



Research Center for Biotechnology and Plant Breeding

25th Colloquium

Crop Plants: Biodiversity & Genomics

November 16th and November 17th 2011

University of Hohenheim

Aula Schloss Hohenheim

ABSTRACTS

Universität Hohenheim, 762 Research Center for Biotechnology and Plant Breeding, Stuttgart, Germany

<https://fsp762.uni-hohenheim.de/>



**PROGRAM
25th COLLOQUIUM**

CROP PLANTS: BIODIVERSITY AND GENOMICS

Venue: Aula at Schloss Hohenheim

The meeting will be held in conjunction with the Society of Plant Breeding (GPZ e.V.)

Talks: November 16, 2011; 13:00 - 18:30 and November 17, 2011; 09:00 - 13:00

Conference dinner: November 16, 19:30

Prof. Dr. Dr. h. c. Adolf M. Steiner:

Dr. Dr. h. c. Hermann Eiselen – his contributions for alleviating hunger in the developing world and his input to plant breeding

Wednesday, November 16; 13:00 - 18:30

13:00 *Opening remarks*

Markus Rodehutschord, Vice-Dean

Gerd Weber, Speaker of the Research Center for Biotechnology & Plant Breeding

13.:30-15:10 BREEDING FOR DEVELOPING COUNTRIES Chair: Bettina Haußmann

13:30 **Mark E. Sorrells**
Association breeding strategies for developing countries

14:20 **Abubaker Touré**
Development of high yielding sorghum varieties for West Africa

15:10 **Peter Craufurd**
Drought tolerance inputs for Asia and Africa in the face of climate change

16:00-16:30 *Coffee break*

Wednesday, November 16 (continued)

16:30 – 18:10 **BIODIVERSITY** Chair: Albrecht E. Melchinger

- 16:30 **Andreas Graner**
*Genomics assisted valorization of plant genetic resources of barley:
Opportunities and constraints*
- 17:20 **Arndt Zacharias**
Utilization of genetic resources in breeding programs
- 18:10 **Karl Schmid**
Population genetics of gene banks: A case study with barley
- 18:50 **Society of Plant Breeding (GPZ e.V.)**
Award ceremony by Chris-C. Schön
- 19:30 *Conference dinner*

Thursday, November 17; 9:00 – 13:00

09:00 -12:30 **GENOMICS** Chair: Karl Schmid

- 09:00 **Harald von Witzke**
World food security: The role of productivity growth and agricultural research
- 09:50 **Tobias Würschum**
Mapping genes in breeding populations
- 10:20-11:00 *Coffee break*
- 11:00 **Stefan Scholten**
Correlation of parental transcriptome and field data for the characterization and prediction of heterosis
- 11:50 **Michele Morgante**
The plant pan-genomes and the creation of novel variation
- 12:30-13:00 **Gerd Weber**
Closing remarks
- 13:00 *End of conference*

Dr. Dr. h. c. Hermann Eiselen – his contributions for alleviating hunger in the developing world and his input to plant breeding

Dinner Speech by Adolf Martin Steiner

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As an eyewitness from the beginning, I was asked to present the Dinner Speech on occasion of the 25th Anniversary of the Colloquium of the Research Center for Biotechnology and Plant Breeding at Hohenheim. Therefore, it is an honor and pleasure for me to report on Dr. Dr. h. c. Hermann Eiselen's life journey, to highlight his contributions for alleviating hunger in the developing world, and to comment on his input to plant breeding. No doubt, without Dr. Eiselen's initiative and ideas, his commitment, dedication, sponsoring and continuous promotion there would never have been such a Research Center and the respective Colloquia now operating over 25 years.

To everybody's sadness, Dr. Eiselen died on summer solstice two years ago at an age of 83. Most of you knew him, and all of us are yet heavy-hearted that he is no longer with us to listen, to discuss, to provide prudent advice and to celebrate cheerfully with us this 25th Anniversary, what he truly would have done. Hence, to bear in grateful remembrance his personality and inspiring example: First, I will draw a brief picture of crucial experiences in Dr. Eiselen's life in order to show, how he eventually became the benefactor he was. Second, I will explain by which means he tried to achieve his aim of fighting hunger and poverty in the developing world. And third, I will describe his input to plant breeding and why biotechnology played such a special role in his thinking. After this, I will end with two quotations of Dr. Eiselen relating to his lifetime aim and his prospect for the future.

On crucial experiences in Dr. Eiselen's life pivotal for becoming a benefactor

Dr. Eiselen was born in 1926 in Nagold, a rural town in the Black Forest. Later in Freudenstadt, he grew up educated by his grandmother in a strict Württembergian- protestant manner and similar surroundings. This meant motivation, industriousness and hard working; punctuality, reliability and trustworthiness; modesty, good manners and thoughtfulness. These nowadays so-called old virtues guided Dr. Eiselen in his activities lifelong.

Between 17 - 19 years of age, Dr. Eiselen experienced the Second World War. As draftee stationed in Berlin he lived and saw emergencies: As an air-raid warden, he faced continuous dangers to his life. Because his commander black-marketed his platoon's food supplies, he and his comrades suffered from hunger. As a Swabian in Berlin he felt homeless and forsaken. Eventually, for a short time he even became a prisoner of war. Thus, already in young years, Dr. Eiselen experienced firsthand: life threatening situations, hunger, loneliness, and imprisonment. As did the old virtues, these grave experiences guided Dr. Eiselen his entire life.

From 1954 - 1980, i. e. for a period of 26 years, Dr. Eiselen acted as chief executive and shareholder in the Company "Ulmer Spatz Vater und Sohn Eiselen" hard working with all duties and responsibilities involved in such a top management position. Finally, this company was sold in 1980. From then on, Dr. Eiselen devoted his life exclusively to what he called his fight against hunger and poverty in the world. However, it was already long before that Dr. Eiselen became a benefactor. The following will show this.

The means by which Dr. Eiselen aimed at alleviating hunger in the developing world

Already in 1960, his father and Dr. Eiselen opened the "Deutsches Brotmuseum" nowadays the "Museum für Brotkultur Ulm". Next, in 1978 the „Vater und Sohn Eiselen-Stiftung“ was founded integrating the Museum. Finally, in 2000 Dr. Eiselen set up his "Stiftung *fiat panis*". Looking at the mission of the two foundations, it becomes apparent that Dr. Eiselen put his activities for alleviating hunger mainly on four pillars. The first pillar represented by the museum accounts for the dissemination of knowledge about worldwide hunger among people, in the public. The second pillar represented by research work accounts for the increase in knowledge for alleviating hunger. The third pillar represented by training of junior scientific staff accounts for the perpetuation as well as the dissemination and the increase of knowledge for alleviating hunger. This includes supporting scientific meetings. The fourth pillar represented by awarding prices accounts for honoring outstanding achievements in alleviating hunger and for making this public. To sum up: Dissemination of knowledge, increase of knowledge, training of staff, and honoring achievements are the basic means by which Dr. Eiselen aimed at alleviating hunger in the developing world.

Dr. Eiselen's input to plant breeding

Dr. Eiselen was actually aware that there existed a multitude of means for alleviating hunger in the developing world. Nevertheless, he placed special emphasis on plant breeding explicitly including biotechnology and gene technology. Dr. Eiselen was convinced that progress in plant breeding plays a key role for increasing agricultural productivity. In addition, he was convinced that it would not be responsible to exclude biotechnology and gene technology as promising options for raising food production as the ultimate prerequisite for alleviating hunger. He wanted to fight hunger by all reasonable means on hand. Thus, in 1985, Dr. Eiselen initiated the research project "Applied Genetics to the Benefit of World Food Supply". This project was up to now the by far largest funding by the Vater und Sohn Eiselen Stiftung granting within 10 years a total of 6.2 Mio Euros. After ending in 1996, this research project continued under the name "Research Center for Biotechnology and Plant Breeding". Today, we celebrate the 25th Anniversary of the colloquia going along with these two projects. The evolution of a continuing research institution developing from an initiative of Dr. Eiselen is characteristic for the wish and vision, which Dr. Eiselen had for fighting hunger and poverty in the world. Of course, many projects running in the Research Center were and are still funded by the Vater and Sohn Eiselen Stiftung and today its successor the Stiftung *fiat panis*.

Today, Dr. Andrea Fadani assisted by Mr. Peter Spiertz are the Executive Secretaries of both foundations. Attorney at law Dr. Klaus Gerstenmaier is Chairman of the two Boards of Trustees. Dr. Eiselen gathered these three persons in charge and the Trustees of the two foundations already a long time ago. They knew Dr. Eiselen and his aim from many years of fruitful cooperation.

Now, they guard his foundations to the best of their knowledge and believe. At Hohenheim University, the Speaker of the Applied Genetics project was Prof. Dr. Dr. h. c. Hartwig Geiger and the Speaker of the succeeding Research Center is Prof. Gerd Weber, both having closely cooperated with Dr. Eiselen. Thus, Dr. Eiselen's heritage is in good hands.

Two quotations of Dr. Eiselen

I had the privilege to read the personal notebook, in which Dr. Eiselen wrote down quotations from others influencing him and his own reflections. I will end this brief commemorative address with two quotations showing Dr. Eiselen's aim of life and wish for the future. These are, concerning his aim of life: "*Freedom from hunger is the most fundamental human right*", and concerning the future: "*I am grateful to see young people following me, which continue building along my beliefs and disseminate my ideas.*"

Bearing Dr. Dr. h. c. Hermann Eiselen in mind, I wish the Center for Biotechnology and Plant Breeding a prospering future.

Association Breeding Strategies for Developing Countries

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Plant breeding strategies are driven by new methods and technologies. Over time breeders have not abandoned old breeding methods but instead have adapted them to new technologies and integrated them into new strategies. In fact, Fischer's 1918 theory of infinitesimal variation is still applicable to breeding populations today. Knowledge of the level of genetic diversity and historical relationships among cultivated wheat germplasm can be effectively exploited for the assessment of genetic variation, association breeding, marker-assisted selection (MAS) and genomic selection (GS) for wheat improvement. Advancements in genotyping technologies are rapidly reducing marker costs and increasing genome coverage allowing the widespread use of molecular markers and methods in plant breeding. These molecular breeding methods greatly facilitate the development of new varieties for developing countries. Major genes can be backcrossed into elite cultivars adapted to the target environments. However, MAS strategies are not well suited for agronomically important complex traits controlled by many genes. Also, quantitative trait loci (QTL) must be identified in segregating populations in the target environment before they can be used in MAS. Genomic selection incorporates genome-wide marker information in a breeding value prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small effect QTL. In GS, a training population representative of the breeding germplasm is genotyped with genome-wide markers and phenotyped in a target set of environments in the developing country or mega-environment. That data is used to train a prediction model that is used to estimate the breeding values of lines in a population using only the marker scores. Prediction models can incorporate performance over multiple environments, G x E effects, specific screening techniques, and novel traits. Because of reduced generation time, annual genetic gain for GS is predicted to be two to three fold greater than for a conventional phenotypic selection program, even with only modest prediction accuracy of 0.50. We developed an analytical framework to compare gains from conventional breeding and GS for complex traits with equal budgets. Results indicate that GS can outperform conventional breeding on a per year basis even at low accuracies. This new approach to crop improvement will facilitate the development of superior varieties for developing countries.

Development of high yielding sorghum varieties for West Africa

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Great potential exists for improving yields and other consumer preferred traits through the use of local landraces in Sorghum. The exploitation of the landraces can lead to cultivars with quite significant improvements that will be productive in West Africa. Different sources of resistance to different sorghum production constraints have been identified. A significant amount of information about key characteristics of landraces has been used successfully as breeding selection criteria. These traditional cultivars have been selected over a long period of time for survival and yield stability over a wide range of environmental conditions. However, these local cultivars have a low yield potential, but are able to survive and produce 'stable yield' under less favorable environments where nutrient and water stresses are acute. Constraints to adoption of the first hybrids and cultivars included lodging, severe leaf diseases, head bugs damage, grain mold, striga, and poor adaptation to soil stresses and poor grain quality. The primary approach is to breed for adapted and vigorous materials. Because West Africa is considered as a center of origin for sorghum, emphasis is made on the use of local germplasm in breeding. Breeding for yield without regard for quality will be a misplaced objective. Farmers will not adopt improved sorghums susceptible to weathering and head bugs and have unacceptable processing and food properties. In West Africa, breeding programs should give major priority in developing improved sorghums resistant to molds, weathering, and head bugs and have or not photosensitivity and good grain and food quality. A significant success of development of sorghum hybrids in West Africa will be achieved when the increase in yield over locals will be significant. Such improved sorghums will provide opportunities to develop new food and industrial products which could enhance demand. These value-added sorghums are the basis for identity –preserved production for use in processing into value added products. The hybrid grown in farmer fields should generate the enthusiasm of the farmer and the interest of government officials and potential seed producers. Improved sorghum seed production and distribution to the farmers is a limiting factor to large scale sorghum production in most West African countries. The existing seed production structures are not well organized to handle F1 hybrid seeds. The success of hybrid production will therefore depend on organizing such structures.

Drought tolerance inputs for Asia and Africa in the face of climate change

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Drought is a common phenomena associated with climate variability, which may be exacerbated in future climates that are warmer and where rainfall patterns and intensity may change. To manage drought effectively a combination of genetic improvement and crop or land management is required, the latter often being the more effective means for smallholder farmers. These paper exams current genetic improvement strategies for drought at ICRISAT in Asia and Africa, focussing on successful examples that link drought physiology to breeding and areas we are currently investing in. These include stay-green QTLs and QTLs that result in conservative water use. Matching crop phenology to available soil moisture and other abiotic and biotic constraints, and maintaining developmental plasticity, remain the most powerful form of drought tolerance. The paper also uses simulation to look at phenological adaptation strategies for current variability and future climates using maize in Africa as an exemplar. Lastly, the potential benefits from genetic improvement vis-a-vis crop/land management strategies are compared.

Genomics assisted valorization of plant genetic resources of barley: opportunities and constraints

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Conventional crop plant breeding essentially rests on repeated cycles of crossing and selection. This approach has warranted the development of superior cultivars over the past decades. However, this approach is only sustainable, if the genetic diversity that is lost in the process of selection is adequately replenished by introducing novel diversity into the gene pool. *Ex-situ* conservation of plant genetic resources represents the major backbone to maintain the intraspecific diversity of many important crop plant species. By the turn of the century than 6 million seed samples were stored in more than 1000 *ex-situ* collections worldwide. However, the vast diversity resting on the shelves of genebanks has been tapped into only marginally. Future challenges regarding the utilization of PGR include trait analysis, gene discovery and the deployment of genetic diversity. As to phenotypic analysis, systematic screens of genebank collections so far remained restricted to simple traits, such as disease resistances, that show a high heritability and can be scored easily. Accurate phenotyping of quantitative traits still represents a major challenge for gene discovery, which represents an entry point for an improved utilization of PGR. The availability of new sensing and imaging technologies is expected to give access to large scale analysis of quantitative traits or components thereof. The availability of an ever increasing amount of sequence information has greatly spurred the development of a comprehensive set of SNP markers. These now allow for high density fingerprinting of large number of individuals and the genetic analysis of quantitative traits by QTL analysis or association mapping. Moreover, the systematic exploitation of intergenomic information will accelerate the isolation of traits by map based cloning, even in complex genomes such as that of barley. The ultimate goal to fully exploit the potential of molecular breeding will be the generation of a high quality genomic sequence of barley which is presently underway. Knowledge of the genes that underlie agronomic traits will allow to systematically sifting through genebank collections for the identification novel alleles.

Population genetics of genebanks: A case study with barley

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The collection of genetic resources and their storage in gene banks has led to very large ex situ collections of modern varieties, land races and wild relatives of many crop species. These resources have been used for a long time in applied plant breeding, and new developments in genotyping, phenotyping and statistical analysis promise new and diversified uses for ex situ plant genetic resources. A key improvement is the ability to analyze genome-wide patterns of genetic variation beyond mere allele frequencies because the historical context of genetic variation can be constructed, for example by characterizing ancestral and derived variation or by analyzing the length and structure of haplotypes. Population genetic methods such as coalescent simulations will contribute to make efficient use of PGR in the construction of core collections for genetic mapping and allele mining, and finally to study the effect of different core collections for different downstream applications such as association studies and 'selection mapping' to identify adaptive genes. We demonstrate some of these developments by analysing genetic variation in wild and cultivated barley and show the limitations of current methods and available data.

Mapping Genes in Breeding Populations

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Association mapping is a powerful tool to unravel the genetic architecture of complex agronomic traits based on phenotypic and genomic data of elite breeding populations. Our objective was to investigate the genetic basis of quality traits (protein and starch content, sedimentation volume, 1000 kernel weight, and test weight), resistance to Fusarium head blight (FHB), heading time, and yield in soft winter wheat (*Triticum aestivum* L.). 455 European elite lines were used for a genome-wide association mapping approach with 115 simple sequence repeat markers randomly distributed across the genome and two allele-specific markers for Rht-B1 and Rht-D1 genes. Field evaluation was done at 2-6 locations with special inoculated trials for FHB resistance. The principal coordinate analysis revealed absence of a clear population but presence of a family structure. Therefore, we used linear mixed models and marker-based kinship matrices to correct for family structure. For all traits, known QTL from linkage mapping could be validated. Furthermore, we identified for all traits new QTL, some of them explaining > 15 % of the genotypic variation. For yield and all quality traits, impact of epistasis was negligible compared to main effect QTL. However, for FHB resistance, the genotypic variance explained simultaneously by individual markers was 36% and increased to 50% when two digenic epistatic interactions were considered, one of them associated with Rht-B1. For heading time, the proportion of genotypic variance explained simultaneously by main and epistatic QTL effects was 93%, substantially higher than the fit with only main effects (46 %). Consequently, for heading time and FHB resistance, it is important to consider epistatic effects for marker-assisted breeding.

Correlation of parental transcriptome and field data for the characterization and prediction of heterosis

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For the characterization of heterosis and the development of transcriptome-based methods to predict hybrid performance, we profiled 21 European maize (14 dent and 7 flint) parental inbred lines at the seedling stage with a 46k oligo microarray. Hybrid performance for grain yield and grain dry matter content as well as heterosis of the corresponding 98 hybrids from flint x dent factorial crosses were assessed in field trials at six locations.

We found that prediction of hybrid performance with transcriptome-based distances of selected transcripts was more precise than earlier prediction models using DNA markers or general combining ability estimates based on field data. Our results suggest that transcriptome-based prediction of hybrid performance and heterosis has a great potential to improve the efficiency of maize hybrid breeding programs.

According to a model of Stupar and Springer, additive expression in hybrids plays a key role in the formation of heterosis, due to its likelihood of falling into a medium, optimal expression range. Based on this model we used calculated mid parental expression levels for correlation analyses with heterosis data. We identified a large set of differentially expressed genes which were highly correlated to heterosis in a linear fashion. These genes indicate important metabolic and regulatory pathways for heterosis and define potential heterosis-associated genomic regions due to their non-random distribution on the maize genome. Transcriptome analyses including hybrids confirmed the predominance of additive expression and showed an inconsistent appearance of non-additive expressed genes among the hybrids. Our results support the existing model with respect to the importance of additive expression for the formation of heterosis. However, instead of a medium optimum expression range, our results prefer a model with heterosis is positively influenced by a shift of absolute expression levels in hybrids.

The plant pan-genomes and the creation of novel variation

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The analysis of variation in plants has revealed that their genomes are characterised by high levels of structural variation, consisting of both smaller insertion/deletions, mostly due to recent insertions of transposable elements, and of larger insertion/deletion similar to those termed in humans Copy Number Variants (CNVs). These observations indicate that a single genome sequence might not reflect the entire genomic complement of a species, and prompted us to introduce the concept of the plant pan-genome, including core genomic features common to all individuals and a Dispensable Genome (DG) composed of partially shared and/or non shared DNA sequence elements. The very active transposable element systems present in many plant genomes may account for a large fraction of the DG. The mechanisms by which the CNV-like variants are generated and the direction of the mutational events are still unknown. Uncovering the intriguing nature of the DG, i.e. its composition, origin and function, represents a step forward towards an understanding of the processes generating genetic diversity and phenotypic variation. Additionally, since the DG clearly appears to be for the most part the youngest and most dynamic component of the pan genome, it is of great interest to understand whether it is a major contributor to the creation of new genetic variation in plant evolution and more specifically in the breeding process. We will discuss the extent and composition of the pan genome in different plant species, the different mechanisms that generate and maintain the dispensable portion, the phenotypic effects of the DG and the rates and modes of creation of new genetic variation due to DG components and whether this could represent an important factor in the breeding process.