplified in potato: I. Effect of selection strategy, implementation stage, and selection intensity on short-term genetic gain
- 10:10 – 10:30 **Azadeh Hassanpour***, University of Göttingen, Germany – Dynamic Optimization for Resource, Allocation in Breeding Programs Using Evolutionary Algorithms (MoBPSopti)

- 10:30– 11:15 Coffee break
- 11:15 – 11:35 **Ravindra Reddy Gundala***, IPK-Gatersleben, Germany – Big Data driven Genomic Predictions for Elevating Genetic Gain in Wheat
- 11:35 – 11:55 **Carina Meyenberg***, University of Hohenheim, Germany – Feature Engineering and Parameter Tuning - Improving Phenomic Prediction Ability in Multi-Environmental Durum Wheat Breeding Trials
- 11:55 – 12:15 **Bright Enogieru Osatohanmwon***, University of Goettingen, Germany – Machine Learning Combined with Locus-Specific Degree of Dominance Transformation for Genomic Prediction in Maize
- 12:15 – 12:35 **Mila Tost***, University of Goettingen, Germany – Identification of polygenic selection for drought stress in European beech populations
- 12:35 – 13:00 Announcements, Awards and Farewell
- 13:00 – Farewell (incl. packed lunch)

*Early Career Researcher

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SESSION 1: MANAGING AND MINING CROP DIVERSITY USING GENOMIC TOOLS

MODERN GENOMIC TECHNOLOGIES TO ACCELERATE CROP GENETIC GAIN

Golicz, Agnieszka A.¹

¹Institute of Agronomy and Plant Breeding I, Justus Liebig University Gießen, Germany

Genomic technologies have become a cornerstone of modern plant breeding. Ongoing improvements in genome sequencing and assembly now allow for the generation of high quality genomes at a fraction of previous computational and monetary cost. The availability of multiple genomes of individuals from the same species facilitates detailed comparative analyses, more precise variant identification and improved marker development.

The term pangenome was introduced to describe a collection of genomic sequence found in the entire population rather than in a single individual. Compared with single reference genomes, pangenomes can represent the entire variation repertoire of a certain

species or genus. By combining the genomic data of multiple accessions, pangenomes allow for the detection and annotation of complex DNA polymorphisms such as structural variations (SVs), one of the major determinants of genetic diversity within a species. From disease resistance to plant morphology and yield, combined with transcriptomic and epigenomic data, pangenomes provide a powerful framework for understanding of variation underlying key traits.

The talk will discuss the most recent developments in genomic data analysis including the concept of pangenome, highlighting their potential practical applications in crop plant research.



@J. Schmid

POLLEN AND ANTHOR MORPHOLOGICAL VARIATION WAS SHAPED BY DOMESTICATION IN RYE (*SECALE CEREALE* L.)

Waesche, Christina¹; Gao, Yixuan¹; Koch, Natalie¹, Gaede, Christin¹, Himmelbach, Axel², Stein, Nils², Mascher, Martin², Boerner, Andreas², Fuchs, Joerg², Dusny, Christian³, Dunker, Susanne⁴, Pillen, Klaus¹, Dreissig, Steven^{1,4}

¹ Martin-Luther University Halle-Wittenberg, Halle, Germany;

² Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany;

³ Helmholtz-Centre for Environmental Research - UFZ, Leipzig, Germany;

⁴ German Centre for Integrative Biodiversity Research (iDiv), Leipzig, Germany

Cross-pollination provides a mechanism to reshuffle genetic variants in a population and enables adaptation to changing environments. In cross-pollinating species, the overall morphology of pollen grains is related to the pollination mechanism, with insect-pollinated species showing extensive sculpting of the outer pollen cell wall (exine), and wind-pollinated species displaying smooth exine structures. While many genes involved in pollen development were identified in Arabidopsis and rice, the genetic architecture underlying intraspecific variation in pollen and anther morphology is not well understood yet. Further on, modulating pollination mechanisms in crops presents an opportunity to improve hybrid breeding programs.

Our study aims to investigate quantitative variations in pollen and anther morphology within an outbreeding and wind-pollinating grass species (*Secale cereale* L.). For this purpose, we analysed 345 rye individuals derived from a diverse set of 65 prior classified rye accessions ranging from domesticated (228), feral (90) and wild-like (27) individuals. A PCA using reduced representation sequencing data (GBS) based on 56,713

SNPs revealed a clustering based on the degree of domestication. We quantified pollen morphology in 286 individuals using high-throughput imaging flow cytometry, and measured anther length via light microscopy in 314 individuals. This analysis revealed that genotypes of a higher degree of domestication displayed higher pollen and anther length compared to genotypes belonging to groups of a lower degree of domestication. We conducted genome-wide association scans and found five and eight genomic regions associated with pollen length and anther length, respectively. A population genomic analysis revealed signatures of selection at one of five loci associated with pollen length, as well as at three out of eight loci associated with anther length indicating a potential indirect selection for larger pollen grains and longer anthers throughout rye domestication.

Our study extends our knowledge of the genetic architecture underlying quantitative variations in pollen and anther morphology and further unravels the domestication history of rye.

UNLOCKING THE POTENTIAL OF WHEAT GENETIC RESOURCES: FINE MAPPING AND VALIDATION OF UNEXPLOITED LEAF AND STRIPE RUST RESISTANCES

Pfrieme, Anne-Kathrin¹; Beukert, Ulrike¹; Schulthess, Albert W.²; Reif, Jochen C.²; Stahl, Andreas¹; Serfling, Albrecht¹

¹ Julius Kühn Institute (JKI) – Institute for Resistance Research and Stress Tolerance, Quedlinburg, Germany

² Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

Several rust-resistance genes for wheat have been identified and cloned in recent decades. Annual infections with leaf rust and yellow rust caused by *Puccinia triticina* and *Puccinia striiformis*, respectively, result in significant yield losses of up to 50% and quality

losses. The integration of unused germplasm shows potential for breeding new cultivars with improved resistance genes. Therefore, identifying genotypes with new, previously unknown resistances is an important task to avoid epidemics caused by cereal

rust and minimize yield losses in an environmentally friendly way. To achieve this, the main goal of the project Genebank is to transform the ex-situ wheat collection of the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben into a collection actively used in breeding. In the first two phases of the project, around 9600 winter wheat and 2700 spring wheat accessions from the IPK Gatersleben ex situ gene bank were tested in field and greenhouse trials for their resistance to defined highly aggressive yellow and leaf rust races. Based on the phenotypic data obtained in combination with whole genome sequencing data, a GWAS identified yellow rust resistance QTL on nearly all wheat chromosomes as well as 194 leaf rust resistance-associated loci on chromosomes 1B, 4A, 4B, 6B and 6D, including resistance sources already used in elite

material. Most of these resistances are active at the seedling stage. Moreover, some unknown resistances could be identified in adult plants in different field trials. The third phase of the project aims to exploit resistances that have not yet been used in breeding. Using the MacroBot platform as a high-throughput phenotyping method, new resistance loci to yellow and leaf rust will be fine-mapped and validated using several races with different virulence patterns. Strategies for validating the resistance associations will be pursued, considering the size of the resistance-associated regions. The goal is to build a publicly accessible library of donors that are carriers of rare resistance loci to different races of powdery mildew, yellow, rust and leaf rust. Furthermore, the genetic background will be analyzed, so that potential candidate genes will be detected.

MEIOSIS GENES VARIATION IN THE TRIANGLE OF U

Schiessl-Weidenweber, Sarah¹; Neuhoff, Maria¹; Zhang, Yuanyuan²; Qian, Lunwen³; Parkin, Isobel⁴; Liu, Zhongsong⁵; Liu, Shengyi²; Jenczewski, Eric⁶; Mason, Annaliese S.⁷

¹ Genetics of Crop Diversity, Justus Liebig University Giessen, Giessen, Germany

² Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences/The Key Laboratory of Biology and Genetic Improvement of Oil Crops, The Ministry of Agriculture and Rural Affairs, Wuhan, China

³ Collaborative Innovation Center of Grain and Oil Crops in South China, Hunan Agricultural University Changsha, Changsha, China

⁴ Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, Canada

⁵ College of Agronomy, Hunan Agricultural University, Changsha, China

⁶ Institut Jean-Pierre Bourgin, Institut National de la Recherche Agronomique, AgroParisTech, Centre National de la Recherche Scientifique, Versailles, France

⁷ Plant Breeding Department, The University of Bonn, Bonn, Germany

Polyploidy is the heritable state of having more than two sets of chromosomes. In plants, it is often linked to higher growth rates and larger biomass, which may explain why many important crops like wheat, potatoes, rapeseed or cotton are polyploids. On the other hand, polyploid formation is difficult and most formation events are unsuccessful. When two species come together to form a new allopolyploid species, correct pairing of homologous chromosomes during meiosis is usually impaired, leading to reduced fertility and eventually extinction. However, successful polyploids must have found a way to overcome this barrier. Here,

we studied variation of 122 meiosis genes within the six species of the triangle of U, *Brassica rapa* (AA), *Brassica nigra* (BB), *Brassica oleracea* (CC), *Brassica juncea* (AABB), *Brassica napus* (AACC) and *Brassica carinata* (BBCC) using publically available resequencing data sets. We found that meiosis genes have lower copy numbers as compared to random genes, but suffer less from gene loss. Meiosis genes were generally more conserved in the polyploids than in the diploids. The results will help to improve interspecific introgression into important crops like *Brassica napus*.

RECENT LANDRACES FROM NOVEL ENVIRONMENTS CAN SERVE AS RESERVOIRS OF GENETIC DIVERSITY IN GRAIN AMARANTH

Singh Akanksha¹, Stetter Markus G.^{1,2}

¹ Institute for Plant Sciences, University of Cologne, Cologne, Germany

² CEPLAS, Cluster of Excellence on Plant Sciences, Cologne, Germany

The predicted climate change will impact worldwide crop yields, requiring shifts and adaptation of crop varieties. The recent global spread of crops across different continents represents an extreme case of expansion, serving as a model to study the factors and sources enabling adaptation to rapidly changing environments. One such spread is the introduction of the nutritious pseudocereal amaranth to India. Grain amaranth has been domesticated over 6,000 years ago in three different regions of the Americas and was only introduced to India approximately 400 years ago. Nowadays numerous local landraces grow throughout the country's wide climatic conditions. We investigate the introduction of grain amaranth to India to understand the factors allowing successful establishment of crops to novel environments, using whole genome sequencing of about 200 accessions from India and more than 100 from the crop's native distribution. The comparison of genetic diversity yielded comparable or even higher diversity in India than in the Americas, despite the likely population bottleneck during the

introduction to India. Surprisingly, the three grain amaranth species that were introduced do not show signs of gene flow, while the strong signals of gene flow were detected in the native range. Correspondingly, the genetic differentiation between grain species was higher within India than within the native range, indicating a strong isolation between otherwise interbreeding populations. The reconstruction of the population history through demographic modelling of different scenarios suggested rapid expansion in the Indian population but a strong bottleneck in the native population, explaining the increase in diversity with isolation. We also identified a few putative genomic loci under selection in India as compared to native range, probably allowing preferential adaptation to the local environment. Our results suggest that introduced crops can act as reservoirs of acquired diversity, providing additional adaptive potential and resilience to future environmental change.

SESSION 2: INNOVATIVE MODELLING STRATEGIES FOR FUTURE CROP IMPROVEMENT

CHALLENGES AND OPPORTUNITIES ARISING FROM Gx E AT DIFFERENT SCALES

Daniela Bustos-Korts¹

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A major objective of plant breeders is to create and identify genotypes that are well-adapted to the target population of environments (TPE). The TPE corresponds to the future growing conditions in which the varieties produced by a breeding program will be grown. A well-adapted genotype can be described as having a better performance than a reference genotype in an environmental range that spans part or whole of the TPE. The identification of genotypes that are well-adapted to the TPE depends critically on the quality of phenotype predictions. These predictions can be made with

models that consider a mixture of statistical, genetic and physiological elements. The selected strategy will largely depend on the amount of Gx E present in the target breeding situation and on trait genetic architecture. This presentation aims at discussing how understanding trait hierarchy can guide the decision-making process of which traits to phenotype in the field and/or platform and how to combine such information to get accurate predictions for the target trait [yield]. These ideas will be illustrated with examples of sunflower and wheat.

LOCATION DETERMINES YIELD PERFORMANCE CONSISTENCY IN WINTER WHEAT (*TRITICUM AESTIVUM* L.): CASE STUDY FROM MULTI-ENVIRONMENT TRIALS AND SIMULATION RESULTS

Wang, Tien-Cheng¹; Chen, Tsu-Wei¹

¹ Albrecht Daniel Thaer-Institute of Agricultural and Horticultural Sciences, Humboldt Universität zu Berlin, Germany

Yield performance results from the intricate interaction between genotype and environments (Gx E), posing challenges to accurately predict crop performance due to plastic responses of plants to environments. To better understand the environmental impacts on complex traits like yield, our research addresses two key questions: How do environmental factors affect the consistency of trait performance (R²trait) in the field? Can physiological relationships between traits across field environments be replicated by theoretical simulation? To explore the Gx E effect on trait performance of yield R²yield, we utilise multi-environment trials (MET) dataset featuring 194 genotypes and 36 environments (spanning three years, four locations and three managements). The management includes combinations of two treatments: total nitrogen fertiliser application (high-HN: 220 kg N ha⁻¹, low-LN: 110 kg

N ha⁻¹) and fungicide application (with-F, without-XF). Resulting three managements are HN_F, HN_XF and LN_XF. R²trait is calculated using standardized major axis (SMA) regression between two environments grouped by three environmental factors: management, location and year. Trait-trait Pearson correlation (r) between eight traits in both field and dataset from simulation in APSIM-Wheat. Our R²yield results across three environmental factors revealed significant differences only between locations. Fungicide addition under high nitrogen or increased total nitrogen under no-fungicide application did not enhance R²yield within the management group, emphasizing location as the predominant determinant. Comparing trait-trait correlations between field and simulation, we found three common correlations: in addition to well known relationships between grain yield, grain number and grain protein, we found a

strong positive association between straw biomass at maturity and grain number ($r > 0.69$). However, the strong positive correlation between flowering time and maturity time in the field ($r = 0.87$) contrasts with the weak and negative correlation in simulation ($r = -0.21$), highlighting the underestimated relationship between

phenology in simulation that warrants re-examination. Toward more precise phenotype prediction and crop modelling, knowledge of environmental influence on trait performance is indispensable. This study suggests the pivotal role of soil properties in determining yield performance consistency.

HIGH-THROUGHPUT FIELD PHENOTYPING TO FACILITATE THE PREDICTION OF CROP PERFORMANCE FOR NEW ENVIRONMENTS AND NEW GENOTYPES IN BREEDING

Roth, Lukas¹; Kronenberg, Lukas^{1,2}; Tschurr, Flavian¹; Hund, Andreas¹; Walter, Achim¹

¹ Institute of Agricultural Sciences, ETH Zurich, Switzerland

² John Innes Centre, Crop Genetics, Norwich NR4 7UH, United Kingdom

Predicting crop performance for new environments and new genotypes is becoming increasingly important in plant breeding. Anticipating future performance is essential in the face of changing climate. Traditionally, multi-environment trials (MET) are combined with statistical models to infer and predict genotype performance in different environments. However, MET data are typically not available for most breeding stages. High-throughput phenotyping offers another perspective to monitor genotype-by-environment (GxE) interactions. The state of a phenotype in a given environment can be viewed as the accumulated response of its genotype to environmental covariates. Modern measurement techniques allow to capture both - environmental covariates and phenotypes - with high temporal and spatial resolution. Here, we provide two use cases that demonstrate the potential of exploring the temporal dimension of plant development in breeding. (1) Temperature is a major driver of plant development in the stem elongation phase of winter wheat. We measured the height development of 352 European cultivars over four years to quantify genotype-specific per se temperature responses. Our results indicate that breeders have influenced the temperature

response through co-selection for phenology in the past. In addition to known major genes related to vernalization, photoperiod, or dwarfing, a GWAS revealed additional unknown loci associated with temperature response. Predictions of phenological stages of winter wheat (jointing, heading, and senescence) with cultivar-specific temperature responses explained GxE interactions better than thermal time. (2) Intermediate traits, such as response parameters, are expected to be more stable across environments than target traits, such as yield. In a second study, we hypothesized that phenomic selection (PS) may allow selection for genotypes with advantageous response patterns in a defined population of environments. A set of 45 winter wheat cultivars was grown at 5 year-sites. A trained PS model predicted overall yield performance, yield stability, and grain protein content with state-of-the-art prediction accuracy. In summary, observing phenotype development over time at a few sites has the potential to reduce the need for large MET trials. However, processing dense time-series data is resource and knowledge demanding. As an outlook, we expect end-to-end image-based approaches to have great potential to facilitate such research.

ROOT TRAITS AS A KEY DRIVER IN ACCELERATING AND STREAMLINING PERENNIAL RYEGRASS IMPROVEMENT

Malinowska, Marta¹; Kristensen, Peter Skov¹; Smith, Abraham George²; Nielsen, Bjarne¹; Fè, Dario³; Greve, Morten³; Lenk, Ingo³; Ruud, Anja Karine^{1,4}; Asp, Torben¹

¹ Center for Quantitative Genetics and Genomics, Aarhus University, Denmark

² Department of Computer Science, University of Copenhagen, Denmark

³ Research Division, DLF Seeds A/S, Denmark

⁴ Department of Plant Science, Norwegian University of Life Sciences, Norway

Perennial ryegrass (*Lolium perenne*), a widely cultivated forage grass, is primarily bred to optimize biomass yield under field conditions. This success relies on the identification of key traits closely associated with desirable agronomic outcomes, particularly early root development traits, which are crucial for establishing efficient nutrient and water uptake networks. However, conventional phenotyping methods for root traits are often labor-intensive, destructive, and time-consuming, hindering their applicability in large-scale breeding programs.

To address these limitations, we developed a novel phenotyping pipeline that combines the fully automated RootPainter tool for extracting root length and our custom-developed SeminalRootAngle tool for determining seminal root angles from images of plants grown in rhizoboxes. This synergistic approach enables rapid and non-destructive phenotyping of large populations, expediting the identification of superior ryegrass genotypes with desirable root characteristics. We further utilized a multitrait modeling approach to investigate the genetic basis of early root development traits obtained from rhizoboxes and their relationship with biomass yield across multiple locations in Europe and over several years. This comprehensive analysis

revealed significant genetic correlations between total root length at the seedling stage and biomass yield, highlighting the potential of total root length as a valuable indicator trait for biomass yield prediction.

Significant correlation between root traits and biomass yield suggests that the use of root traits for pre-breeding selection can help to identify superior genotypes early in the breeding cycle. This can expedite the selection process and save time and resources by eliminating inferior genotypes from further breeding efforts. This approach holds the potential to improve and streamline perennial ryegrass breeding, paving the way for the development of more productive, sustainable, and resilient varieties.

These findings underscore the critical role of root architecture in enhancing perennial ryegrass productivity and stress tolerance. By employing efficient and non-invasive phenotyping methods, such as our novel pipeline, breeders can prioritize root development and expedite the development of superior ryegrass varieties that are adaptable to a changing climate and can flourish in diverse environments.

SESSION 3: ACCELERATING CROP BREEDING FOR IMPROVED CLIMATE RESILIENCE AND SUSTAINABILITY

FOOD AND NUTRITION SECURITY IN THE GLOBAL SOUTH: CROP IMPROVEMENT INTERVENTIONS BY CGIAR AND PARTNERS

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The Consultative Group on International Agricultural Research (CGIAR) is the largest public breeding institution working with developing and least developed countries, through their National Agricultural Research and Extension Systems (NARES), in the global south. The CGIAR and its partners work with about 21 crops, some of which are not attractive to seed companies, and are also custodians of germplasm for these crops in Genebanks. The CGIAR is known for initiating the 'green revolution' in wheat and rice in the 60's. Since this initial success, the production environments that the CGIAR targets have become more complex with many

challenges mostly driven by climate change, increasing populations, reducing land, conflicts, among other challenges affecting livelihoods. These challenges have forced the CGIAR and its partners to restructure and redefine their mode of operations to create a cohesive global breeding function that ensures an all-inclusive food and nutrition secure world. In this talk, I will discuss how the CGIAR and its partners are leveraging on systems, partnerships and modern technologies to drive the development of high yielding, nutritious and climate resilient crops.

DWARFING GENES IN WHEAT, TRITICALE AND RYE HINDER GENETIC GAIN IN FUSARIUM HEAD BLIGHT RESISTANCE

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Fusarium head blight (FHB) is a devastating disease of all cereals in temperate regions that reduces grain yield and quality and leads to mycotoxin contamination of the harvest. Maximising genetic gain is the ultimate goal of breeding. However, in selection for resistance to FHB, the widespread use of the dwarfing genes Rht-B1 and Rht-D1 in wheat hinders genetic gain by significantly increasing susceptibility. This was shown by a comparison of near-isogenic lines with different dwarfing alleles, an analysis of resistance trials within the German VCU trials over the last 20 years, and a genome-wide association study (GWAS) of 400

European winter wheat cultivars. Similarly, the dwarfing gene Ddw1 in triticale increased FHB severity by 20-30%, delayed heading and reduced plant height by an average of 22-29 cm in two segregating bi-parental populations. A preliminary study in rye also showed that hybrids with a dwarfing gene were significantly more susceptible to FHB than tall hybrids. Solutions to increase the genetic gain for FHB resistance could be (1) to use alternative dwarfing genes that do not affect FHB resistance, (2) to select for anther extrusion in wheat, or (3) to accumulate FHB resistance loci in the genetic background by genomic selection.

INTROGRESSING CROP WILD DIVERSITY TO IMPROVE ALFALFA DROUGHT TOLERANCE FOR KAZAKHSTAN AND KYRGYZSTAN

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The rapid onset of climate change in Central Asia has had a large impact on summer rainfall, snow deposition, glacial ice melt and the subsequent availability of irrigation water for agriculture. As a result, farming systems in Kyrgyzstan and southern Kazakhstan are transitioning from full irrigation to rainfed or partially irrigated as water becomes scarce. The Crop Trust Biodiversity for Opportunities, Livelihoods and Development (BOLD) alfalfa project aims to use crop wild relative (CWR) diversity to develop climate adapted varieties of alfalfa that help small holder farmers adapt to their changing environment.

Pre-breeding lines developed for this project by introgressing CWR into lines with advanced genetic backgrounds have been made available for order at Genesys (<https://www.genesys-pgr.org/>).

Chromosome doubling diploid CWR alfalfa collected from desert environments has been widely employed to generate autotetraploids to facilitate the development of wide-genome hybrids. The generation time of this development is being shortened by learning from new approaches to speed breeding, with the use of LED lighting in CER rooms to promote early flowering for crossing to develop hybrid populations.

An additional subset of diverse alfalfa populations, identified from climate searches on Genesys to reveal populations of plants collected from their most extreme environments, has been identified, acquired and is now being multiplied for distribution (available for order from May 2023). This subset includes plants collected from a range of environments that include -30 to 4000m elevation, <200mm annual precipitation, and within the arctic circle.

A core set of 80 pre-breeding lines, wild accessions

and land races are being evaluated in Kazakhstan and Kyrgyzstan in partnership with smallholder farmers. The project partners all use GRID Score to collect, share and upload data associated with trial evaluation and characterisation of individual plant selections. The data is then in the correct format to load onto Germinate (James Hutton Institute), where it can be shared with the global research community.

Severe drought in 2021 to 2022 had a devastating effect on agriculture in southern Kazakhstan but provide an excellent opportunity for selecting alfalfa plants that survived the drought conditions. The surviving 238 plants were selected and transplanted from Makulbek and Tlemis Batyr in a nursery at the Amalybaq research station near Almaty. The plants are now being phenotyped and genotyped (for analysis of diversity and identification of CWR introgression) to identify parents for a new variety for this region. The new variety will target improved autumn and spring production, to make more efficient use of natural rainfall and available irrigation water that occurs outside of the hot, dry summer conditions.

Acknowledgement: This work was undertaken as part of the initiative "Biodiversity for Opportunities, Livelihoods and Development" (BOLD) which is supported by the Government of Norway. The project aims to strengthen food and nutrition security worldwide by supporting the conservation and use of crop diversity. BOLD is managed by the Global Crop Diversity Trust and implemented in partnership with national and international genebanks and plant breeding institutes around the world. For further information, go to the project website: <https://www.croptrust.org/work/projects/the-bold-project/>

EVALUATION OF GENETIC DIVERSITY AND GENOME-WIDE ASSOCIATION STUDIES OF RESISTANCE TO BACTERIAL WILT DISEASE IN POTATO

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Potato is a significant food crop worldwide, after wheat and rice. The development of novel and improved varieties adapted to constantly unstable environmental conditions is made possible by the genetic diversity of breeding materials. The use of wild and landrace populations by breeding programs for germplasm improvement is a reality for breeders through gene banks and germplasm collections around the world. However, there are still significant hindrances to breeding gains in potato attributed to its autotetraploid and highly heterozygous genome. This study evaluated the genetic variation in tetraploid potato genotypes and identified associations with bacterial wilt disease using genome wide association studies (GWAS). A total of 192 International Potato Center (CIP) clones were evaluated genotypically by DArT-Seq, resulting in 9,250 high-quality dosage single nucleotide polymorphisms (SNPs). The same clones were phenotyped for *Ralstonia solanacearum* resistance over two trials. Bacterial wilt disease symptoms were assessed for four weeks at intervals of five days. Bacterial wilt incidence was rated

on a scale of 0 to 4, and the area under the disease progression curve (AUDPC) for GWAS. High heritability ($H^2=0.91$) was observed for AUDPC. At 5 days after infection (DAI), the infected potato clones did not exhibit any signs of wilting. Twenty-six potato clones remained asymptomatic upon disease evaluation. Genetic diversity analysis revealed three major clusters, with subgrouping mostly related to clone familial origin. All the highly resistant, moderately resistant, and susceptible genotypes were clustered among the three subgroups in varying numbers. The families Rodriga x CIP509509.6, CIP394895.7 x CIP509509.6, and others had the highest number of highly resistant clones. There were five major hits among the significant SNPs linked to AUDPC that were within the false discovery rate (FDR) threshold and in all eight GWASpoly models: chromosome 4 (2-dom-ref), chromosome 5 (2-dom-ref), two hits on chromosome 8 (2-dom-ref), and one hit on chromosome 9 (2-dom-alt). These results represent a significant advancement in the development of marker-enabled potato breeding.

NEW STRATEGIES OF THE GLOBAL BARLEY BREEDING PROGRAM OF THE CGIAR TO ACCELERATE GENETIC GAINS UNDER CLIMATE CHANGE

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Barley cultivation in the Developing World is facing new challenges linked to Climate Change. To accelerate the development of new cultivars and better adapted cultivars, the Global Barley Breeding Program of the CGIAR (GBBP) uses new technologies to rapidly

mobilize and incorporate new useful diversity into newly developed varieties that fit farmer's needs. To accelerate the deployment of new diversity, the GBBP has been using Speed Breeding, a rapid generation advancement strategy that allows advancing 4-5

generations in merely one year, coupled with selection for highly heritable traits such as disease resistance, as its main segregating generation advancement technique for the last 3 years. The results show that, despite the absence of field selection during generation advancement, no significant increase in the proportion of undesired plant types related to plant height, lodging or phenology was observed. In addition, the exposure of the segregating generation to diseases under Speed Breeding suggests increased resistance to common diseases like net form of net blotch and others.

When aiming to develop new high yielding varieties adapted to a changing environment, breeding programs must often choose between increasing testing locations or entries number, especially at early testing stages.

This is even more important for international breeding programs targeting several countries with highly diverse environments. For it, the GBBP implements since 2021 a genomic-assisted sparse multi-location approach, an experimental design that allows breeders to test thousands of entries under multi-location trials having only a fraction of the genotypes present in all environments. Using low density genotyping the program can predict traits of interest of thousands of non-planted lines across 8 locations in 4 countries representing relevant growing areas. This approach yields medium to high cross-validation accuracies ($r=0.20-0.55$) at target environment for grain yield while allowing to recover entries lost due to extreme climatic events, and evermore common situation when breeding under Climate Change.

BIODIVERSITY FOR OPPORTUNITIES, LIVELIHOODS AND DEVELOPMENT (BOLD): HARNESSING CROP DIVERSITY TO MITIGATE THE EFFECTS OF CHANGING CLIMATE - FINGER MILLET COMPONENT

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Finger millet is the most important millet in East Africa (EA) for food and nutrition security, feed, income and adaptation to adverse conditions. It has an impressive nutritional profile with 5–8% protein, 15–20% fiber, 2.5–3.5% minerals, high degree of unsaturated fatty acids mainly linoleic (40.3–51.7%), oleic (20.2–30.6%) and linolenic acid (2.3–5.8%). The problem is yields are low, ≤ 1.3 t/ha compared to a potential of up to 10 t/ha due to biotic and abiotic stresses including blast disease, Striga, drought, and poor soils. Research has focused on mitigation of the constraints. The Crop Trust initiative started with the Crop Wild Relatives project in 2016 which enabled screening wild relatives, landraces, and farmer varieties for blast, Striga, and drought resistance. Resistant products were intermitted to result into resilient pre-breeding lines which are currently at advanced generations and being deployed in breeding programs in Kenya, Tanzania, and Uganda. The BOLD-WP2 on Finger millet targets: (i) exploitation

of existing introgression lines and new germplasm for enhanced biotic and abiotic stresses resistance, (ii) Identification of superior pre-bred genotypes and availing them to farmers and breeders, (iii) Genetic characterization of traits of interest, and (iv) Establishment and optimization of finger millet hybridization to enable routine trait introgression. This has resulted in generation of new crosses for different traits such as blast diseases, drought and striga tolerances. Where, the plastic bag technic was used for the first time in Tanzania; advancement of cross products made under CWR to F3 and F4 generations; constitution and implementation of Pre-PVS trials; screening of pre-bred lines for abiotic and biotic stresses across the three countries. The pre-PVS trial in Kenya contained 37 lines plus 12 parental checks; in Tanzania 36 lines; in Uganda 25 lines. Preliminary results suggest potential for identification of superior varieties. Genotyping data of 94 finger millet genotypes using

the mid-density panel (MDP) developed on the DARt-tag platform by ICRISAT. Out of the 50 markers tested across 188 East African genotypes, 4 (snpEC00250, snpEC00253, snpEC00254, snpEC00258) did not

amplify. The remaining 46 performed extremely well with 38 of them having a PIC value of more than 0.25, therefore considered very informative.

UNRAVELING THE FUNCTION OF THE CYST NEMATODE RESISTANCE GENE HS4 IN DIFFERENT GENOMIC BACKGROUNDS

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Plant-parasitic nematodes are major pests in agriculture. The beet cyst nematode (BCN) *Heterodera schachtii* is the main pest of sugar beet (*Beta vulgaris*) and many other species from the *Amaranthaceae* and *Brassicaceae* plant families. After completing their life cycle in the plant's roots, the females stay attached to the roots and form a cyst filled with several hundred eggs that can survive in the soil for up to ten years. Sugar beet and its close relatives are highly susceptible to the BCN, while distant relatives from the genus *Patellifolia* are fully resistant. Sugar beet lines carrying translocations from the *P. procumbens* chromosome 1 are resistant to the BCN. Recently, the Hs4 gene was cloned from a *P. procumbens* translocation attached to the beet chromosome 9. The gene encodes an ER-bound rhomboid-like protease. A homolog with 60 % polypeptide similarity is present in *B. vulgaris*. The Hs4 gene was expressed in susceptible sugar beet hairy roots resulting in resistance to the BCN.

In an ongoing project, we searched the genomes of different *Beta* and *Patellifolia* species for the presence of Hs4 or its homolog. We found that all *Patellifolia* contained the Hs4 gene and the homolog could be detected in all *Beta* species. Then, we studied the expression of these two genes in several *Beta* and *Patellifolia* species. While Hs4 is expressed more prominently in *Patellifolia* roots compared to leaves, the homolog is expressed conversely in beets.

We were also questioning whether Hs4 functions in distantly related species. We therefore transformed the gene into the model plant *Arabidopsis thaliana* under the transcriptional control of two different promoters. Hs4-transgenic T3 lines showed significantly reduced cyst numbers. Moreover, the Hs4 expression correlated with the cyst number indicating that the Hs4 gene confers resistance even in distantly related species. Recently, we started transforming oilseed rape (*Brassica napus*) using the same Hs4 constructs.

BREEDING FOR STABLE DISEASE RESISTANCE: A COMMERCIAL WHEAT BREEDING CASE STUDY USING GENOMIC PREDICTION

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Traditionally, wheat breeders screen and select for disease resistance using dedicated disease nurseries in the field. While an effective approach, there are many challenges and limitations, such as cost, high labour intensity, sufficient disease infection and data reliability. Genomic selection (GS) presents an alternative and complimentary approach that mitigates the limitations of phenotypic selection and is now routinely deployed in commercial breeding programs. GS models that incorporate Genotype x Environment (GxE) interaction terms are typically reserved for the highly complex trait, yield. Yet, the expression of disease resistance is often influenced by variation in the pathogen population across locations/years and environmental factors, such as rainfall and humidity. Thus, GS approaches aiming to breed varieties with enhanced resistance stability could also benefit. In a collaboration between the Australian commercial plant breeding company, InterGrain, and the University of Queensland, this study surveys the level of GxE interaction for LR and YR in a large-scale wheat breeding population and explores the impact

on prediction accuracy from fitting more complex GS models that include GxE, Genotype x Pathotype (GxP) and Genotype x Environment x Pathotype interaction terms. The multi-environment trial analysis, spanning several years and nurseries, revealed high levels of GxE interactions for both the LR and YR datasets. For LR, a significant prediction accuracy improvement was achieved when fitting a GxE model within a one-stage GBLUP framework (r 0.8) compared to a traditional two-stage GBLUP model (r 0.4), however there was no substantial differences in prediction accuracy between the one-stage GBLUP GxE, GxP and GxExP models. This is likely a result of the one-stage approach leveraging precision in prediction through using relationships in the genomic relationship matrix to account for minimal replication in the datasets. Based on learnings from this study, we propose a framework that could be applied to breeding of any crop-patho system, and we highlight the need for more detailed environment and pathotype information to accelerate the development of crops incorporating effective and durable resistance.

SESSION 4: DESIGNING FUTURE CROPS USING MODERN BREEDING TECHNOLOGIES

TRANSFORMING VEGETABLE BREEDING

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Vegetables by Bayer R&D has twenty-two vegetable and fruit crops in its portfolio all of which are transforming their breeding processes with new technologies to meet the grower and consumer demands for high-yield and high-quality vegetable varieties.

Shortening breeding cycles is key, but acceleration of shortening cycle time must go in tandem with the other variables in the breeder's equation to substantially increase genetic gain. Selection accuracy depends on several factors including consistent trait measures, preferably quantitative (e.g. digital phenotyping) rather than subjective scores (e.g. height ratings). Accurate and cost-effective genomic tools are paramount to achieving mass characterization of breeding lines. Selection intensity can be altered by increasing the number selection candidates through rapid inbreeding methods. Finally, diversity can be influenced by introducing new genetics. These fundamental concepts are known, yet routine application at scale remains challenging mainly due to the logistics of implementing technologies. Breeding program simulations assist

the choices between speed, accuracy, resources, and genetic gain. Timely discovery and integration of native traits is crucial to success in most vegetable markets. Is the recent rapid progress in genome sequencing technologies, genome editing, and Pangenome analytics poised to transform vegetable breeding?

Bayer is building genomic, phenotypic, analytic, digital, and logistic resources to enable transformations in a broad set of breeding pipelines and global environments. Environments of course differ across regions, and, increasingly, they vary more widely within region due to climate change requiring more resilient and adaptable varieties. How do we best strike a balance between global and local focus?

Solving these complex issues requires collaborations between industry and academia. No organization has all the answers and ongoing engagement as well as co-designed projects are needed to meet grower demands for productive varieties and consumer demands for sustainably grown nutritious food.

ADAPTING TO THE HEAT: STRESS RESPONSE AND REPRODUCTIVE SUCCESS IN BARLEY

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High ambient temperature is one of the leading abiotic stresses impacting crop yield. Enhancing the thermal resistance and yield stability has become a pivotal target in crop breeding, especially in temperate cereals like wheat and barley. The major photoperiod-responsive

gene, PHOTOPERIOD-H1 (PPD-H1), accelerates flowering time under long-day conditions and thus promotes adaptation to marginal environments with terminal stress. Furthermore, we found that a natural mutation at CCT domain of ppd-h1, prevalent in spring barley

cultivars, causes a delay in flowering and a strong reduction in grain number in response to high ambient temperature. By contrast, genotypes carrying the wild-type Ppd-H1 allele accelerate flowering and maintain grain number under high ambient temperature. Moreover, microscopic phenotyping revealed that PPD-H1 controls floret fertility by modulating anther and pollen development in response to high ambient temperature.

Global transcriptome profiling on developing inflorescences and leaves of genotypes differing at

PPD-H1 under control and high ambient temperatures, demonstrated that PPD-H1 controlled overall stress resistance and energy metabolism. PPD-H1- and temperature-dependent differences in stress gene expression were linked to changes in carbohydrate metabolism, spike development, and hormone homeostasis as supported by hormone level changes in leaves and meristems. We, therefore, propose that PPD-H1 controls overall stress resistance, thereby affecting carbon metabolism, inflorescence development, and grain yield.

GENOMIC PREDICTION OF APPLE TRAITS INTEGRATING ENVIRONMENTAL COVARIABLES AND NON-ADDITIVE EFFECTS

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Genotype by environment interactions ($G \times E$) result in changes in the extent of phenotypic differences between genotypes cultivated in diverse environments. The multi-environmental apple reference population (apple REFPOP) represents an opportunity to broaden our understanding of $G \times E$, particularly when incorporating $G \times E$ into genomic prediction. To study the $G \times E$, conventional statistical models can be extended to include not only additive effects but also non-additive effects, environmental covariables and their interactions with genotypes. Additionally, deep learning, which enables the integration of data from various sources and allows for multi-environment prediction, has recently emerged as a viable alternative to statistical genomic prediction. Here, we compared conventional statistical genomic prediction models with their extended versions that incorporate modeling structures to accommodate additive, non-additive and environmental sources of variation, as well as with a hybrid deep learning alternative based on two genotypic and two environmental input streams. The study evaluated the performance of genomic predictions on

the apple REFPOP dataset. The dataset consisted of 534 genotypes, 303K single nucleotide polymorphisms, and eleven traits related to phenology, yield, and fruit quality, which were phenotyped in up to 25 environments (combinations of locations and years). The proportions of variance components associated with additive, non-additive, and environmental sources of phenotypic variation were reported, shedding light on how $G \times E$ affects the studied traits. The differences in predictive ability among the compared statistical models were marginal, and the statistical model containing the main additive effects and $G \times E$ showed the best performance. The applied deep learning approach demonstrated a comparatively lower predictive performance than statistical models, except for the trait harvest date, where deep learning exhibited a considerable advantage with a 0.1 higher predictive ability than the statistical models. The obtained insights about the impact of $G \times E$ on the studied traits and model performance will inform future modelling decisions in the field of genomic prediction in apple.

GENETIC VARIABILITY OF DROUGHT RESPONSES AND ROOT TRAITS IN WILD VITIS SPECIES WITH AN INTEREST TO BE USED AS GRAPEVINE ROOTSTOCKS

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Grapevine is one of the world's most important fruit crops with, approximately 7 million hectares planted in 2021. It is grown as a grafted vine almost everywhere in the world, but the most commonly used rootstocks were selected in the late 19th and early 20th centuries and are based on reduced genetic diversity. Climate change leads to new threats to viticulture, such as more intense and frequent drought events. As the roots have an essential function in the uptake of water and mineral nutrients, the choice of rootstocks selected for their drought tolerance is an important option in the adaptation of viticulture to climate change. In addition, breeding rootstocks adapted to drought conditions could allow maintaining the typicity induced by cultivars. However, one of the main challenges in rootstock breeding in accessing roots in the field, which makes phenotyping very time consuming and makes it difficult to study the root system on a large scale. To overcome the issue of phenotyping root traits in a perennial specie, we hypothesized that metabolites can be used as biomarkers of complex root traits.

The aim of this study was to correlate root traits

(morphological and molecular) with drought responses and to estimate the genetic variability of these traits. We evaluated 12 wild *Vitis* species (3 - 5 accessions per species = 50 accessions; n = 3). We performed a water deficit pot experiment in controlled conditions with 6-month-old cuttings. During the experiment, gas exchanges and shoot growth were measured on the aerial parts. Root morphological features were extracted using two image analysis softwares (SmartRoot and Rhizovision). We characterized osmotic adjustment in roots and targeted and non-targeted metabolic profiles. We used mixed models to extract the best linear unbiased predictors (BLUPS) and broad-sense heritabilities. Using genetic correlations and multivariate predictive analysis we established the link between root traits genetic variation and drought responses or metabolite profiling. Specifically, root osmotic adjustment was negatively correlated with specific root length. These results will enable the development of methods for high-throughput phenotyping of roots and the identification of accessions to be used into new grapevine rootstock breeding programs.

EARLY MATURITY 7 (EAM7) IS A MODULATOR OF PHOTOPERIOD SENSITIVITY IN BARLEY

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Flowering in the most favorable seasonal conditions is essential for a plant's reproductive success and ensures high crop yields. Photoperiod is one of the most important environmental cues to regulate the timing of flowering in response to seasonal changes.

Agronomically important temperate cereal crops, such as barley and wheat, are long-day plants requiring day lengths above 12 hours to induce reproductive development. In barley, PHOTOPERIOD 1 (Ppd-H1) has been identified as a key player in photoperiodic

flowering. Nonetheless, large parts of the genetic networks controlling reproductive development in response to day length remain to be elucidated in barley.

Plants carrying a mutation at the early maturity 7 (eam7) locus are characterized by early flowering under non-inductive short-day conditions. Utilizing a biparental mapping population, we identified LIGHT-REGULATED WD 1 (LWD1) as a promising candidate gene for the eam7 locus. Complementation tests between eam7 mutants and CRISPR/Cas9-generated *lwd1* mutants confirmed LWD1 as the gene underlying the eam7 locus. Diurnal gene expression patterns revealed that LWD1

acts as an upstream night-time repressor of *Ppd-H1* and the circadian clock gene EARLY FLOWERING 3 (ELF3). Genetic interactions between *lwd1* and *Ppd-H1* resulted in the photoperiod-independent induction of florigen FLOWERING LOCUS T1 (FT1) and early flowering under short days. We thus concluded that LWD1 controls the light input into the circadian clock and photoperiod-dependent flowering in barley.

These findings extend our knowledge of photoperiodic flowering and may be useful in modulating photoperiod insensitivity to improve crop performance in areas with short growing seasons.

USING CRISPR/CAS FOR PLANT BREEDING: FROM GENE EDITING TO CHROMOSOME ENGINEERING

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Till today CRISPR/Cas nucleases have been applied to plants mainly to mutate genes for the improvement of traits. As these enzymes are originating from human photogenic bacteria, their activity optimum is far above plant cultivation temperatures. By mutagenesis we were able to optimize Cas12a enzymes for plants use, resulting in much higher frequencies of mutation induction but also gene targeting by homologous recombination. Besides improving single traits, breeding also requires the breaking or establishing genetic linkages on the chromosome level. Using CRISPR/Cas, we were able to change genetic linkages by inducing heritable translocations in the Mb range between heterologous chromosomes in *Arabidopsis*

thaliana. Recent improvements in sequence analysis of crop plants reveal that multi Mb long inversions occur with high frequency between different genotypes, leading to crossover suppression. We were not only able to demonstrate that inversions up to almost chromosome size can be achieved in *Arabidopsis*, but also meiotic recombination can be redirected this way. Thus, on one side a recombination dead region could be reactivated after 5000 years and on the other almost a complete chromosome could be excluded from genetic exchange. In the future, CRISPR/Cas-mediated chromosomal engineering will allow us to restructure plant genomes according to our needs for breeding.

GENOME SPECIFIC ASSOCIATION STUDY (GSAS) FOR EXPLORATION OF INTRAVARIETAL VARIABILITY IN HEMP (*CANNABIS SATIVA*)

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Hemp (*Cannabis sativa* L.) stands as a versatile crop with substantial economic potential. However, its intravarietal phenotypic and genetic variability remain inadequately elucidated. Here, we employed a population derived from a single plant to extensively explore variability in plant growth, development, reproductive patterns, as well as genetic variability. Furthermore, we found statistically significant single nucleotide variants (SNVs) and haplotypes associated with traits of interest identified through the innovative implementation of a genome-specific association study (GSAS) framework. The GSAS methodology consolidates a streamlined generation of a single phenotyped population, selection of alleles

heterozygous in the parent plant, and application of a model conducive to the polygenic association of studied traits. The GSAS approach emerges as a pivotal tool capable of significantly advancing our foundational comprehension of the genetic determination of intravarietal phenotypic variability in hemp and in other highly heterozygous crops. Findings of prospective GSA studies hold the potential to be harnessed for the marker-assisted breeding of new cultivars with enhanced uniformity and improved performance in traits relevant to various applications, ranging from pharmaceuticals to manufacturing of materials of superb properties, such as hempcrete or bioplastics.

UNRAVELLING THE GENETICS OF MUNGBEAN CANOPY DYNAMICS USING UAV-DERIVED PREDICTION MODELS

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Mungbean is a high-value export pulse crop grown in subtropical farming systems globally. Their indeterminate growth behaviour is a major physiological constraint negatively impacting yield, as it results in the accumulation of vegetative and reproductive components simultaneously. Understanding canopy dynamics can provide new insight to increase yield potential by improving resource accumulation, remobilisation, and light interception. Additionally, understanding the genetics underpinning these complex traits would allow breeders to strategically target improved phenotypes that could enhance mungbean productivity. However, due to the current phenotyping bottleneck that exists, screening these

traits particularly at a large-scale remains a challenge, thereby limiting our understanding of their genetics. In this study, a diverse nested association mapping (NAM) population was evaluated across multiple environments in QLD, Australia and imaged using a drone fitted with a multi-spectral camera flown regularly throughout development. Several vegetative indices and geometric traits were extracted from each flight and used to establish biomass prediction models. Spline curve fitting was used to integrate the predicted values from single flights into a continuous time course to calculate canopy dynamic traits such as maximum accumulation rate. Undertaking a local genomic estimated breeding value approach for the first time in mungbean, we were

able to identify haploblocks associated with these dynamic traits which can be explored further to develop cultivars with optimised canopy development patterns. The identification of these haploblocks establishes

a catalogue of chromosome segments that can be leveraged for the enhancement of mungbean breeding and crop performance.

EXPLORING THE (EPI)GENETIC DIVERSITY IN GRAPEVINE

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Riesling is one of the economically most important white vine varieties and is at least 500 years old being first documented in 1453. Since then a wide spectrum of clonal variation has developed which is represented in the Riesling clone collection at Geisenheim University where more than 1400 different Riesling clones are grown and monitored. These varieties differ in cluster architecture growth behavior bud burst and ripening characteristics as well as berry color. The genetic and epigenetic causes for this variation so far remain mostly unknown. For this reason the institute of grapevine breeding is working on sequencing a significant number of the clonal population to uncover the genetic differences within the genomic population. Therefor

we are using a combination of short read and Oxford Nanopore based long read sequencing techniques to uncover not just small genomic differences like single nucleotide polymorphisms and small InDels but also larger duplications, deletions and rearrangements by doing de-novo genome assemblies of representative clones and using these as references for aligning and analyzing the short read data generated from a larger number of clones. Furthermore, the use of Oxford Nanopore Long-Read sequencing and specialized short read sequencing technologies enables simultaneously analyzing the epigenetic variation in the population and helps explaining which traits are caused by somatic and which by epigenetic mutations.

SESSION 5: PREDICTING A PATH FOR FUTURE CROP IMPROVEMENT

RETHINKING THE “BREEDER’S EQUATION”: EMERGING OPEN QUESTIONS

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The “breeder’s equation”, in its many forms, provides a framework for design, optimisation and evaluation of population level genetic gain over cycles of a breeding program. Empirical results demonstrate it has served us well to date. Plant breeding programs take on different forms based on the details of the

target crop species, accessibility of technologies to manipulate genetic variation and the on-farm Target Population of Environments (TPE) within which genetic gain must have impact. Theoretical considerations, based on knowledge of trait genetic architecture and the details of the structure of the TPE,

and complementary simulation investigations, inform breeding program design. However, empirical results from long-term selection experiments and commercial breeding programs are the foundations on which such investigations should be conducted. Further, the consequences of climate change necessitate consideration of a future TPE that can impose different crop adaptation and performance requirements from the recent (last few decades) and deep (last century) past. Experience from maize hybrid breeding in the US corn-belt, based on both long-term genetic gain

for yield and more recent breeding to accelerate improvement of yield stability for drought-prone on-farm environments, provide a foundation to define emerging “open questions” that should be considered when contemplating breeding for a future TPE under the influences of climate change. We will consider some of these emerging “open questions” and discuss their implications for the design of breeding programs to achieve long-term genetic gain for the global needs of this century.

FROM BITTER TO BETTER: OPTIMIZING THE TASTE OF RAPESEED PROTEIN FOR HUMAN CONSUMPTION BY APPLIED GENOME RESEARCH

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The demand for plant protein for human nutrition is rising due to concerns about food security, animal welfare, and human health. In this context, rapeseed as a local protein source with high bioavailability is of high relevance. The use of its protein for food is, however, limited by the presence of bitter-tasting flavonols in the seeds. Therefore, one aim is to reduce or ideally eliminate these taste-impairing flavonols. This requires a comprehensive understanding of flavonol biosynthesis in rapeseed. In related species, flavonol derivatives are synthesized by the sequential activity of flavonol synthases (FLS) and subsequent glycosylation by flavonol glycosyltransferases (FGTs). The expression of FLS and FGTs is primarily regulated by MYB transcription factors. The aim of this work is to characterize these structural and regulatory genes in rapeseed with regards to their contribution to flavonol biosynthesis in order to develop targeted breeding strategies.

Candidate genes involved in flavonol biosynthesis were identified and selected candidates were characterized

in terms for their functionalities. We showed that the rapeseed FLS gene family comprises 13 members (Schilbert et al., 2021). Five FLS genes were active in the seed. Of these, two have FLS and flavanone 3-hydroxylase (F3H) activity (FLS1-1 and FLS1-2), two have F3H activity only, and one has neither FLS nor F3H activity. We identified homozygous fls1 1/fls1-2 rapeseed mutants, which showed a significant reduction in all bitter-tasting flavonol derivatives. In addition, we could identify eriodictyol as antagonist for bitter-tasting flavonols. The endogenous production of eriodictyol was studied in a related plant species (Schilbert et al., 2023). The identified candidate genes can contribute to the breeding optimization of flavonol composition and content of rapeseed seeds. Overall, the results can be used to breed elite rapeseed varieties with reduced levels of bitter-tasting flavonols, thus making rapeseed protein more suitable for human consumption.

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GENETIC GAIN IN SPRING BARLEY AND GENOMIC PREDICTION STRATEGIES FOR EFFICIENT BREEDING OF YIELD IN DIFFERENT ROW TYPES

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Genomic prediction (GP) has the potential to be a cost efficient and accurate tool in breeding for complex traits. With the advent of GP usage in plant breeding programs there is an expectation of increased variety performance, however the rate of improvement in current market spring barley varieties is not known. Here, the genetic gain of yield in spring barley in the last 20 years was estimated by using historical data from field trials from 2014-2022 with 22-60 market varieties grown per year. This resulted in an estimated genetic gain of 1.07% per year for all lines and a 0.94% increase per year of the top performing lines. Using GP to specifically breed for targeted regions could

enhance yield output in released cultivars and reduce phenotyping costs. In this study, 376 breeding lines of two-row and six-row barley tested in multi-environment trials were used to develop and test GP models, resulting in a prediction accuracy of 0.63 for yield (kg/ha). The genetic diversity of the row-types was explored and used as a factor in the evaluation of the predictions. In addition, the potential to predict untested locations using yield data from other locations was explored. This article investigates historical and current genetic gain trends in spring barley and how accounting for population stratification in a breeding population can improve GP results in a spring barley population.

OPTIMAL IMPLEMENTATION OF GENOMIC SELECTION IN CLONE BREEDING PROGRAMS— EXEMPLIFIED IN POTATO: I. EFFECT OF SELECTION STRATEGY, IMPLEMENTATION STAGE, AND SELECTION INTENSITY ON SHORT-TERM GENETIC GAIN

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Genomic selection (GS) is used in many animal and plant breeding programs to enhance genetic gain for complex traits. However, its optimal integration in clone breeding programs (for example potato) that up to now rely on phenotypic selection (PS), requires further research. In

this study, we performed computer simulations based on an empirical genomic dataset of tetraploid potato to (i) investigate how the weight of GS relative to PS, the stage of the GS implementation, the correlation between an auxiliary trait and a target trait, the variance

components, and the prediction accuracy affect the genetic gain of the target trait, (ii) determine the optimal allocation of resources maximizing the genetic gain of the target trait, and (iii) make recommendations to breeders how to implement GS in clone and especially potato breeding programs. In our simulation results, any selection strategy involving GS had a higher short-term genetic gain for the target trait than Standard-PS. In addition, we showed that implementing GS in consecutive selection stages can largely enhance short-term genetic gain and recommend the breeders

to implement GS at single hills and A clone stages. Furthermore, we observed for selection strategies involving GS that the optimal allocation of resources maximizing the genetic gain of the target trait differed considerably from those typically used in potato breeding programs and, thus, require the adjustment of the selection and phenotyping intensities. Therefore, our study provides new insight for breeders regarding how to optimally implement GS in a commercial potato breeding program to improve the short-term genetic gain for their target trait.

DYNAMIC OPTIMIZATION FOR RESOURCE ALLOCATION IN BREEDING PROGRAMS USING EVOLUTIONARY ALGORITHMS (MOBPSOPTI)

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With the rise of genomics and new breeding technologies, breeding programs have undergone significant transformations over the past few decades that allow for more complex and advanced designs. As a result, the optimization of modern breeding programs involves many interdependent decisions on how to allocate resources, to obtain both short-term genetic and long-term sustainability. Significant benefits can be achieved by linking stochastic simulation with simulators such as MoBPS with a family of optimization techniques to identify breeding programs that make the best use of resources, achieve optimal outcomes for a given budget, and provide effective trade-offs between competing objectives. Since there is a significant amount of randomness in both, simulations and real-world breeding programs, we have developed a new optimization framework that integrates the use of evolutionary algorithms to iteratively optimize breeding programs and subsequently apply kernel regression in a complementary manner to minimize the stochasticity in data patterns and ensure accurate outcome predictions.

To do this, we initially choose parameter settings randomly from the entire range of potential breeding programs. Parameter settings with the best value of the objective function (e.g. genetic gain or loss in genetic diversity) will be selected as parents. The “offspring” settings are created either by “recombination”, which involves taking two existing parents and combining their information to create a new parameter setting, “mutation”, which introduces small, random changes to a single parent, or by introducing new parameter settings randomly to overcome the problem of convergence to a local maximum. Following that, the optimal parameter settings will undergo simulation, iterating through this process until convergence is attained. Our optimization pipeline benefits from the automation provided by the Snakemake workflow management system, which can easily integrate with our iterative optimization approach, simplifying the execution of a set of tasks that need to be run in a specific order regularly. Our algorithm proved successful in a toy breeding program, highlighting its effectiveness.

BIG DATA DRIVEN GENOMIC PREDICTIONS FOR ELEVATING GENETIC GAIN IN WHEAT

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Prediction ability is an important factor that can positively influence genetic gain under genomic selection. Prediction ability can be increased by enhancing the training set size and the diversity within the training set. Therefore, we collected phenotypic and genotypic data from four breeding companies and five historical datasets and integrated them into Big Data. Finally, we assembled around 13,846 inbred lines yield data that is coming from ~ 700 thousand plots. Our results show that combining datasets into a

training set best predicts each company's genotypes compared to the same company dataset as the training set. Furthermore, the cumulated training set gives 24 to 157 % improvement in the prediction ability compared to the single company dataset as the training set when predicting the performance of released varieties that are tested in official trials. In summary, using big data in predictive breeding contributes to a higher genetic gain, thus representing an exciting option for wheat breeding.

FEATURE ENGINEERING AND PARAMETER TUNING - IMPROVING PHENOMIC PREDICTION ABILITY IN MULTI-ENVIRONMENTAL DURUM WHEAT BREEDING TRIALS

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The success of plant breeding programs depends on efficient selection decisions. Phenomic selection (PS) has been proposed as a tool to predict genotype performance based on near-infrared spectra (NIRS) to support selection decisions. In this talk, you will learn about our latest research, in which we tested the performance of PS in multi-environment durum wheat breeding data for three wheat breeding scenarios and used feature engineering as well as parameter tuning to improve the phenomic prediction ability. In addition, we investigated the influence of genotype and environment on the phenomic prediction ability for agronomic and quality traits.

We found that preprocessing based on a grid search

parameter tuning over the Savitzky-Golay parameters based on 756,000 genotype best linear unbiased estimate (BLUE) computations, improved the phenomic prediction ability up to 500 %. Furthermore, we showed by using feature engineering that the preprocessing should be optimized depending on the data set, trait, and model used for prediction to yield the highest prediction ability. The three phenomic prediction scenarios based on our durum breeding program resulted in low to moderate prediction abilities with the highest and most stable prediction results when predicting new genotypes in the same environment as used for model training. This is consistent with the finding that NIRS capture both genetic and environmental information.

MACHINE LEARNING COMBINED WITH LOCUS-SPECIFIC DEGREE OF DOMINANCE TRANSFORMATION FOR GENOMIC PREDICTION IN MAIZE

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The genetic architecture of a trait plays a vital role in the predictive ability of genomic models. Previous studies have used and reported different methods of accounting for the genetic architectures of traits. In this study, we combined three machine learning methods: Support Vector Machine (SVM), Light gradient boosting machine (LGBM) and eXtreme Gradient Boosting (XGBoost) with locus-specific weighted dominance effect (a new method of capturing dominance effects) for use in the genomic prediction of maize yield. The results of the machine learning combined model were also compared with classical methods, amounting to a total of nine (9) models: [1] SVM combined with locus-specific weighted dominance effects, [2] LGBM combined with locus-specific weighted dominance effects, [3] XGBoost combined with locus-specific weighted dominance effects, [4] SVM only, [5] LGBM only, [6] XGBoost only, [7] Genomic Best Linear Unbiased Prediction (GBLUP) model with additive effects only,

[8] GBLUP model including additive and dominance effects, [9] GBLUP combined with locus-specific weighted dominance effects. The preliminary results show that the machine-learning model outperforms the classical models by a 2% increase in predictive ability. Combining locus-specific weighted dominance effects with either machine or classical methods decreased the predictive ability, which shows limitations for this parameterisation. Overall, the dominance variance of yield in this data set was low, and models including dominance effects did not have a significant advantage. However, they showed higher stability for predictive ability. These methods will be further analysed in other traits and species, considering different marker densities and sample sizes.

KEYWORDS: *Machine learning, dominance effects, maize, yield, genomic prediction, gradient boosting, genetic architecture*

IDENTIFICATION OF POLYGENIC SELECTION FOR DROUGHT STRESS IN EUROPEAN BEECH POPULATIONS

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Determining the genetic basis of polygenic traits is crucial in forest genetics. Tree breeding is an extremely long and tedious process. Therefore, it is necessary to know how promising the selection will be before programs are implemented. To study the genetic basis of polygenic traits, field experiments are implemented. These experiments are costly. Phenotypic results on traits that are measured at maturity are only available after a long time and juvenile-mature correlations are often unknown. G^{\wedge} is a method that identifies selection on complex traits by evaluating the relationship between genome-wide changes in allele frequency and their estimates of effect sizes. Genotypic and phenotypic data were previously collected from 100 individuals per stand in 5 locations in Braşov (Romania) along an altitudinal gradient which is associated with precipitation and temperature. Different traits related to drought stress or tree physiology were collected. G^{\wedge} usually uses the allele frequency change calculated between two groups that faced different selection scenarios. We calculated allele frequency change as a slope of the linear relationship between the allele frequency in the different populations along the precipitation/temperature gradient. To evaluate the

effects on G^{\wedge} , we additionally tested 100 randomly generated traits. G^{\wedge} uses a simple permutation-based test for significance that also takes into account the effective number of independent markers. The effective number of independent markers is approximated by estimating the LD decay over the entire genome. The calculated number of effective markers was 838,522, which corresponds to the number of total markers. Consequently, 91 and 87 of our randomly generated traits were significantly under selection when calculating G^{\wedge} . Therefore, we tested all possible values (800,000 to 1,000) as effective markers. With 7000 effective markers, we never observed more than 10 randomly generated features that were significantly under selection. Finally, we calculated G^{\wedge} for the measured traits related to drought stress or physiology. Significant selection was observed for diameter at breast height (DBH), leaf carbon content and water use efficiency measured as $\delta^{13}C$, while no selection was observed for stomata density. In a further analysis, we want to find out whether stomata density is really not under selection or whether it is simply not as polygenic as DBH, leaf carbon content and $\delta^{13}C$ and therefore cannot be detected.

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SESSION 3: ACCELERATING CROP BREEDING FOR IMPROVED CLIMATE RESILIENCE AND SUSTAINABILITY

POSTERS – QUANTITATIVE GENETICS AND BREEDING

1. OPTIMIZING WHEAT BREEDING STRATEGIES FOR ENHANCED GENETIC GAIN THROUGH COMPUTER SIMULATIONS

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Plant breeding programs are often complex and require breeders to make strategic decisions to allocate the available resources effectively. Computer simulations provide a rapid and inexpensive means of assessing the potential for implementing changes in a breeding scheme to achieve higher genetic gain within the given constraints. In this project, we evaluated different crossing strategies in Agroscope's winter and spring wheat breeding schemes to identify possible improvements that can deliver higher rates of genetic gain in the breeding program. To do this, we defined a grid of possible scenarios that included different combinations of number of genitors, number of crosses and progeny per cross. This grid was constrained by the capacity of the breeding program in the early stages before pure line selection (250k and 100k plants for winter and spring wheat, respectively). The

scenarios were evaluated using stochastic simulations in AlphaSimR over a period of 50 breeding cycles. Our results indicate that reducing the current number of genitors by 40% can lead to an expected increase in the rate of genetic gain of 15% and 20% for spring and winter wheat, respectively. This improvement is likely due to an increase in selection intensity. No improvement was observed by changing the number of crosses and progeny per cross, these seem to have little or no effect on the rate of genetic gain in the long term (50 cycles). This study identified optimal crossing strategies to increase genetic gain in Agroscope's wheat breeding pipelines. The results provide useful insights for optimizing breeding schemes that could contribute to the development of more productive and resilient crops for the future.

2. GENOMIC PREDICTION ABILITIES IN THE UNDERUTILIZED CROP QUINOA (*CHENOPODIUM QUINOA* WILLD.)

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Quinoa (*Chenopodium quinoa* Willd.) is a low-demand, climate-resilient, and healthy pseudo grain. While demand for quinoa is increasing worldwide, breeding methodology is still in its infancy. Genomic prediction has emerged as a valuable component in a growing number of breeding programs. However, no applications of genomic prediction in quinoa have been reported in the literature. We calculated genomic prediction abilities

for different prediction models and traits with and without accounting for population structure. Substantial differences were found between the prediction abilities of different traits, while differences between different prediction models were relatively small. Within an F2 population, where population structure can be neglected, prediction abilities were consistently positive with peaks around 0.6. Similar predictive

abilities were found in a structured diversity panel when population structure was ignored. However, the predictive ability decreased when population structure was taken into account by making predictions within and across groups. Therefore, it is highly advisable

to consider population structure when working with diverse quinoa material. It can be concluded that, just considering prediction abilities, genomic prediction might be a useful tool for future quinoa breeding programs.

3. GENOMIC PREDICTION WITH HAPLOTYPE BLOCKS IN WHEAT

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Haplotype blocks are characterized by combinations of SNP markers or combinations of the variants of alleles on a single chromosome. They might carry additional information compared to single SNP markers and have therefore been proposed for use as independent variables in genomic prediction. Studies across various species resulted in more accurate predictions than with single SNP markers in some traits but not in others. In addition, the optimal construction of haplotype blocks for maximizing prediction accuracies remains an open question. Our objective was to compare the results of genomic prediction with different types of haplotype blocks to single SNP markers in 11 traits in winter wheat. To achieve this, haplotype blocks were constructed using marker data from 361 winter wheat lines. Four distinct methodologies were employed for block generation: LD-based construction, fixed SNP numbers, fixed lengths in cM, and implementation with the R package HaploBlocker. To compare these blocks we conducted a cross-validation study with 1000 runs for predictions with RR-BLUP, an alternative method (RMLA) that allows for heterogeneous marker variances

and GBLUP performed with the software GVCHAP. The greatest prediction accuracies for resistance scores for *B. graminis*, *P. triticina*, and *F. graminearum* were obtained with LD-based haplotype blocks. Conversely, blocks with fixed marker numbers and fixed lengths in cM resulted in the greatest prediction accuracies for plant height. Haplotype blocks constructed with HaploBlocker performed better than other methods in predicting protein concentration and resistance scores for *S. tritici*, *B. graminis*, and *P. striiformis*.

We hypothesize that the observed trait-specific prediction accuracies were caused by properties of the haplotype blocks that have overlapping and contrasting effects. The ability of haplotype blocks to capture local epistatic effects and ancestral relationships may contribute to improved predictions in certain traits compared to single SNP markers. However, the multi-allelic nature of haplotype blocks could potentially introduce unfavorable characteristics in the design matrices of prediction models, leading to reduced accuracy under certain circumstances.

4. ACCELERATING QUINOA BREEDING PROGRAMS FOR TEMPERATE REGIONS USING GENOMIC TOOLS

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Quinoa (*Chenopodium quinoa* Willd.) can offer an alternative staple food considering its tolerances to abiotic stresses and high seed nutritional quality. Despite the long history of this crop and the worldwide growing interest for its cultivation, quinoa breeding is still in its infancy. The main breeding aims for quinoa in temperate regions are to develop short, high-yielding varieties with high protein, low saponin content and improved tolerance to abiotic and biotic stresses. Because quinoa is primarily a short-day species, it must be adapted to long-day conditions when grown in temperate climates and high latitudes such as northern Germany. High photoperiodic sensitivity and as its consequence, low yield are the major factors that limit quinoa cultivation in regions outside its center of origin. However, there are a few photoperiod-insensitive quinoa accessions originated from the coastal regions in southern Chile, which provide a narrow genetic basis for European quinoa cultivars developed in the last decades. To broaden the genetic diversity of quinoa germplasms in temperate regions, we selected 48 quinoa accessions using a selection index through simultaneous selection for thousand kernel weight, seed yield, days to flowering, plant

height, mildew susceptibility and saponin content. Next, we investigated these accessions for their genotypes at loci associated with days to flowering, days to maturity, plant height, seed weight and saponin content, previously identified through a genome-wide association study in our group. The ten selected accessions were then used for developing 12 segregating populations for quinoa breeding programs in temperate regions. We propagated these populations using the single-seed-descent method producing more than 3000 families currently in F6 (5 crosses), F5 (5 crosses) and F4 (2 crosses) generations, to increase the genetic gain through acceleration of the breeding program. The F5 and F6 lines from these crosses are currently tested in field trials in different locations in Germany. Moreover, these lines will be screened for agronomical and quality traits based on the available genomic data using molecular markers. Finally, the best lines will be introduced as new quinoa cultivars with enhanced agronomic and quality performance for cultivation in temperate regions and for creation of genetic diversity through crossing in quinoa breeding programs.

5. BREEDING PROGRESS FOR STEM WATER-SOLUBLE CARBOHYDRATES IN EUROPEAN WINTER WHEAT

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Plant breeding has contributed to a steady yield progress in European winter wheat varieties released since the 1960s. This progress was particularly driven by improving sink-related traits like grain number per spike. Since yield formation relies on complex source-sink interactions throughout the entire vegetation period, an additional investigation of source-related traits is essential for understanding and further improving yield progress in wheat breeding.

Accumulation of stem water-soluble carbohydrates (SWSC) is one determinant for source capacity after the shift to generative growth and is known to be a key factor for yield formation. To assess the SWSC concentration in the context of genotype-environment-interactions, 50 well-characterized, elite European winter wheat varieties representing the last five decades of breeding progress were sown in a field trial with two irrigation treatments (rainfed and additional irrigation) at our

field station in Gross Gerau. Plant samples were taken at four timepoints (flag leave, anthesis, milk/dough stage, maturity) to investigate the temporal dynamics of the SWSC under abiotic stress conditions. Besides the classical chemical analysis (anthrone method) of SWSC, NIR-spectra of the plant samples were taken in order to develop calibration equations for the establishment of a high-throughput analysis method for samples from field trials in multiple years, locations and treatments. As expected, preliminary results of the field trial in 2023 confirmed the increasing yield performance of the varieties over the year of registration. Moreover, the concentration of SWSC showed a similar progress over the registration years and was correlated to grain

yield under both irrigation treatments. Modern varieties tend to have higher yields as well as a higher source capacity than older varieties. Therefore, we assume that SWSC as a source-related trait is a key factor that has contributed to yield progress in winter wheat breeding. However, this needs to be validated with further sample analysis and multi-location field trials in 2024. By setting up high-throughput phenotyping for SWSC, we will be able to collect large amounts of data that will provide valuable insight into the complex genotype-environment-interactions affecting yield performance, especially under abiotic stress conditions. Ultimate, this will facilitate a more direct approach to selection for yield improvement in future wheat breeding programs.

6. FEATURE SELECTION IMPROVES PREDICTIONS IN LARGE PLANT BREEDING POPULATIONS

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Artificial intelligence (AI) employs a broad spectrum of statistical techniques that may be able to detect uncommon allelic diversity and investigate the relationships between a crop's genetic composition and its interaction with the environment. Robust algorithms, like Machine learning (ML), possess the ability to acquire knowledge from training population input data sets and forecast results in correlated genotypes. To gain a better understanding of nonlinear interactions from plant breeding data sets, we investigated a range of ML models including random forests, neural networks and gradient boosting machines. The ability of ML-based feature selection to distinguish between positive alleles and the genetic background was demonstrated

by investigations of two different breeding populations. On the one hand we used a spring-type oilseed rape (*Brassica napus*) population comprising 950 F1 hybrids obtained by crossing between two male sterile testers and a diverse population of 475 pollinators. The second population was a diversity panel of 191 genetically diverse cultivars of winter wheat (*Triticum aestivum*). Our findings demonstrate that ML models combined with feature selection techniques can – in some cases – perform better than existing linear methods, improve the detection of significant alleles involved in qualitative or quantitative features, increase prediction accuracies, and significantly reduce computing time for genomic predictions.

7. MIXED MODELING ANALYSIS FOR AUGMENTED ROW-COLUMN DESIGN TRIALS IN POTATO – GENOTYPES DERIVED FROM *S. CAJAMARQUENSE* FOR RESISTANCE TO LATE BLIGHT

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Early Generation Variety Trials are an integral part of plant breeding programs. These trials represent the initial opportunity for breeders to select key quantitative

traits. To establish an appropriate and replicable analysis procedure for trials in early generations with unbalanced designs, we worked with a population

called HERLB, which has an introgressed gene from wild *S. cajamarquense* resistance to late blight. The traits considered were i) late blight resistance as area under the disease progress curve (AUDPC) ii) total tuber weight per plot (TTWP) and iii) total commercial tuber weight per plot (MTWP). The experimental design used was the 'augmented row-column'. All analyses were performed using R software. Phenotypic data were fitted in a mixed model analysis, using restricted maximum likelihood (REML) implemented with the `asreml` and `lmer` functions available in "ASreml-R" and "lme4" packages, respectively. The best model was selected using the Akaike information criterion (AIC) followed by the estimation of the Best Linear Unbiased Estimators (BLUEs) and predict Best Linear Unbiased Predictors (BLUPs). The pedigree matrix (A-matrix) was included in the random model and the heritability was calculated. Additionally, a compressed process was performed using the H2cal function available in the "inti R package", which adjusts the model, detects outliers, and calculates heritability and repeatability, all implemented in the same function. In a preliminary

analysis, the correlation between AUDPC BLUEs and AUDPC BLUPs using both packages are around 0.971 and 0.989, respectively. The correlation between AUDPC and the other variables were negative. The heritability for AUDPC and MTWP was 0.60 and 0.88. The correlations between BLUEs and BLUPs of AUDPC (R=0.70) and TTWP (R=0.90) confirm these values. Although the results using the different packages are similar, the time spent is less when using ASreml-R, but often a license is not available. For those unfamiliar with statistical concepts, packages, and the R environment, the H2cal function of the inti package may be of interest. If a spatial analysis is needed, the packages lme4 or inti are limited as they do not have an argument able to define the output structure of the residuals. A solution for these cases can be the statgenSTA package. We have presented a simplified outline of the process of mixed model analysis of a phenotypic dataset from an early generation variety trial with an unbalanced design, emphasizing the available tools that can be used in different scenarios faced during the analysis.

8. HAPLOBLOCK-BASED AUTOENCODERS FOR DIMENSIONALITY REDUCTION

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The rapid advancement of genotyping technologies has enabled the widespread establishment of genomic prediction with high-dimensional marker data in plant breeding programs. The use of genomic datasets with tens or even hundreds of thousands of DNA markers requires increasing amounts of computational time and power for training of genomic prediction models.

Combining several markers in linkage disequilibrium (LD) based haplotype blocks has been proposed as a way to reduce the dimensionality of genomic data. However, multiple variants usually exist for every single haplotype block in breeding populations, which enter as input variables into prediction models. Thus, the high number of existing haplotype block variants counteracts dimensionality reduction. Novel tools are needed to handle the complexity of genomic data and efficiently exploit haplotype block information. One possible option to address this issue is the use

of autoencoders, which are a type of neural network designed for data compression.

Our study presents an approach for combining autoencoders for dimensionality reduction with the concept of LD-based haplotype blocks. By training small-scale autoencoders for each haplotype block, our method condenses complex genetic information from several haplotype block variants into single variables. We applied our method to a maize and a rapeseed dataset and evaluated its performance by (i) measuring the dimensionality reduction of the datasets, (ii) comparing the prediction accuracy for hybrid yield with the reduced and the full datasets and (iii) comparing model training time for both full and reduced datasets. We used Genomic Best Linear Unbiased Prediction (GBLUP) and Gradient Boosting Machines (GBM) as prediction models for hybrid yield.

The autoencoder achieved a reduction in the

dimensionality of the genomic data for both maize and rapeseed of more than 90%, with no loss in prediction accuracy. Both the computation of the relationship matrices for GBLUP and the GBM model training were considerably faster with the reduced datasets. The GBM model did not outperform the GBLUP model in terms of

prediction accuracy. We conclude that our proposed autoencoder approach effectively addresses the dimensionality problem inherent in haplotype block based models while retaining the essential genetic information necessary for genomic prediction.

9. SELWINEQ: QTL ANALYSIS ON A HIGH-DENSITY GENETIC MAP BASED ON FULLY INFORMATIVE HAPLOPHASES FOR MAPPING WINE QUALITY TRAITS

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The evaluation of new grapevine genotypes regarding their potential to produce high quality wines is the time limiting factor in the process of grapevine breeding. Young seedlings need three to four years on average to produce sufficient yield for micro-vinification (small-scale winemaking) and sensory evaluation. Hence, the development of quality-related markers that can be used in marker-assisted selection (MAS) as well as prediction models for this bottleneck trait, will tremendously enhance breeding efficiency. To achieve this goal, SelWineQ evaluates quality related aspects: (1) the genetic quality potential (irrespective of the environment), (2) the metabolic quality potential (genotype by environment interaction) of grapevine must, and (3) the wine quality (analytical and sensory properties).

A training set of a segregating white wine F1 population (150 F1 genotypes = POP150; `Calardis Musqué` x `Villard Blanc`) was deeply phenotyped and genotyped. An improved high-density integrated genetic map consisting of highly informative haplotype-based markers (HBMs) from a genotyping by sequencing (GBS) approach was developed and used for QTL mapping of the collected phenotypic traits.

We identified a major impact of the grapevine véraison locus Ver1 regulating the onset of ripening on many important quality attributes of the population. Traits directly affected are sugar content, organic acid concentrations, pH value and important aroma compounds. For some of these constituents the Ver1

locus shows the highest genetic impact in QTL analysis (i.e. tartaric acid, malic acid, pH) when véraison variation is not respected as covariate.

This makes véraison a central adjusting screw for the development of climate-adapted varieties with enhanced quality potential. Resulting grapes have balanced sugar and organic acids concentrations with no need of additional effort of adjustments during the vinification process (sugar enrichment/deacidification) under regular local growing conditions. Additionally, an optimal aroma characteristic has to be reached. Sensory evaluation indicated aroma compounds of the monoterpene group (in particular linalool and cis-rose oxide) to be of major importance for quality rating in this population. Beside of the strong influence of Ver1, additional important loci were detected indicating for candidate genes of the terpenoids biosynthetic pathway.

Applying genetic markers for the onset of ripening could therefore be a powerful tool in marker-assisted breeding (MAS) to develop climate-adapted varieties with high wine quality potential. Prior to that, these molecular markers will be validated for their applicability on broader genetic background. This knowledge will accelerate breeding for high quality and climate-adapted grapevine varieties with improved fungal disease resistances to be cultivated in a pesticide-reduced and sustainable viticulture.

10. BELOWGROUND BIOMASS IS AS HERITABLE AS ABOVEGROUND BIOMASS IN *MISCANTHUS SINENSIS*

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Miscanthus biomass is an interesting ecological alternative for renewable energy, green chemistry, and bio-sourced products. This perennial grass efficiently recycles nutrients and reduces the need for nitrogen fertilization, minimizing its environmental impact. *Miscanthus x giganteus* is interesting due to its high biomass production and efficient nitrogen recycling. However, the crop in Europe is mostly based on a single clone of *Miscanthus x giganteus*. This presents a risk at the slightest hazard. Therefore, it is necessary to increase the varietal offer in miscanthus, as this sterile interspecific hybrid is known to have a narrow genetic background. For that purpose, *Miscanthus sinensis* is a good alternative for nitrogen recycling as well as biomass production (Leroy et al., 2021), but the genetics of nitrogen recycling remains unknown. Our objective was to explore the genetic variance and heritability of nitrogen recycling by studying nitrogen fluxes between aboveground and belowground parts at different times of the growing season. As nitrogen fluxes calculations are based on biomass characterization and nitrogen concentrations, we presented here the first results regarding biomass in the aboveground and belowground parts of the plant.

Eighty genotypes of a diploid *Miscanthus sinensis*

progeny were established in the field in 2018. We characterized biomass in both the aboveground and belowground parts of the plants at four key sampling periods for the dynamics of the nitrogen fluxes. We calculated heritability and genetic parameters using linear mixed models for the corresponding traits.

We highlighted high genetic variance in both aboveground and belowground biomass across the three first sampling periods. We also found a high correlation between the two variables across the same periods [0.76, 0.69, and 0.64]. Regarding the aboveground biomass, high individual plant broad sense heritability values (H²sl) were obtained across these periods, ranging from 0.60 to 0.80. Interestingly, for the belowground biomass, high values were also obtained, ranging from 0.86 to 0.90. We observed higher progeny mean broad sense heritability (H²Pi) for both traits in each period.

These results highlighted that belowground biomass was as heritable as aboveground biomass. Considering it has not been explored in *Miscanthus* before, the notably high heritability of belowground biomass is particularly encouraging for further genetic studies related to nitrogen recycling.

11. GENOMIC PREDICTION IN HYBRID CROPS

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We have developed a model for prediction of additive, epistatic, and dominance effects in hybrid crops. The hybrids are produced by crossing inbred lines from two different heterotic groups. The model enables prediction of the total genetic values of potential or realized hybrids as well as prediction of the breeding values of parental lines within each of the heterotic groups.

The model was evaluated using data from commercial breeding programs for rye (from Nordic Seed) and for sugar beet (from DLF Beet Seed). For each of the crops, parental lines of ca. 600 three-way hybrids were genotyped for ca. 6.000 polymorphic SNPs, and yield of the hybrids was recorded in multi-location field trials over several years. For both grain yield in rye and root

yield in sugar beet, estimated genetic variances of general combining abilities (additive and within-group epistasis) were considerably larger than variances of specific combining abilities (across-group epistasis and dominance). The hybrid performance could be predicted quite accurately in both crops based on the genotypes of the parental lines.

Thus, the model can facilitate selection of the best parental lines of the hybrids within the two heterotic groups. Furthermore, the combination of parental lines across the heterotic groups that will produce hybrids with the highest non-additive effects can be predicted. Thereby genetic gain can be increased in breeding programs.

12. PHOSPHATE STARVATION INDUCES MORPHOLOGICAL AND HERITABLE RESPONSES IN *SORGHUM BICOLOR* ROOTS

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Phosphorus (P) deficiency and finite P reserves for fertilizer production pose a threat to future global crop production. Understanding root system architecture (RSA) plasticity is central to breeding for P-efficient crops. Sorghum is regarded as a P-efficient and climate-smart crop with strong adaptability to different climatic regions of the world. Here we investigated early genetic responses of sorghum RSA to P deficiency and identified genotypes with interesting root phenotypes and responses under low P. Diverse sorghum lines (n=285) genotyped using *DarTSeq* generated over 12,472 quality genome-wide single-nucleotide polymorphisms. Root phenotyping was performed in a paper-based hydroponic rhizotron system under low and normal P nutrition in controlled greenhouse conditions. Genotypic and P-response variations were observed for multiple root-related traits at 21 and 42 days after germination. High broad sense heritability was observed for the number of roots, volume, root

surface area, root network area, root dry weight, and root dry weight/ total plant weight. Although multivariate analysis revealed four major clusters defining distinct sorghum RSA types, genotypes nevertheless clustered separately under low and normal P conditions, indicating genetic control of root responses to P availability. Association studies identified many quantitative trait loci (QTL) and genes potentially involved in P transport and stress responses. Several pleiotropic QTL for RSA were found on different chromosomes at the two time points, providing a starting point for gene identification and genomic selection of beneficial RSA traits for low-P conditions. The genetic determination of key factors underlying RSA and P efficiency could enable selection at earlier growth stages, reducing phenotyping costs and time. Selected elite lines with interesting RSA traits for low P environments will be incorporated into current sorghum breeding programs.

13. IDENTIFICATION OF A MAJOR QTL FOR CADMIUM ACCUMULATION IN OAT GRAINS

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Oats (*Avena sativa*) rank sixth in worldwide cereal production after maize, rice, wheat, barley and sorghum, with the European Union being the biggest producer of oats. After a decline in oat production and demand since

the late 1960s, the healthy cereal is gaining attention and popularity again. Oats are rich in β -glucans, the essential fatty acid linoleic, antioxidants, alpha-tocotrienol, alpha-tocopherol and avenanthramides,

minerals and vitamins. The range of oat-based products for human consumption is constantly growing. Additionally, its health benefits have been discovered by the cosmetics industry. Cadmium (Cd) is a highly toxic non-essential, ubiquitous heavy metal, that is taken up by plants through the root system and eventually accumulated in leaves and storage organs, e.g. grains. High amounts of Cd negatively impact germination, root elongation, and overall growth in plants. Humans take up Cd through consumption of contaminated food. Cd accumulation in humans has been linked to kidney failure, bone demineralisation, as well as lung, bladder and breast cancer. Several protein families and genes have been reported for Cd uptake and translocation in rice, wheat and barley, i.e. are zinc-regulated transporter (ZRT)/ iron-regulated transporter (IRT) like proteins (ZIP), natural resistance-associated macrophage proteins (NRAMP), or low-affinity cation transporters (LCT), heavy metal ATPase (HMA) family, and PLANT CADMIUM RESISTANCE 2 (HvPCR2). Little

research has been done in oats so far.

We have analysed 620 spring oat lines from Lantmännen's breeding programme, tested for Cd grain content between the years 2015 to 2021. The lines were genotyped with the 7k Illumina Oat array. Subsequent SNP quality filtering led to 3322 informative SNPs, which were mapped against the latest version of the Sang genome. Bayesian clustering for analysis of ancestry revealed an optimal k value of 2, with a small peak of k = 5, however, most lines showed admixed ancestry (ancestry coefficient <0.8). PCA showed a weak population structure as most lines clustered together. The first two principal components explained 10.97% and 6.09% of the phenotypic variance, respectively. LD across genomes decayed at 31.6 Mbp. GWAS for Cd grain content revealed a major QTL on chromosome 3D, as well as several minor QTL, of which many were located on chromosomes of the D genome. This is a first step into identifying the genetics of Cd accumulation in oat grains.

14. SELECTION RESPONSE DEPENDING ON GENOMIC ESTIMATES OF THE SEGREGATION VARIANCE AND THE FAMILY SIZE

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Standard theory for truncation selection is valid for a single population of infinite population size. In breeding programs, promising genotypes are usually selected from a population consisting of multiple sets of genotypes derived from different crosses with varying means and segregation variances. Moreover, breeders need to consider technical, biological, and budget restrictions in terms of number of crosses that can be made, number of offspring that can be generated from a set of crosses, and individuals that can be selected for further intensive testing.

Formulas for predicting means and segregation variances of crosses based on marker effects from genomic selection have been developed. However, studies on how these formulas can be used to optimize resource allocation and selection in breeding programs are scarce. Moreover, analytical solutions for predicting selection gain for selection from multiple crosses with finite population size are still lacking.

We present formulas for predicting order statistics for the selected fraction from a population consisting of offspring from several crosses with varying mean and segregation variance and finite population size, and demonstrate how these formulas can be used for optimizing breeding program design and selection gain under budget restrictions. For illustration, we use a data set from barley resistance breeding consisting of DH families derived from 20 crosses of elite lines and resistance donors.

We implement the analytical formulas in user-friendly R code, employ them to determine the population sizes and sizes of the selected fraction per cross that maximize selection differential and response to selection for a given total population size N and total size of selected fraction S, and select an optimal set of crossing partners from all potential pairs of parents. Computer simulations based on the derived optimal crossing criteria will provide further insights into the

long-term effects on response to selection and diversity in comparison to already existing strategies. The presented formulas extend existing theory for directional truncation selection, have the potential to

increase selection gain, and are ready to be applied in practical breeding programs for optimizing resource allocation to crosses.

15. MACHINE LEARNING COMBINED WITH LOCUS-SPECIFIC DEGREE OF DOMINANCE TRANSFORMATION FOR GENOMIC PREDICTION IN MAIZE

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The genetic architecture of a trait plays a vital role in the predictive ability of genomic models. Previous studies have used and reported different methods of accounting for the genetic architectures of traits. In this study, we combined three machine learning methods: Support Vector Machine (SVM), Light gradient boosting machine (LGBM) and eXtreme Gradient Boosting (XGBoost) with locus-specific weighted dominance effect (a new method of capturing dominance effects) for use in the genomic prediction of maize yield. The results of the machine learning combined model were also compared with classical methods, amounting to a total of nine (9) models: (1) SVM combined with locus-specific weighted dominance effects, (2) LGBM combined with locus-specific weighted dominance effects, (3) XGBoost combined with locus-specific weighted dominance effects, (4) SVM only, (5) LGBM only, (6) XGBoost only, (7) Genomic Best Linear Unbiased Prediction (GBLUP) model with additive effects only,

(8) GBLUP model including additive and dominance effects, (9) GBLUP combined with locus-specific weighted dominance effects. The preliminary results show that the machine-learning model outperforms the classical models by a 2% increase in predictive ability. Combining locus-specific weighted dominance effects with either machine or classical methods decreased the predictive ability, which shows limitations for this parameterisation. Overall, the dominance variance of yield in this data set was low, and models including dominance effects did not have a significant advantage. However, they showed higher stability for predictive ability. These methods will be further analysed in other traits and species, considering different marker densities and sample sizes.

KEYWORDS: *Machine learning, dominance effects, maize, yield, genomic prediction, gradient boosting, genetic architecture*

16. MULTI-TRAIT GENOMIC PREDICTION BY DEEP LEARNING

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Thanks to developments in digital phenotyping and sequencing technology we now have access to ever-increasing volumes of objective and high-quality data. However, to derive useful insights from this data we also need improved analytical methods. Neural networks are the state of the art in many domains such as image analysis and natural language processing. As was demonstrated earlier, neural networks can also be used for genomic prediction. They can learn highly non-linear relations and often outperform traditional genetic prediction approaches. However, this comes at the cost of interpretability. The way in which the input signal (individual SNPs) is influencing the output signal (a predicted trait) remains hidden in the complexity

of the network. Here, we tried to get a sneak peek into this 'black box' using techniques borrowed from image classification. First, a model was trained to predict multiple traits. Subsequently we tried to visualize the genetic patterns that positively influenced these predictions. The resulting patterns of SNPs largely overlap with those detected using a GWAS approach. Crucially, there were also regions that were not detected by GWAS but that the model nonetheless learned to be relevant for the trait of interest. Altogether, this appears to be a promising technique for detecting non-linear (epistatic) marker effects and gaining more insight in complex trait architecture.

17. PHENOMIC SELECTION FOR HYBRID RAPESEED BREEDING

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Phenomic selection is a recent approach suggested as a low-cost, high-throughput alternative to genomic selection. Instead of using genetic markers, it employs spectral data to predict complex traits using equivalent statistical models. Phenomic selection has been shown to outperform genomic selection when using spectral data that was obtained within the same generation as the traits that were predicted. However, for hybrid breeding, the key question is whether spectral data from parental genotypes can be used to effectively predict traits in the hybrid generation. Here, we aimed to evaluate the potential of phenomic selection for hybrid rapeseed breeding. We performed predictions for various traits in a structured population of 410 test hybrids, grown in multiple environments, using near-infrared spectroscopy data obtained from harvested

seeds of both the hybrids and their parental lines with different linear and non-linear models. We found that phenomic selection within the hybrid generation can outperformed genomic selection for complex traits, even when spectral data was collected at single locations, while being less affected by population structure. Furthermore, we demonstrate that phenomic prediction across generations is feasible, and selecting hybrids based on spectral data obtained from parental genotypes is competitive with genomic selection. We conclude that phenomic selection is a promising approach for rapeseed breeding that can be easily implemented without any additional costs or efforts as near-infrared spectroscopy is routinely assessed in rapeseed breeding.

18. OPTIMIZING CROSS EFFICIENCY AND SEED MULTIPLICATION IN FABA BEAN VIA INSECT POLLINATION AND RETROSPECTIVE GENOTYPING

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Faba bean is a promising crop, which can help to meet the growing demand for plant protein and reduce reliance on soy imports, due to its high protein yield under temperate climatic conditions and low nitrogen inputs. However, faba bean suffers from low yield stability due to poor heat and drought adaptation. To improve stress adaptation, we aim to employ genomic prediction in new breeding families that exhibit broad genetic variance from offspring of multiparental crosses, including parents with drought tolerance characters. However, achieving effective recombination for complex traits in multiparental crosses requires large cross families. These are normally difficult to achieve in faba bean because crossing is very challenging and offspring have a low seed multiplication rate. To overcome these bottlenecks, we used bumblebees in enclosed greenhouse chambers for mass crossing among genetically diverse F1 plants. After harvesting all seeds from each maternal plant, seed-chipping

was employed to extract DNA and genotype each seed with a genome-wide selection of cost-effective, locus-specific KASP markers. The marker data from the parents and offspring allowed the pollen donor of each seed on each mother plant to be identified, enabling us to assign every harvested seed to a family of either (1) F2 siblings from a self-pollinated maternal plant, or (2) a specific F1*F1 double-cross combination. Using "speed breeding" all families will be advanced to recombinant inbred lines (RIL). In contrast to standard crossing and RIL production in faba bean, which typically result in small families with limited recombination, this procedure enables us to rapidly generate a very large and diverse base population of biparental F2 and multiparental families as a basis for future breeding. Subsequent genotyping of RILs with a new, genome-wide SNP chip will lay a foundation for genetic mapping along with marker-assisted and genomic selection to advance genetic gain in faba bean.

19. IDENTIFICATION OF QUANTITATIVE TRAIT LOCI AND GENOMIC PREDICTION OF VASE LIFE IN CARNATION

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Vase life is a key trait that determines quality and therefore commercial value in cut flowers. Over the years, efforts by the cut flower industry have focused on improving vase life through control of the immediate environment or the use of post-harvest floral preservatives. To date, no studies have been conducted for the improvement of vase life in carnation that are based on genetic/genomic analyses. The objectives of this study were: (1) to identify quantitative trait loci (QTL) for vase life in carnation, and (2) to evaluate the potential of genomic prediction for this trait.

In the current study, a genetic linkage map was constructed based on two segregating F1 spraycut

carnation populations, of sizes 88 and 75 respectively. With this map, QTL-mapping using interval mapping was conducted for each population independently. A genome wide association study (GWAS) based on ridge regression-best linear unbiased prediction (RR-BLUP) was conducted with both populations combined. Genomic prediction was carried out with RR-BLUP. Markers showing high association to vase life, in the GWAS, were added as fixed effects into the genomic prediction model to evaluate their effect on prediction accuracy.

The constructed map comprised 3727 SNP markers spanning 1152.6 cM across 15 linkage groups. In the

QTL analyses, peaks suggesting the presence of a QTL were observed only on different regions between the two populations. Moreover, based on a permutation test, none of the peaks markers were significant. From the GWAS, we observed 85 SNP markers with high association to vase life on 11 out of the 15 linkage groups. Genomic prediction had an accuracy close to 0.8. Including between 5 to 25 peak markers, detected by the GWAS, as fixed effects into the model, increased prediction accuracy. In contrast, progressively adding more peak markers, beyond 25, decreased prediction accuracy.

Results from QTL-mapping and GWAS confirm previous reports on the quantitative nature of vase life, where the trait is controlled by many minor QTL instead of a few major ones.

This makes genomic prediction a compelling approach for genetic gain in vase life. We could corroborate this, based on the high prediction accuracy observed from our results. Furthermore, adding known QTL (e.g. peak GWAS markers) into the genomic prediction model, can potentially improve prediction accuracy of vase life in carnation.

20. ACCURATE PREDICTION OF QUANTITATIVE TRAITS WITH FAILED SNP CALLS IN CANOLA AND MAIZE

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In modern plant breeding, genomic selection is becoming the gold standard to select superior genotypes in large breeding populations that are only partially phenotyped. Many breeding programs commonly rely on single-nucleotide polymorphism (SNP) markers to capture genome-wide data for selection candidates. For this purpose, SNP arrays with moderate to high marker density represent a robust and cost-effective tool to generate reproducible, easy-to-handle, high-throughput genotype data from large-scale breeding populations. However, SNP arrays are prone to technical errors that lead to failed allele calls. To overcome this problem, failed calls are often imputed, based on the assumption that failed SNP calls are purely technical. However, this ignores the biological causes for failed calls - for example: deletions - and there is increasing evidence that gene presence-absence and other kinds of genome structural variants can play a role in phenotypic expression. Because

deletions are frequently not in linkage disequilibrium with their flanking SNPs, permutation of missing SNP calls can potentially obscure valuable marker-trait associations. In this study, we analyze published datasets for canola and maize using four parametric and two machine learning models and demonstrate that failed allele calls in genomic prediction are highly predictive for important agronomic traits. We present two statistical pipelines, based on population structure and linkage disequilibrium, that enable the filtering of failed SNP calls that are likely caused by biological reasons. For the population and trait examined, prediction accuracy based on these filtered failed allele calls was competitive to standard SNP-based prediction, underlying the potential value of missing data in genomic prediction approaches. The combination of SNPs with all failed allele calls or the filtered allele calls did not outperform predictions with only SNP-based prediction due to redundancy in genomic relationship estimates.

21. GENOMIC ESTIMATED GENOTYPIC VALUES FOR FREEZING TOLERANCE OF WINTER FABA BEANS: DÉBUT

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Vicia faba, a grain legume with a high seed protein content (ca. 30%), is valuable for animal feed and human consumption. The interest in winter faba bean, characterized by a higher yield potential compared to spring faba bean, continuous to increase in many northern EU countries. However, insufficient winter hardiness and unpredictable winter conditions constrain its large-scale production. Winter hardiness and freezing tolerance, in particular, are genetically complex traits. Selection is difficult, as differentiating winter conditions occur rarely and thus artificial screening is a common approach. Genomic selection based on such data should generate substantial progress in winter faba bean breeding.

We hence screened two sets of winter faba bean inbred lines (Association-set, N=188 lines; Validation-set, N=64 lines) in two series of climate chamber experiments. Juvenile plants of each set were tested in two treatments: winter-frost and late-frost (mimicking frost in spring). Traits were plant height (PH), freezing injury (LossTC), frost survival (DtS), and regrowth (REG). GBLUP models were trained on the Association-set employing either the 17k, 15k, 10k, 5k, or 1k SNP set and checked via 5-fold cross-validations. The

accuracy of predictions was ultimately validated via the Validation-set (per treatment, trait, and SNP set).

We observed large phenotypic variations and rather high trait heritabilities ($0.69 \leq h^2 \leq 0.92$). Within the Association-set, the prediction accuracy ranged from 0.36 to 0.49 (REG; LossTC) in winter-frost and from 0.28 to 0.46 (LossTC; PH) in late-frost across all SNP sets. However, these models utilized only 80% of the Association-set lines in our 5-fold cross-validations. For the ultimate validation, in contrast, GBLUP models were trained with all Association-set lines to predict the Validation-set. Resulting prediction accuracies ranged from 0.17 to 0.41 (DtS; LossTC) in winter-frost and from 0.34 to 0.55 (LossTC; REG) in late-frost treatment across all SNP sets, respectively. The SNP set size had only small effects on the trait prediction accuracy, except for the 1k SNP sets, which had very low prediction accuracies.

Our findings suggest that already 5k to 10k SNPs can be sufficient to predict these traits with reasonable high accuracy. Furthermore, genomic prediction proofed to be promising for implementation in winter faba bean breeding and selection for freezing tolerance as component of winter hardiness.

22. A RAPID CYCLING SELECTION EXPERIMENT IN MAIZE LANDRACES

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To avoid depletion of genetic diversity in advanced cycle breeding populations it is common practice to introgress genetic material from resources exhibiting a substantial yield gap. In this study we worked with maize landraces adapted to Central European growing conditions and established a rapid cycling genomic selection (GS) program to target traits with limited genetic variation in elite European Flint germplasm.

The experiment comprises three cycles of GS

without retraining the prediction model. As a training population for genomic selection, we selected a flint doubled-haploid (DH) library (N = 899) derived from the three landraces Petkuser Ferdinand Rot, Kemater Landmais Gelb and Lalin which has been characterized extensively for more than 50 phenotypic traits and has been genotyped with a 600k SNP array. A subset of this DH library (N = 420) was used to train the selection model. The selection was based on multi-trait genomic

breeding values based on test cross performance for total dry matter yield (TDMY). To avoid an unfavorable correlated response, a selection index comprising TDMY, plant height and female flowering time was constructed. To initiate the selection scheme, 10 DH lines from the Petkuser landrace library (N = 188) were selected, crossed in a diallel scheme and selfed to produce 1000 S1 progenies to form the selection units in cycle C1. Applying genome-based prediction, the best 30 individuals were selected and recombined to generate the 1000 selection units of cycle C2. These were again subjected to GS and recombined to obtain

the genotypes of cycle C3. From each cycle, 100 DH lines were random sampled and crossed to a tester. In 2023, the test crosses and DH-lines were phenotyped in multi-environmental trials to evaluate the outcome of the rapid cycling GS program.

Based on adjusted means, we observe a significant increase in TDMY from cycle C0 to C1. From cycle C1 to C2 we did not observe a change in the selected trait, while from cycle C2 to C3 again a significant increase was observed. We will present a comprehensive analysis of the potential of rapid cycling GS for total dry matter yield in landrace derived material.

23. MOLECULAR CHARACTERIZATION OF A RAPID CYCLING SELECTION EXPERIMENT IN MAIZE LANDRACES

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Maize landraces constitute a valuable source of genetic variation for plant breeding. The challenges of incorporating this variation into elite germplasm are heterogeneity, heterozygosity, and abundance of unfavorable alleles. Utilization of landrace diversity requires efficient selection approaches over multiple generations based on phenotypic and genotypic data. A rapid cycling experiment was performed in landrace-derived material. The experiment comprised three genome-based selection steps. The selection scheme was replicated three times. In two of the replications, the selection was based on line per se performance, while in the third replication, it was based on test cross performance. In each of the three replications, diallel crosses were performed on 10 DH lines selected from landrace Petkuser based on multivariate genomic breeding values calculated from multi-environment phenotypic data of cycle 0 (C0); C1-S0 progenies were selfed, and the best 30 C1-S1 genotypes were selected with genome-based prediction. Genome-

based prediction was carried out a second time on the resulting C2-S0 individuals. The recombination of the selected C2-S0 produced C3-S0 individuals. For each of the three replications, 100 doubled haploid (DH) lines per selection cycle were produced and tested with a random sample of 100 DH lines and 10 selected DH lines from C0 in large-scale field trials in 2022 and 2023. Cycle 0 lines were genotyped with the 600k SNP array. In addition to the C1-S1 and C2-S0 genotypes, 100 DH lines produced from each cycle were genotyped with a 15k SNP array. We calculated population genetic summary statistics and analyzed linkage disequilibrium (LD) structure among the genotyped populations. We will analyze the overall genomic constitution of the selected lines, identify which regions were under selection, and determine how genomic selection affected the genetic variance in each cycle. The rapid cycling experiment holds unique genetic material for future experiments and genome-based pre-breeding optimization.

24. EXPLORING NATURAL GENETIC VARIATION IN PHOTOSYNTHESIS-RELATED TRAITS OF BARLEY IN THE FIELD

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To satisfy the increasing demands for agricultural products, at constant crop production areas, crop yields need to be increased by the year 2050 by about 25%-70%. Photosynthesis efficiency, as one of the main factors contributed to potential genetic yields, is considered an important strategy for improving crop yields to ensure food security. To evaluate the potential of using photosynthesis-related parameters in crop breeding programs, we conducted chlorophyll fluorescence measurements along with growth-related and morphological traits of 23 barley inbreds across different developmental stages in field conditions. We found that the photosynthesis-related parameters were highly variable, changing with light intensity and developmental progression of barley. Yet, the variations in photosystem II (PSII) quantum yield observed among the inbreds in the field largely reflected the variations in CO₂ assimilation properties in controlled climate chamber conditions, confirming that the chlorophyll fluorescence-based technique can provide

proxy parameters of photosynthesis to explore genetic variations under field conditions. We also observed that heritability (H²) of the photosynthesis-related parameters in the field ranged from 0.16 for the quantum yield of non-photochemical quenching to 0.78 for the fraction of open PSII center. Two parameters, the maximum PSII efficiency in light-adapted state (H² 0.58) and the total non-photochemical quenching (H² 0.53), showed significant positive and negative correlations, respectively, with yield-related traits (dry weight per plant and net straw weight) in the barley inbreds. These results indicate the possibility of improving crop yield through optimizing photosynthetic light use efficiency by conventional breeding programs. In addition, if the breeding program is directly targeting at high photosynthesis efficiency, the rapid expansion phase is the developmental stage of choice to take measurements in barley because of the observed high heritability of photosynthesis-related parameters.

25. CREATING NESTED ASSOCIATION MAPPING POPULATIONS OF AFRICAN SPIDER PLANT USEFUL FOR TRAIT MAPPING SUCH AS C4 PHOTOSYNTHESIS AND BIOMASS.

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The African spider plant *Gynandropsis gynandra* (L.) Briq (2n=34) is a member of the *Cleomaceae* family which is a sister family of the Brassicaceae (Hoang et al., 2023). It is endemic to tropical Africa and south east Asia (Omondi et al., 2017) but is now well spread across the world in tropical and subtropical regions including Australia, South and Latin America and India. Depending on its location, it is either considered as a weed such as in Australia (Saifullah et al., 2023) or as a crop (Africa) (Houdegbe et al., 2018).

G. gynandra is enriched in nutrient such as carotenoids

(pro-vitamin A, vitamine E and C), minerals such as iron, zinc, and proteins (Omondi et al., 2017). It is therefore cultivated or simply gathered as a source of food in Africa. The tender leaves and young shoots are harvested before the flowering stage and boiled in stew or sauce. (Sogbohossou et al., 2018). The sale of the plant also provides a valuable income for the farmer and contribute to the local economy.

G. gynandra is considered as an orphan species (i.e. an under-utilized or unimproved crop which is only consumed locally) and as such has received little

scientific interest.

In recent years, acknowledging the importance of the species to feed the local population in Africa and to fight hunger, efforts were made to generate knowledge related to the agronomy (e.g. fertilisation, planting density, pest management) and breeding (heterosis studies, studies of natural variation). Recently, a reference genome comprised of 17 pseudomolecules with a length of 740Mb was released by Hoang et al. (2023) allowing trait mapping techniques to be performed.

In that direction, we are developing three Nested Association Mapping (NAM) populations of *G. gynandra* to dissect the genetic architecture of complex traits of agricultural relevance such as edible biomass, germination and flowering date. The accessions composing each NAM are widely diverse and encompass the three geographic groups (East and South-Africa, Asia, and West-Africa) that clustered apart for morphological and molecular parameters (Sogbohossou et al., 2020).

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26. A NEW SELECTION CRITERION TO ACCELERATE COMMERCIAL GENETIC PROGRESS BY PROJECTING USEFUL DIVERSITY INTO THE FUTURE

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Selection decisions traditionally rely on expected offspring performance, hence parent average breeding values. By also considering the expected Mendelian sampling variance of a mating or a cross, the probability to produce offspring with very high performance can be increased, which means a shift in the planning horizon of the breeding objective by one generation. This idea has been proposed by animal and plant breeders in the past. We extended this idea to multiple generations. Thus, by extending the planning horizon, our selection criterion allows to maximize genetic gain in several generations ahead. We tested our newly developed criterion against previously developed criteria, namely selection based on: 1) breeding values, 2) the probability to select top offspring, 3) the expected breeding value of selected offspring, and 4) a recently published index that describes the linearized probability to produce top offspring. Comparisons were based on a

simulated recurrent selection breeding scheme using the software MoBPS. We explored our new criterion in an ideal breeding program with known QTL effects and linkage information to test the theoretical benefit without errors induced by estimating QTL effects and haplotypes. Our criterion achieved higher genetic gain compared to all other criteria while maintaining more genetic variance and achieving lower inbreeding levels relative to selection based on breeding values, both after 5 and 20 generations. This is because our criterion allows to consider the diversity that is present in the current generation to project how it can be turned into genetic gain in a certain generation in the future. Though developed for animal breeding schemes, our selection criterion is a general method that may also be applied in plant breeding programs, especially for rapid cycling schemes. In conclusion, our criterion allows faster genetic progress without compromising diversity.

POSTERS – GENOMICS

27. HIGH-QUALITY GENOMES UNRAVEL THE UNIQUE GENOMIC LANDSCAPE OF BASMATI RICE

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Aromatic rice is an important subgroup of *Oryza sativa*. India boasts the largest assortment of aromatic rice landraces, including the globally acclaimed Basmati. Basmati rice is globally admired for its exceptional organoleptic qualities, which include a pleasant aroma, a rich texture post-cooking, and a distinct taste. Basmati rice has enjoyed popularity right since its initial cultivation in ancient India, well before 1700 AD. Traditional Basmati varieties, however, were not suitable for large-scale commercial cultivation due to their low yield, proneness to lodging, and lengthy maturation period. It wasn't until the 1960s that efforts to improve these low-yielding traditional Basmati varieties began at IARI, New Delhi. After more than two decades of extensive and meticulous breeding efforts the first improved variety, Pusa Basmati 1 (PB1) was developed in 1989. This involved a complex hybridization scheme, combining traditional Basmati lines (Basmati370 and Type 3) with high-yielding, non-aromatic varieties (Taichung Native 1, IR8, and IR22). Unlike its predecessors, PB1 was a semi-dwarf (lodging resistant), photoperiod-insensitive (early maturing) cultivar with high yield potential. It also laid the foundation for development of numerous superior Basmati varieties characterized by enhanced yield, early maturity, and premium grain quality. Consequently, India's Basmati production has expanded substantially in the last few decades, a testament to over five decades of meticulous breeding efforts. The market demand for aromatic rice is

still surging in the international market, with Basmati's market value projected to hit \$31.6 billion by 2027. India dominates Basmati exports, commanding over 65% of the global share, making Basmati rice an extremely valuable agricultural commodity for the country. With the escalating global demand for Basmati rice and the challenges posed by shifting climate conditions, there's an imperative need to adopt advanced genomics-assisted breeding techniques for genetic improvement of Basmati rice. However, high-quality genomes for Indian Basmati rice are still not available, hindering use of advanced genomics methods for Basmati improvement. Consequently, our study has generated high-quality genomes of Basmati rice, encompassing both a traditional Basmati variety (Taraori Basmati) and a widely cultivated improved Basmati variety (Pusa Basmati 1121) leveraging accurate long read sequencing and other state of the omics technologies. These genomes unraveled the unique genomic landscape of Basmati rice which bestows Basmati rice with premium characteristics. Further, the comparative genomics analysis utilizing these genomes also provides novel insights into genetic basis of Basmati improvement. We believe the insights from the current study will also prove vital for rapid improvement of the plethora of unique short-grain aromatic rice landraces available in the Indian subcontinent, which still remains neglected. Therefore, this study is expected to serve as an invaluable resource for future aromatic rice research.

28. DECIPHERING THE FABA BEAN GENOME: HIGH-QUALITY ASSEMBLIES AND RESOLUTION OF HAPLOTYPES

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Faba bean (*Vicia faba*) is an agriculturally important crop plant with a large diploid genome. Its haploid size is estimated to comprise 13 billion base pairs (Gb, n=6), with one chromosome larger than the entire human genome. Faba bean has also one of the highest percentage of repeats among crop plant genomes. While assembling genomes representing completely homozygous lines is conceptually most straight forward, in real world breeding material a range of different levels of heterozygosity can be observed. This feature can make faba bean genomes more challenging to assemble, with haplotype resolved assemblies

requiring further validation.

In our faba bean pangenome project we used Pac-Bio HiFi sequencing (30X coverage) and assembled genomes from six diverse faba bean lines representing breeding material and spanning a range of heterozygosity. By assessing heterozygosity and repeat percentage, we examine the challenge of haplotig purging in this large genome, ensuring the accurate separation of haplotypes in our assemblies with different approaches. In this work we evaluated the quality of haplotype-resolved assemblies for a very large, highly repetitive genome.

29. GENETIC RELATEDNESS OF IN VITRO CASSAVA (*MANIHOT ESCULENTA* CRANTZ) ACCESSIONS BASED ON QUANTITATIVE MORPHOLOGICAL CHARACTERIZATION AT TISSUE CULTURE LEVEL AND DARTSEQ SNP MARKERS

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Deep knowledge of the structure and potential of genetic variability in breeding programs and gene bank management is critical for achieving genetic gain and managing genebanks for genetic diversity. This study assessed the genetic relatedness and pinpoint duplicates using quantitative morphological characters (plant height, number of roots, root length, leaf width, leaf length, number of leaves, and number of leaf lobes) and DArTseq SNP markers of 101 in vitro cassava (*Manihot esculenta* Crantz) accessions from IITA, Genetic Resources Centre, in 2023. Evaluated traits were analyzed using R software version 4.3.0 (R Development Core Team, 2023) and TASSEL 5.0 version for molecular study. Morphologically, Analysis of variance (ANOVA) revealed significant difference (P<0.01) of all traits across accessions and weeks. Root length and number of leaf lobes proved significant

differences (P<0.01) across interaction between accession and weeks, with mean squares of 6.19*** and 0.871***, respectively. Cluster analysis identified four distinct clusters. The accessions TMe-3373 and TMe-4132 had the closest similar phenotypes (< 1.0 of height dissimilarity Euclidian distance) followed by TMe-178 and TMe-892. Principal Component Analysis (PCA) indicated that three principal components significantly contributed 67.26% to the total variations observed among the accessions with 30.72% of PC1, 20.47% of PC2 and 16.06% of PC3. The number of leaf lobes (NLL) and number of leaves (NL) had the highest eigenvalues of -0.002 and -0.142 respectively in principal component 1 (PC1). Relationship between leaf width and leaf length was the highest significant and positive (r=0.81***). Molecular study confirmed 4 clusters as morphological study showed, 3 first

principal components contributed 23.44% of the total variation. 17 duplicates (TMe-4547 and TMe-11373, TMe-1128 and TMe-2966, TMe-1437 and TMe-1230, TMe-3235 and TMe-3252, together with TMe-70, TMe-148, TMe-3314, TMe-743, TMe-1074, TMe-2215, TMe-4562, TMe-3398, and TMe-1572) were found out of 89 accessions using 0.15 IBS distance as a threshold. This study recommends to use Molecular Data (SNP Markers) to confirm the accuracy of phenotypic data

since they are influenced by the environment while accessing the genetic diversity of cassava. Cassava accessions with similar genetic profiles can undergo further characterization to confirm their identities prior to removal from the genebank. These findings provided insights into the genetic diversity of in vitro cassava accessions and offer a foundation for further breeding and conservation efforts.

30. EVALUATING GENETIC VARIATION OF CARAWAY (*CARUM CARVI*) AS PREREQUISITE TO BREED NEW VARIETIES FOR FUTURE NEEDS AND CHALLENGES

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Caraway (*Carum carvi*, Apiaceae) is used as a spice and in pharmacy to ease gastrointestinal afflictions. With an annual nationwide demand of about 10,000 tons it is one of the most important aromatic plants in Germany. However, prolonged drought and heat events of previous years led to devastating yield losses. This makes German and global cultivation more risky under changing climatic conditions.

For caraway, biennial ecotypes with vernalization requirement and winter-hardiness as well as summer-annual ecotypes without vernalization requirement and winter-hardiness are available. Both, biennial and summer-annual cultivation suffer from climate change. Breeding of winter-annual varieties could increase yield stability. By sowing in autumn, the usually higher precipitation from autumn to early spring can be used for germination and vegetative development. Moreover, flowering and seed filling appear earlier and are less prone to heat and drought stress.

To breed winter-annual varieties winter-hardiness of the biennial gene pool and missing or reduced vernalization requirement of the annual gene pool should be combined. Furthermore, several other traits have to be considered: High essential oil content is necessary for the pharmaceutical market. A low shattering rate

increases yield stability. The stalk attachment rate to the grains should be low for marketing. Early flowering and ripening as well as high thousand-grain weight and high plant height are associated with higher yields.

However, neither phenotypic nor genetic data of the annual and biennial gene pool were available, which would have allowed an informed selection of parental material for new breeding programs. Therefore, we genotyped 137 wild to cultivated caraway accessions using genotyping by sequencing (GBS) and phenotyped them in two years at the JKI location in Quedlinburg. Principal coordinate analysis (PCoA) of GBS-data revealed two subpopulations associated with ecotype. The phenotyping showed a high variability of all traits with medium to high heritability (0.52-0.95). Principal component analysis (PCA) of traits revealed traces of domestication and breeding. Correlation analysis between traits provided useful findings for future breeding programs. In several cases, the genetic substructure was associated with some clusters within the phenotypic data.

These studies lay the foundation for current (projects: FNR22023215, FNR2220NR103A) and future breeding programs of caraway.

31. GENOTYPING FOR DIVERSITY AND PHENOTYPING FOR PHOSPHORUS UTILISATION EFFICIENCY IN IPK'S MEDICAGO GERMLASM COLLECTION

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Phosphorus (P) is a macronutrient essential for the growth of plants. Its limited availability in soils can hinder the optimal growth of crops, affecting e.g. yield and nutritional quality of forage crops. Notably, in the case of legumes like alfalfa (*Medicago sativa* L.), P plays a crucial role in nodule formation, essential for nitrogen fixation. Optimising phosphorus utilisation efficiency (PUE) is vital for agriculture, as it not only minimises environmental impact by reducing P loss by leaching but also supports reduced P fertilizer input and therefore costs for farmers. This study is focused on exploring the diverse germplasm within a large Medicago collection to elucidate and exploit traits related to PUE.

The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) has been conserving Medicago genetic resources for several decades. Currently, the collection comprises 741 Medicago accessions of *M. sativa* and *M. × varia* which can be used for fodder production. All accessions were genotyped using genotyping-by-sequencing (GBS). The obtained data were de novo assembled, resulting in approximately 10,000 loci and more than 122,000 single nucleotide polymorphisms (SNPs). These SNPs were utilised to assess the genetic diversity within the collection. Based on this dataset, 200 diverse accessions were chosen for PUE

phenotyping. The selection process was based on a bootstrap resampling method using a fast-heuristic search and a parsimony-based optimality criterion.

The selected accessions were phenotyped for biomass formation under a high P supply (1 g P as TSP per 7-liter pot) and low P supply (0.05 g P as TSP per 7-liter pot) using a low P substrate. The shoot dry matter ranged from 2.48 g to 7.42 g with an average of 4.81 g and 1.65 g to 5.86 g with an average of 3.67g under high P and low P conditions, respectively (ptreatment < 0.001, paccession < 0.001). Similarly, the root dry matter ranged from 0.51 g to 2.33 g with an average of 1.43 g and 0.37 g to 2.17 g with an average of 1.10 g in high P and low P conditions, respectively (ptreatment < 0.001, paccession < 0.001). There was a wide range in the responsiveness of different accessions to the low P treatment, showcasing the adaptability of these plants to P-limited conditions.

A final genome-wide association study (GWAS) in this diverse germplasm using GBS-derived SNPs and phenotypic trait data will enable the identification of genetic variations associated with traits related to PUE. These findings are crucial for advanced breeding strategies aiming at developing alfalfa varieties with enhanced PUE.

32. DETECTION OF GENETIC VARIATION FOR HEAT AND DROUGHT STRESS RESPONSE IN *VICIA FABA*

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Faba beans (*Vicia faba*) have a cultivation area of approximately 71,000 ha in 2022 (BMEL), making them the most important large-grain legume grown in Germany after the pea. Growing faba beans has several advantages, including (i) enriching the soil with nitrogen fixed from the air, (ii) interrupting dense cereal crop rotations and (iii) contributing to the domestic protein supply. However, faba beans are particularly

sensitive to abiotic stresses heat, and drought during flowering. The foreseeable increase in climate change-induced dry and hot growing seasons therefore requires the breeding of adapted genotypes with appropriate tolerance strategies. The primary objective of this work is to evaluate and pinpoint genotypes that exhibit robust stress resilience, thereby establishing a solid base for subsequent genetic studies. This poster describes the

preliminary results of a comprehensive phenotyping of a diversity panel of 80 genotypes for tolerance to abiotic stress in *Vicia faba* using a systematic, multi-stage methodology, the study begins by exposing these genotypes to controlled abiotic stress conditions in two climate chambers with different temperatures (20°C vs. 28°C) during flowering. Preliminary results show that the heat stress condition reduced seed yield of all tested lines but increased pod number of about 20 lines. In parallel, the same genotypes were cultivated in the plant array, a modern phenotyping platform for tracking transpiration in extremely high frequency under controlled conditions. Based on the

data, genotype-specific transpiration profiles can be generated, allowing the determination of water uptake and transpiration efficiency of all genotypes. This parallel execution of experiments should contribute to disentangling heat and drought stress responses. In the subsequent phase, populations going back to extreme genotypes will be used to detect chromosomal regions responsible for heat and/or drought stress by genetic mapping. The anticipated outcomes of this study hold substantial promise in fortifying the resilience of Faba beans against a spectrum of environmental stressors, thereby contributing significantly to the sustainability and productivity of this pivotal crop.

33. DEVELOPMENT OF AN AUTOMATED FRAMEWORK FOR THE IDENTIFICATION AND CLASSIFICATION OF PLANT GENE FAMILY MEMBERS AT THE PAN-GENES LEVEL

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Genome data has accumulated rapidly in recent years due to the influx of next-generation sequencing technologies. A plethora of plant genomes are now available in public databases. Plants are constantly exposed to a variety of environmental stresses, prompting the evolution of several mechanisms and gene families to confer tolerance and resistance against these stresses. In the past few years, numerous gene families have been studied and published using the datasets available in public databases. The genome-wide Identification (GWI) studies aid in identifying and characterizing gene members, providing insights into their structural and functional diversity, as well as their expression patterns under stress conditions. These in-silico analyses provide an initial framework for further functional elucidation and breeding research. However, these GWI studies are often single-reference-based, which is insufficient to capture the genetic diversity of multiple individuals within a species. Additionally, the GWI of gene family members is time-consuming and requires significant effort. Manual handling of numerous files also increases the likelihood of errors and biases. Therefore, our aim is to develop a pipeline that automates the identification of gene family

members from multiple plant genomes and classifies these members into pan-gene sets.

In the first module, the gene members from multiple genomes will be identified through alignment, filtering, and domain profiling. In the next module, these members will be categorized at the pan-gene level into Core, Accessory, and Unique genes. Finally, the categorization of these pan-genes will be visually represented through summary tables, bar plots, upset plots, and Venn diagrams. For validation of this pipeline, an assessment will be conducted on both simpler (*Arabidopsis*, 2n with genome size in Mbp) and complex (*Arachis*, both 2n and 4n with genome size in Gbs) genomes.

This pipeline will be a single command-line-based, easily executable pipeline with scripts written in the Python programming language and Bash scripting. It will enable quicker and automated identification of gene family members from multiple related genomes at the pan-gene level. Moreover, it will facilitate further diversity and functional (breeding) studies such as crop improvement by targeting the stress-resistant gene families.

34. LINKING GENOMIC VARIATION TO TRANSCRIPT EXPRESSION USING PANGENOME GRAPHS

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Structural variations (SVs) are large genomic alterations including deletions, insertions, and duplications of DNA segments (>50 bp). Due to their size, they can have a greater impact on traits than single nucleotide polymorphisms (SNPs) and smaller InDels, leading to changes in gene expression, protein function, and cellular behaviour.

Brassica napus has an allotetraploid genome (2n = 38, AACG), and different accessions harbour extensive genomic variation including SVs. Some of the SVs have been shown to affect candidate genes associated with important agronomic traits. However, this extensive variation can lead to biased variant detection and transcript expression quantification. Therefore, pangenome graphs, which capture species-wide genomic variation in a single data structure, provide an excellent framework for expression quantitative trait loci (eQTL) analyses, facilitating the association between SVs/SNPs and transcript expression. This project is to understand the impact of genomic variations on transcript expression and transcriptional regulation using pangenome graphs to overcome the linear reference bias in oilseed rape.

To construct the pangenome graphs, we used long-read datasets from Oxford Nanopore sequencing and short-read datasets from Illumina. Long reads were mapped

to the *B. napus* reference genome (Express617) using minimap2. SVs were identified using cuteSV. A final, non-redundant SV set was used for pangenome graph construction. SVs were genotyped from short reads using Paragraph and VG call for comparison. Spliced pangenome graph was constructed with VG autoindex using non-redundant SVs, SNPs, and available Express617 annotation. RNA-Seq reads were aligned to the spliced pangenome graph reference using VG mpm. Graph-based expression quantification performed using RPVG was compared with linear reference-based quantification performed using Kalisto. eQTL analysis was performed with matrixEQTL, accounting for population structure and hidden variables.

In this study, we confirmed that pangenome graphs reduce reference bias, enable SVs genotyping, and improve transcript expression quantification for eQTL analyses. SVs genotyping from short and long reads compared to get confident SVs genotyping. Our analysis revealed that a substantial proportion of variants found in long reads could not be genotyped from short reads even using pangenome graph reference. Thanks to functional analyses, we further interpreted the potential impact of structural variations on agronomic traits.

35. GENETIC DIVERSITY IN JUVENILE STAGE FOR FROST SURVIVAL IN SORGHUM

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To adapt to climate change and increase biodiversity, it is necessary to implement new, robust crops into local agriculture. Grain sorghum (*Sorghum bicolor* L. Moench), a multipurpose and drought-tolerant crop, offers numerous agro-ecological advantages to farmers. Furthermore, it can also represent a risk protection for farmers during drought conditions and enable the establishment of new regional value chains. Due to its tropical origin, sorghum is sensitive to cold. Hence, sorghum is sown usually several weeks later

than maize, implying a reduced growth period on the expense of yield potential and maturity. This highlights the necessity to find genotypes with enhanced cold tolerance at the juvenile stage, including the ability to survive short frost events, which are typical for late spring in Central Europe. In two semi-controlled experiments, juvenile frost tolerance was analyzed in a broad diversity set (n=285). For this purpose, the seedlings were grown under favourable conditions and then exposed to frost (up to -3°C) for two nights. Ten

days after stress exposure, survival rate was scored. A high phenotypic variation among the different sorghum inbred lines was observed for this trait, with the mean survival rate (67 %) being higher than expected and several genotypes showing surprisingly high frost tolerance (almost 100% survival). These results were also used for genetic studies. Genetic regions influencing this trait were identified by genome-wide association studies (GWAS). Furthermore, the results

show a rather quantitative trait architecture for frost tolerance. Additionally, an early sowing trial was carried out, enabling the identification of genotypes with the ability to both emergence in cold soils after early sowing and withstand frosts during juvenile stages. These results will contribute to the breeding of varieties with improved cold tolerance, allowing for better adaptation to temperate latitudes and earlier sowing.

36. IDENTIFYING STRUCTURAL VARIATION USING NEXT GENERATION SEQUENCING DATA IN FABA BEAN

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Plant-based protein provides essential amino acids for human nutrition and valuable stock feed for livestock farming. The demand for plant-based proteins is increasing, so there is a need to diversify the domain of legume-based plant proteins by adding new protein crops. Faba beans have a high protein content and good nutritional profiles but suffer from high yield instability due to low breeding efforts in the last few decades. Its huge, complicated genome, which is one of the largest diploid crop genomes with 13 GB spread over six chromosomes, is one of the reasons for minimal breeding efforts. The main reason for its large genome size is due to a high concentration of transposable elements, which can result in structural variations, mostly tandem duplications. Tandem duplication (TD) is a structural variant event where a segment of the DNA is duplicated and inserted serially into the original segment. This type of variation can have a significant impact on phenotypic traits and is therefore important for breeding. The best method to detect structural variants is long-read sequencing, but the respective methods still do not allow high throughput as required in a breeding context. However, next-generation

sequencing technology also allows us to detect SVs at a reasonable quality with the help of strategies that include paired-end mapping, read depth, and split read. To detect TD, several pipelines, such as DINTD, Delly, TARDIS, dudeML, and TIDDIT, have been developed with reference to the human genome and are able to detect TD with good precision and accuracy. In this project, we will test the suitability of different pipelines to detect structural variants in the faba bean genome at a reasonable throughput. For this purpose, we use publicly available data from 197 accessions published by Jayakodi, M., Golicz, A.A., and Kreplak, J. (2023), with Hedin as a reference genome. We focus on identifying TD regions with the inference of their breakpoints for these accessions from short sequencing reads using the above-mentioned pipelines. The detected SVs can be helpful in understanding their role in the phenotypic variation of Faba bean, and they can also be utilized in detecting candidate regions that are linked to important agronomic traits by combining the information of SVs and genome-wide association studies together to accelerate the breeding process in Faba bean.

37. GWAS IN WINTER FABA BEAN (*VICIA FABA* L.) FOR GRAIN YIELD AND FURTHER AGRONOMIC TRAITS USING DATA FROM 189 INBRED LINES AND THEIR PROGENY ACROSS 16 YEARS: DÉBUT

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Faba bean (*Vicia faba* L.) is a globally grown grain legume, standing out by its high protein content, high symbiotic performance and climatic adaptation. In Germany, although it experienced an expansion of cultivation area in the last years, its acreage is still relatively low, partly because of yield instability and high seed cost. Winter faba bean especially, is little cultivated because of the high risk of winter kill caused by harsh winter conditions.

This study aimed to perform the first genome-wide association study (GWAS) in winter faba bean for a total of 28 traits, based on historical field data of 189 inbred lines and their open-pollinated progeny across 16 years. Among the 18 field trials studied, two were located in Hohenlieth (Schleswig-Holstein), and the remaining 16, at the experimental station of the University of Göttingen, Reinshof (Niedersachsen). We focused on six traits: plant height, beginning of flowering, lodging, maturity, grain yield and thousand grain weight. We observed a high broad sense heritability for all traits, ranging from 0.76 to 0.94 in the inbred line dataset, and from 0.63 to 0.90 in the progeny dataset. Genotyping was performed on all inbred lines using the “Vfaba_v2” Axion SNP array, which contains

approximately 60K probes. After filtering, 17,227 SNPs remained to be employed in the GWAS analysis.

A total of 27 single nucleotide polymorphism (SNP) markers were significantly associated with the traits using the inbred line dataset, and 17 using the progeny dataset, of which 4 were identified for grain yield, explaining around 33% of the phenotypic variation explained (PVE). The detected SNP markers have the potential to be used by breeders for marker-assisted selection (MAS).

Furthermore, the data of the inbred lines and their progeny will be used as training population in the scope of the Abo-Direkt project (<https://orgprints.org/id/eprint/45126/>), to develop genomic prediction in winter faba bean. The prediction model will then be validated using phenotypic and genotypic data of random highly inbred genotyped individuals of the Göttingen winter bean population (GWBP).

In the end, the study will allow us to identify breeding-relevant genotypes among the individuals of the GWBP, and globally support the breeders in optimising the selection of winter faba bean for several traits, through MAS and genomic selection.

38. BIOINFORMATICS ANALYSIS OF GENOMES AND TRANSCRIPTOMES FOR LUPIN BREEDS

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The P³roLucas initiative, a part of BioSC, is dedicated to enhancing the cultivation of lupins through the Optimization of plant performance and products for the lupin cascade. Various lupin species, such as *Lupinus albus* (white lupin), *Lupinus angustifolius* (narrow-leafed lupin), *Lupinus luteus* (yellow lupin), and *Lupinus mutabilis*, find applications in agriculture. Lupins are considered a valuable source of high-quality protein suitable for human consumption and represents

a sustainable alternative to soybeans. Due to their unique ability to convert atmospheric nitrogen into ammonia via rhizobium-root nodule symbiosis, they are well-suited for growing in infertile soils and play a crucial role in reclaiming barren and poor-quality lands. *Lupinus mutabilis*, which originates from the Andes, is of particular interest for agricultural use in Europe due to its high tolerance to cold stress.

While comprehensive genomic resources have been

established for *Lupinus angustifolius* and *Lupinus albus* at the pan-genome level, a genome assembly for *Lupinus mutabilis* is still missing. Therefore, we produced the first draft genome assembly for *Lupinus mutabilis*, utilizing Oxford Nanopore sequencing in conjunction with chromosome conformation capture sequencing to arrange and align the sequence contigs. The preliminary assembly consists solely of ONT reads, and we used the Helixer gene prediction tool to identify genes based on the DNA sequence alone, without any extrinsic data. We further refined this gene annotation to include splice variants and isoform derived from RNA-seq data. The preliminary assembly, composed solely

of ONT reads, shows promising results, and we have employed the Helixer gene prediction tool to identify genes based on the DNA sequence. Our early assembly of *Lupinus mutabilis* exhibits a BUSCO completeness of 98.8%, comparable to the pan-genome level assemblies of other lupins. We conducted a functional classification of proteins using Mercator4 and integrated a portion of the alkaloid pathway into the MapMan software. These novel resources are intended to propel advancements in lupin breeding and cultivation, ultimately contributing to the development of sustainable regional agriculture in the future.

39. GENOMIC ADVANCEMENTS IN FABA BEAN BREEDING: INSIGHTS FROM WHOLE GENOME SEQUENCING, SNP CALLING, AND PRACTICAL HAPLOTYPE GRAPHS

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Faba bean (*Vicia faba*) is becoming increasingly important globally as a crucial legume crop. To further the precision of faba bean breeding, we conducted a thorough genetic analysis using advanced technologies. Our study takes a comprehensive approach to understand the genetic makeup of faba bean by combining Whole Genome Sequencing (WGS), Single Nucleotide Polymorphism (SNP) identification, and the development of Practical Haplotype Graphs (PHG) using twenty diverse faba bean accessions. These tools together provide a detailed framework for precise breeding, giving us valuable insights into the genetic architecture of faba bean.

We aim to provide a resource for faba bean researchers and breeders seeking to accelerate the development of varieties with enhanced resilience, yield, and nutritional profiles. To that end, we constructed a faba bean

Practical Haplotype Graph (PHG) database using the genomic variation data from these twenty accessions. The PHG, a cost-effective genotyping tool, combines WGS data into a database to capture main haplotype groups within a breeding program or species. Sequences and consensus haplotypes stored in the PHG can then serve as a foundation for genomic prediction. This faba bean PHG database contains variant and haplotype information for the mentioned accessions, enabling the imputation of SNPs and haplotypes from low-coverage data and predicting genotypes for a breeding population.

By reducing input sequence requirements, the PHG can decrease the cost of genotyping, make genomic selection more feasible, and facilitate larger breeding populations.

40. EPICBEET – GENOME WIDE ANALYSIS OF EPIGENETIC PATTERNS IN SUGAR BEET

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Epigenetic modifications affect phenotypes and influence an enormous variety of plant traits [1]. It is known that epigenetic factors play an important role in adaptation to environmental stresses [2]. They also can be stably inherited in plants [3]. Nevertheless, the mechanisms of DNA methylation pattern heritability and the genome wide pattern itself are still largely unexplored, especially in cultivated crops. Consequently, epigenetic markers are not applied in breeding programs yet.

The aim of the EpicBeet project is to investigate the occurrence, stability and heritability of DNA methylation patterns in sugar beet (*Beta vulgaris* subsp. *vulgaris*). Epigenetic modifications could be beneficial to widen the domestication bottle neck that occurred during the relatively young breeding history of sugar beet.

A main focus is the epigenetic impact on phenotypic plasticity and transposable element (TE) activity with respect to future breeding approaches. Our joined project deals with genome wide calling and mapping of 5mC DNA methylation patterns in both wildtype and mutant genotypes in CpG, CHH and CHG context.

The impact of three genes, namely MSH1, MET1 and DDM1, are of main interest in the project. In *Arabidopsis thaliana* these genes are known to affect DNA

methylation and its heritability. Since a dysfunction of these genes resulted in hyper- or hypomethylated genomic regions, a sugar beet mutant population was screened to identify plants with modifications in the three candidate genes, either STOPs or amino acid exchanges in relevant domains [4][5][6].

For the molecular characterisation, high molecular weight DNA is isolated from single plants and subjected to Oxford Nanopore Technologies (ONT) sequencing. This sequencing method allows to simultaneously call the bases and their modifications (mainly 5-methyl cytosine, 5mC). The data sets are mapped to high-continuous genome sequence assemblies of the reference genotype KWS2320 and/or corresponding mutant background genotypes [7]. The bioinformatics pipeline to analyse the ONT data uses DeepSignal Plant, as this program is specialized and trained in calling 5mC in resequenced plant data sets [8].

The goal is to detect whether, how and to what extend DNA methylation patterns are heritable and how they are connected to TE mobilisation. Moreover, we want to investigate epigenetically relevant genomic regions with regard to phenotypic variation and promising marker candidates for future epigenetic breeding.

41. GWAS BASED ON INDIVIDUALS OF PLANT POPULATIONS, USING SNPS AND USING HAPLOTYPES

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Plant genome-wide association studies (GWAS) usually employ sets of inbred lines phenotyped in plots of field trials. Developing and phenotyping such sets of lines costs considerable time and money. Gyawali et al. (2017) reported a faster, cheaper GWAS approach: Using for genotyping and phenotyping individuals from a randomly mating maize population. This approach

identified significant and promising SNP associations with plant height. However, their GWAS was conducted in but one population (Shoeppeg maize). Hence, their approach should be validated and expanded.

To this end, we investigated the effectiveness of such an Individual Plant Genome-Wide Association Study (IP-GWAS). We used 330 individuals from a diverse set of

40 European maize landrace populations (EMLP). GBS yielded 152671 SNP markers; single-plant phenotypes were recorded for cob weight, grain yield, plant height, leaf width, and leaf length. We compare SNP-based and haplotype-based GWAS. So far, SNP-based IP-GWAS identified a number of N significant SNPs associated for all traits: cob weight (N=15), grain yield (N=13),

plant height (N=11), leaf width (N=11), and leaf length (N=10). We are further investigating haplotype-based GWAS, since it should be superior to SNP in detecting QTL with very rare minor alleles. This study will markedly contribute to assess advantages and disadvantages of IP-GWAS and SNP- vs. Haplotype-based analyses.

42. ANALYSIS OF REGULATORY SNPS WITH AGREG-SNPDB-PLANTS AND ITS APPLICATION TO OIL CONTENT AND -QUALITY OF RAPESEED (*BRASSICA NAPUS* L.)

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Transcriptional regulation of gene expression in higher organisms is fundamental for numerous biological processes. These processes are mainly controlled by a special class of regulatory proteins, the transcription factors (TFs), and their combinatorial interplay.

Various genetic programs, such as environmental adaptation, tissue development, or disease control, are governed by the binding of TFs to short DNA motifs, called transcription factor binding sites (TFBS), in the regulatory regions of their target genes. Single nucleotide polymorphisms (SNPs) located in promoter regions can alter TFBSs leading to a change in the binding affinity of TFs and, thus, affect gene expression. Such SNPs are referred to as regulatory SNPs (rSNPs). In recent years, rSNPs have come into the focus of research, and the underlying mechanisms have been studied for many traits and diseases mainly in humans or model organisms. However, these studies mostly concentrate on single rSNPs and do not include systematic analyses. Thus, there is still a lack of comprehensive analyses and genome-wide collections of rSNPs.

In this work, we developed a pipeline for the detection of rSNPs and created the database agReg-SNPdb-Plants, storing genome-wide collections of rSNPs and

their predicted effects on TF binding for agricultural plant species. agReg-SNPdb-Plants includes 13 crop species and subspecies, namely African rice, Asian rice (with its subspecies Indica and Japonica), barley, bread wheat, durum wheat, grape, maize, rapeseed, sorghum, sunflower, tomato, and wild rice.

Out of all species stored in agReg-SNPdb-Plants, rapeseed holds a special role. In contrast to the remaining species, where we used the data from Ensembl Plants as basis, in rapeseed, to date, there is no genome-wide collection of SNPs available. Therefore, we used a previously published data set based on different resequenced *Brassica napus* L. cultivars for the identification of rSNPs. Based on this data set, we investigated the regulatory mechanisms in two cultivars, namely Zhongshuang11 (ZS11) and Zhongyou821 (ZY821), which are characterized by high and low oil content, respectively. In this way, we demonstrate the application of rSNPs together with multi-omics data to perform a systematic analysis of the complex interplay between rSNPs, TFs, and differentially expressed genes (DEGs) in four tissues (flower, leaf, stem, and root) which are underlying the oil content and -quality in rapeseed.

43. DECODING THE COMPLEXITIES OF SAFFRON CROCUS: CHALLENGES IN POLYPLOID GENOME ASSEMBLY

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Saffron (*Crocus sativus*), a triploid and male sterile plant with 24 chromosomes (2n = 3x), is a clonal line, originated around 4000 years ago, spreading globally through human cultivation. This widespread cultivation serves as a unique long-term experiment, showcasing epigenetic differentiation, adaptation, and human-driven selection. Investigating saffron's genomics becomes crucial for understanding the processes during and after triploidization and clonal adaptation to diverse climates. In the absence of parental lines, the progenitor of saffron becomes a valuable benchmark. Earlier investigations, including analysis of chloroplast genomes, genome-wide DNA polymorphisms, and comparative multicolor fluorescent in situ hybridization (FISH), have suggested that the autotriploid saffron originates from a hybridization event involving diverse *C. cartwrightianus* cytotypes that evolved in Attica, Greece. Our recent efforts in genome assembly aim to unravel the complexities of saffron and its progenitor. The challenge lies in the large, highly heterozygous triploid genome, deviating from conventional diploid genome assembly

methods. Additionally, variations in chromosome size and structure present challenges for achieving a haplotype-resolved assembly (1x = 8 chromosomes). To address this, we employed a combination of PacBio HiFi, Oxford Nanopore, HiC, and bisulphite sequencing. Through validation of various assemblers, we generated a draft pseudo-haplotype genome assembly (N50 of approximately 300 Mbases) for both *C. sativus* and *C. cartwrightianus*. The continuity of the assembly was confirmed cytologically by anchoring the two largest scaffolds (490 Mb and 350 Mb) to chromosomes using Fluorescent In Situ Hybridization (FISH) with 54,000 unique oligonucleotide probes designed to span the first big scaffolds. This robust assembly pipeline not only validated the genome continuity but also enabled an in-depth epigenetic analysis of 5mC methylation across different *C. sativa* cultivars. Our findings shed light on the complex genetic and epigenetic landscape of saffron, contributing to a comprehensive understanding of its evolution and adaptation.

44. EFFICIENT MACHINE LEARNING MODEL FOR ADAPTIVE PLANT BREEDING IN DYNAMIC CLIMATES

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The escalating unpredictability of climates poses a substantial risk to plant production, necessitating adaptive approaches in breeding initiatives. The performance of selected genetics in plant breeding cycles displays variability influenced by these shifting climates. This investigation addresses the imperative

for efficient machine learning models to unravel intricate climate patterns and precisely forecast traits in unknown environments. To establish a forecasting model, data on flowering time traits and 400,000 chip SNP markers were gathered from around 1,500 Barley samples from the 25 families of HEB-25 populations

across 4 continents (Asia, Europe, Africa, and Australia) over two years. By employing a machine learning (ML) algorithm, we formulated a predictive model proficient in accurately predicting trait values for unknown environments, achieving an impressive Pearson correlation coefficient of 0.82 when incorporating environmental features, such as temperature. The interpretable nature of the ML model facilitates the identification of markers linked to the trait. Notably, these markers coincide with genes previously cloned, such as Ppd-H1, denso/sdw1/GA20ox2, Vrn-H1, or Vrn-H3/FT1, in distinct chromosomes associated

with the trait. Interestingly, several key markers in the ML model were also significant in linear genome-wide association analysis. We further interpreted the model using Shapley additive explanation values to understand the impact of each feature on the traits, including the effects of individual alleles. This predictive model not only enhances the accuracy of flowering time prediction in unknown environments but also empowers breeders to select genetic material more efficiently, potentially reducing the overall duration of the breeding program.

45. TOWARDS MOLECULAR MARKER BASED DIFFERENTIATION OF RACES AND SUB-RACES OF DIFFERENT CEREAL RUST SPECIES

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Among the phytopathogens, the rusts (*Pucciniales*) play a decisive role as obligate biotrophic fungi. Having a broad host spectrum rusts are mainly responsible for the worldwide considerable yield losses. In German agriculture, yellow rust (*Puccinia striiformis*) and leaf rust (*Puccinia hordei*) are particularly prevalent, frequently infecting wheat and barley crops, respectively. Classification of environmental rust species into races or sub-races with specific virulence patterns requires skilled people for single-spore multiplication and time-intensive bioassays on the host species differential sets. To fasten and facilitate this process we aimed to design molecular markers based on single nucleotide polymorphisms (SNPs) using the approach of genotyping by sequencing (GBS) to differentiate races and sub-races of different rust species. In a first question we investigated the extent to which sub-races of wheat yellow rust within the Warrior(-) race, which only differ phenotypically on an expanded differential set, can be genetically differentiated. The samples were

collected from infected fields in Germany (as part of the project “RustWatch”), France (INRAE) and the UK (United Kingdom Cereal Pathogen Virulence Survey, UKCPVS) spanning several years of collection (2017-2022). In a second research question, the aim was to genetically differentiate races of barley leaf rust originating from a core collection at the JKI in Quedlinburg, but also to investigate the relationship between SNPs in the fungal genomes and the breakage of certain resistance genes in a barley differential set. With regard to the differentiation of the sub-races of yellow rust in wheat and the races of leaf rust in barley, the limitations of GBS for resolving marginal genetic differences were clearly evident. Thus, the sub-race differences could not be completely resolved using GBS; however, this was possible for the race differences. In addition, significant SNPs in coding regions of the fungal genome might indicate loci responsible for leaf rust resistance breakages of Rph1, Rph2 and Rph9 in barley.

46. BENCHMARKING THE TOOLS AND PIPELINES FOR PANGENOME ASSEMBLY

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Pangenomes are crucial for understanding species-wide genetic diversity, delineating core and variable genes. This study rigorously benchmarks three key pangenome assembly pipelines: Minigraph, PGGB, and Cactus-Minigraph, using publicly available Sorghum data. We introduce tailored metrics for comprehensive pangenome graph evaluation, including completeness, duplication levels, and fidelity of structural variants. By assessing the tools on Sorghum datasets, we gauge their efficacy in handling diverse genomic features. The analysis provides detailed insights into the strengths and limitations of Minigraph, PGGB, and Cactus-

Minigraph, aiding researchers in informed tool selection. The metrics developed contribute to standardizing pangenome graph assessments, enabling robust and objective tool comparisons. In conclusion, this benchmarking study advances our understanding of pangenome assembly tools and establishes a foundation for standardized evaluation metrics. We plan to further use these insights to optimize tool selection for specific applications, such as genome wide association studies, improving the accuracy of downstream analyses in our research on pangenomics of *Sorghum*.

47. EXPLORING GENETIC AND EPIGENETIC DIVERSITY WITHIN CLONAL POPULATIONS OF MAJOR PINOT VARIETIES OF GRAPEVINE (*VITIS VINIFERA* L.)

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Grapevine is vegetatively propagated to maintain genetic integrity, preserving favourable agronomical and oenological traits that are also crucial for regional wine identities. Major ancient cultivars, like Pinot, have been grown and propagated for over two thousand years. Over this long period, somatic mutations have shaped the genome of Pinot, resulting in a substantial amount of clonal variation for economically important traits, such as yield, sugar content, cluster architecture or budding time. In order to systematically explore and exploit such diversity for trait improvement, the grapevine breeding department at Geisenheim University has assembled and maintained a large and diverse population of over 260 Pinot clones, collected from different origins, which show substantial variation

for important viticultural traits. Several key traits such as yield, juice quality parameters have been recorded for over a decade. The aim of this project is to analyse the genetic and epigenetic diversity within this large Pinot collection, firstly to understand the extent and the nature of it, and subsequently connect mutations and epi-mutations to trait variation. The outcome will clarify the role of genetic and epigenetic mutations in clonal variation and will identify molecular variants to be used in future clonal selection, finally leading to improved clones of Pinot that enable improved sustainability and climate adaptation in viticulture.

POSTERS – PHENOTYPING

48. INNOVATIVE PHENOTYPING APPROACHES OF *SCLEROTINIA SCLEROTIUM* IN SUNFLOWERS

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Sclerotinia sclerotiorum is a fungal pathogen with a broad host spectrum that is of great importance in sunflower cultivation worldwide. It can cause stem and flower basket rot, which leads to negative effects on seed weight and oil quantity, while stem breakage can lead to yield losses of up to 100%. Resistance to *Sclerotinia* is also of particular importance in breeding programs, as the fungus forms sclerotia that remain in the soil as permanent stages and there is a lack of effective fungicides to control the disease. Complete *sclerotinia* resistance has not yet been described in cultivated sunflowers, but there are varietal differences in susceptibility.

The ProSun project is dedicated to the identification of genetic resources for *sclerotinia* resistance in sunflowers and the elucidation of molecular mechanisms underlying this resistance. In a first step, a set of 300 genotypes (lines, RILs, NILs, semi-dwarfs) will be tested for *Sclerotinia* resistance under defined environmental conditions in the greenhouse using two high-throughput methods. The pathogenicity and aggressiveness of the isolates used will be investigated based on their spread after inoculation on stems of the sunflower genotypes and infection

and resistance-specific wavelengths will be identified non-destructively in a reflection range from 405 nm to 2500 nm using hyperspectral analysis (BBCH 30). In parallel, leaf material of the genotypes is inoculated with the corresponding isolates and the infection is automatically and quantitatively analysed at several points in plant development (BBCH 15, BBCH19, BBCH 39) using high-throughput technology (Macrobot, Lueck et al., 2019). With a sufficiently high correlation ($r > 0.8$) to stem infestation this method can be used to accelerate and automatically analyze a large number of genotypes at different stages of development. Subsequently, resistant and sensitive genotypes are exposed to different levels of drought stress and simultaneously to the most aggressive *Sclerotinia* isolate in order to test the influence of the environmental factor water status on plant resistance.

The findings of this work should not only contribute to the identification of resistant genotypes, but also provide insights into the molecular mechanisms of *Sclerotinia* resistance in sunflowers under different environmental conditions, especially in relation to water status.

49. SHOOT-LEVEL PHENOTYPING REVEALS ADAPTIVE VARIATION IN THE GRASS GENUS HORDEUM

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After its emergence in the Middle East around 9.5 million years ago, the *Hordeum* genus, which includes domesticated barley, spread across the Americas and Eurasia, adapting to diverse climatic conditions.

The spread of *Hordeum* into new environments was accompanied by rapid speciation and ecological diversification. The *Hordeum* species are thus an interesting clade to study traits and trait complexes

underlying ecological diversification, including life-history variation and local adaptation.

In this study, we investigated the phenotypic and genetic variation within and between annual and perennial species of the grass genus *Hordeum*, including the economically important crop barley (*H. vulgare* L.). We trialled 56 annual and perennial *Hordeum* accessions, comprising 18 species of the *Hordeum* clade, in a common garden experiment at the University of Düsseldorf, Germany, between the 2021 and 2023 growing seasons. We scored 22 shoot traits at the vegetative and reproductive stages and identified genome-wide genetic variation between and within the species. We tested whether specific climatic variables contributed to phenotypic variation when accounting for geographic distances and phylogenetic structure.

Genotype-environment association analyses using redundancy analysis support our hypothesis that local climatic differences contributed to patterns of adaptive divergence among the species across America and Eurasia. Seasonal variation in temperature and precipitation were implicated as primary climatic variables linked to phenotypic variation. We found that variations in plant height, days to flowering, and shoot biomass at harvest are associated with temperature and rainfall seasonality. This study provides insight into genotype-environment interaction and potentially adaptive traits in the *Hordeum* clade. This work represents a promising starting point for dissecting genetic variation underlying adaptive variation in important life-history traits.

50. EXPLORATION OF DROUGHT STRESS-RESPONSE OF WINTER WHEAT USING ADVANCED GRAVIMETRIC PHENOTYPING TECHNOLOGY

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Winter wheat (*Triticum aestivum*) is the most important crop, cultivated widely in Germany. Similar to other crops, winter wheat production is heavily influenced by changing weather conditions such as the amount and distribution of precipitation. The efficient utilization of water is crucial to achieve enhancements in wheat yield. Yield performance is the result of plant transpiration rate (TR), water use efficiency (WUE) and harvest index. Providing insight into transpiration and understanding its relationship with Vapor Pressure Deficit (VPD) are particularly important to improve drought stress tolerance in winter wheat. Restricting the maximum TR in the presence of elevated VPD is recognized as a water conservation strategy. Genotypes that exhibit this characteristic are desirable, particularly in high VPD environments where water deficit occurs later in the growing season.

The objective of the current study is to investigate the transpiration response to soil water deficit and VPD among 30 selected modern winter wheat genotypes using an advanced gravimetric phenotyping platform

(Plantarray®) to identify genotypes that use water more efficiently under drought stress at earlier growth stages. The setup is a pot experiment with an alpha-lattice design under controlled environmental conditions. It involves two irrigation scenarios as treatments, representing 70% and 35% soil water capacity with two replicates and initially 50 plants per pot. When the plants reach the 2-3 leaf stage after germination, pots are exposed to vernalization at 4°C for 8 weeks. Then, the pots are placed in the Plantarray®. At the end of the establishment period and before applying 35% soil water capacity, the number of plants per pot is reduced to 10. Besides the automatic data measurements and calculations by Plantarray® e.g., TR and VPD, the chlorophyll content is also recorded using SPAD device. The experiment will be concluded at the stem elongation stage and the above-ground biomass is measured. In this way, it is expected that the complex relationships of drought stress tolerance can be better disentangled, and the underlying sub-traits associated with breeding progress for better drought stress tolerance can be

identified. The results will give valuable insights into the drought tolerance and form the basis for further genetic studies.

Keywords: *evapotranspiration, abiotic stress, stomatal regulation, water loss dynamics, phenotyping, winter wheat*

51. EXPLORING DROUGHT RESPONSE IN WILD POTATO GERMPLASM

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Climate change imposes new environmental scenarios with a scarcity of rainfall for agriculture. These conditions, combined with the narrow genetic base of potato cultivars, pose a challenge to global production. Wild potato species serve as sources of genetic diversity where genes associated with a favorable response to drought may be present.

Twenty-eight genotypes from 12 wild potato species putatively tolerant to drought (*S. boliviense*, *S. infudibuliforme*, *S. lignicaule*, *S. raphanifolium*, *S. tacnaense*, *S. tarapatanum*, and *S. bukasovii*) were selected, along with genotypes with a known response to stress conditions, to be validated for this trait under greenhouse conditions experiment. Three irrigation treatments (RN=normal irrigation, RR=restricted irrigation, and SS=severe drought) were implemented in a split-plot design in a randomized complete block arrangement. The objective was to identify genotypes and species exhibiting a favorable response under water deficit conditions by measuring physiological variables such as chlorophyll amplitude (ChlSPAD_{max}), stomatal conductance, leaf temperature differential, and agronomic variables such as total and stratified dry biomass. Tolerance indices associated with physiological and agronomic variables were also calculated and, through principal component analysis, categorized into groups based on productivity and resilience.

The results of the analysis indicated that accession CIP761364 of *S. boliviense* exhibited the highest values of ChlSPAD_{max} overall. Additionally, genotypes CIP761786.005 and CIP762833.025 of the species *S. raphanifolium* and *S. tarapatanum*, respectively, displayed outstanding performance under RR and SS conditions, as evidenced by increased greenness, reduced leaf length, and total aboveground biomass accumulation. Furthermore, genotype CIP762830.004 of the species *S. lignicaule* demonstrated the highest yields under both RR and SS conditions. Although the reduction in stratified biomass yield corresponded to the severity of stress, it was observed that more limited water resource conditions had a greater impact on tuber production in *S. lignicaule*. Wild species with early maturity, such as *S. boliviense*, allocate more resources to aboveground biomass than the harvestable product. In the group of late-maturing wild species, genotype CIP762866.038 of the species *S. tacnaense* exhibited good yields under RR and SS conditions. It showed the least reduction in tuber yield, despite its low aboveground biomass. On the other hand, the species *S. tarapatanum* accumulated the highest aboveground biomass, even under SS conditions. These characteristics may be attributed to the late maturity of these species, which allows for balancing the effects of drought between the exponential and maximum growth of coverage and tuber yield.

52. FROM CONTROLLED ENVIRONMENT TO FIELD: CONFOUNDING FACTORS IN CONTAINER TRIALS

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Global climate change models predict an increase of extreme weather events, among them drought and heat. Potato is one of the big five food crops and produces maximum calories per volume water. However, potato is drought sensitive. Maintenance of agricultural yield thus requires breeding of resilient cultivars. The bottleneck in drought tolerance breeding is phenotyping in managed field environments. Fundamental research on drought tolerance uses container-based test systems in controlled environments as a proxy. However, breeders debate the portability of results from these systems to performance under field conditions. Thus, we analysed the effects of climate conditions, container size, starting material, and substrate on yield and drought tolerance assessment of potato genotypes in pot trials compared to field trials. The tolerance ranking in the

field was obtained from seven multisite-multiyear trials. The tolerance ranking in controlled environments was highly reproducible, but weakly correlated with field performance. Changing to variable climate conditions, increasing container size and substituting cuttings by seed tubers did not improve the correlation between pot and field results. Substituting horticultural substrate by sandy soil resulted in yield and tuber size distributions similar to those under field conditions. However, as the effect of the treatment × genotype × substrate interaction on yield was low, drought tolerance indices that depend on relative yields can be assessed on horticultural substrate too. Realistic estimates of tuber yield and tuber size distribution, however, require the use of soil-based substrates.

53. FROM PAST TO PRESENT: INVESTIGATING PLASTIC RESPONSES OF STOMATA TO LIGHT AND TEMPERATURE FLUCTUATIONS IN WINTER WHEAT (*TRITICUM AESTIVUM* L.)

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Unraveling the adaptive traits of stomata is crucial for enhancing resilience in winter wheat breeding in response to climate change and increasing weather extremes. In this study, we examined the plasticity of stomata's morphology of winter wheat in response to light and temperature variations, using a panel of 50 cultivars, representing the German breeding history. Seedlings were subjected to two contrasting conditions: source-limited (high temperature, low light: 32/28°C day/night temperatures, 50 $\mu\text{mol m}^{-2}\text{s}^{-1}$ PAR) and sink-limited (low temperature, high light: 16/12°C day/night temperatures, 550 $\mu\text{mol m}^{-2}\text{s}^{-1}$ PAR). A handheld digital microscope (ProScope HR2) equipped with an x400 magnification lens was used to capture 11,520 images of leaf surfaces. These were processed using a customized algorithm of object detection to analyze stomatal traits—length (μm), width (μm), count, and stomata covered area (mm^2)—on both sides of the 3rd leaf. Among both source and sink limited conditions,

stomatal covered area was higher in the source-limited condition ($0.189 \pm 0.018 \text{ mm}^2$) compared to the sink-limited condition ($0.134 \pm 0.10 \text{ mm}^2$). Conversely, stomatal length was greater in the sink-limited condition ($40.6 \pm 0.88 \mu\text{m}$) than the source-limited condition ($34.7 \pm 1.2 \mu\text{m}$). Stomatal count exhibited a robust positive correlation with stomatal covered area (mm^2) ($R = 0.96$), a strong negative correlation with stomatal length ($R = -0.90$), and a weak negative correlation with stomatal width ($R = -0.19$). Furthermore, plasticity in stomatal covered area correlated strongly with plasticity in stomatal count between source and sink limited conditions ($R = 0.69$), while demonstrating a weak negative correlation with plasticity in stomatal length between source and sink limited conditions ($R = -0.37$). We detected that no stomatal trait has been selected by breeding, allowing for the tailored development of strategies to optimize stomatal traits independently, addressing specific climatic stressors effectively.

54. ARCHITECTURAL PLASTICITY IN RESPONSE TO PLANT DENSITY INCREASES CANOPY LIGHT INTERCEPTION

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With rising population levels and increased pressure on our agricultural system due to climate change, a key challenge is increasing crop productivity. High planting density in winter wheat (*Triticum aestivum* L.) increases yield potential per ground area, but also enhances intra-genotypic competition that can cause yield penalty. To understand the balance between yield potential and penalty, we phenotyped 200 winter wheat genotypes in response to three planting densities (30, 89 and 270 plants m⁻²) using the high-throughput phenotyping platform PHENOARCH (INRAE, Montpellier). The image data and ground truth measurements allowed to quantify dynamic changes of multiple categories of functional and architectural traits during four weeks experimental period, such as plant height, tiller number, leaf area and angle parameters, fresh and dry biomass, light interception and extinction coefficients, as well as the degree of self-shading. Interestingly, the development of leaf area was fastest under intermediate density, suggesting competition-driven plasticity in biomass allocation and/or in leaf mass per area. Biomass and tiller number per plant decreased

with increasing density and the degree of this plasticity differed largely between genotypes. High correlation between plasticity of biomass and tillering suggests that biomass of genotypes maintaining tiller development under high density was least affected by planting density, probably by increasing light interception per plant. To prove this, we conducted in silico experiments simulating the effects of architectural plasticity in response to density on light interception at individual and canopy levels. This was achieved by coupling the 3D plant architecture models obtained from the experiment with a light model. Interestingly, increasing density without architectural adaptation of individual plants reduces canopy light interception in most of the studied genotypes. This indicates that architectural plasticity in response to high planting density is not purely a “selfish” behavior, but also beneficial to canopy light interception and therefore productivity. Our results highlight how non-invasive phenotyping in combination with 3D modeling can reveal the important functions of phenotypic plasticity for canopy productivity.

55. FEMALE FLORAL ORGANS CONTROL SEED SET AFTER REPRODUCTIVE COLD STRESS IN SORGHUM

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The significance of cold tolerance in sorghum (*Sorghum bicolor* L. Moench) for expanding cultivation in temperate regions is gaining increasing scientific and agricultural interest. Due to its versatility in end-uses (food, feed, and industrial applications), high drought tolerance, nutrient efficiency, and resistance to *Diabrotica virgifera*, sorghum represents a promising novel crop for Central Europe.

However, cold, particularly in temperate regions, but also in tropical highlands, presents a major challenge. Sorghum is not only sensitive during the germination

stage but also exhibits increased susceptibility to cold stress during the reproductive phase, significantly affecting crop yields.

Our research project aims to deepen the understanding of reproductive cold tolerance and decipher the underlying mechanisms to further advance breeding efforts. To achieve this, cold-tolerant and cold-sensitive parental lines, as well as their reciprocal F1 hybrids, were subjected to cold stress at various stages of reproductive development, with a focus on pollen fertility and the female reproductive organ. While existing

literature primarily attributes reduced pollen fertility as the cause of decreased seed set, this study reveals that the female reproductive organ is significantly more affected than previously assumed. It is evident that the initiation of generative tissue formation until BBCH39 is the most cold-sensitive developmental stage, and in

the inheritance of cold tolerance QTLs, neither maternal nor paternal effects predominate.

These results provide valuable insights for the development of cold-tolerant sorghum varieties, aiming to expand cultivation in colder regions and increase crop yields in temperate climates.”

56. IDENTIFYING DIVERSITY FOR DROUGHT STRESS TOLERANCE IN FABA BEAN (*VICIA FABA* L.) BY DIGITAL AND PHYSIOLOGICAL PHENOTYPING

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Drought stress is one of the most crucial abiotic stress factors threatening the worldwide cultivation of faba beans. In the face of climate change, breeding for drought stress tolerant genotypes is growing even further in importance under increasing temperatures and longer drought periods. The aim of this study is to identify drought stress tolerant *Vicia faba* genotypes within a diverse genotype panel as a knowledge base for selection of crossing parents and for subsequent selection based on morphological and physiological traits associated with relevant drought stress tolerance characters.

A diverse set of genotypes were grown in 240 large containers with a 90 cm deep soil profile in our phenotyping (DroughtSpotter XXL) facility. This fully automated drought phenotyping platform automatically and accurately measures the weight of each container every five minutes 24/7, enabling precise gravimetric recording of water use and stress responses. It simultaneously enables individual irrigation of each container, allowing simulation of specific drought

stress conditions. Furthermore, fully automatic non-destructive measurement of complex above-ground plant architecture was assessed in a high resolution using a vertical multispectral PlantEye 3D scanner across the whole plant development.

The scanner not only enables the capture of the normalized difference vegetation index, normalized pigment chlorophyll ratio index, plant senescence reflectance index, and Hue but also seizes specific traits regarding plant morphology and their changes over time. Connecting precise phenotypic and plant performance data obtained under relevant drought stress conditions allows identification of target traits for efficient field selection and breeding lines capable of sustaining yield under limited water availability.

The study revealed clear differences in plant indices between the irrigation schemes and between genotypes. Based on specific plant indices, significant variations were observed in relation to yield components, grain quality and water uptake as a basis to design future selection strategies.

57. A FIRST LINE OF DEFENCE – GRAPEVINE RIBBON TRICHOMES AS A PHYSICAL BARRIER AGAINST DOWNY MILDEW INFECTION

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Trichomes are hair-like epidermal structures on the surface of different plant organs and are of diverse morphology, ontogeny and function. For grapevine (*Vitis* spp.), trichome types are described as either non glandular, including ribbon trichomes and simple trichomes (bristles), or glandular. Ribbon trichomes are flat and elongated and their occurrence varies in extent from absent to sporadic up to a dense hydrophobic indumentum within the range of grapevine wild species and varieties. When present in high density on the abaxial leaf surface this trichome type acts as a physical barrier against infection with *Plasmopara viticola*, since the causal agent of grapevine downy mildew requires the presence of liquid water, enabling its zoospores to reach the stomata, through which they penetrate the leaf. Thus, ribbon trichomes can be considered as a first line of defense acting upstream and complementary to genetic resistances (Rpv loci - resistance against *P. viticola*). The resilience conveyed by the ribbon trichomes has the advantage that it cannot be overcome by the pathogen, is therefore particularly durable and should be made genetically accessible for grapevine breeding.

To achieve this goal the present study aims at mapping of genetic loci that are associated with the formation

of grapevine ribbon trichomes. A high throughput phenotyping pipeline was developed for the evaluation of abaxial ribbon trichome density on leaves and applied to a high number of F1 individuals from several mapping populations. This incorporates automated photography of leaf discs using a stereo microscope and a quantitative rating based on artificial intelligence (ResNet CNN). A major locus on chromosome 5, known as Leaf Hair 1 (LH1) from 'Muscat of Alexandria', was identified in further glabrous varieties by QTL mapping using three independent F1 populations and upon further investigation of the locus six candidate genes were designated. Moreover, two SSR markers are proposed for potential application in marker assisted selection (MAS) enabling a negative selection for absence of ribbon trichomes as conveyed by the LH1 locus.

Identification of loci responsible for the presence of ribbon trichomes are expected out of a mapping approach using rhAmpSeq marker based genetic maps of interspecific F1 populations of the type *V. labrusca* x *V. vinifera*. Accessions of *V. labrusca* a North American wild species exhibit a dense indumentum on their abaxial leaf blade.

58. CHARACTERIZING THE INDIVIDUAL EFFECT OF FLUCTUATING LIGHT AND TEMPERATURE ON SOURCE ACCLIMATION ON WINTER WHEAT

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Improving our understanding of plant photosynthetic acclimation to environmental fluctuations is a crucial aspect to develop crop varieties adapted to future climatic conditions. Here we propose a theoretical model of photosynthetic protein turnover that explains photosynthetic acclimation as the accumulated effect of light and temperature on the synthesis and degradation of photosynthetic proteins in three functional pools: carboxylation, electron transport,

and light harvesting. However, parameterizing this model across a wide panel of winter wheat varieties is challenging due to the number of genotype-specific parameters. Consequently, we propose hyperspectral phenotyping as a high-throughput approach for indirect assessment of parameters such as maximum carboxylation rate (V_{cmax}), maximum electron transport rate (J_{max}), and chlorophyll concentration. In order to determine the individual effect of light and

temperature fluctuations, we are conducting a series of experiments growing 50 winter wheat genotypes covering the recent German breeding history in a controlled environment with different combinations of varying and constant conditions. These experiments aim to characterize the three protein pool dynamics

through periodic measurements of pigment content, chlorophyll fluorescence and gas exchange; and establish correlations between this ground truth and hyperspectral data, which will be instrumental in understanding how breeding has affected the photosynthetic acclimation.

59. ASSESSING DROUGHT STRESS RESPONSES IN OILSEED RAPE USING HIGH THROUGHPUT PHENOTYPING AND MACHINE LEARNING

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Drought is a global threat to crop yields worldwide, hence ensuring stable yields while consistently increasing yield levels is a crucial process in plant breeding. Oilseed rape exhibits considerable genotype by environment interaction. To predict the performance of oilseed rape under drought stress and thus ensure the accurate identification of drought-tolerant breeding lines, the STRESS-STOPP project aims to link multidimensional phenomic, spectral and genomic datasets using machine learning techniques, considering G*E interactions. The project utilizes multiple levels of phenotyping platforms ranging from controlled drought trials to large scale multi-environmental trials. The high-throughput phenotyping platform DroughtSpotter XXL is being used in concurrent studies at Justus Liebig University Giessen in 2024 to simulate drought stress during the flowering period in a foil house experiment. In this platform, plants are cultivated in oversized containers with arable soil,

ensuring high comparability with field performance data. Gravimetric transpiration monitoring occurs at 5-minute time intervals throughout the entire growing season. The vapor pressure deficit is recorded and the water use efficiency is calculated. Simultaneously, an automated dual PlantEye F600 3D laser scanner is implemented to determine morphological and spectral characteristics throughout the growing season. Traits assessed include digital biomass, leaf area and normalized vegetation index. Collating all data from different controlled-environment trials and field phenotypes (also including multispectral image data) results in an extensive phenotypic catalogue. Ultimately, this catalogue will be linked to the yield under various drought conditions using cutting edge machine learning pipelines to capture and describe G*E. The findings will be implemented in breeding to improve breeding populations for robust reactions on drought stress and for increased yield.

60. GENETIC DIVERSITY AND PHENOTYPIC VARIATION IN *SOLANUM TUBEROSUM* L. FOR PHOSPHORUS (P) EFFICIENCY

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Potatoes (*Solanum tuberosum* L.) require an optimal amount of phosphorus (P) for growth, tuber production and starch quality. But their small and shallow root system makes it difficult to acquire nutrients from the deeper level of soils. Our study aimed at exploring the phenotypic and genotypic variation among potato genotypes and identifying significant markers associated with phosphorus stress tolerance. We screened a set of 183 potato accessions of the Gross Luesewitz Potato Collections (GLKS), along with 17 modern starch potato cultivars, for their response to P stress in a sand hydroculture pot experiment. Two phosphorus treatments (high and low P) were applied to the plants as KH₂PO₄ in the nutrient solution in amounts of 15 mg l⁻¹ (high P) and 3 mg l⁻¹ (low P), respectively. After four weeks, shoots, roots, and tubers (if produced) were harvested and dried (60 °C) and the dry matter was determined. P concentration was measured by ICP method. DNAs isolated from invitro plantlets were genotyped by sequencing, leading to the identification of 56,738 SNPs. The genetic structure among the genotypes was estimated (PCA) based on the genetic distance between individuals, as well as by admixture analysis. A genome-wide association

studies (GWAS) was conducted on the phenotypic traits and the filtered SNP set using FarmCPU model. Results from the pot experiment showed a reduction of shoot biomass by an average 67.1 % under low P conditions, while root biomass was only reduced by, on average, 39.8 %. P uptake varied between 0.71 and 5.76 mg pot⁻¹ under high P and between 0.18 and 1.33 mg pot⁻¹ under low P. The extent of reduction in shoot and root dry weight was genotype dependent, with the majority showing increased root: shoot ratios under low P conditions. After phenotypic screening, we were able to identify outstanding genotypes such as variety 'Kristall' (GLKS 11578) with a shallow but very dense root system or 'Tiger' (GLKS 10591) with a long and extensive root system. A GBS based PCA identified distinct genetic clusters of cultivated and of wild entries. GWAS revealed a total of 33 significant marker-trait associations (MTAs), the majority of which were linked with phosphorus utilisation efficiency (PUE) and shoot biomass of the genotypes. In conclusion, we observed high phenotypic and genotypic variability among the potato accessions, forming a good basis for breeding towards P efficient potatoes.

61. UNVEILING GRASSPEA (*LATHYRUS SATIVUS* L.) POTENTIAL BY AGRO-MORPHOLOGICAL, MOLECULAR, AND BIOCHEMICAL CHARACTERIZATION OF DIVERSE GERMPLASM

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Grasspea is a versatile legume crop with exemplary nutritional profile and a spectacular choice as climate smart species to overcome malnutrition. A total of 168 diverse germplasm including four checks (Ratan, Prateek, Mahateora, and Narayangon) were evaluated for 14 quantitative and 20 qualitative traits using an

augmented block design at Pusa Farm, ICAR-NBPGR, New Delhi, India over two consecutive rabi seasons (2019-20 and 2020-21). The promising accessions for important traits such as 100-seed weight – IFLA1439 (14.02 g), IFLA432 (13.38 g), IC0634674 (13.38 g); early flowering – BANG31 (64 days), IC525179

(63 days), BANG208 (69 days); higher plant height – BANG285 (119.45cm); number of pods per plant – IFLA276 (87 pods), IC489623 (86 pods); and early maturity – BANG31 (112 days) were identified. Modified DNA isolation protocol was standardized for this crop and out of 70, 20 SSR markers were polymorphic. PIC value ranged from 0.02 to 0.67, and heterozygosity ranged from 0 to 0.5. K means clustering as per population structure analysis using the STRUCTURE and PCoA analysis were performed. Molecular diversity studies further categorized germplasm into three principal clusters. Notably, the observed similarity between the morphological and molecular cluster dendrogram indicated that accessions with higher days to maturity and 100-seed weight were grouped in the same clusters. The sample selection was by the FOSS NIRS 6500 for biochemical analysis for both seed and leaf for proximate parameters like protein, starch, sugar, phenol, moisture, ash, TDF, minerals like

Fe, Cu, Zn, Ca, and Mg along with amino acid profiling and β-ODAP estimation using UPLC with agilent ZORBAX Eclipse Plus C18 and SB C18 column, respectively. We observed a significant difference for ODAP content from 0.074 to 0.34 mg/kg in seed and 0.03 to 0.287 mg/kg in leaves. Low β-ODAP in the seeds of IC525182 (0.074), IC0634662 (0.078), and IFLA2924 (0.088) and in leaves of IFLA1193 (0.030), IC470982 (0.040), and IC208430 (0.040) was observed. This nutritional profiling has resulted in identification of accessions which are having superior agro-morphological traits like early maturity, more pods per plant, more seeds per pod, and better seed size along with high protein and minerals and low ODAP content for both seed and leaf. These accessions are IC208430, IC0634654, IC0634662, IC0634674, BANG285, BANG31, IFLA143, and IFLA1193. These accessions can be used in grasspea breeding programmes for the development of low ODAP and agronomically superior varieties.

62. PHENOTYPIC DIFFERENTIATION BETWEEN HIGHLAND AND COASTAL QUINOA ECOTYPES UNDER COLD STRESS CONDITIONS

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Quinoa (*Chenopodium quinoa* Willd.) is a genetically diverse Andean crop with important implications for food security. It has gained worldwide attention not only due to its nutritional value and health benefits but also due to its adaptations to a wide range of agro climatic conditions like frost, drought, heat, and salinity. Consequently, quinoa might be suitable as an alternative crop for marginal lands in Europe and Mediterranean regions. Here, we investigated the germination and phenotypic variation of 60 quinoa accessions from highland and coastal environments under low temperature conditions. The hypothesis is that highland quinoa accessions are better adapted to cold stress, especially during early growth stages, because of their adaptation to thrive at higher altitudes characterised by lower and fluctuating temperatures, as compared to coastal regions. We first conducted a field experiment where seeds were sown at three distinct time points representing late winter (T1), early

spring (T2), and spring (T3) conditions. Second, we investigated germination under laboratory conditions at standard (18.3 °C) and cold (4.4 °C) conditions where germination progress was documented daily. To process the large amount of germination images we developed a deep-learning image analysis pipeline. Our findings showed that T1 plants experienced cold stress during early stages, resulting in delayed germination and lower germination percentages compared to T2 and T3 plants. Surprisingly, despite the poor germination due to low temperatures, the T1 plants recorded more total yield of 64 g compared to the plants of T2 (46 g) and T3 (35 g). We furthermore observe significant differences between highland and coastal accessions, with highland accessions exhibiting early germination and high germination percentages and coastal accessions early maturity and higher yield across all time points. The results of the laboratory seed germination experiment were consistent with the field experiment,

also demonstrating that highland accessions exhibit superior germination traits. Evaluations of our newly developed deep-learning image analysis pipeline with manually recorded data revealed high accuracy and effectiveness making it a valuable novel image analysis technique for future germination studies. The results indicate distinct adaptation patterns, where various

advantageous adaptations for cultivation in Europe are observed in both highland and lowland accessions that could be combined by breeding and selection. This research also contributes valuable insights into quinoa adaptation to low-temperature conditions, emphasizing its potential as a resilient and versatile crop for diverse agro-climatic settings.

63. EXPLORING DROUGHT RESPONSE FROM WILD POTATO GERMPLASM

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Climate change imposes new environmental scenarios with a scarcity of rainfall for agriculture. These conditions, combined with the narrow genetic base of potato cultivars, pose a challenge to global production. Wild potato species serve as sources of genetic diversity where genes associated with a favorable response to drought may be present.

Twenty-eight genotypes from 12 wild potato species putatively tolerant to drought (*S. boliviense*, *S. infudibuliforme*, *S. lignicaule*, *S. raphanifolium*, *S. tacnaense*, *S. tarapatanum*, and *S. bukasovii*) were selected, along with genotypes with a known response to stress conditions, to be validated for this trait under greenhouse conditions experiment. Three irrigation treatments (RN=normal irrigation, RR=restricted irrigation, and SS=severe drought) were implemented in a split-plot design in a randomized complete block arrangement. The objective was to identify genotypes and species exhibiting a favorable response under water deficit conditions by measuring physiological variables such as chlorophyll amplitude (ChISPAD_{max}), stomatal conductance, leaf temperature differential, and agronomic variables such as total and stratified dry biomass. Tolerance indices associated with physiological and agronomic variables were also calculated and, through principal component analysis, categorized into groups based on productivity and resilience.

The results of the analysis indicated that accession CIP761364 of *S. boliviense* exhibited the highest values of ChISPAD_{max} overall. Additionally, genotypes CIP761786.005 and CIP762833.025 of the species *S. raphanifolium* and *S. tarapatanum*, respectively, displayed outstanding performance under RR and SS conditions, as evidenced by increased greenness, reduced leaf length, and total aboveground biomass accumulation. Furthermore, genotype CIP762830.004 of the species *S. lignicaule* demonstrated the highest yields under both RR and SS conditions. Although the reduction in stratified biomass yield corresponded to the severity of stress, it was observed that more limited water resource conditions had a greater impact on tuber production in *S. lignicaule*. Wild species with early maturity, such as *S. boliviense*, allocate more resources to aboveground biomass than the harvestable product. In the group of late-maturing wild species, genotype CIP762866.038 of the species *S. tacnaense* exhibited good yields under RR and SS conditions. It showed the least reduction in tuber yield, despite its low aboveground biomass. On the other hand, the species *S. tarapatanum* accumulated the highest aboveground biomass, even under SS conditions. These characteristics may be attributed to the late maturity of these species, which allows for balancing the effects of drought between the exponential and maximum growth of coverage and tuber yield.

64. IMPACT OF ELEVATED CO₂ ON LEAF RUST RESISTANCE IN EUROPEAN WINTER WHEAT (*TRITICUM AESTIVUM* L.): GREENHOUSE VS. FIELD STUDIES

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Common wheat (*Triticum aestivum* L.) is one of the most important crops for human nutrition worldwide. However, leaf rust infections caused by *Puccinia triticina* can lead to yield losses up to 60%. Breeding and cultivation of resistant varieties is the most effective and environmental friendly strategy to secure yield. The atmospheric CO₂ concentration has almost doubled since the pre-industrial time and it can be firmly assumed, that the CO₂ concentration will continue to increase in the years to come.

Although a large number of studies have analysed the effects of elevated atmospheric CO₂ concentration, to our knowledge no study has investigated the effects of elevated atmospheric CO₂ concentration (eCO₂) on the infection and resistance behaviour of a larger number of varieties yet.

In the WheatFACE project, we are strive to gain a better understanding of the influence of eCO₂ on the resistance behaviour of winter wheat.

Therefore, it is investigated whether eCO₂ leads to increased susceptibility, for example because CO₂ fertilisation increases biomass growth, or whether

fungal invasion is reduced, for example by stronger closed stomata or improved plant resistance. To analyse this, two different winter wheat populations with 200 and 370 genotypes are exposed to different CO₂ concentrations (410 ppm vs. 800 ppm) and inoculated with two particularly aggressive leaf rust isolates.

Leaf rust infestation is assessed both by manual evaluation and by digital quantification of the infested leaf area using high-throughput technology. The results provide information on the influence of eCO₂ on the extent and intensity of leaf rust infection in wheat.

Based on these results, twelve varieties were selected that showed contrasting resistance behaviour at different CO₂ concentrations. These are cultivated over the two years in a free air carbon dioxide enrichment (FACE) facility under field conditions. The preliminary data show a comparatively high repeatability (h²: 0.6 to 0.9) of the respective experiments. The study provides an unprecedented insight of the effect of CO₂ on leaf rust infection and forms the basis for further genetic studies.

POSTERS – CROP IMPROVEMENT

65. HARNESSING THE BENEFITS OF CROP WILD RELATIVES FOR AFRICAN DRYLAND FARMERS

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The genebank of the international Centre for Agricultural Research in the Dry Areas (ICARDA) holds the second-largest collections of barley (*Hordeum*) and the fourth-largest collection of wheat (*Triticum*) species globally, maintaining over fifty thousand accessions. Thus, it offers unparalleled opportunities for cereal pre-breeding activities. However, the effective identification of useful material and its rapid introgression into elite germplasm remain challenging. In this context, we investigate the deployment of the Focused Identification of Germplasm Strategies (FIGS) as a strategic solution to create sub-sets of landraces with an increased probability of harbouring useful genes. Beyond FIGS, the secondary and tertiary gene pools provide even greater opportunities for the identification of novel alleles. *Hordeum bulbosum* L. is the only known secondary crop wild relative (CWR) of barley and has very low crossability. By testing Bulbosum-derived accessions in multi-location field trials across

Morocco we discovered that certain introgressions can improve straw and grain production under drought, heat, and low input soil conditions. Similarly, durum wheat derived from various CWRs has been performing exceedingly well when tested under severe heat and drought stress. Results from breeding trials using this germplasm support the strong need to expedite the usage of CWRs to address the future challenges caused by global climate change. Farmers, as the ultimate beneficiaries of this work, were engaged through participatory selection in the trials. This ensures that the novel germplasm developed meets their needs and facilitates rapid adoption of novel varieties. We found that selections made by farmers from African drylands cannot fully be explained by physiological parameters measured in experimental fields, posing the challenge of how to incorporate farmer preference in breeding and pre-breeding pipelines.

66. CHARACTERISING STAY-GREEN IN BARLEY ACROSS DIVERSE ENVIRONMENTS: UNVEILING NOVEL HAPLOTYPE

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Barley is considered one of the most naturally resilient crops making it an excellent candidate to dissect the genetics of drought adaptive component traits. Stay-green, is thought to contribute to drought adaptation, in which the photosynthetic machinery is maintained for a longer period post-anthesis increasing the photosynthetic duration of the plant. In other cereal

crops, including wheat, stay-green has been linked to increased yield under water-limited conditions. Utilising a panel of 397 diverse barley breeding lines from a commercial breeding program we aimed to characterise stay-green in four environments across two years. Phenotype data was collected using an unmanned ariel vehicle (UAV) with a fixed Micasense

multi-spectral camera from which vegetative indices were extracted. Spatio-temporal modelling was used to accurately model senescence patterns from flowering to maturity characterising the variation for stay-green in barley for the first time. Environmental effects were identified, and multi-environment trait analysis was completed for stay-green characteristics during grain filling. A consistently positive though environmentally varied genetic correlation was found between yield and stay-green. Twenty-two chromosomal regions with

large effect haplotypes were identified across and within environment types, with ten being identified in multiple environments. Stacking of multiple desirable haplotypes showed an opportunity for improved stay-green phenotype. This study is the first of its kind to model barley stay-green in a large breeding panel and has detected novel, stable and environmentally specific haplotypes. This will provide a platform for breeders to develop Australian barley with custom senescence profiles for improved drought adaptation.

67. EFFECTS OF HIGH AMBIENT TEMPERATURE ON PLANT GROWTH AND REPRODUCTIVE DEVELOPMENT IN BARLEY

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The increase in the average ambient temperatures due to climate change threatens crop production on a global scale. As one of the most demanded cereal crops, barley (*Hordeum vulgare*) is an important target to generate cultivars that are resistant to high ambient temperatures. In the model plant *Arabidopsis thaliana*, phytochromes and the circadian clock genes control the growth and development in response to high ambient temperatures. In barley, PHOTOPERIOD RESPONSE 1 (PPD H1) and EARLY FLOWERING 3 (ELF3) have been implicated in the control of development under high ambient temperatures. However, the genetic

control of flowering time and reproductive development in response to different ambient temperatures in barley remains unclear. We tested the effects of PHYTOCHROME C (HvPHYC) and its interactions with PPD H1 on development under high ambient night and day temperatures. For this purpose, we analysed the genetic, hormone and metabolite networks in the leaves and shoot apical meristem (SAM) which control flowering time, spike development and floret fertility downstream of PHYC and PPD-H1 and in response to high ambient temperatures.

68. ENHANCING YIELD POTENTIAL AND YIELD STABILITY IN DURUM WHEAT, BARLEY AND LENTIL USING CROP WILD RELATIVE CROSSES, AND PARTICIPATORY ASSESSMENT OF MOROCCAN FARMERS PREFERENCES

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Crop wild relatives (CWRs) are an important source of genetic diversity for crop improvement. Maintaining

high grain yield and genotype performance stability with good nutritional quality under changing climatic

conditions remain challenging. Here, 19 durum wheat, 24 barley, and 24 lentil elites, with CWR in pedigrees, were tested against commercial checks across 19 environments located in Morocco, Ethiopia, Lebanon, and Senegal. Using the additive main effects multiplicative model wide adaptation index (AWAI), six CWR elites were identified for each crop matching or superior to the best check. Regression analysis using a climate matrix revealed that grain yield was mostly influenced by the maximum daily temperature and soil moisture. These climatic factors were used to define five clusters of mega-environments. The CWR elites significantly outperformed the checks in E1, E2, and E4 for durum wheat, and in E2 for both barley and lentil. The germplasm was also assessed for several food transformation characteristics. For durum wheat, one accession (Zeina) originating from *T. araraticum* was significantly superior in mixograph score to the best check, and three accessions originating from *T. araraticum* and *T. urartu* were superior for Zn concentration. For barley, 21 accessions derived from *H. spontaneum* were superior to the checks for protein content, six for Zn content, and eight for β -glucan. For lentil, five to ten accessions originating from *Lens orientalis* were superior to the check for protein content,

Zn and Fe. Building on these findings, three to four CWR elites per crop were selected for further testing across 19 farms representing four agroecological zones of Morocco. Farmers' preferences were gathered through socio-economic participatory weighted selection (PWS) and participatory varietal selection process (PVS). Results revealed that farmers prioritized high yield potential, abiotic stress tolerance, and good nutritional quality for the three crops. A comparison among biophysical performances, PVS, and PWS demonstrated harmonious alignment for durum wheat, where Nachit, Jabal, and Zagherin2 emerged as the best met the farmers' targeted traits. For lentil, the commercial check cultivar, Bakria, appeared as the optimal choice, demonstrating a consistent alignment across the three approaches. Notably, certain differences emerged for barley, with PWS proving more congruent with actual biophysical trials than PVS. Evidence was observed of the effectiveness of PWS approach in capturing farmers' preferences for the three crops, surpassing the more demanding PVS strategy. This study, the first time of its kind in Morocco, provides a valuable trait list for breeders to enhance crop development adoption rates, and offers insights into bridging the gap between breeders' objectives and farmers preferences.

69. CANDIDATE REGIONS FOR ABIOTIC STRESS TOLERANCE ADAPTATION IDENTIFIED BY SELECTIVE SWEEP ANALYSES IN *CHENOPODIUM PALLIDICAULE*

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Chenopodium pallidicaule also known as canihua is a relatively unknown orphan crop from the Andean region. It is a close relative to the better known *Chenopodium quinoa*. Canihua is only a semi-domesticated crop, that lacks strong artificial selection. In contrast canihua is highly adapted to growth at high altitudes of up to 4500 meters. The high tolerance to cold, drought and salt stress suggests selection on these traits. Genomic studies on canihua are still scarce, but previously conducted genetic differentiation studies between samples collected from farmer's fields in Puno Peru and samples from germplasm collections revealed differentiation between the two groups. Here, we used the same data to screen the genome of canihua for signatures

of selection. This was done to verify the differences between the two genetic groups. Additionally, we investigated if there are detectable signatures at all and if yes, where in the genome and which genes they affect. The target of interest were selective sweeps. Selective sweeps are a phenomenon that occurs during the fixation of an allele, resulting in specific patterns in the diversity, site frequency spectrum and linkage disequilibrium, allowing for their identification. Our hypothesis was that we would discover selective sweeps in regions connected to abiotic stress tolerance. This assumption was made based on the selective pressures by the harsh environment canihua is cultivated in. In this study SweepFinder2 and RAiSD

were used to detect selective sweeps. Selective sweeps were required to have signals in the top 0.5% of both tools in the same region. Using these criteria 12 selective sweeps were discovered. The discovered selective sweeps were checked for gene content using the annotated reference genome of canihua. Field and germplasm samples showed differential selective sweeps. Additionally the largest selective sweep discovered contained multiple genes involved

in abiotic stress responses. Among those genes was a homolog of the SCAB1 gene from *Arabidopsis thaliana* that is involved in stomata closing processes and can lead to differential adaptation to drought stress. These results allow for future experiments to be conducted on the exact mechanisms involved in the abiotic stress tolerance of canihua. This could ultimately lead to targets for selection in breeding programs for canihua.

70. FROM BITTER TO BETTER: OPTIMIZING THE TASTE OF RAPESEED PROTEIN FOR HUMAN CONSUMPTION BY APPLIED GENOME RESEARCH

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The demand for plant protein for human nutrition is rising due to concerns about food security, animal welfare, and human health. In this context, rapeseed as a local protein source with high bioavailability is of high relevance. The use of its protein for food is, however, limited by the presence of bitter-tasting flavonols in the seeds. Therefore, one aim is to reduce or ideally eliminate these taste-impairing flavonols. This requires a comprehensive understanding of flavonol biosynthesis in rapeseed. In related species, flavonol derivatives are synthesized by the sequential activity of flavonol synthases (FLS) and subsequent glycosylation by flavonol glycosyltransferases (FGTs). The expression of FLS and FGTs is primarily regulated by MYB transcription factors. The aim of this work is to characterize these structural and regulatory genes in rapeseed with regards to their contribution to flavonol biosynthesis in order to develop targeted breeding strategies.

Candidate genes involved in flavonol biosynthesis were

identified and selected candidates were characterized in terms of their functionalities. We showed that the rapeseed FLS gene family comprises 13 members (Schilbert et al., 2021). Five FLS genes were active in the seed. Of these, two have FLS and flavanone 3-hydroxylase (F3H) activity (FLS1-1 and FLS1-2), two have F3H activity only, and one has neither FLS nor F3H activity. We identified homozygous fls1 1/fls1-2 rapeseed mutants, which showed a significant reduction in all bitter-tasting flavonol derivatives. In addition, we could identify eriodictyol as antagonist for bitter-tasting flavonols. The endogenous production of eriodictyol was studied in a related plant species (Schilbert et al., 2023). The identified candidate genes can contribute to the breeding optimization of flavonol composition and content of rapeseed seeds. Overall, the results can be used to breed elite rapeseed varieties with reduced levels of bitter-tasting flavonols, thus making rapeseed protein more suitable for human consumption.

71. BREEDING IN WINTER WHEAT (*TRITICUM AESTIVUM* L.) CAN BE FURTHER PROGRESSED BY TARGETING PREVIOUSLY NEGLECTED COMPETITIVE TRAITS

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Breeders adapt winter wheat genotypes for high planting densities to pursue sustainable intensification, aiming to maximize canopy productivity. Although the effects of plant-plant competition under high planting density have been extensively reported, the quantitative relationship between competitiveness and plant performance is still very limited.

Here we introduced a shoot competitiveness index (SCI) to quantify the degree of competitiveness of a genotype and studied the dynamics of ten competitiveness-related traits in 200 winter wheat genotypes grown in heterogeneous canopies in two planting densities. Higher planting density resulted in increased plant length but reduced biomass, tiller numbers, and leaf mass per area (LMA) and the plastic responses of our traits showed a minimum of 41% differences between genotypes. Surprisingly, genotypes with higher

LMA in low planting density exhibited greater LMA decrease under high density, challenging conventional expectations derived from game theory. Regression analysis identified that the key traits tiller number, LMA and plant length strongly influence wheat genotype performance under high density. Contrary to our hypothesis, early competitiveness did not guarantee sustained performance, revealing the dynamic nature of competitiveness.

Evaluation of breeding progress across our panel revealed a declining trend in SCI ($R^2 = 0.61$). This aligns with the broader breeding objective of minimizing individual competitiveness to enhance overall canopy productivity. The simultaneous absence of historical trends in pivotal architectural traits and their plasticities, tiller number and LMA, suggests their potential for further crop improvements.

72. HIGHER SEED YIELD THROUGH SELECTION FOR REDUCED SEED SHATTERING IN ITALIAN RYEGRASS

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Seed yield is an important factor for economic seed production of Italian ryegrass (*Lolium multiflorum* Lam.). The realized seed yield can be lowered by several factors such as unsuccessful pollination and fertilization, abortion of seeds during development as well as seed shattering. Seed shattering, i.e., the loss of seeds at ripening stage shortly before or during seed harvest, was found to be the main factor limiting seed yield in Italian ryegrass breeding germplasm of Agroscope. The aim of this study was to evaluate the possibility to reduce seed shattering through recurrent phenotypic selection on spaced plants. To phenotype seed shattering, inflorescences of each plant were bagged after flowering to capture shattered seeds.

Plants were harvested when they reached a given sum of temperature calculated from their start of flowering to eliminate any effects of earliness. Seed shattering was calculated as the proportion of shattered seed mass over total seed mass. Starting from a founder population of 300 plants serving as FO population, two cycles of phenotypic selection for high and low seed shattering, including a neutral selection at each cycle, were conducted. The resulting five populations were compared in a spaced plant nursery trial as well as in plot trials with sown swards. A significant effect of selection was observed in spaced plants, with lowest seed shattering observed in the population selected twice for decreased shattering (15.3 %) and highest

seed shattering (47.9%) for the population selected twice for increased shattering. The same ranking of the five F2 populations was observed in the trial with sown plots. Using the applied phenotyping method, recurrent phenotypic selection on single spaced plants allows to efficiently reduce seed shattering and, therefore, increase seed yield in plots of sown swards.

Analysis of correlations revealed that selection for reduced shattering did not compromise agronomical important traits such as vigor or maturity. The recurrent phenotypic selection in spaced plants presented here is effective to create new cultivars with reduced seed shattering and increased harvestable yield.

73. IMPROVING YIELD PREDICTION OF SYNTHETIC CULTIVARS IN CASE OF PARTIAL ALLOGAMY

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Finding an adequate breeding strategy for a partially allogamous crop is challenging. In faba bean (*Vicia faba*), hybrid cultivars cannot be bred since no mass-pollination control is feasible, whereas line cultivars do not use heterosis. In this crop, synthetic cultivars are bred. Synthetics are populations, composed of selected inbred lines, grown as open-pollinated mixture to initiate the population.

For creating such synthetics, selection of parents which lead to the best-performing synthetic population is crucial. To thus predict the performance of a synthetic from data of parents, current theory includes number of parents, their degrees of cross-fertilization, their per-se performances, and their GCA effects. So far, it has been assumed that all parents contribute the same amount of pollen to cross-fertilization. Yet, recent findings indicated that faba beans differ in their success rates as pollen donors, i.e., in paternal outcrossing success. Hence, previous predictions were obviously ignoring such relevant feature. To make yield predictions more precise, we advanced the algebraic basis of prediction by considering paternal outcrossing success as additional parameter.

Here, we present extended algebra allowing to predict the performance (grain yield) of partially allogamous

synthetics in Syn-1. Simulations were conducted to inspect the impact of genetic variation in paternal outcrossing success on the precision of predictions. $N=3200$ fictive inbred lines were created, with appropriate variances for per-se performance, GCA, degree of cross-fertilization, and paternal outcrossing success. With these lines, we composed synthetics from $k=4$ or $k=8$ parents. Then, we estimated the performance of synthetics in Syn-1 based on (i) 'complete' information vs. (ii) gradually less information, i.e. setting the variation of one or several parameters to zero. From comparing the respective R^2 , the importance of parameters was judged. We found that per-se performance and GCA effect were most important (each explaining ~ 67% of the variance between synthetics), followed by degree of cross-fertilization (~ 30%). Paternal outcrossing success was least important (< 15%).

Considering the effort in estimating these parameters and acknowledging their limited R^2 , breeders will probably mainly use per-se performance of inbred lines and/or polycross-progenies for selection and add rather degree of cross-fertilization than paternal outcrossing success as additional parameter.

74. LEVERAGING A 32-PARENT MAGIC POPULATION FOR ENHANCED DISEASE RESISTANCE AND YIELD STABILITY IN WINTER BARLEY BREEDING

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In the quest for sustainable barley production, enhancing yield stability and resilience to abiotic and biotic stressors remains a pivotal challenge. Traditional methods, such as introgressing resistance genes or quantitative trait loci (QTL), have made strides in disease resistance. However, backcrossing of resistance donors into elite lines inevitably lead to strong selection signatures and conserved, low-diversity linkage disequilibrium (LD) blocks in the genome. Addressing this, our study proposes to utilize a Multi-parental Advanced Generation Inter-Cross (MAGIC) population, which facilitates precise mapping of QTL and allows dissection of complex traits and the exploration of epistatic interactions.

Here we present the preliminary findings from analyzing a 32-parent winter barley MAGIC population, consisting of 1838 double haploid (DH) lines derived from 41 progenies and 138 full siblings with identical crossing schemes. Representing the genetic diversity

of 227 German winter barley varieties (1914-2007), the population was evaluated through a strongly unbalanced design, involving 1000 DH lines across three locations in a two-year field trial. Our results indicate significant quantitative differences among the parents and DH lines in their susceptibility to leaf rust, powdery mildew, net blotch, and Rhynchosporium leaf blotch. Additionally, we observed notable variations in yield, yield stability, and drought stress response.

The anticipated results of a thorough analysis of the MAGIC population will likely reveal quantitative resistance loci and their epistatic effects, alongside assessing the environmental impact on resistance efficacy. It can be expected that some DH lines might combine favorable resistance loci with positive epistatic interactions. The results are intended to lead to a better understanding of the inheritance of essential traits and contribute to more resilient and productive cultivars in the face of growing environmental challenges.

75. EXPLOITATION OF PLANT GENETIC RESOURCES FOR SUSTAINABLE SWEETNESS OF *LUPINUS ANGUSTIFOLIUS* L.

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Due to the increasing demand for high quality plant-based proteins narrow leafed lupin (NLL) as a domestic legume with high protein content, is a crop of great interest. It is well adapted to light soils with shallow groundwater levels and can even improve soil quality with its ability to fix nitrogen due to the symbiosis with nodule forming bacteria (Rhizobium). However, its use as feed and food is limited by the alkaloid content of the seeds (reference thresholds: 0.05 % for feed, 0.02 % for food). The selection of sweet plants in the 1930s led to a genetic bottleneck, narrowing the genetic base further breeding progress. Thus, a wide range of sweet and bitter varieties, gene bank material, landraces and mutant lines of different origins have been collected

in order to increase the genetic diversity of the current breeding material and include previously unused genetic resources for the further improvement of NLL as a crop with high yields and high quality.

To achieve this, we intend to (1) conduct a genome-wide association study with a focus on alkaloid content in a diverse set of sweet and bitter NLL accessions (N = ~300), (2) regard the functional background of alkaloid biosynthesis by transcriptome analysis, (3) develop molecular markers for marker-assisted selection and linkage analysis, (4) create segregating populations for genetic mapping of specific loci and (5) stack gene variants for low alkaloid content. Preliminary results showed that mutant lines and older sources of sweet

NLL-varieties do not possess the most prominent low alkaloid allele known as iucundus and differences in alkaloid stability in several environments suggest that there might be additional mutations involved in very stable low alkaloid lines.

With these potentially new sources of genes and mutations for low alkaloid content in so far unused plant genetic resources, we aim to improve future breeding programs and secure the application of NLL in the feed and food industry.

76. *HORDEUM ERECTIFOLIUM*, A NEW GENOMIC RESOURCE: UNDERSTANDING PERENNIALITY AND ADAPTATIONS TO DROUGHT.

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Annual crops require intensive labor and environmental resources for sowing, tilling, pesticide applications, and irrigation. To address these challenges and enhance food security, the development of low-input, robust, and adaptive perennial crops is crucial. The *Hordeum* genus, comprising of both annual and perennial species including the annual crop barley offers a unique opportunity to uncover the genetic basis of perennial growth and stress adaptation.

Perennial plants live over many years and seasons and are therefore adapted to recurring stresses. Understanding and leveraging seasonally recurring (phenological) patterns of physiological stress acclimation can facilitate climate change adaptation and mitigation. Delving into how perennial wild crop relatives overcome temporary unfavorable environmental conditions will generate new ideas and genetic resources to improve crop resilience and yield stability during transient stresses.

Within the PanHordeum consortium, we have generated reference assemblies for several annual and perennial

Hordeum species. Here, we focus on the perennial *Hordeum erectifolium*, endemic to Argentina, which has evolved a number of adaptive traits, including an altered leaf anatomy supporting rapid leaf rolling under drought stress. The genome was assembled to pseudochromosomes with long-read Oxford Nanopore Technologies, Bionano optical mapping, and Hi-C. The gene annotation was complemented with PacBio IsoSeq high-quality full-length transcripts. Using genomic and transcriptome data we report on comparative genomic and transcriptomic analyses with *Hordeum vulgare*.

By harnessing the resilience of perennials, we can cultivate more sustainable, productive, and resilient food systems, addressing the challenges posed by transient stresses such as drought. *H. erectifolium* will serve as a valuable platform to discover new genetic adaptations and will give us a first glance into the biodiversity and genomics of a perennial *Hordeum* species.

77. GENERATIONAL IMPROVEMENT IN FERTILITY IN DE NOVO ALLOHEXAPLOID BRASSICA OCCURS INDEPENDENTLY OF SELECTION

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Polyploidy is widespread in plants with common examples including agronomically important crops such as wheat, rapeseed and cotton. Diploid (AA, BB and CC) and allotetraploid (AABB, AACC and BBCC) species of the genus *Brassica* within the Brassicaceae (cabbage) family exist in nature, but no allohexaploid *Brassica* (2n = AABBCC) exists.

Allohexaploid *Brassica* can however be artificially synthesized via crossings between the diploid and/or allotetraploid species, and may have agronomic advantages associated with increased ploidy level and with heterosis conferred by the extra set of alleles present in the additional subgenome. However, like many newly formed polyploids, *Brassica* allohexaploids usually have unstable meiosis, hindering establishment of these novel hybrid types.

In this study we tested if meiotic chromosome pairing behaviour improves with fertility-based selection over three generations in a segregating allohexaploid population derived from the cross [*B. napus* (2n = AACC) × *B. carinata* (2n = BBCC) × *B. juncea* (AABB)] × [*B. juncea* (AABB) × *B. oleracea* (CC)]. Inheritance of specific alleles contributed by each of the four parent

species and five parent genotypes was investigated, as well as frequency and location of chromosome rearrangement events. Fertility varied widely in each generation. The average pollen viability in the F2 experimental population was 54%, ranging from 8 - 88% with significant variation between individuals (p < 0.001, one-way ANOVA), while seed set averaged 181 seeds/plant (range 0 - 826). We selected the seven most fertile and nine least fertile F2 plants as parents of the F3 generation, based on seed production. Interestingly, there were no fertility differences between progeny of parents selected for low or high fertility. Maximum pollen viability and seed set nevertheless improved to 98% and 2869 seeds respectively from the first to second generation. No clear correlation was observed between fertility measures and meiotic behaviour in the F2 generation. Our results suggest that selection for improved stability and fertility may be operating independently of observable measures such as pollen fertility or seed set in these newly formed allopolyploid hybrids, and highlight the complexity of selection in polyploid systems.

78. IDENTIFICATION OF PROMISING GRASSPEA INTERSPECIFIC DERIVATIVES FOR LOW ODAP CONTENT

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Grasspea is one of the most resilient and versatile legume crops that can survive in extreme environments. It is valued for its nutritional significance as food, feed, and fodder crop mainly due to its high protein content and biomass. These abilities make it a crop of choice for adaptation to changing climate. Despite its virtues, grasspea cultivation is limited due to the presence of β-N-Oxalyl-L-α,β-diaminopropionic Acid which can cause neurological disorders if it is consumed by an undernourished person as a primary diet for an extended period. Therefore, breeding efforts in grasspea have focused on developing high-yielding varieties with low ODAP content. Traditional cultivars of grasspea contains 0.5-2.5% ODAP content. In contrast, crop wild relatives emerge as a rich reservoir of rare alleles for low ODAP content upon the evaluation of 490 accessions of *Lathyrus* species. We observed significant variation from 0.024 to 0.456% with low ODAP accessions in *Lathyrus annuus*, *L. cicera*, and

L. gorgoni. To develop low ODAP varieties we utilized crop wild relatives in ICARDA breeding program with support from the Crop Trust which have resulted in the development of prebreeding lines from *L. sativus* × *L. cicera* crosses. These lines were advanced using the single seed descent (SSD) method of breeding via speed breeding. The estimation of ODAP content in the seeds of 131 prebreeding lines showed a wide range of variation for ODAP content (0.02 to 0.11%), suggesting a successful introgression of alleles associated with ODAP content. A set of 21 promising CWRs-derived lines have been shared with the national partners in Bangladesh, India, and Nepal under the BOLD project to assess their performance and stability in the targeted environments during the current season. This will open opportunities to regain the grasspea area lost in the past as these prebred lines would be safe for human consumption.

79. BREEDING PROGRESS OF THE NEW RUBBER PRODUCING CROP RUSSIAN DANDELION (*TARAXACUM KOKSAGHYZ*)

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In recent years, Russian dandelion (*Taraxacum koksaghyz*, Tks) has proven to be one of the most promising alternative resources for natural rubber for temperate climates, enhancing the independence from subtropical rubber tree (*Hevea brasiliensis*) plantations and adding to a sustainable production to meet future demands.

Starting from scratch with wild plant material, we

constantly worked hard on progressing Russian dandelion into a commercial viable crop together with our project partners along the value chain in the meanwhile fourth subsequent project (TAKOWIND IV), funded by the Federal Ministry of Food and Agriculture. As part of the JKI Institute for Breeding Research on Agricultural Crops, we focus on developing molecular markers and population genetic tools in order to support

and accelerate the breeding progress.

On that account, because Russian dandelion is an outcrossing diploid species, we first developed a segregating F1 population for the quantitative trait rubber content, which we used for creating high-resolution genetic maps with markers from genotyping-by-sequencing and performed the first QTL-analysis based on obtained phenotypic data from extensive field trials. In the meantime, we were able to develop a more sophisticated F2 mapping population based on higher differentiating parents concerning the rubber content and overcoming the self-incompatibility of Russian dandelion by applying the so-called mentor pollen effect. With the advent of more and more genomic resources like the reference genome of Russian dandelion on a pseudo chromosome level (Lin et al., 2022) we were now able to accurately map QTL regions for rubber content and identified several QTL in close distance to genes related with rubber biosynthesis. In combination with markers obtained from differential

expression analysis we are currently developing a set of markers which are applicable in breeding programs and examine possibilities to apply genomic prediction models in the future.

Additionally, we provide genetic background information on several accessions of Russian dandelion and other *Taraxacum* species, especially *Taraxacum officinale* based on sequencing data. Recent results have shown, that the genetic diversity of Russian dandelion might be limited because of its relatively small region of origin. Although it was possible to drastically increase the rubber content through breeding efforts, the plants still show weak growth and low competitiveness in the field. Thus, especially for agronomic reasons, we plan to develop interspecific hybrids and combine high rubber producing qualities with increased biomass from related *Taraxacum* species. The first interspecific hybrids could successfully be developed but many challenges remain, which we try to overcome by a systematic approach and marker-assisted breeding.

80. PARTICIPATORY APPROACH FOR DEVELOPING IMPROVED RICE VARIETIES UNDER THE BOLD-RICE PROJECT IN VIETNAM

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Rice production plays a vital role in Vietnam's agricultural landscape, providing food and income to a significant portion of the population. However, the sector grapples with escalating challenges from climate change-threatening crop yields. Under the BOLD-Rice project, a participatory evaluation approach is being followed to assess the agronomic performance of rice pre-breeding lines derived from the Crop Wild Relatives (CWRs) across diverse agroecological zones for potential release as variety(ies) for large-scale cultivation at farmers' fields in Vietnam. Under the CWR Initiative, preliminary evaluation of a set of 110 CWR-derived pre-breeding lines at Mekong Delta led to the identification of 10 promising high-yielding lines tailored to specific farmer-identified needs by scientists. Within the collaborative framework of the BOLD-Rice project, involving farmers, researchers, and extension workers, the study employs a participatory methodology for the extensive

evaluation of the promising pre-breeding lines in the North, South, Center, and Central highlands of Vietnam. Ten seed clubs, strategically distributed across Vietnam—three in the North, two in the central region, and five in the Mekong Delta, actively participate in the evaluation process, offering valuable insights derived from practical experiences and local knowledge. These seed clubs closely collaborate with local extension centers and seed centers to identify climate-resilient rice varieties. This collaboration empowers farmers in communities to make informed decisions about crop selection tailored to their unique environmental contexts, facilitated through a meeting called the farmer field day, where feedback is gathered and the lines are ranked by local farmers based on performance at specific locations. Efforts are also in progress to characterize the farmers preferred landraces and the germplasm from national genebanks to important biotic

(blast, brown plant hopper, bacterial blight) and abiotic (drought, salinity) stresses as well as nutrition-related traits. The well-characterized germplasm will be used as donors in breeding programs for developing new high-yielding, nutrient-rich rice varieties with improved tolerance or resistance to important abiotic and biotic stresses following a participatory evaluation approach. The participatory evaluation approach significantly contributes to the development of context-specific recommendations for sustainable rice farming practices in Vietnam. By fostering collaboration among farmers,

researchers, and stakeholders, the study advocates for a holistic and adaptive strategy to address challenges arising from climate change and other stressors in rice production. This participatory framework not only enhances the evaluation's reliability but also facilitates knowledge exchange, empowering local communities to adapt to changing environmental conditions. Ultimately, the research presents a model for inclusive and community-driven agricultural research, demonstrating its applicability in regions confronting similar challenges.

81. POTATO CROP WILD RELATIVES NEW SOURCES OF RESISTANCE TO LATE BLIGHT (LB) AND PURPLE TOP DISEASE (PPT) IN ECUADOR

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In Ecuador, LB (*Phytophthora infestans*) and PPT (*Phytoplasmas* and *Candidatus liberibater solanacearum*) transmitted by *Bactericera cockerelli* (Bc), are the main constraints. The method of control is based on weekly applications of pesticides. However, it is not a sustainable solution. Genetic resistance is the best option. For this reason, Crop Wild Relatives (CWR) of potato could be an important alternative. With the support of CIP, INIAP develops activities to find new sources of resistance: i) Select CWR progenies with LB resistance developed by CIP and ii) Morphological and molecular characterization of Ecuadorian potato WR. LB resistant CWR progenies (29 families) from CIP were evaluated under field conditions. The area under the disease progress curve (AUDPC) was calculated. Yield and number of tubers were evaluated. Tubers were characterized. Evaluation of the antibiosis against Bc was performed in 8 selected progenies. For activity (ii), 91 accessions were selected: *S. acaule* (1), *S. albicans* (4), *S. albornozii* (13), *S. andeanum* (24), *S. chilliasense* (4), *S. chomatophilum* (?), *S. colombianum* (24) and *S. minutifolium* (14). Two molecular markers (mm) for LB were selected, 76-2SF2/76-2SR and Prp1. Ploidy was determined using Cyflow Space. For the morphological

characterization 39 descriptors were used.

Large variation for AUDPC among and within families were observed. More than 88% of progenies had LB resistance. The yield had a variation from 0 to 2.5 kg/plant. Over 25% of progenies had yield > 0.94 kg/plant. For LB resistance, agronomic and tuber quality traits 129 progenies were selected. All the progenies showed characteristics of antibiosis against Bc. Using mm for LB, amplification of the 76-2S was obtained in 46% of the accessions, and for the Prp1 in 31%. There were 21% that had both genes, and 44% that did not have any gen. Ploidy level established that 81% of *S. andeanum* accessions 100% of *S. chilliasense*, 90% of *S. minutifolium*, 78%, *S. albornozii*, 50% of *S. chomatophilum*, were diploid and 50% triploid, *S. albicans* 50% was hexaploid, while the *S. acaule* was tetraploid. Morphological and molecular characterization are in the process of analysis.

Large variation for LB resistance, yield, number of tubers and quality traits was observed in the CWR progenies, most of them had LB resistance. Tuber quality traits suit the Ecuadorian consumer preferences in the selected CWR progenies. Progenies showed characteristics of resistance against Bc.

82. BREEDING CLIMATE RESILIENT WHEAT FOR THE HEAT AND DROUGHT PRONE ENVIRONMENTS OF UGANDA

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Wheat production in Uganda is currently limited to the highland environments above 1600 masl. The low domestic wheat production coupled with turbulent global wheat grain supply and prices, demands that wheat production in Uganda be expanded to non-traditional areas to reduce on imports. However, the mid and low altitude environments with large chunks of land are characterized by frequent droughts and high night temperatures that cause crop failure. This study was conducted to develop high yielding bread wheat varieties adapted to the heat and drought prone mid-altitude (1400masl) and lowland (1000masl) areas of Uganda. Bread wheat germplasm with tolerance to abiotic stresses mainly drought and heat (50 entries from 18th Dryland Spring Bread Wheat Yield Trial and 50 from 18th Elite Spring Bread Wheat Yield Trial were introduced from ICARDA and evaluated through standard breeding procedures. The initial screening

conducted in two sites; Bulegeni (1400 masl) and Namulonge (1000 masl) under rainfed conditions with two replications arranged in 5 by 5 blocks in alpha lattice design resulted in selection of 19 promising entries in terms of yield and rust resistance. The selections were evaluated in multiple locations; Ngenge & Ikulwe – lowland (1000 masl), Bulegeni & Rwebitaba – mid altitude (1400 – 1500 masl), Kalengyere – highland (2400 masl) in RCBD for three seasons. Four adapted candidate wheat lines (VAR-29156, VAR-27521, VAR-29229 and VAR-29141) with adequate rust resistance and grain yields above 2.5 t/ha have been identified and selected for cultivation in the mid and low altitude agro ecologies so as to increase domestic wheat production in the country. A considerable quantity of seed of these varieties is being multiplied for quick promotion and dissemination.

83. SYNERGISM BETWEEN GENETIC AND AGRONOMIC BIOFORTIFICATION TO INCREASE ZN/FE CONCENTRATION IN WHEAT

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Biofortification of cereal crops like wheat is considered as a reasonable solution to prevalent Zn deficiency problem in the human population of developing world. As an International group, HarvestPlus breeding program has developed and released several high Zn wheat genotypes for the South Asian region including north India and Pakistan. However, due to adverse soil and climatic conditions of the target areas these genotypes may not be able to perform according to the genetic potential without application of Zn fertilizers. Zn applications also decrease Cd uptake and accumulation in plants consequently reducing the Cd concentration in grain.

Current research aimed to study the synergistic effect of genetic and agronomic biofortification by evaluating the performance of the high Zn biofortified genotypes with several soil and foliar Zn fertilizer application. Ten HP-biofortified genotypes and two conventional varieties (as check) were tested in greenhouse conditions under four fertilizer treatments i) deficient soil Zn ii) foliar Zn application iii) adequate soil Zn application iv) both adequate soil and foliar Zn. The results indicate that biofortified lines have higher capacity to absorb and accumulate Zn in grain from soil and foliar Zn fertilizer as compared to check cultivars. No negative correlation was observed in grain yield and grain Zn concentration

of biofortified lines. As an average of all genotypes, 21% increase in yield and 3.5 folds increase in grain Zn concentration were recorded with the application of both soil and foliar fertilizers. Application of soil and foliar Zn also significantly increased the Fe concentration more than 28% and reduced the Cd concentration in grains up to 61.8%. Highest grain yield was achieved by a biofortified Pakistani genotype (NR-488), and highest grain Zn and Fe concentration with lowest grain Cd was observed in an Indian biofortified genotype (HPBW-01)

with both soil and foliar Zn application.

The results conclude that genetic and agronomic biofortification strategies are not separate but synergistic and complementary to each other. In Zn-deficient calcareous soils of south Asian countries like India and Pakistan, integrated strategy of growing genetically biofortified wheat cultivars with an added application of Zn in soil and foliar form is the best approach to improve yield and grain Zn/Fe accumulation, and hence to overcome the malnutrition problem

84. INCREASING THE PROTEIN USE EFFICIENCY OF THE MAGIC-WHEAT-POPULATION WM-800

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Background: Winter wheat holds a crucial position in German agriculture, constituting the primary cereal both in terms of cultivation area (long-term average: 3.0 million hectares) and harvest quantity (long-term average: 23.1 million tons). Approximately one-third of the annual harvest is allocated to human consumption, particularly in bread and bakery products. However, the attainment of high quality standards demanded by the industry involves significant nitrogen (N) fertilizer inputs, leading to environmental challenges.

Objective: This study aims to explore the genetic regulation of winter wheat for enhanced baking quality and protein use efficiency (ProtUE = loaf volume divided by the amount of grain protein content).

Methods: The investigation leverages the winter Wheat MAGIC-Population WM-800, characterized by

an eight way cross of eight German elite varieties. The resulting 800 RILs allow precise QTL mapping with reduced linkage disequilibrium. Previously identified candidate genes are now being validated by creating Heterogeneous Inbred Families (HIFs). Furthermore, a subset of the WM-800 with diverging baking quality parameters will be tested in multiple field studies under reduced N fertilization.

Project goals: The study aims to identify potential genotypes with improved baking quality and ProtUE under reduced N fertilization to mitigate the crop's carbon footprint. Proteomic and metabolomic analyses will provide insights into the genetic regulation of baking quality, ProtUE, and metabolite profiles influenced by N fertilization.

POSTERS – CANDIDATE GENES

85. LANDING CWR NEW GENES FOR LATE BLIGHT RESISTANCE ON POTATO FARMER FIELDS

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Participatory selection is part of the breeding process at CIP with the understanding that it must begin and end with the farmer. In the Central Highlands of Peru, farmers from Andean communities' demand for high yielding potato varieties with late blight resistance. To address this demand, a comprehensive breeding strategy, using late blight resistant genes from s. cajamarquense through embryo rescue followed polyploidization, and through a meticulous selection process allowed to deliver a set of 16 4x hybrids for Participatory Variety Selection (PVS). Our objective was to select genotypes with better performance for further utilization in breeding, or even releasing as variety with support of farmers and under their management practices. We performed two seasons of PVS trials in five localities, considering sex-disaggregated preferences. Evaluations were performed at flowering, harvest, and post-harvest stages. We observed that trait criteria and degree of importance varied more across localities than between gender groups within localities. Gender differences were observed generally in the order of trait importance. For instance, women preferred traits such as broad leaves, tuber shape, large number of colored tuber eyes, LB resistance, and frost tolerance. Men want thick stems, poor or profuse flowering, large tuber size and uniformity, and tolerance to frost and weevils.

There were only two traits (i.e., large number of eyes and tolerance to hailstorm) selected by women that were not considered important by men although both traits were of secondary importance at the time of scoring them by women. Although farmers demand a set of traits, i.e., up to 23 traits, their selection requirements could fall into four main characteristics: vigorous plants, attractive tubers of high marketable yield, organoleptic attributes, and suitable storage capacity. In general terms they preferred a yellow-fleshed and floury texture, present in local native varieties, and shallow-eyed-large tuber uniformity of improved ones. The success of pre-breeding lies on defining a target environment and address farmers' traits for adaptation and market demands that will facilitate farmers to adopt a variety. Two new hybrids CIP512010.20 and CIP512010.1, were selected as promising by farmers. The clone CIP512010.20 was released in 2023 named CIP-Matilde. They showed good storage capacity and high marketable yield and stability, only the former showed organoleptic traits as good as those of their native local varieties. Landing of variability for late blight resistance and genetic diversity on farmers' field entailed selection of organized communities of disadvantaged smallholder farmers that seek to expand market options to improve their incomes.

86. VALIDATION OF NITRATE TRANSCRYPTOR NPF2.12 TO IMPROVE NITROGEN USE EFFICIENCY IN WHEAT

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Nitrogen is an essential nutrient and often limits crop growth, but excessive fertilization is harmful to the environment. Therefore, it is imperative to develop cultivars with increased Nitrogen Use Efficiency (NUE) under normal and water scarcity conditions.

A preliminary GWAS study using 221 winter wheat cultivars identified the NPF2.12 gene, encoding a nitrate transceptor homolog, to regulate NUE at different levels of nitrogen supply. Allelic variants in the NPF2.12 promoter region were found to control root growth as well as nitrate uptake and translocation. Two distinct haplotypes (Hap1 and Hap2) were identified in winter wheat. Notably, Hap2 exhibited superior root development and higher nitrogen accumulation in the plant leaves under low nitrogen conditions.

In our current study, we will characterize the root and yield traits of a set of selected genotypes showing extreme phenotypes. The root morphological and anatomical traits will be collected and the NUE will be evaluated. The segregation of the Hap1 and Hap2 of the NPF2.12 gene will be determined to validate previously

reported association to root development and NUE.

For a better mechanistic understanding, tissue specific NPF2.12 expression will be analyzed. By increasing the variability via genome-editing approaches, we intend to develop various alleles that will permit analysis of the regulatory mechanisms and selection of more efficient allelic variants.

Further, we are interested to estimate the dependency of NPF2.12 dependent NUE upon water availability. For that, the extreme genotypes will be grown under different nitrogen levels both under drought and control conditions.

The gained knowledge aims to support the development of winter wheat cultivars with improved nitrogen use efficiency, particularly under low N and limited water availability.

Keywords: Nitrogen use efficiency, winter wheat, root traits, NPF2.12 gene, nitrate transceptor, allelic variation, expression patterns, transport activity

87. DISSECTING CHLOROPLAST DEVELOPMENT IN BARLEY VIA FUNCTIONAL CHARACTERIZATION OF HVLST AND HVCMF GENES

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Although genes encoded in the plastome are responsible for plastid gene transcription, translation, and photosynthesis, chloroplast biogenesis is mainly governed by genes encoded in the nucleus through the interaction of nuclear and chloroplast genomes. Loss of function in the underlying genes can compromise normal chloroplast development, resulting in reduced photosynthetic efficiency, albino seedlings, plants with variegated leaves, or even lethal

effects. Previously, mutant collections were screened using low resolution genetic mapping, whole-genome re-sequencing and comparative functional analyses to identify candidate genes controlling chloroplast development and thylakoid structure in barley. Consequently, the CCT Motif Family genes HvCMF3 and HvCMF7 were identified and functionally characterised via random mutagenesis (EMS TILLING) and CRISPR-Cas9 mediated precise genome editing. Using a similar

approach, the ATP-Dependent Clp Protease Subunit C1, HvClpC1 was subsequently proposed as a candidate for the variegation mutant termed luteostrians (LST). In this project we aim to further elucidate chloroplast development in barley by inducing CRISPR-Cas9

mediated loss-of-function mutations in three and ten homologs of the HvLST and HvCMF gene families, respectively. Induced functional mutations within the targeted genes will shed light on their possible dosage-dependent role in this context.

88. NOVEL PHOTOPERIOD-1 GENE VARIANTS ASSOCIATE WITH YIELD-RELATED AND ROOT-ANGLE TRAITS IN EUROPEAN BREAD WHEAT

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The sequence diversity of three homeologous copies of the PHOTOPERIOD-1 gene in European winter wheat was analyzed by Oxford Nanopore amplicon-based multiplex sequencing and molecular markers in a panel of 194 cultivars representing breeding progress over the past five decades. A strong, consistent association with an 8% increase in grain yield was observed for the PpdA1-Hap1 haplotype across multiple environments. This haplotype was found to be linked in 51% of cultivars to the 2NS/2AS translocation, originally introduced from *Aegilops ventricosa*, which leads to an overestimation of its effect. However, even in cultivars without the 2NS/2AS translocation, PpdA1-Hap1 was significantly associated with increased grain yield, kernel per spike,

kernel per m² and harvest index under optimal growth conditions, conferring a 4% yield advantage compared to haplotype PpdA1-Hap4. In contrast to Ppd-B1 and Ppd-D1, the Ppd-A1 gene exhibits novel structural variations and a high number of SNPs, highlighting the evolutionary changes that have occurred in this region over the course of wheat breeding history. Additionally, cultivars carrying the photoperiod-insensitive Ppd-D1a allele not only exhibit earlier heading, but also deeper roots compared to those with photoperiod-sensitive alleles under German conditions. PCR and KASP assays have been developed that can be effectively employed in marker-assisted breeding programs to introduce these favorable haplotypes

89. EFFECT OF A QTL ON WHEAT CHROMOSOME 5B ASSOCIATED TO WITH ENHANCED ROOT DRY MASS ON TRANSPIRATION AND NITROGEN UPTAKE UNDER CONTRASTING DROUGHT SCENARIOS IN WHEAT

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A sufficient nitrogen supply is crucial for high-quality wheat yields. However, the utilization of nitrogen fertilization can adversely affect ecosystems through leaching or volatile atmospheric emissions. Drought events, increasingly prevalent in numerous crop production areas, have a significant impact on nitrogen uptake. Breeding more efficient wheat varieties is imperative to attain acceptable yields with limited nitrogen and water. Crop root systems play a pivotal role as the primary organ for absorbing water and nutrients. To investigate the impact of an enhanced root system on nitrogen and water use efficiency in wheat under various irrigation conditions, this study conducted two experiments using precision phenotyping platforms for controlled drought stress treatment. Experiment 1 involved four contrasting winter wheat genotypes, including the Chinese variety Ning0604, harbouring a quantitative trait locus (QTL) on chromosome 5B associated with higher root dry biomass, and three elite German varieties, Elixer, Genius, and Leandrus. Experiment 2 compared near-isogenic lines (NIL) of the three elite varieties, each containing introgressions of

the QTL on chromosome 5B linked to root dry mass. In both experiments, nitrogen partitioning was tracked via isotope discrimination after fertilization with 5 Atom % ¹⁵N-labeled KN03-. In Experiment 1, quantification by ¹⁵N isotope discrimination revealed significantly ($p < 0.05$) higher nitrogen derived from fertilizer in the root organ for Ning0604 compared to those of the three German varieties. In Experiment 2, two out of three NILs showed a significantly ($p < 0.05$) higher uptake of N derived from fertilizer than their respective recipient line under well-watered conditions. Additionally, significantly lower transpiration rates ($p < 0.1$) were observed in one NIL compared to its respective recipient. The combination of the DroughtSpotter facility with ¹⁵N tracer-based tracking of N uptake and remobilization provides further insights into the impact of genetically altered root biomass on wheat NUE and WUE under different water availability scenarios. The study demonstrates the potential for how a modified genetic constitution of the locus on wheat chromosome 5B can reduce transpiration and enhance N uptake.

90. VC2 IS A SECOND VICINE LOCUS RESPONSIBLE FOR BASELINE CONTENT IN LOW VICINE FABA BEAN

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Faba bean is a valuable legume crop desired globally for its high nutritional composition, offering a significant source of both food and feed. Nonetheless, the presence of vicine-convicine in the seeds reduces the nutritional quality of faba bean protein and poses health risks for humans and animals. Eliminating these compounds is essential for enhancing its suitability in food and feed. Recent findings revealed that the VC1 gene encodes a bi-functional riboflavin protein, RIBA1, responsible for initiating the vicine-convicine biosynthetic pathway. In low vicine-convicine cultivars, a 2 bp inactivating insertion in this gene results in loss of its function. However, as this mutation does not completely eliminate vicine-convicine biosynthesis, the involvement of other genes or gene copies remains unclear. In this study, our objective was to identify active RIBA1 genes and functional polymorphisms underlying vicine-convicine biosynthesis. Here, we show that VC2 is the second RIBA1 gene in faba bean. VC1 and VC2

share highly identical RibA domains, which encodes GTP cyclohydrolase II directly involved in vicine-convicine biosynthesis. Gene expression analysis revealed a genotype-specific differential expression of VC1 while VC2 exhibited uniform expression pattern across genotypes. However, VC1 showed significantly higher expression than VC2, indicating a major effect of VC1. VC2 constitutes approximately 5-10% of total RIBA1 transcripts and correlates with observed differences in vicine-convicine between low and high vicine-convicine genotypes. Furthermore, cDNA analysis revealed that VC2 does not carry an inactivating mutation and appears to be the functional RIBA1 gene responsible for the baseline contents in low vicine-convicine cultivars. Finally, we demonstrated that VC1 has multiple copies, and this poses a significant challenge when employing marker-assisted selection in faba bean. We recommend VC2-based SNPs which can accurately predict vicine-convicine contents.

91. IDENTIFICATION AND DISSECTION OF A GENOMIC REGION AFFECTING EARLY DEVELOPMENT AND MAXIMUM QUANTUM YIELD OF PHOTOSYSTEM II (FV/FM) IN MAIZE GENETIC RESOURCES

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In maize (*Zea mays* L.), landraces harbor genetic diversity that is barely captured in today's elite germplasm. In a genome-wide association study we identified two QTL in close proximity controlling the traits early plant height (QTL 1) and maximum quantum yield of photosystem II (Fv/Fm) (QTL 2) in a library of doubled-haploid (DH) lines derived from the Austrian landrace 'Kemater Landmais Gelb' (KE). We developed a bi-parental mapping population from a cross of two DH lines with contrasting alleles for both QTL. Based on

data from multi-environment field experiments we fine-mapped QTL1 to 1.4 Mb containing 51 gene models and validated it in a second mapping population derived from a different cross. QTL 2 was fine-mapped to a 1.7 Mb genomic segment containing 101 gene models. Based on functional annotation and differential protein expression revealed by leaf proteome analyses, light harvesting chlorophyll a/b binding protein6 (Lhcb6) was identified as candidate gene for QTL 2. Lhcb6 is part of the C2S2M2-type LHCII supercomplex, which is associated with photosystem II and involved in light

harvesting and non-photochemical quenching (NPQ). Whole genome sequencing data using PACBio Hifi long reads were generated for both parental DH lines revealing structural variation in the promoter region of the candidate gene, likely causing the differences

in protein expression and eventually Fv/Fm due to impaired LHCII supercomplex formation. Our work is an example of successfully identifying genes controlling quantitative traits of interest for breeding in European maize landraces.

92. GENETIC MAPPING OF A CHEMICALLY INDUCED PENDANT AWN MUTANT IN BARLEY (*HORDEUM VULGARE*)

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Awns are widespread across cultivated cereal crops and their wild relatives. While their significance is a subject of debate, they play crucial roles in photosynthesis and transpiration, particularly in challenging environments. Their development and morphology are influenced by multiple genes and their interactions. Despite extensive genetic characterization in rice, similar insights are often lacking in other cereal crops, such as barley. This study focuses on genetically mapping a unique pendant awn trait identified in an ethyl methanesulfonate (EMS)-mutagenized barley population of the cultivar Igri. The trait is characterized by shorter, thinner, brittle awns that do not uniformly point upwards, giving them a pendant appearance and are apparently associated with fewer, longer, and thinner seeds. The first stage of this study involved a comprehensive visual characterization of the mutant, using microscopy to examine the characteristics of both the awns and mature seeds of the mutant and wild type. Afterwards, using a segregating biparental population (F2) with 147 individuals derived from the EMS mutant and the cultivar Alraune, a 1:3 inheritance pattern was observed, consistent with monogenic

inheritance. Using genotyping-by-sequencing data from the F2 population, the trait was mapped to a 441 Mbp region on chromosome 3H containing 3296 genes. Following this, whole genome sequencing data of the mutant and Alraune were generated. Currently, a KASP assay in the F2 population is applied using custom-designed primers representing markers that are polymorphic in the EMS mutant and the wild-type cross parents within the region previously identified as containing the polymorphism. This approach aims to fine-map the specific genomic region that harbours the gene responsible for the pendant awn trait. Additionally, based on the identified region and the whole genome sequencing data, the genes located in the region are screened for their potential as candidate genes. In-silico analyses have revealed one gene with missense mutations, as well as SNPs up- and downstream of genes influencing the floral development in the region on chromosome 3H. This holistic approach enhances the understanding of awn development and morphology in barley and will benefit breeding, by offering valuable insights for understanding crop performance, especially in challenging environments

93. CANDIDATE GENES FOR STEM RUST RESISTANCE IN ITALIAN RYEGRASS REVEALED BY NESTED ASSOCIATION MAPPING

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Italian ryegrass (*Lolium multiflorum* Lam.), an obligate outcrossing species, is widely cultivated due to its high biomass yield and good forage quality. Although Italian ryegrass is subject to intense selection activities within different breeding programs, stem rust caused by *Puccinia graminis* ssp. *graminicola* is still a major issue, especially during seed production. Stem rust infects leaf sheaths and inflorescences at the time of seed formation and consequently reduces seed yield. The increasing daily average temperatures due to climate change will further increase stem rust disease pressure. Until now, the knowledge on the genetic control of stem rust resistance in Italian ryegrass was limited. The aim of this study was to identify stem rust resistance genes within breeding material for efficient resistance breeding. We used a nested association mapping (NAM) population consisting of 708 F2 individuals, derived from crossing 23 diverse founders with one common founder, followed by an open pollination among F1 plants. Multisite field phenotyping as well as

in vitro inoculation of leaf segments were conducted and revealed a high phenotypic variation for stem rust resistance. For genotyping, restriction site associated DNA sequencing resulted in 4,762,767 single nucleotide polymorphism (SNP) markers at affordable costs. Using all field phenotyping data combined with the genotypic data revealed three quantitative trait loci on chromosomes 6 and 7. On chromosome 7, SNPs significantly associated with resistance caused missense mutations within two receptor-like serine/threonine protein kinase predicted genes next to each other. Receptor-like serine/threonine protein kinases are known to confer resistance to many pathotypes of stem rust in other species such as barley. This study shows that a NAM population is suitable to find new resistance sources for stem rust in outcrossing species such as Italian ryegrass. Our findings can be either directly implemented by marker-assisted selection in breeding programs or used for functional validation of the candidate genes identified.

POSTERS – OTHERS

94. EFFORTS TO DEVELOP MOLECULAR MARKERS FOR SHARKA RESISTANCE IN EUROPEAN PLUM (*PRUNUS DOMESTICA* L.)

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Despite increasing demand, production of the European plum (*Prunus domestica* L.) is still limited in Europe. The reasons for this are certainly manifold. However, one of the main reasons is the increasing threat to German plum production from Sharka disease that is caused by the Plum pox virus (Ppv). This disease was first described in Eastern Europe in 1917, has since spread, and can now be observed throughout Europe as well as on other continents like Northern and Southern America, Asia and Africa. The Ppv is infectious to European and Japanese plum as well as to apricot and peach. Infected plants show yellow ring spots and distortions on leaves and fruits. Fruits show pockmarked indentations, and strong premature drop of fruit occurs frequently. Since there are only preventive measures available to control Sharka infestations, breeding Sharka-resistant varieties that either show no symptoms, or show a strong hypersensitive response against the pathogen, is a very important goal. The challenges of such a breeding program lie in the fact that only few resistances are

known so far, as well as in the polyploidy nature of the European plum's genome.

In order to increase effective selection in breeding populations, we aim to identify genomic regions that can be associated with Sharka resistance. Therefore, a segregating F1 population as well as a diverse set of lines that are potential breeding parents in existing breeding programs were investigated in this project. Both sets of lines were genotyped by genotyping-by-sequencing (GBS). In parallel, the population was phenotyped for Sharka resistance in greenhouse experiments with a method that includes a virus-infected intermediate grafting step. The genotypic and phenotypic data will be used to identify genomic regions that are associated with hypersensitivity against the Sharka disease. With the results of this study we aim to be able to provide molecular markers, which will facilitate breeding European plum cultivars that are less susceptible to Sharka disease.

95. THE USEFULNESS OF DEFEATED RESISTANCE LOCI TO PLASMOPARA VITICOLA (RPV) IN DOWNY MILDEW-RESISTANT GRAPE VARIETIES (*VITIS* SPP.)

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Grape downy mildew, caused by *Plasmopara viticola*, is one of the main diseases affecting viticulture worldwide and its control usually relies on frequent sprays with agrochemicals. New grapevine varieties resistant to *P. viticola* represent an effective solution to control epidemics and reduce the environmental impact of viticulture. Loci of resistance to *P. viticola* (Rpv) have been introgressed from wild *Vitis* species and some of them, like Rpv1, Rpv3.1 and Rpv10, currently represent the most utilized genetic resources for resistance breeding. However, in the last years, *P. viticola* strains able to overcome Rpv-mediated resistances have been isolated, making the corresponding resistant varieties susceptible. One strategy to increase the durability of resistance is to pyramidize several resistance loci in

new varieties. However, the breakdown of a number of Rpv genes raises the question as to whether defeated Rpvs may still be of interest in pyramiding strategies. In our study, we generated a segregating population for three Rpvs (Rpv1, Rpv3.1 and Rpv10) and performed phenotyping of offspring resistance in laboratory conditions with two *P. viticola* strains: an avirulent strain and a Rpv10-virulent strain. By phenotyping all Rpv combinations with the two *P. viticola* strains, we discovered that a defeated Rpv can significantly contribute to control the relative virulent *P. viticola* strain when the locus is used in specific pyramiding combinations. This discovery provides useful knowledges and perspectives for breeding grapevine varieties resistant to *P. viticola*.

96. FINE-TUNING TISSUE CULTURE AND GENETIC TRANSFORMATION PROTOCOL FOR FABA BEAN (*VICIA FABEA* L.)

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Faba bean (*Vicia faba* L.) is an economically significant and nutritionally valuable leguminous crop that contributes significantly to global food security. Nevertheless, its productivity is impeded by various obstacles, such as vulnerability to diseases, adverse environmental conditions, slow growth, and restricted genetic variability. The presence of self-incompatibility, which further complicates breeding, is an additional obstacle. In order to fully harness the capabilities of faba beans, it is imperative to refine the processes of tissue culture and genetic transformation. Our research was centered on the enhancement of protocols for genetic transformation and tissue culture of faba beans. Embryos were used as explants in the tissue culture of 37 different cultivars of faba beans. Furthermore, we designed the genetic transformation protocols for the Tiffany and Hedin/2 cultivars by inserting a GFP construct into their embryos via particle bombardment.

In tissue culture, we determined that the regeneration efficiency of faba bean cultivars was nearly 95%, while the transformation efficiencies of Tiffany and Hedin/2 were, respectively, 75.5 and 66.66%. The present study investigated the impact of various parameters on the efficiency of regeneration and transformation. Our objective was to enhance the overall success rates through the improvement of tissue culture and genetic transformation methodologies applicable to a diverse range of cultivars, such as Tiffany and Hedin/2. The purpose of this project was to provide plant breeders and researchers with standardized techniques that would aid future efforts in the development of faba beans. This research highlights the criticality of employing resilient tissue culture and genetic transformation methodologies in order to fully harness the sustainable food production capabilities of faba beans.

97. INTEGRATIVE MULTI-OMICS ANALYSIS REVEALS MOLECULAR NETWORKS UNDERLYING POWDERY MILDEW RESISTANCE IN THE BARLEY HEB-25 POPULATION

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Exploring the relationship between genetic variants and traits, as well as unraveling the molecular mechanisms behind the emergence of these traits, is key for precision breeding and trait engineering. Recently, the successful application of multi-omics approaches in plant genomic studies has been effective in characterizing such mechanisms. In this study, we investigated the molecular mechanisms behind genotype-phenotype associations through the intermediate molecular traits, namely the metabolome, of the Barley Nested Association Mapping population. We employed a nonlinear predictive method, XGBoost [“eXtreme Gradient Boosting”], an implementation of gradient-boosted decision trees designed for

efficient selection of predictive features in multi-omic data. XGBoost models of depth 2 or higher efficiently captured interactions between input features and provided high prediction accuracy. The analysis was complemented with the SHAP algorithm to rank feature importance and identify optimal feature sets. Furthermore, we constructed a three-way network for 14 barley quality traits, linking key phenotypes, such as pathogen resistance, with their genetic and metabolic determinants. The presented multi-omics implementation of XGBoost has not only enabled the effective identification of key genetic traits in Barley but also offered insights into the intricate relationships between these traits and various molecular features.

98. BIOCHEMICAL AND MOLECULAR PROFILING OF INDUCED HIGH YIELDING M3 MUTANT LINES OF TWO *TRIGONELLA* SPECIES: INSIGHTS INTO IMPROVED YIELD POTENTIAL

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Trigonella, commonly known as Fenugreek, is among the most promising medicinal herbs consumed worldwide due its protein rich dietary contributions. In this study, induced mutagenesis was conducted on two *Trigonella* species using caffeine and sodium azide as mutagens, leading to the isolation of nine high-yielding mutant lines in the M3 generation. To investigate the genetic divergence among the control and mutant lines, molecular characterization was carried out using SCoT markers, revealing a high polymorphism percentage of 28.3% and 46.7% in PEB and Pusa kasuri, respectively. Similarity correlation indicated that the highest similarity was between mutant A and mutant C (0.97); between mutant J and mutant O (0.88). Conversely, the lowest similarity was between mutant B and mutant F (0.74); between control and mutant L (0.58). There observed a wide range of variability in the quantitative parameters, chlorophyll, carotenoid, proline, protein, and mineral contents in the mutant lines comparative to their respective controls. Assessment of stomatal

and seed characteristics using scanning electron microscopy may lead to improved physiological processes and distinction at the interspecific level, respectively. Methanolic extracts of the control and the mutant lines of both the species were subjected to gas chromatography-mass spectrometry (GC-MS) analysis, revealing 24 major phytochemicals known for their pharmacological activities (antioxidant, antimicrobial, anti-inflammatory, anticancer, etc.). Statistical methods such as pearson correlation heatmap and pairwise scatter plot matrix provided insights into the correlations and linear associations among the parameters of both PEB and Pusa kasuri. The strong correlation between iron content and seeds per pod in the mutant lines suggests a promising avenue for further research studies. Continued research and breeding efforts using these mutants can lead to significant advancements in agriculture and medicine, benefiting farmers, consumers, and industries alike.

99. GENOTYPE-SPECIFIC RESPONSES TO PHOSPHORUS DEFICIENCY IN *B. RAPA*, *B. OLERACEA* AND THEIR SYNTHETIC RAPESEED HYBRIDS

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Synthetic rapeseed, an allotetraploid resulting from the cross of *B. rapa* (AA) and *B. oleracea* (CC), offers a source for introducing novel traits into existing cultivars to enhance performance and resilience, particularly in response to environmental stresses like nutritional deficiencies. Phosphorus (P) is an essential macronutrient and constituent of plant structural components such as membrane lipids, nucleic acids, enzymes, and ATP. While P deposits are globally limited, threatening agricultural productivity in the near future, P is also considered an important pollutant of open water bodies. Therefore, on demand P-fertilization and high P-use efficiency are critical for more sustainable agriculture. As phosphorus is essential for DNA synthesis, polyploid organisms, which have more DNA per cell, might be expected to exhibit increased P requirement and hence show increased sensitivity to its limitation. However, this hypothesis has rarely been tested.

This study investigates the phenotypic and physiological responses to phosphorus deficiency in nine synthetic rapeseed genotypes and their diploid parents. A glasshouse pot-based experiment was conducted with soil of 165 g/100mg phosphorus used

for the control group and no phosphorus application used as treatment group. Garzweiler loess (the loess comes from a C horizon at a depth of 5 meters) which contains 0.0013g P per 100mg was used as the substrate.

The morphological traits of plant height, biomass, leaf area, and root surface area significantly decreased under P-deficient conditions relative to control conditions, while root network length increased. Remarkably, Synthetic lines showed little effect of phosphorus deficiency relative to the control treatments. Notably, there were no significant differences in root morphological and anatomical traits between synthetic rapeseed lines and their respective parental lines in control and treatment.

As some synthetic lines also outperformed their parents for a number of morphological traits (Biomass, leaf area etc.) under control conditions, hybrid vigour may be responsible for the frequent observation of phosphorus-efficiency in the synthetics. These findings contribute valuable insights into the molecular mechanisms underlying phosphorus use efficiency and suggest novel strategies for improving phosphorus utilization efficiency in rapeseed.

100. DEEP-HPI-PRED: AN R-SHINY APPLLET FOR NETWORK-BASED CLASSIFICATION AND PREDICTION OF HOST-PATHOGEN PROTEIN-PROTEIN INTERACTIONS

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Host-pathogen interactions (HPIs) are vital in numerous biological activities and are intrinsically linked to the onset and progression of infectious diseases. HPIs are pivotal in the entire lifecycle of diseases: from the onset of pathogen introduction, navigating through the mechanisms that bypass host cellular defenses, to its subsequent proliferation inside the host. At the heart of these stages lies the synergy of proteins from both the host and the pathogen. By understanding these interlinking protein dynamics, we can gain crucial insights into how diseases progress and pave the way for stronger plant defenses and the swift formulation of countermeasures. In the framework of current study, we developed a web-based R/Shiny app, Deep-HPI-pred, that uses network-driven feature learning method to predict the yet unmapped interactions between pathogen and host proteins. Leveraging citrus and CLas bacteria training datasets as case study, we spotlight the effectiveness of Deep-HPI-pred in discerning Protein-protein interaction (PPIs) between them. Deep-HPI-pred use Multilayer Perceptron (MLP) models for HPI prediction, which is based on a comprehensive evaluation of topological features and neural network architectures. When subjected to independent validation datasets, the predicted models consistently surpassed a Matthews correlation coefficient (MCC) of

0.80 in host-pathogen interactions. Remarkably, the use of eigenvector centrality as the leading topological feature further enhanced this performance. Further, Deep-HPI-pred also offers relevant gene ontology (GO) term information for each pathogen and host protein within the system. This protein annotation data contributes an additional layer to our understanding of the intricate dynamics within host-pathogen interactions. In the additional benchmarking studies, the Deep-HPI-pred model has proven its robustness by consistently delivering reliable results across different host-pathogen systems, including plant-pathogens (accuracy of 98.4% and 97.9%), human-virus (accuracy of 94.3%), and animal-bacteria (accuracy of 96.6%) interactomes. These results not only demonstrate the model's versatility but also pave the way for gaining comprehensive insights into the molecular underpinnings of complex host-pathogen interactions. Taken together, the Deep-HPI-pred applet offers a unified web service for both identifying and illustrating interaction networks. Deep-HPI-pred applet is freely accessible at its homepage: <https://cbi.gxu.edu.cn/shiny-apps/Deep-HPI-pred/> and at github: <https://github.com/tahirulqamar/Deep-HPI-pred>.

101. MULTI-OMICS DATA INTEGRATION FOR MAPPING THE CIS-REGULATORY ARCHITECTURE OF *BRASSICA NAPUS*

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The highly dynamic genome of the allotetraploid rapeseed (*Brassica napus*, AACC, 2n = 38) is an ideal model to study the role of regulatory region activity in a complex genome. A key step towards this goal is a comprehensive identification and annotation of cis-regulatory elements (CREs; promoters, enhancers and silencers), including their roles in modulating gene expression in a tissue- or developmental stage- specific manner.

For this purpose, five different sample types of the German winter rapeseed accession 'Express 617' were selected: leaves, roots, seedlings, immature floral buds and immature siliques. Chromatin accessibility, closely correlated with active regulatory elements presence, was assessed with ATAC-seq. DNA methylation was detected by WGBS (Whole Genome Bisulfite Sequencing) and confirmed the low-to-no methylation status of a considerable portion of the identified open chromatin regions (OCRs). Finally, concomitant mRNA sequencing allowed for a direct validation of gene

expression modulation, supporting the predicted regulatory function of these sequences towards nearby genes. Functional annotation of OCRs confirmed an overlap with known cis-regulatory elements, while also identifying novel tissue- and stage-specific enhancers and silencers.

To date, several studies in both model and crop plants have confirmed that intra-species genetic variations in known CREs can result in relevant and subtle phenotypic effects, that are often tissue or environment specific. Integration of this newly generated *B. napus* CRE map with an eQTL analysis from 100 rapeseed genotypes has enabled for the identification of several regulatory variants affecting both physiological and metabolic traits.

Overall, these data have resulted in a comprehensive annotation of cis-regulatory elements and affected genes, furthering our understanding of their contribution to crop evolution and performance.

102. MEIOTIC STABILITY IN RESYNTHESIZED WINTER RAPESEED

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Allopolyploids need to stabilize meiosis by preventing non-homologous chromosome pairing associations between different subgenomes. However, little is known about control of meiotic chromosome pairing behavior in most allopolyploids. *Brassica napus*, commonly known as canola or rapeseed (AACC, 2n = 4x = 38) is an interesting model system to study meiotic stability in allopolyploids: although established rapeseed has relatively stable meiosis, synthetic rapeseed (produced by crossing between progenitor species *B. rapa* and *B. oleracea*) is usually unstable, with frequent non-homologous chromosome pairing. Recently, we identified putatively stable and unstable synthetic

lines (derived from homozygous spring-type parents *B. rapa* and *B. oleracea*) based on novel accumulation of copy number variants (CNVs). The present study aimed to cytologically characterize meiotic chromosome pairing behavior in these lines. We observed that putatively stable lines exhibited predominantly normal meiosis and regular bivalent formation (average 84%), as compared to putatively unstable lines, which had high frequencies of multivalent formation at diakinesis and fewer bivalents (61% on average). Surprisingly, univalent chromosomes were rare in Metaphase I, and chromosome laggards and chromosome bridges were also seldom observed in Anaphase I. These results

suggest that frequent multivalent formation is the primary cause of chromosome rearrangements (as detected by novel CNVs) in synthetic rapeseed. Future work will focus on investigation of allosyndetic (A-

C) chromosome pairing frequencies using molecular cytogenetics, and will dig deeper into the genetic factors affecting meiotic stability in synthetic rapeseed.

103. UNCOVER THE SECRETS OF CROP DIVERSITY WITH GENESYS TOOLS

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Genesys (www.genesys-pgr.org) is the global portal on plant genetic resources for food and agriculture in genebanks worldwide. It is a common platform through which genebanks make the data on their collections publicly available to external users, including breeders. As of December 2023, Genesys held passport information on over 4,300,000 active accessions in international, regional, and national genebanks.

For users of genebanks, and users of genebank data, this makes Genesys a powerful tool for finding the specific crop diversity they need for research or breeding. The data in Genesys includes, in addition to passport data, over 150,000 images, 400 characterization and evaluation datasets (C&E), and 250 core collections and other interesting subsets of plant genetic resources. Breeders and researchers can download the data to conduct their analyses for their specific purposes.

Once users have found the crop diversity they need, they can submit a request for the germplasm to most of the participating genebanks directly through Genesys or contact the genebank curators.

In 2023, Genesys launched two major tools that are particularly interesting for plant breeders: the Subsetting Tool and Searchable Trait Datasets.

The Subsetting Tool, allows Genesys users to use

combinations of abiotic factors to create subsets of accessions that can grow under specific environmental conditions.

The tool considers only accessions that include the coordinates of their collecting site in the passport data. 20 agroclimatic indicators related to the site of collecting can be used to do the subsetting, grouped into six categories: drought, flooding, heat, photoperiod, soil and (depending on the species) additional crop-specific indicators. The tool then groups the accessions according to their similar agroclimatic conditions. The breeder gets to specify which of the variables to consider in order to create a subset relevant to their needs, and also how many subsets the tool should create.

Characterization and evaluation (C&E) data stimulates the use of germplasm collections. Since 2018, Genesys has provided access to C&E datasets from various genebanks for download and analysis by users. But querying trait data directly in Genesys required some database magic. As of 2023, Genesys provides just that: it is now possible to search the C&E datasets for specific traits through the recently developed Searchable Trait Data functionality of Genesys.

104. PERFORMANCE OF LANDRACES, WILD RELATIVES, AND CULTIVATED INTER-CROSSES LINES IN THE FINGER MILLET BREEDING PROGRAM IN KENYA

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Finger millet (*Eleusine coracana*) is the most important millet in East Africa (EA) for food, feed and cash, even though the yields are extremely low at ≤ 1.3 t/ha. It is a nutritious and climate-resilient cereal of significant importance in Kenya. Various biotic and abiotic stresses are responsible for the low yield in comparison to its potential >5 t/ha. The global warming phenomenon is an emerging threat to agriculture production. Food production systems are very susceptible to climate variation, and production of finger millet is no exception. Breeding climate resilient crop varieties is one of the strategies to combat effects of climate change. Initial finger millet breeding efforts in Kenya in the 1980s resulted in the release of the first variety P-224 in 1991. Subsequent efforts lead to pioneering finger millet hybridization effort in 2005 and release of ten more varieties to date, four of which are products of the pioneering hybridization breeding effort between adapted x adapted. In an effort to create more diversity, in 2016, with the support of the Crop Trust, 92 accessions

composed of landraces, farmer adapted varieties, and wild relatives were screened for blast disease and Striga resistance. In 2018, 19 accessions were identified as blast disease resistant, and 22 as Striga resistant. The resistant accessions were intercrossed within their resistance categories. A total of 241 crosses were made for blast and 278 for Striga. Seed was harvested from each crossed panicle and planted head to row in 2019. Morphological markers were used to pick out probable true crosses and a total of 51 plants were picked out as true F1 plants. These were planted out head to row for F2 population. The F2 were advanced to F3 by advancing three selected plants head to 10m row. F3 row yield was recorded and used to appraise yield performance per line. A number of wild x adapted lines showed potential yield superiority. The best 37 cross combinations were entered in a preliminary yield trial with adapted parental checks and preliminary results indicate potential to identify new varieties superior to the current adapted farmer varieties.

105. INTRODUCING THE NEW HORIZON EUROPE PROJECT GRAPEBREED4IPM

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Biodiversity loss and ecosystem collapse are major threats facing humanity in the next decades and massive consumption of chemical pesticides in agriculture is a significant contributing factor. Viticulture ranks high among the crops that depend on a massive consumption of chemical pesticides, making it a priority target for reducing the use of chemical plant protection products. At the same time, grapevine is economically and culturally important in the EU, with wine being the largest EU agri-food sector.

Recent advances and new perspectives in grapevine breeding have opened the possibility for GrapeBreed4IPM to address the reduction of fungicides and preserve biodiversity. Lessons learned from past experience in viticulture have shown that success in improving sustainability relies on global involvement of

all actors. This project brings together the top European research groups in grapevine breeding and involves different stakeholders along the grapevine industry value chain in a multi-actor and co-design approach to produce the best insights for maximum impact. The project will develop grapevine varieties with resistance to relevant diseases, adapted to local environmental and pedoclimatic conditions, and with the goal of reducing reliance on chemical pesticides. In addition, the project will provide farmers, winegrowers and advisers with best practices and guidelines for integrated pest management, adapted to disease-resistant varieties, as ingredients for their largest possible adoption and leading to a long-awaited more environmentally friendly and sustainable viticulture in Europe.

106. EFFECTS OF BIOLOGICALS ON EARLY DROUGHT STRESS UNDER FIELD CONDITIONS

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Increased occurrence of heat, drought or flooding are key challenges of agriculture. In Germany, the amount of precipitation has declined by 10-25 % during the period from 2018-2022 compared to the reference period 1961-1990 (UBA, 2023) potentially leading to a yield reduction of up to 40 % (Daryanto et al., 2017). Besides, political regulations and requirements regarding the use of synthetic chemical pesticides like the EU-wide “Farm-to-Fork” strategy must be met by farmers. As one consequence, the importance of biologicals increases due to their environmental preserving properties. Biologicals can improve the stress resilience of plants in extreme weather conditions. However, the underlying physiological background and genetic determinants are not well understood yet. Therefore, the aim of this study was to analyse the effects of four different biologicals on drought stress for a diverse set of spring barley (*Hordeum vulgare* L.) genotypes. In our study, ten genotypes with different drought tolerance levels were selected from a set of 200 genotypes of the IPK_SB224-panel for field trials. Field experiments were conducted at two locations for two years. Drought stress started at BBCH 13 for six weeks with and without spray-application of four different biologicals. Traits involved in photosynthesis like the chlorophyll content were measured at three time points. Flag

leaves were harvested for proline and soluble sugar content analysis and mature plants were harvested to investigate the effect of biologicals on yield related traits. Additionally, quality attributes of grains were determined such as raw protein and starch content. Notable results were the high heritability of heading time ($h^2=0.9-0.95$), plant height ($h^2=0.89-0.96$), full ears ($h^2=0.51-0.94$), thousand grain weight ($h^2=0.67-0.89$), raw protein ($h^2=0.75-0.81$), and starch content ($h^2=0.79-0.92$) for all treatments. One biological showed a significant ($p<0.01$) effect on the increase of the chlorophyll content among all genotypes for all three measured time points under drought stress. Another interesting result was the significant ($p<0.05$) increase of the grain biomass among all genotypes after treatment with three of the biologicals under drought stress. However, the level of the increase depended on the genotype and location for all traits. The raw protein content was significantly ($p<0.05$) increased by the use of one biological under drought stress and starch content was enhanced by all biologicals in a genotypic dependent manner. Overall, our results highlight the potential of biologicals for an improved drought stress performance in spring barley, however, further research regarding the genotype and environment specificity is still necessary.

107. GOING FOR BOLD – SUPPORTING THE BIODIVERSITY FOR OPPORTUNITIES, LIVELIHOODS AND DEVELOPMENT PROJECT WITH GERMINATE AND GRIDSCORE

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The Biodiversity for Opportunities, Livelihoods and Development Project (BOLD; <https://bold.croptrust.org>) coordinated by the Crop Trust and funded by the Government of Norway is a USD 80 million project. The ‘Use Component’ of BOLD is supporting pre-breeding projects on seven important crops across 20 countries. These projects aim to utilise beneficial traits from crop wild relatives and landraces into their modern breeding programmes. Through thousands of crosses and backcrosses between domesticated species and their wild relatives, the project partners are generating huge volumes of characterisation, evaluation, genotypic and phenotypic data which needs to be made easily available to plant breeders and scientists. This data is collected across several countries and under various environmental conditions. Collecting and managing the data is difficult but analysing can pose an even larger challenge. This however must be addressed if pre-breeding is going to

contribute to the development of sturdier, more adapted crops for changing environments. Germinate (<https://germinateplatform.github.io/get-germinate>) allows these pre-breeding projects to present their experimental data in a common platform which is continually evolving with both data and the features that it makes available to users. We are developing a community of species which contribute to this global initiative and the use of Germinate means that this data will be available quickly and in meaningful ways for plant breeders and scientists. Tools like GridScore also help partners collect their field trial data in a standard and consistent way. We are developing Germinate instances in alfalfa, barley, finger millet, grasspea, rice and wheat that complement the resources already in place through the CWR project (<https://cwr.croptrust.org>). These resources will be made freely available to the community.

108. BREAKING THE BOTTLENECK: EXPLORING QUANTITATIVE GENETICS TO UNLOCK THE POTENTIAL OF SYNTHETIC HEXAPLOID WHEAT

Tally Wright¹

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For over a decade NIAB has been creating ‘diversity-enriched’ wheat with the aim of targeting the diversity bottleneck in modern cultivars. Synthetic Hexaploid Wheat (SHW) is created through resynthesizing the hybridisation events that formed modern wheat, using a diverse collection of different accessions of the D genome donor *Ae. tauschii*. NIAB has formed a large, diverse, and powerful Nested Association Mapping (NAM) resource that consists of 3241 individuals from 54 SHW BC1 populations which exploit untapped D

genome diversity. The resource is a powerful tool with high allele richness for discovering novel genes and haplotypes from ancestral wheat backgrounds. We have explored the panel by growing large scale field trials and are mapping genes linked to important traits such as disease resistance that are under exploited in UK elite wheat backgrounds. Historically, implementing genomic selection in pre-breeding has been challenging due to linkage-drag with undesirable characteristics from exotic material.

We are investigating methods of prediction that could reduce the need to phenotype at such large scale. As part of the BBSRC Designing Future Wheat project, due to a desirable combination of competitive grain yield and high genetic diversity, UK based wheat breeders

have actively incorporated this novel material into their own pre-breeding programs. Continued exploration will increase our understanding of the large and significant resource that NIAB has created over the last decade.

109. MOLECULAR STUDIES ON ROOT LESION NEMATODE RESISTANCE IN CEREALS

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Our study addresses the urgent need for a swift and accurate diagnostic method to tackle the damage caused by Root Lesion Nematodes (RLN), specifically *Pratylenchus neglectus*, in German cereal production, intensified by climate change. A DNA-based assay was developed to measure RLN infection in cereal roots efficiently. A *P. neglectus*-specific primer combination was used to detect and quantify *P. neglectus* using an RT-qPCR detection assay in infected barley and wheat roots. The assay's exceptional sensitivity allows the detection of a single nematode's DNA in water and as few as ~250 nematodes in an infected root. Importantly, it surpasses traditional visual counting by identifying eggs and inactive/dead nematodes. Simultaneously, the study explored the impact of different pre-cultivations on the pathogenicity of *P. neglectus*. We found that the commonly used monoxenic culture of nematodes on carrot calli reduces the nematode's pathogenicity. We hypothesize that the decline in pathogenicity

may be linked to changes in the microbiota of the nematode. Furthermore, a genome-wide association study was conducted with a global barley collection infected with *P. neglectus*. The RT-qPCR detection assay facilitated faster and more reliable quantification, revealing significant SNPs on chromosome 3H. Thirty-eight potential genes associated with resistance were identified, including six genes related to plant defense and disease resistance, offering promising avenues for future research on plant-nematode interactions.

This integrated approach, encompassing diagnostic assay development, comprehension of pathogenicity, tripartite interaction of plant-nematode-microbiome, and genetic marker identification, propels RLN research forward. The findings hold potential for practical applications in plant breeding, facilitating routine measurements, selecting resistant plants, and assessing nematode screening in farmland through the RT-qPCR detection assay.

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