

**10. GPZ Haupttagung**  
**Freising-Weihenstephan**  
**15. - 17. März 2010**

***'Innovations in Breeding Methodology'***

**MONDAY, 15.03.2010**

Zentrales Hörsaalgebäude, HS16, Maximus-von-Imhof-Forum 6, 85354 Freising  
Conference office opens at 10:30

***Opening***

**13:00**      **Friedel Cramer**, Leiter des Referats Acker- und Pflanzenbau, BMELV

***Multi-environment experiments, chair: H.-P. Piepho***

**13:30**      **Fred van Eeuwijk**, Biometris, Wageningen, The Netherlands  
Modern regression techniques for new perspectives at multi-environment trials

**14:10**      **Heiko Parzies**, University of Hohenheim, Stuttgart, Germany  
Stability analysis of pearl millet (*Pennisetum glaucum*) and Sorghum (*Sorghum bicolor*) based on multi-environment field trials in West Africa

**14:35**      **Beat Boller**, Agroscope Reckenholz-Tänikon ART, Switzerland  
Agronomic performance of meadow fescue ecotypes does not reach cultivars and is negatively correlated with the nature value of the sites of origin

**15:00**      **Ralf Uptmoor**, Leibniz University Hannover, Germany  
Discovering the genetic basis of complex traits by linking crop modelling with QTL analyses

15:25-15:55    Coffee Break

***New resources, chair: M. Frisch***

- 15:55**      **Laima Kott**, University of Guelph, Canada  
New twists on classical breeding
- 16:35**      **Thilo Wegenast**, University of Hohenheim, Stuttgart, Germany  
Comparison of breeding schemes and selection strategies for hybrid maize breeding with doubled haploids
- 17:00**      **Bianca Büttner**, Christian-Albrechts-University Kiel, Germany  
A second bolting factor in *Beta vulgaris* that acts epistatically to the bolting gene B

17:25-18:00 Break

**18:00-19:30 Akademische Feier zur Verleihung des Günter und Anna Wricke-Forschungspreises**

**TUESDAY, 16.03.2010**

Zentrales Hörsaalgebäude, HS16, Maximus-von-Imhof-Forum 6, 85354 Freising

***Lessons from natural selection, chair: C. Jung***

- 8:30**      **Pierre Saumitou-Laprade**, University of Lille, France  
Genetics and evolution of adaptation to zinc polluted soils in *Arabidopsis halleri* (Brassicaceae)
- 9:10**      **Diro Terefe**, Leibniz University Hannover, Germany  
Dissecting rose NBS-LRR encoding genes by means of an exon based SSR marker
- 9:35**      **Karl Schmid**, University of Hohenheim, Stuttgart, Germany  
Haplotype-based detection of natural and artificial selection: A simulation study

10:00-10:30 Coffee break

***Gene introgression and pyramiding major genes, chair: F. Ordon***

- 10:30**      **Richard Visser**, University of Wageningen, The Netherlands  
Genomics assisted breeding: know your alleles
- 11:10**      **Eva Herzog**, Justus-Liebig-University Gießen, Germany  
Using high-throughput marker systems for efficient marker-assisted backcrossing
- 11:35**      **Aneela Yasmin**, Leibniz University Hannover, Germany  
Identification of a major rose resistance gene to black spot
- 12:00**      **Marion van de Wal**, Nunhems, The Netherlands  
Marker development and implementation in vegetable breeding
- 12:40-14:00    Lunch break at the Mensa

***Poster Session***

14:00-15:00

***Association and QTL mapping, chair: C.-C. Schön***

- 15:00**      **Michael McMullen**, USDA-ARS, Columbia, USA  
Genetic diversity and the genetic architecture of complex agronomic traits in maize
- 15:40**      **Christiane Gebhardt**, MPI Köln, Germany  
The molecular basis of complex traits in potato as prerequisite for 'Precision Breeding'
- 16:05**      **Pasam Raj Kishore**, IPK, Gatersleben, Germany  
Whole genome association mapping in spring barley cultivars
- 16:30-17:00    Coffee break

**17:00**        **Roland Kölliker**, Agroscope Reckenholz-Tänikon ART, Switzerland  
Marker assisted breeding of forage crops: past achievements and future challenges

**17:40**        **Monika Spiller**, Leibniz Universität Hannover, Germany  
QTL mapping of scent metabolites in the rose genome

**18:15-19:45 GPZ Mitgliederversammlung**

20:00        Conference dinner at the Bräustüberl Weißenstephan

**WEDNESDAY, 17.03.2010**

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***Association and QTL mapping; chair: K. Pillen***

**8:30**        **Laurence Moreau**, Agropolis-INRA, France  
QTL detection in intermated and multiparental populations.  
Consequences for selection

**9:10**        **Christiane Kelm**, Martin-Luther-Universität Halle, Germany  
Multiple QTL mapping of resistance to *Septoria tritici* blotch in a DH population of hexaploid wheat

**9:35**        **Wolfgang Ecke**, University of Göttingen, Germany  
Mapping QTL for phenological, morphological and quality traits by whole genome association analysis in canola quality winter rapeseed (*Brassica napus L.*)

10:00-10:30 Coffee break

***Genome-wide prediction and selection, chair: J. Léon***

- 10:30**      **Georg Thaller**, Christian-Albrechts-University Kiel, Germany  
Genomic selection in dairy cattle: Methods, current status and consequences
- 11:10**      **Boby Mathew**, University of Bonn, Germany  
An efficient adaptive MCMC algorithm for the prediction of breeding values in self-pollinating crops
- 11:35**      **Alexander Thiemann**, University of Hamburg, Germany  
Prediction of maize hybrid performance with transcription profiles of parental inbred lines
- 12:00      Closing remarks
- 12:15      End of conference