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27th Colloquium

Genomic Selection in Plant Breeding

20. November 2014

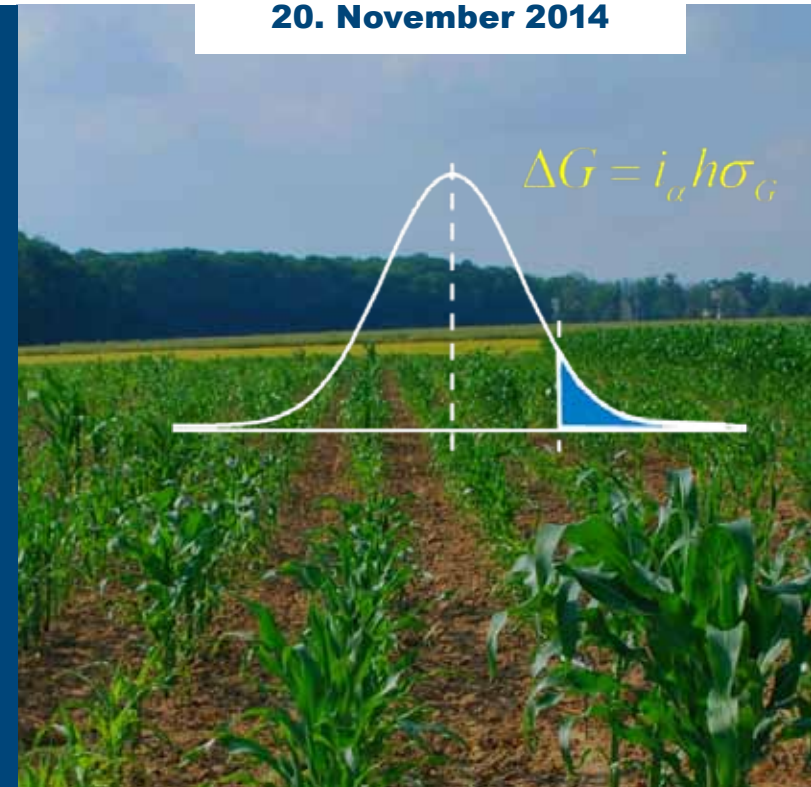
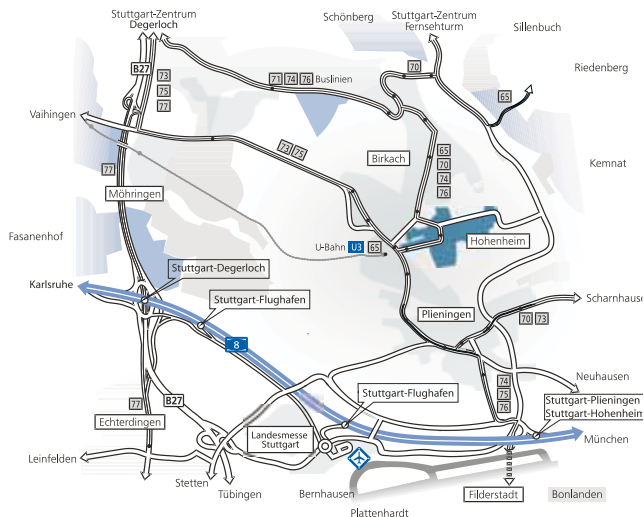
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Chair of program committee:
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- Deutsche Saatveredelung AG, Lippstadt
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- KWS LOCHOW GMBH, Wohld
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is gratefully acknowledged



Aula, Castle Hohenheim
11:00 – 19:00

WELCOME

Genomic Selection in Plant Breeding

Biometrics – Experiments – Breeding plans

Genomic selection is a form of marker-assisted selection where genetic markers covering the whole genome are used so that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker. This approach has become feasible thanks to the large number of single nucleotide polymorphisms (SNP) discovered by genome sequencing and new methods to efficiently genotype large number of SNP.

In our 27th Colloquium, we will present the biometric foundations as well as simulation and experimental results from various crops and discuss the major implications of genomic selection for plant breeding in future.

The colloquium will be held in honor of Prof. Dr. H.F. Utz to recognize his outstanding contributions to academic teaching and research related to selection theory in plant breeding at the University of Hohenheim. He joined the Institute of Plant Breeding in 1964 and was a pioneer in developing software for the design and analyses of agronomic experiments and QTL studies. Prof. Utz is still active in research and supports generously the members of the Center of Competence of Plant Breeding at Hohenheim in his fields of expertise as he practiced during the past 50 years with generations of students and researchers.

PROGRAM

- 11:00** **Welcome and opening address**
Prof. Dr. Stephan Dabbert, President, University of Hohenheim
Prof. Dr. Karl Schmid, Speaker of the Research Center for Biotechnology & Plant Breeding, University of Hohenheim

Biometric foundations of genomic selection

Chair: Prof. Dr. Albrecht E. Melchinger

- 11:15** Genomic selection in animal breeding: Current state of the art and perspectives
Prof. Dr. Jörn Bennewitz, University of Hohenheim
- 11:45** Ridge regression methods with heteroscedastic marker variances for genomic prediction
Prof. Dr. Matthias Frisch, Justus-Liebig-Universität Gießen
- 12:15** Building a unified framework for prediction of complex phenotypes
Prof. Dr. Chris-Carolin Schön, Technische Universität München
- 12:45** *Lunch break (Snacks)*

Genomic selection and breeding methods

Chair: PD Dr. Tobias Würschum

- 13:45** Estimation of heritability and prediction accuracy
Prof. Dr. Hans-Peter Piepho, University of Hohenheim
- 14:15** Genomic prediction in hybrid breeding
Prof. Dr. Albrecht E. Melchinger, University of Hohenheim

- 14:45** Assessment of factors contributing to accuracy of genomic prediction
M.Sc. Pascal Schopp, University of Hohenheim
- 15:15** Prediction accuracy of genomic selection in highly diverse panels and multiparental designs
Dr. Laurence Moreau, INRA Science and Impact, France
- 15:45** *Coffee break*

Genomic selection in plant breeding programs

Chair: Prof. Dr. Chris-Carolin Schön

- 16:15** Hybrid wheat: Optimum breeding strategies and genomic selection
Dr. Friedrich Longin, University of Hohenheim
- 16:45** Genomic selection in barley
M.Sc. Patrick Thorwarth, University of Hohenheim
- 17:15** Genomic selection in hybrid breeding: lessons learned from practical experience
Dr. Andres Gordillo, KWS LOCHOW GMBH
- 17:45** Genomic predictions in a commercial maize breeding program
Dr. Christian Riedelsheimer, DuPont Pioneer
- 18:15** 50 years of service to Plant Breeding at the University of Hohenheim
Laudatio for Prof. Dr. H. Friedrich Utz by Prof. Dr. Albrecht E. Melchinger
- 18:35** *End of Colloquium*
- 19:00** **Reception and supper**
Balcony and Blue room, Hohenheim castle