DIGITAL BREEDING

Program

February 11-13, 2020 | Tulln – Austria
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Internationales Symposium der
Gesellschaft für Pflanzenzüchtung e.V. (GPZ)

International Symposium of the
Society for Plant Breeding e.V. (GPZ)

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Internationales Symposium der Gesellschaft für Pflanzenzüchtung (GPZ) gemeinsam mit der Vereinigung der Pflanzenzüchter, Saatgutproduzenten und Saatgutkaufleute Österreichs

International Symposium of the Society for Plant Breeding e.V. (GPZ) in cooperation with Saatgut Austria

February 11-13, 2020 | Tulln – Austria
https://gpz2020.boku.ac.at/

hosted by:
University of Natural Resources and Life Sciences, Vienna

Scientific Committee
Andreas Graner, IPK Gatersleben
Frank Ordon, JKI Quedlinburg
Tim Beissinger, University Göttingen
Rod Snowdon, University Giessen
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Dear colleagues,

over the past decades, Vienna has become a European beacon of fundamental and applied plant research. Therefore, I am pleased that the GPZ Symposium on Digital Breeding will be organized and hosted by our colleagues at the University of Natural Resources and Life Sciences (BOKU).

The Society for Plant Breeding e.V. (GPZ) aims at advancing fundamental and applied research into plant breeding and strengthening the interaction between plant breeders and academia. GPZ was founded in Göttingen in 1991 and has more than 850 members at present. Every two years, the society organizes a scientific symposium at different locations covering topical issues of plant breeding. This year´s conference sets a historic landmark because it is the first general symposium held outside Germany.

Agriculture faces humongous challenges in terms of food security, sustainability, biodiversity and global change. We are not going to solve any of these issues at the national level. The quest for innovation in plant breeding is a global mission. Against this backdrop, this conference will be a platform to foster scientific collaboration in the emerging field of Digital Breeding at the European level.

Our thanks go to the local organizers, especially to Prof. Dr. Hermann Bürstmayr and his team, who have put together an exciting program. It features outstanding keynote presenters from the international arena along with a lineup of young scientists from a wide range of institutes.

Again, a warm welcome to Vienna and best wishes for a rewarding conference.

Andreas Graner

Andreas Graner
President of the GPZ

Dear colleagues and participants,

with great delight we took over the mission to host the 2020 General Plant Breeding Conference under the auspices of the Society for Plant Breeding e.V. (GPZ) at the Campus Tulln of the University of Natural Resources and Life Sciences Vienna (BOKU).

The general motto of the conference DIGITAL BREEDING seems to be a perfect choice as we received a total of 114 contributions, which underlines the spiritedness and engagement of the plant breeding community. We especially thank all of you who have responded to our invitation to submit abstracts of your latest research results to discuss these here with a broader audience. GPZ symposia are always highly inspiring as we can enjoy an interesting mix of contributions covering a broad range of crops and topics while at the same time giving both early stage and senior scientists the opportunity to present and critically discuss their recent work. A notable proportion of the scientific presentations comes thus from early stage researchers, some of whom get the chance to present their results for the first time at a high-level scientific meeting, and I personally always enjoy the enthusiasm and devotion of the younger generation. An outstanding feature of GPZ symposia is that its attendees represent numerous sectors, such as applied breeding, academia, administration or NGOs. It is you who make this symposium a fascinating and inspiring one!

I sincerely acknowledge all colleagues who served in the scientific advisory board for their recommendations and guidance in designing the program, and particularly for their active contributions as abstract reviewers for the numerous oral and poster contributions.

At the same time, I thank the local organizing committee and our student helpers for their active role in the planning and implementation of this conference. My particular thanks deserve Mrs. Suanne Weber, our conference secretary, whom many of you had contact with. Susanne’s support and enthusiasm were the cornerstones when managing the conference preparations in a smooth and successful manner.

Lastly, without sponsoring and industry support we would not be able to realize this symposium. Therefore, I express my sincere appreciation to all sponsors, supporters and exhibitors.

Hermann Bürstmayr

Hermann Buerstmayr
and all members of the local organizing committee

Oral Presentations

Tuesday, February 11, 2020			
09:00-13:00	Registration, Poster Setup		
11:30-13:10	Lunch, Registration, Poster Setup		
Opening Ceremony			
13:10-13:15	Christian Obinger	Vice Rector for Research, BOKU	**Welcome to the Symposium DIGITAL BREEDING**
13:15-13:20	Michael Gohn	President of Saatgut Austria	**Welcome to the Symposium DIGITAL BREEDING**
13:20-13:30	Andreas Graner	President of the GPZ	**Opening of the Symposium DIGITAL BREEDING**
Keynote Lecture			
Chair: Andreas Graner			
13:30-14:10	Theo Meuwissen	Norwegian University of Life Sciences	**Past experiences and future directions for genomic selection in animal breeding**
Phenomics & Breeding			
Chair: Frank Ordon			
14:10-14:45	Astrid Junker	Leibniz Institute of Plant Genetics and Crop Plant Research	**Using advanced digital phenotyping to identify novel breeding targets: stories about controlled environmental fluctuations, multi-trait dynamics and acclimation capacity**
14:45-15:05	Ulrich Schurr	Forschungszentrum Jülich	**Phenotyping for crop improvement - technologies - access - knowledge**
15:05-16:40	Coffee Break & **Poster Session 1 - Genomics & Breeding** - *odd numbers P1-P81*		
Chair: Chris Schön			
16:40-17:00	Karin Köhl	MPI of Molecular Plant Physiology	**Can phenotypic marker-assisted selection for drought tolerance replace stress-trials in potato?**

17:00- 17:20	Tsu-Wei Chen	Leibniz University Hannover	**Field phenotyping identifies the architectural and physiological functions determining canopy light interception and light use efficiency in winter wheat**
17:20- 17:40	Pernille Sarup	Nordic Seed	**Using NMR metabolomics in breeding for malt quality in spring barley**
Chair: Thomas Debener			
17:40- 18:00	Roland Geyer	lifespin GmbH Regensburg	**Analysis of drought tolerance in perennial ryegrass (*Lolium perenne* L.) with methods of metabolite profiling and systemic metabolite markers**
18:00- 18:20	Svenja Diehl	Wintersteiger | Sponsored Talk	**Easy Breed - The flexible software solution for the entire breeding process**
18:20- 20:30	Reception with Snacks & GPZ General Assembly (UFT-Tulln)		

Wednesday, February 12, 2020			
Biotechnology & Breeding			
Chair: Christian Jung			
08:45- 09:20	Brigitte Poppenberger	Technical University Munich	**Establishing tools for a fast-track genetic improvement of the wild crop species *Crassocephalum crepidioides*, to realize its potential as a nutritious, leafy vegetable**
09:20- 09:40	Nirosha L. Karunarathna	Christian-Albrechts-University of Kiel	**Mutations in SEED FATTY ACID REDUCER genes increase seed oil content in oilseed rape**
09:40- 10:00	Annaliese Mason	Justus Liebig University Giessen	**Hybrid speciation in Brassica**
10:00- 10:45	Coffee Break & **Poster Session 2** – *all posters*		
Genomics & Breeding			
Chair: Klaus Pillen			
10:45- 11:20	Cristobal Uauy	John Innes Centre Norwich, UK	**Unlocking the polyploid potential of wheat through genomics**

11:20-11:40	Laura Morales	School of Integrative Plant Science, Cornell University, Ithaca, NY	**Characterization of a large panel of maize nested association mapping near-isogenic lines (NAM NILs)**
11:40-12:00	Maria Buerstmayr	University of Natural Resources and Life Sciences, Vienna	**Progress in Fusarium head blight resistance breeding in wheat (2009-2019) – *a review***
12:00-14:30	Lunch Break & **Poster Session 3 – Biotechnology & Breeding, Phenomics & Breeding, Predictive Breeding** - *even numbers P2-P82*		
Chair: Albrecht Melchinger			
14:30-14:50	Jenny HueyTyng Lee	Justus Liebig University Giessen	**Genomic and epigenomic patterns in novel heterotic pools of winter rapeseed (*Brassica napus*)**
14:50-15:10	Steven Dreissig	Martin Luther University Halle-Wittenberg	**Exploring natural genetic variation in meiotic recombination rates in barley**
15:10-15:30	Ali Ahmad Naz	Universtiy of Bonn	**A novel wild allele improves drought adaptation and yield sustainability in cultivated barley**
15:30-15:50	Antonia Lisker	Martin Luther University Halle-Wittenberg	**Genetic interplay of yield, baking quality and resistance in the MAGIC winter wheat population WM-800**
15:50-16:35	Coffee Break & **Poster Session 4** – *all posters*		
Chair: Rod Snowdon			
16:35-16:55	Ravi Koppolu	Leibniz Institute of Plant Genetics and Crop Plant Research	**Tissue specific global transcriptomes of barley meristems**
16:55-17:15	Max Haupt	University of Hohenheim	**Landscape genomics identifies the genetic architecture of soybean environmental adaptation and genetic resources suitable for Central European soybean breeding**
17:15-17:35	Harmeet Singh Chawla	Justus Liebig University Giessen	**Widespread gene-scale structural variants revealed by long-range sequencing**
17:35-17:55	Dietmar F. Schulz	Leibniz University Hannover	**Association studies in roses reveal robust markers for flower traits**
17:55-18:15	Matteo Schiavinato	University of Natural Resources and Life Sciences Vienna	**Analysis of subgenome structure and evolution in allopolyploid plants**

18:15- 19:30	Recreation Break
19:30- 20:15	**Günter and Anna Wricke prize awarding to Martin Mascher, IPK Gatersleben** for his exceptional achievements in bioinformatics and genomics of crop plants
20:15- 24:00	**Symposium Dinner at Atrium Tulln** Minoritenplatz 1, 3430 Tulln

Thursday, February 13, 2020

Predictive Breeding

Chair: Jens Leon

09:00- 09:35	Timothy Beissinger	Georg-August-University Göttingen	**Reverse genomic prediction: identifying important traits in breeding populations**
09:35- 09:55	Rodrigo Jose Gala¡n	State Plant Breeding Institute, University of Hohenheim	**Integration of genotypic, hyperspectral, and phenotypic data to improve biomass yield prediction in hybrid rye**
09:55- 10:40	Coffee Break & **Poster Session 5** – *all posters*		

Chair: Timothy Beissinger

10:40- 11:00	Christian Werner	The Roslin Institute, University of Edinburgh	**The relevance of dominance to genomic selection in clonal breeding programs**
11:00- 11:20	Sebastian Michel	University of Natural Resources and Life Sciences, Vienna	**Ten years of genomic selection in an applied wheat breeding program - from expectations to experience**
11:20- 11:40	Tobias Schrag	University of Hohenheim	**Omics-based prediction of hybrid performance in maize**
11:40- 12:00	Stefanie Griebel	Georg-August-University Göttingen	**Quantifying the contribution of epistasis to quantitative trait variation with Epistasis Mapping Populations**
12:00- 12:20	Dilan S.R. Patiranage	Christian-Albrechts-University of Kiel	**Genome-wide association mapping of agronomically important traits in quinoa**
12:20- 14:20	Lunch & Farewell		

Poster Presentations

Genomics & Breeding, Tuesday, Feb. 11, 15:05-16:40			
P-1	Stjepan Vukasovic	Justus Liebig University Giessen, Department of Plant Breeding	Increasing root biomass production in European winter wheat for improved drought-stress tolerance and nitrogen use efficiency
P-3	Oyiga Benedict	Rheinische Friedrich-Wilhelms-Universität Bonn	*hap3A.1* is a novel genetic determinant for grain yield and stability performance in wheat
P-5	Manuel Geyer	Bayerische Landesanstalt für Landwirtschaft, Freising	Genetic basis of the trade-off between grain yield and baking quality in winter wheat
P-7	Saida Zulfuqarova	Azerbaijan National Academy of Sciences, Institute of Molecular Biology & Biotechnologies, Baku	Determination of *HSP16.9* gene using allele-specific primer and membrane thermal stability in different wheat genotypes
P-9	Samira Rustamova	Azerbaijan National Academy of Sciences, Institute of Molecular Biology & Biotechnologies, Baku	Expression divergence of the *DREB* transcription factor among contrasting wheat genotypes under drought stress
P-11	Salma Benaouda	Rheinische Friedrich-Wilhelms-Universität Bonn	A stable and novel QTL on chromosome 3A induces early heading in winter bread wheat
P-13	Said Dadshani	Rheinische Friedrich-Wilhelms-Universität Bonn	Sustainable increase of nitrogen and phosphorus efficiency in winter wheat through effective root-soil interactions
P-15	Dominic Dennenmoser	University of Kassel, Section Organic Plant Breeding and Agrarbiodiversity	Association analysis in lines derived from winter wheat CCPs—comparing four different populations stratification methods
P-17	Benjamin Wittkop	Justus Liebig University Giessen, Department of Plant Breeding	High-resolution mapping of rachis nodes per rachis, a critical determinant of grain yield components in wheat
P-19	Turana Isgandarova	Azerbaijan National Academy of Sciences, Institute of Molecular Biology & Biotechnologies, Baku	Changes in some antioxidant enzymes activity of wheat genotypes under drought stress during leaf senescence

P-21	Leonhard Sommer	Martin Luther University Halle-Wittenberg, Chair of Plant Breeding	MAGIC-RESIST - Identification and mapping of resistances against fungal diseases in the MAGIC-WHEAT population WM-800
P-23	Maria Buerstmayr	University of Natural Resources and Life Sciences, Vienna (BOKU)	Fine-mapping *Qfhs.ifa-5A* revealed two tightly linked QTL both affecting resistance against initial infection and anther extrusion
P-25	Barbara Steiner	University of Natural Resources and Life Sciences, Vienna (BOKU)	Isolating the wheat gene enhancing mycotoxin detoxification at the major Fusarium resistance QTL *Fhb1* – a progress report
P-27	Christian Wagner	University of Natural Resources and Life Sciences, Vienna (BOKU)	Fusarium head blight resistance in winter wheat: Insights from genome-wide transcriptome analysis
P-29	Rizky Pasthika Kirana	University of Natural Resources and Life Sciences, Vienna (BOKU)	Improving Fusarium head blight resistance in durum wheat through introgression of resistance alleles from relatives
P-31	Rizky Pasthika Kirana	University of Natural Resources and Life Sciences, Vienna (BOKU)	*Fusarium graminearum* and deoxynivalenol resistance in *Aegilops tauschii*
P-33	Magdalena Ehn	University of Natural Resources and Life Sciences, Vienna (BOKU)	Common bunt resistance in winter wheat – a cross-chromosome journey
P-35	Andreas Maurer	Martin Luther University Halle-Wittenberg, Chair of Plant Breeding	Insights into the genetic control of flowering time based on a worldwide series of field trials with the barley NAM population HEB-25
P-37	Timm Bernhard	Justus Liebig University Giessen, Department of Plant Breeding	Broadening the genetic basis for hybrid breeding in winter barley
P-39	Ehsan Fatemi	Christian Albrechts University of Kiel, Plant Breeding Institute	Quantification of root lesion nematodes by RT-qPCR in the roots of cereal plants
P-41	Nazanin Pesaran Afsharyan	Rheinische Friedrich-Wilhelms-Universität Bonn	A systemic approach to identify the gene underlying flowering-delaying epistatic QTL “Hvheading”
P-43	Smit Shah	Christian Albrechts University of Kiel, Plant Breeding Institute	QTL mapping and Genome wide association mapping of root lesion nematode resistance genes in barley

P-45	Nikolaj Meisner Vendelbo	Nordic Seed A/S & Aarhus University	Analysis of population structure and genetic diversity within hybrid rye elite breeding component lines
P-47	Julia Mauser	University of Hohenheim	Exploring molecular markers in conjunction with traditional DUS traits for managing reference collections in European rye varieties
P-49	Subhadra Chakrabarty	Justus Liebig University Giessen, Department of Plant Breeding	PEGASUS: Prediction and exploitation of gene bank accessions – a study in Ugandan sorghum
P-51	Jan E. Neuweiler	University of Hohenheim, State Plant Breeding Institute	Long-term trends and genetic architecture of seed characteristics and grain yield components in triticale (×*Triticosecale* Wittmack)
P-53	Mauricio Orantes Bonilla	Justus Liebig University Giessen, Department of Plant Breeding	Assembling the restructured genome of a novel synthetic *Brassica napus* with diverse genome donors
P-55	Elizabeth Ihien	Justus Liebig University Giessen, Department of Plant Breeding	Can resynthesized rapeseed be genomically stable?
P-57	Paul Vollrath	Justus Liebig University Giessen, Department of Plant Breeding	Quantitative blackleg resistance and gene presence-absence variation in elite *Brassica napus*
P-59	Daniela Quezada-Martinez	Justus Liebig University Giessen, Department of Plant Breeding	Towards a stable and diverse *Brassica* hexaploid crop
P-61	Isabelle Deppé	Justus Liebig University Giessen, Department of Plant Breeding	Genetic variation for seed protein traits in diverse *Brassica napus* germplasm
P-63	Miroslav Poláček	Gregor Mendel Institute, Vienna	Annual tree-ring detection and segmentation using deep learning
P-65	Sandra Färber	Julius Kühn Institute (JKI), Institute for Breeding Research on Horticultural Crops, Quedlinburg	Mapping of resistance genes against *Aphanomyces euteiches* in pea
P-67	Nathaly Maldonado	Christian Albrechts University of Kiel, Plant Breeding Institute	Towards understanding the phenological development of quinoa by expression analysis of putative flowering time genes
P-69	Elena Pestsova	Forschungszentrum Juelich GmbH, Germany	Transcriptome resources for successful breeding of non-food bioenergy crop *Silphium perfoliatum*

P-71	Avneesh Kumar	Christian Albrechts University of Kiel, Plant Breeding Institute	Characterizing a wild beet translocation in sugar beet conferring resistance to the beet cyst nematode
P-73	Vinicius Vilperte	Leibniz University Hannover, Institute of Plant Genetics	Glutathione S-transferase as a potential marker for mutation breeding in poinsettia (*Euphorbia pulcherrima* Wiild. ex Klotsch)
P-75	Felix L. Wascher	University of Natural Resources and Life Sciences, Vienna (BOKU)	Population analysis of sugar beet and wild beets
P-77	Heinz Himmelbauer	University of Natural Resources and Life Sciences, Vienna (BOKU)	Quinoa sequencing and detection of haplotype blocks for genome scaffolding
P-79	Lisa Blazek	University of Natural Resources and Life Sciences, Vienna (BOKU)	Evolutionary dynamics of the repeat landscape in sugar beet and its wild relatives
P-81	Sebastian Urzinger	Technical University Munich (TUM)	Fine mapping of a genomic segment associated with the traits carbon isotope composition, water use efficiency and drought sensitivity in maize (*Zea mays* L.)
P-83	Giedrius Petrauskas	Lithuanian Research Centre for Agriculture and Forestry	Red clover: breeding strategy based on plant phenotyping and cpDNA genotyping
P-85	Jose Moreno-Amores	University of Natural Resources and Life Sciences, Vienna (BOKU)	Plant height and heading date as covariates to predict Fusarium head blight in durum wheat
P-87	Rebecca Tacke	Georg-August-Universität Göttingen	Fine-mapping of two bi-parental crosses to zoom into the genomic vicinity of the major QTL for very low vicine & convicine seed content in faba bean (*Vicia faba* L.)
Phenomics & Breeding, Wednesday, Feb. 12, 12:00-14:30			
P-2	Paul Herzig	Martin Luther University Halle-Wittenberg, Chair of Plant Breeding	Genetic dissection of grain elements predicted by hyperspectral imaging associated with yield-related traits in a wild barley NAM population

P-4	Laura Schmidt	Martin Luther University Halle-Wittenberg, Chair of Plant Breeding	MAGIC-EFFICIENCY: Genetic analysis of nitrogen efficiency regulation and selection of efficient winter wheat varieties from the MAGIC-WHEAT population WM-800
P-6	Gwendolin Wehner	Julius Kühn-Institut (JKI), Institute for Resistance Research and Stress Tolerance, Quedlinburg	Breeding for priming triggered leaf rust resistance in barley
P-8	Ulrike Beukert	Julius Kühn-Institut (JKI), Institute for Resistance Research and Stress Tolerance, Quedlinburg	Automated phenotyping to identify leaf and stripe rust resistances in wheat genetic resources
P-10	Aydinli Lale	Azerbaijan National Academy of Sciences, Institute of Molecular Biology & Biotechnologies, Baku	Ascorbate-glutathione cycle for scavenging H_2O_2 in bread wheat genotypes (*Triticum aestivum*) during drought stress and following recovery
P-12	Julia Hagenguth	Georg-August-Universität Göttingen, Abteilung für Zuchtmethodik der Pflanze	Breeding tomatoes with improved flavour using a breeders' sensory test
P-14	Thanh Chi Tran	Georg-August-Universität Göttingen, Abteilung für Zuchtmethodik der Pflanze	Improving pea production – Yield and nitrogen content of pea cultivars with different leaf types
P-16	Johann Vollmann	University of Natural Resources and Life Sciences, Vienna (BOKU)	Soybean stem termination gene *Dt2* affecting agronomic characters and stress tolerance in early maturity genotypes
P-18	Sandra Cvejić	Institute of Field and Vegetable Crops, Novi Sad, Serbia	Use of digital image analysis for the flower color evaluation in ornamental sunflower
P-20	Andreas Eckert	Justus Liebig University Giessen, Department of Plant Breeding	Assessment of plant architectural traits by processing 3D scanned point clouds of *Brassica napus*
P-22	Peter Stasnik	AIT - Austrian Institute of Technology, Center for Health and Bioresources, Tulln	Exploring *Camelina sativa* stress tolerance mechanisms for future breeding approaches

P-24	Karl Schmid	University of Hohenheim	Genetic contributions to tolerance for downy mildew pathogen *Peronospora variabilis* in a South American panel of quinoa.
P-26	Christoph Korte	Rheinische Friedrich-Wilhelms-Universität Bonn	Laying a cornerstone for cup plant breeding
P-28	Ronja Schmitz	Julius Kühn-Institut für Rebenzüchtung	Establishment of an image-based, high-throughput phenotyping system to monitor grapevine root architecture
P-30	Sara Francesconi	Department for Agriculture and Forest Sciences (DAFNE), University of Tuscia, Viterbo, Italy	FHB early detection by in-field phenomics
P-32	Wiebke Sannemann	Martin Luther University Halle-Wittenberg	Genetic dissection of anther extrusion in the MAGIC-WHEAT population WM-800
Biotechnology & Breeding, Wednesday, Feb. 12, 12:00-14:30			
P-34	Sara Francesconi	Department for Agriculture and Forest Sciences (DAFNE), University of Tuscia, Viterbo, Italy	Effectiveness of chitosan hydrochloride on organic control of Fusarium head blight of wheat
P-36	Manar Makhoul	Justus Liebig University Giessen, Department of Plant Breeding	Challenges in converting single nucleotide polymorphisms into KASP markers in polyploid wheat
P-38	Almuth Müllner	University of Natural Resources and Life Sciences, Vienna (BOKU)	Identification of common bunt resistance gene *Bt12* in wheat
P-40	Almuth Müllner	University of Natural Resources and Life Sciences, Vienna (BOKU)	Comparative mapping of bunt resistance QTL in wheat
P-42	Srijan Jhingan	Christian Albrechts University of Kiel, Plant Breeding Institute	Breeding oilseed rape (*B. napus*) with lower glucosinolate content through functional analysis and mutagenesis
P-44	Asis Shrestha	Rheinische Friedrich-Wilhelms-Universität Bonn	The role of ABA-responsive element binding factors in proline biosynthesis in Arabidopsis and barley

P-46	Aylin Kabas	Akdeniz University, Turkey	Morphological and molecular characterization of some wild tomato genotypes
P-48	Sebastian Schultheiss	Computomics GmbH	The power of big data integration in phenotype predictions
P-50	Martin Greve	Rheinische Friedrich-Wilhelms-Universität Bonn	Towards speeding up the breeding process of the perennial cup plant (*Silphium perfoliatum* L.)
P-52	Adebimpe N. Adedeji-Badmus	TUM School of Life Sciences Weihenstephan, Biotechnology of Horticultural Crops,	Natural variation in seed development and germination capacities of *Crassocephalum* species and their implication for the domestication of these orphan crops
P-54	Victoria Armario-Najera	University of Lleida-Agrotecnio Center, Department of Plant Production and Forestry Science, Lleida, Spain	Experimental field trial of a triple combination anti-HIV microbicide produced in rice endosperm
P-56	Johannes Wanner	Georg-August-Universität Göttingen, Abteilung für Zuchtmethodik der Pflanze	The ProFaba project in SusCrop (ERA-NET) started: Improving *Vicia faba* breeding practices and genotypes to promote climate-friendly and vegetable protein production in the European Union
P-58	Tahmina Islam	Christian Albrechts University of Kiel, Plant Breeding Institute	CRISPR-Cas-mediated genome editing for the improvement of oilseed rape
P-60	Norman Warthmann	IAEA Laboratory Seibersdorf	Mutation breeding creates desired traits in African sorghum – semi-dwarf and early maturing
Predictive Breeding, Wednesday, Feb. 12, 12:00-14:30			
P-62	Ana Marjanović Jeromela	Institute of Field and Vegetable Crops, Novi Sad, Serbia	Dealing with HTTP data in modern crop breeding programs
P-64	Mathias Gemmer	Martin Luther University Halle-Wittenberg, Chair of Plant Breeding	Genomic prediction of flowering time and yield through SNP and metabolite analysis in the barley NAM population HEB-25
P-66	Sebastian Michel	University of Natural Resources and Life Sciences, Vienna (BOKU)	Improving and maintaining winter hardiness and frost tolerance in bread wheat by genomic selection

P-68	Jakob Seereiter	University of Natural Resources and Life Sciences, Vienna (BOKU)	Molecular-genetic analysis of FHB resistance in a CIMMYT spring wheat line
P-70	Stephan Greiner	Max Planck Institute of Molecular Plant Physiology	Dissection of the cytoplasmic effects of chloroplasts and mitochondria uncovers a remarkable contribution of the chloroplast to plant reproductive traits
P-72	Iulian Gabur	Justus Liebig University Giessen, Department of Plant Breeding	Genome-wide association studies and genomic selection for disease resistance in *Brassica napus*
P-74	Katharina Tyson	Justus Liebig University Giessen, Department of Plant Breeding	High-throughput phenotyping and genetic analysis to promote breeding for enhanced nitrogen use efficiency in winter oilseed rape
P-76	Norman Warthmann	IAEA Laboratory Seibersdorf	kWIP: the k-mer weighted inner product, a de novo estimator of genetic similarity
P-78	Vichai Puripunyavanich	Thailand Institute of Nuclear Technology, Nakhon Nayok, Thailand	On the first step of tropical tulip breeding in hot and humid country as Thailand
P-80	Vuk Djordjevic	Institute of Field and Vegetable Crops, Novi Sad, Serbia	Different approaches to genomic prediction model validation in soybean
P-82	Charlotte D. Robertsen	Sejet Plant Breeding, Denmark	Perspectives on genomic selection and marker-assisted selection of malt quality traits in winter barley
P-84	Daniel Valle Torres	Technical University Munich (TUM)	Optimizing the construction of haplotype blocks to increase genomic prediction accuracy across maize landraces
P-86	Carla Colque-Little	University of Copenhagen	Developing image analysis for phenotyping quinoa-downy mildew pathobiome

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Eppendorf	www.eppendorf.com
Harvest Master	www.harvestmaster.eu
Illumina	www.illumina.com
New England Biolabs	www.neb-online.de
Wintersteiger	www.wintersteiger.com/en/Plant-Breeding-and-Research

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