



DIGITAL BREEDING

Book of Abstracts

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

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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.

A handwritten signature in black ink, reading "Andreas Graner". The signature is written in a cursive, flowing style.

Andreas Graner
President of the GPZ

Dear colleagues and participants,

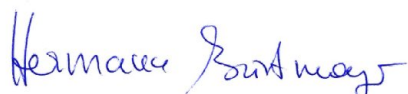
with great delight we took over the mission to host the 2020 General Plant Breeding Conference under the auspices of the Society for Plant Breeding e.V. (GPZ) at the Campus Tulln of the University of Natural Resources and Life Sciences Vienna (BOKU).

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 Buerstmayr
and all members of the local organizing committee

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Poster 62

Dealing with HTTP data in modern crop breeding programs

Ana Marjanović Jeromela¹, Miroslav Zorić¹, Dragana Rajković¹, Sreten Terzić¹, Ankica Kondić Špika¹, Dragana Miladinović¹, Sandra Cvejić¹, Vuk Đorđević¹, Johann Vollman²

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Modern crop breeding programs are data-driven. A breeder's decisions are based on the prediction of the genotype performance from a large number of field trials. These trials should account for environmental variability of the target region, and more importantly, they should possess a high degree of accuracy. In recent years, different robotic and sensor technologies for collecting high-throughput field-based plant phenotyping (HTTP) data have been developed. Thereby, the possibility for gaining higher overall precision, as well as data and decision accuracy from crop breeding field trials was gained. Prediction of end-of-season yield and quality will become faster with the use of cameras for hyperspectral imaging, which is important for large scale producers. Comparing big sets of images generated in the field with results of classical chemical analyses serves as an advanced crop quality prediction tool for breeders. Important steps in such data analysis are calibration, noise reduction and the search for the most significant relations. Nevertheless, assessing phenotypic traits within genetic collections is made more accurate with the aid of phenotyping platforms that record plant growth from germ to seed. Like many types of phenotypic data, HTTP data collected from the images may also have some amount of unknown variability. This type of variability can introduce bias prior to integration with phenotypic and genomic data for a final prediction model. Application of statistical procedures for outlier detection and testing for normality is required, as well as visualization tools in order to attain an optimal level of data quality. Considering the volume and frequently high correlation of HTTP data, data reduction techniques and shrinkage regressions are required for an efficient selection of the most important HTTP variables for inclusion in the statistical model. Further development of new tools for HTTP data analysis is needed for big data interpretation. Choosing the appropriate statistical model should enable relevant analyses of the obtained data to breeders and provide assistance in the decision-making process during plant breeding.



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A close-up photograph of several green leaves, likely from a plant, showing their veins and texture. The leaves are arranged in a fan-like pattern, with some overlapping. The lighting is bright, creating a soft glow around the edges of the leaves.

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