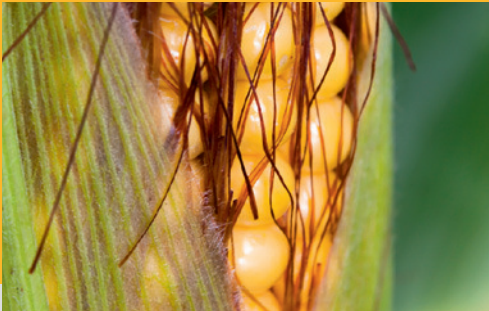


Aktuelles in der Maiszüchtung



11.-12. Juni 2012

Stuttgart-Hohenheim
Akademie der
Diözese Rottenburg-Stuttgart



**Gesellschaft für
Pflanzzüchtung e.V.**



Deutsches Maiskomitee e.V. (DMK)

Programm

Montag, 11.06.2012

11:30–14:00 | Registrierung

12:30 | Begrüßungsimbiss

13:30 | Begrüßung und Eröffnung

Session 1: Aktuelle Zuchtziele in Mais

(Diskussionsleitung: Prof. Dr. A. E. Melchinger, Stuttgart und Dr. R. Leipert, Einbeck)

13:45 Uhr | Prof. Dr. Jim Holland – Department of Crop Science, North Carolina State University, Raleigh | *Genome-wide and nested association mapping in maize*

14:45 Uhr | Prof. Dr. Markus Rodehutschord – Institut für Tierernährung, Universität Hohenheim, Stuttgart | *Maize quality from the viewpoint of animal nutrition*

15:30 Uhr | Kaffeepause

16:00 Uhr | M.Sc. Christoph Grieder – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Genetic analysis of traits relevant for biogas production in maize*

16:30 Uhr | Dr. Matthias Martin – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Breeding maize for resistance to ear rot caused by *Fusarium graminearum**

17:00 Uhr | Prof. Dr. Frank Hochholdinger – Institut für Nutzpflanzenwissenschaften und Ressourcenschutz, Rheinische Friedrich-Wilhelms-Universität, Bonn | *Transcriptomic complexity of reciprocal hybrids and their parental inbred lines*

17:30 Uhr | Dr. Christoph-Martin Geilfus – Institut für Pflanzenernährung und Bodenkunde, Christian-Albrechts-Universität, Kiel | *Growth disturbance in maize induced by soil salinity*

Kulturprogramm

18:30 Uhr | Dr. Klaus Herrmann – Institut für Agrartechnik, Universität Hohenheim, Stuttgart | *Führung durch das Deutsche Landwirtschaftsmuseum der Universität Hohenheim. Die Führung erfolgt in deutscher und englischer Sprache.*

20:00 Uhr | Abendessen im Dt. Landwirtschaftsmuseum

Dienstag, 12.06.2012

Session 2: Genetische und biologische Ressourcen bei Mais

(Diskussionsleitung: Prof. Dr. C.-C. Schön, Freising)

08:00 Uhr | Dr. Alain Charcosset – INRA, Le Moulon, Gif-sur-Yvette | *Assembling new flint and dent maize association genetics panels for cooperative research: first results from the CornFed project*

08:45 Uhr | Dr. Milena Ouzunova – KWS Saat AG, Einbeck | *New technologies supporting a maize breeding program – current applications and future demands*

09:15 Uhr | M.Sc. Alexander Strigens – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Genetic and phenotypic diversity in DH lines derived from European landraces*

09:45 Uhr | Kaffeepause

Session 3: Kartierung und genetische Karten bei Mais

(Diskussionsleitung: apl. Prof. Dr. T. Miedaner Stuttgart)

10:15 Uhr | Dr. Eva Bauer – Lehrstuhl für Pflanzenzüchtung, TU München, Freising | *The landscape of recombination and variation in a European nested association mapping population*

10:45 Uhr | M.Sc. Michael Stange – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Chromosomal recombination and comparison of mapping functions in maize populations of DH lines*

11:15 Uhr | Dr. Claude Lebreton – Limagrain SA, Colmar | *Application of genome wide approaches to maize breeding using historical and de novo data*

Session 4: Genomische Selektion und Vorhersage in der Maiszüchtung

(Diskussionsleitung: Prof. Dr. F. Hochholdinger, Bonn)

11:45 Uhr | Prof. Dr. Chris-Carolin Schön – Lehrstuhl für Pflanzenzüchtung, TU München, Freising | *Genome-based prediction of genetic values in highly structured maize populations*

12:15 Uhr | M.Sc. Christian Riedelsheimer – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Whole-genome and metabolic prediction of testcross performance in maize*

12:45 Uhr | M.Sc. Frank Technow – Kompetenzzentrum für Pflanzenzüchtung, Universität Hohenheim, Stuttgart | *Genomic prediction of hybrid performance*

13:15 Uhr | Abschließende Worte | Prof. Dr. Chris-Carolin Schön

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Genome-wide and nested association mapping in maize

Jim Holland¹ and The Maize Diversity Project²

QTL mapping with biparental populations has limited reliability and inference, restricting its utility to breeding for complex traits. The maize Nested Association Mapping (NAM) population was developed to incorporate substantial genetic diversity into a large scale mapping resource to help overcome these problems. QTL mapping with NAM has facilitated high resolution genetic mapping of complex traits and the extensive functional allelic variation in maize. Recent efforts involve integrating high density polymorphism information from the Maize HapMap to enable Genome-Wide Association Study (GWAS) in NAM. GWAS in NAM is complementary to GWAS in maize diversity panels, and NAM has several important features: (1) NAM has a known population structure, (2) it permits excellent control of genetic background effects, and (3) accurate imputation of high density founder variation information on progeny lines by use of linkage information. Disadvantages of NAM compared to diversity panels are its relatively limited sample of allelic variation and the maintenance of longer range linkage disequilibrium that hinders association resolution. Sampling larger numbers of founders in future NAM-type studies would be advantageous. Identification of specific causal variants underlying complex traits in maize will permit breeders to know their distribution in the germplasm and direct selection of favorable alleles. This strategy can be carried out complementary to ge-

nomous selection for polygenic background effects, and may be most important in the introgression of favorable alleles from otherwise unfavorable exotic germplasm backgrounds.

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² *www.panzea.org*

Ihre Notizen

Maize quality from the viewpoint of animal nutrition

Markus Rodehutschord

Maize is highly relevant in animal nutrition for reasons that are different depending on animal species. Maize silage is very popular in ruminant feeding, especially in cattle. It is a good source of metabolizable energy, but also contributes to the physical structure of the diet, which is needed to maintain rumen functions. Since decades, nutritionists and maize breeders successfully collaborate in improving the nutritional value of maize silage as a compromise between starch content by higher proportion of the cob and high digestibility of the fibre fractions in the residual plant.

The high starch content together with low content of protein and antinutritional non-starch polysaccharides makes the maize kernel an energy source of high value for many animal species. Maize starch is highly digestible in poultry and pigs. In the rumen, maize starch is degraded by microorganisms at a lower rate and extent than starch from wheat or barley. This is highly relevant in the feeding of high-performing dairy cows because using maize helps to avoid the disliked acidosis in the rumen and at the same time improves glucose supply to the cow. The variation in ruminal degradation of starch between maize genotypes and the linkage with ruminal protein degradation are only rarely investigated and in the focus of current collaborative research projects.

High-oil maize is of value in the feeding especially of poultry. The oil fraction is highly digestible and the increase in the oil content is mirrored in an increased content of metabolizable energy, the most relevant factor in the linear programming of compound feeds. It is advantageous that the oil content is positively correlated with the protein content, the next important factor in feed compounding. Results of a meta-analysis on this subject will be part of the presentation. Specific fatty acids can become the limiting factor for the use of high-oil maize in certain feeding situations.

Among amino acids, lysine is first-limiting in pig feeding and second-limiting in poultry feeding.

Genotypes with improved lysine concentration can therefore help to reduce the feeding of protein-rich feeds such as those produced from soybeans. However, lysine and other amino acids are available as feed additives, and these are widely used for optimizing the dietary amino acid profile, with the exception of organic farming.

Phosphorus also plays a major role in animal feeding. The supplementation of diets with feed phosphates is expensive and the global raw phosphate deposits are limited. Phytate is the major storage form of phosphorus in the maize kernel. Phytate is hardly digestible in pigs and poultry. Low-phytate maize has higher phosphorus availability than conventional maize, and feed phosphate supplementation can be reduced. Here again feed additives are available to improve phosphorus availability as an alternative to using low-phytate maize.

It is concluded that the definition of "quality" of maize should consider traits that are different for different animal species (ruminants vs. non-ruminants) and physiological situations.

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Genetic analysis of traits in maize with influence on biogas production

Christoph Grieder

The area of maize (*Zea mays* L.) grown for production of biogas has tremendously increased in Germany during the past decade. A high methane yield per area (MY), which depends multiplicatively on dry matter yield (DMY) and methane fermentation yield (MFY, i.e. the amount of methane produced per dry matter), is required to ensure the efficiency of biogas maize cultivation. However, information on the targeted biogas maize ideotype is still missing and estimates of relevant quantitative genetic parameters for representative material are required to design optimum breeding strategies. To provide these information, we conducted a large field experiment with a very diverse set of 300 dent inbred lines and their 600 testcross progenies with two single-cross testers, grown at three locations during two years. For analysis of MFY, samples of a diverse core set of 16 inbred lines and their 32 testcrosses were analyzed using the Hohenheim Biogas Yield Test, a discontinuous, laboratory fermentation assay. The kinetics of methane production was assessed by non-linear regression. Estimates of heritability (h^2) for MFY measured after short fermentation time (3 days) were high, but genotypic variance (σ^2_g) and, therefore, also h^2 decreased towards the end of the fermentation period (35 days). This was presumably the consequence of a nearly complete degradation of all chemical components during the long fermentation period. This interpretation was supported by strong correlations of MFY with

chemical components and metabolizable energy concentration (MEC) for the early, but not the late fermentation stages. Based on the samples in the core set, NIRS calibrations were developed for MFY and chemical composition. Performance of NIRS to predict MFY on day 35 ($R^2_v = 0.77$) was lower than for MFY on day 3 ($R^2_v = 0.85$), but still at a satisfactory level.

For performance of the testcrosses, estimates of variance components from the main experiments revealed that general combining ability (GCA) was the major source of variation. The very tight correlation of MY with DMY but not with MFY (on day 35) indicated that variation in MY was primarily attributable to differences in DMY. Compared to MEC, an important parameter in ruminant nutrition, MFY showed a weaker association with chemical composition. Correlation of MFY with starch was even not significant and indicated a lower importance of high cob proportions for biogas maize than for forage maize. Results for inbred line per se performance largely confirmed results from testcrosses. Hence, to improve MY, selection should primarily focus on increasing DMY and biogas maize varieties can be expected to diverge more clearly from forage maize in the future.

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Ihre Notizen

Breeding maize for resistance to ear rot caused by *Fusarium graminearum*

Matthias Martin¹, Thomas Miedaner², Bettina Kessel³, Milena Ouzunova³
and Albrecht E. Melchinger¹

Gibberella ear rot (GER) of maize is mainly caused by *F. graminearum* Schwabe. This ear rot leads to contamination of the grains with deoxynivalenol (DON) and zearalenone (ZEA), two mycotoxins, which adversely affect the health of humans and animals. Cultivation of maize varieties resistant to GER and mycotoxin contamination is the most promising option for a sustainable solution to this problem. Classical phenotypic selection for resistance to GER is however expensive because of the need to conduct multi-environment testing and laborious artificial inoculations. An increase of selection efficiency might be achieved by a combination of classical phenotypic and marker-assisted selection based on QTLs for GER resistance and reduced mycotoxin contamination, which were identified recently in populations derived from multiple crosses of flint lines. Furthermore, costs should decrease by indirect selection for resistance to mycotoxin accumulation on the basis of visual ear rot ratings, because genotypic correlations between these traits are very strong. As correlations between line and testcross performances tend to be moderate or low, field testing should focus on testcrosses. Only few elite sources of superior resistance are available, but our results indicate that sustainable improvement of resistance might be possible without detrimental effects on other important agronomic traits, such as grain yield.

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Ihre Notizen

Transcriptome complexity in maize (*Zea mays* L.) hybrids and their inbred parents

Anja Paschold^{1*}, Yi Jia^{2,3,#,*}, Caroline Marcon¹, Steve Lund⁴, Nick B. Larson⁴, Cheng-Ting Yeh², Stephan Ossowski^{5,†}, Christa Lanz⁵, Dan Nettleton⁴, Patrick S. Schnable^{2,3}, Frank Hochholdingen¹

Typically, F1-hybrids are more vigorous than their homozygous, genetically distinct parents, a phenomenon known as heterosis. Despite its large agronomic importance, the molecular mechanisms underlying the manifestation of heterosis are only poorly understood. In the past it was demonstrated that in addition to above-ground traits such as plant size and yield which emerge late in development, already the young root system shows heterosis. In the present study the transcriptomes of the reciprocal maize (*Zea mays* L.) hybrids B73xMo17 and Mo17xB73 and their parental inbred lines B73 and Mo17 were surveyed in primary roots early in the developmental manifestation of heterosis. Four-fold biological replication and subsequent analyses established that ~35,000 (i.e., 89%) of all high-confidence maize genes were expressed in at least one genotype. Consistent with the dominance model (i.e., complementation) for heterosis >800 genes were expressed in only one of the two parents, but in the hybrids. For 50 genes it was shown that this was a consequence of complementation of presence/absence variation. For dozens of other genes, alleles from the inactive inbred were activated in the hybrid, presumably via interactions with regulatory factors from the active inbred. As a consequence of these types of complementation, both hybrids expressed more genes than did either parental inbred. Finally, in hybrids >10% of expressed genes exhibited allele-specific

expression (ASE) levels that differed significantly from the parental-inbred expression ratios, providing further evidence for interactions of regulatory factors from one parental genome with target genes from the other parental genome.

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Ihre Notizen

Salinity differentially affects growth promoting agents in leaves of maize hybrids contrasting in salt resistance

Christoph-Martin Geilfus¹, Dietrich Ober², Karl Hermann Mühling¹ and Christian Zörb^{1, 3}

Salt-sensitive crop plants such as maize (*Zea mays* L.) show a strong and rapid growth reduction in response to NaCl-induced stress. Wall-loosening agents such as expansins are of major impact for cell wall extensibility and growth. Elucidation of the way that salinity affects expansin proteins in leaves is of great importance for a better understanding of processes that contribute to the inhibition of leaf growth under salt stress. For this purpose, the abundance of growth-mediating β -expansin has been compared between a salt-sensitive and a salt-resistant maize hybrid under condition of salinity. Several expansin isoforms were monitored by gel-based 2D proteomics and a subsequent 2D western blot. The abundance of the growth-mediating β -expansin isoform 6 (ZmEXPB6) was decreased in growth-inhibited leaves of the salt-sensitive maize hybrid. Treating these growth-inhibited leaves that lack this β -expansin isoform 6 with recombinant *Zea mays* EXPB6 protein produced in *E. coli* improved leaf growth under saline conditions. Expansins were formerly reported to be pH-dependent proteins, being activated by an increased acidity. Camera-based real-time *in planta* ratio imaging of the pH revealed an apoplastic acidification in the leaves of the salt-resistant maize hybrid that maintained growth under NaCl stress, whereas the apoplastic pH of the growth-reduced leaves of the salt-sensitive hybrid did not change. Acidifying the leaf apoplast of the salt-sensitive hybrid using an ATPase activator caused an improved growth under salinity.

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Ihre Notizen

Assembling new flint and dent maize association genetics panels for cooperative research: first results from the CornFed project

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Following Discovery of Americas, Maize was rapidly cultivated at significant scales in several European regions and then spread over time. Traditional European maize open pollinated varieties (OPVs) have been instrumental for the development of hybrid breeding in northern Europe, leading to the European Flint x American Dent heterotic pattern. We will present marker based analyses of diversity evolution within these two genetic pools, from OPVs to inbred lines recently developed by public institutes. A specific focus will be made on two panels of inbred lines created by public institutes and representing these two pools. These panels were recently assembled within the CORNFED project, a trinational initiative involving 14 public and private partners from Spain, Germany and France. Based on the analysis of an array representing 49 585 SNP markers, we will illustrate the respective contributions of ancestral diversity structure and more recent pedigree breeding of inbred lines on the present organization of diversity within these genetic pools. We will then present preliminary results on the use of these panels for association genetics studies to discover loci affecting the variation of traits of interest. Finally we will present optimization methods aiming at defining a set of reference lines in view of heavy phenotyping for physiological traits, that lead to best genomic based prediction of non phenotyped inbred lines.

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New technologies supporting a maize breeding program – current applications and future demands

Milena Ouzunova

KWS is investing substantially into the development of biotechnological breeding tools, including genomics programs for its major crop plants. Major prerequisites for a successful molecular breeding program to support maize breeding are (i) cost efficient high throughput SNP based genotyping platform and (ii) strong biostatistics covering multi-line cross QTL, association mapping, joint linkage and association mapping, and whole genome selection approaches. Significant progress has been achieved recently in both areas. Examples for the impact of an advanced genotyping platform on genomics based molecular breeding approaches will be presented for monogenic and polygenic inherited traits in maize.

In order to meet the future technological demands the maize genomics research will focus on genotyping by sequencing and the utilisation of allelic diversity through re-sequencing approaches as well as on efficient systems for data management and data processing. Future strengthening of the maize molecular breeding programs will require significant efforts in the areas of efficient selection for must-have alleles based on information from QTL/GWAS studies, genomic prediction of test-cross performance, genomic prediction of hybrid performance and control of genetic diversity. As a consequence, novel alleles for introgression into elite germplasm, allele-specific molecular mark-

ers and selection indices for multiple traits will be made available to maize breeders, all potentially applicable for increasing the selection gain in the breeding process.

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Ihre Notizen

Genetic and phenotypic diversity in doubled haploid lines derived from European maize landraces

A. Strigens¹, T. Presterl², W. Schipprack¹ and A. E. Melchinger¹

Since maize has been introduced to Europe in the 15th century, European landraces, mainly of flint type, had plenty of time to get adapted the cooler climatic conditions of Central and Western Europe. The needs and preferences of farmers shaped a broad range of landraces expected to harbor much more diversity than the modern flint breeding pool. This also includes negative properties which hamper efficient use of this germplasm in breeding. The use of the *in-vivo* haploid technology has been proposed to get efficient access to this genetic resource. Negative or lethal recessive alleles would come to expression in the haploid stage and thus be removed from the population. At the same time, the remaining genetic diversity of the landrace can be immortalized in inbred lines in only few steps. Characterization and maintenance of the obtained doubled haploids (DH) would be much easier and identified properties might be rapidly introduced in modern germplasm. Thus, we evaluated 130 DH lines from three European flint landraces in multi-location trials together with 240 modern flint and dent inbred lines for morphological and agronomical traits. The original landraces, as well as “synthetic” landraces re-composed from the respective DH lines were evaluated in the same environments. The inbred and DH lines were further genotyped for 56110 SNP markers. Our aims were to (i) assess the phenotypic diversity within and between the DH-populations in comparison to modern germplasm, (ii) compare population

structure based on phenotype and SNP markers, (iii) look for any “sweep” of alleles during the haploid production and re-synthesis of the landrace, and (iv) evaluate the potential contribution of the landraces to improve the flint breeding pool.

First results show that the phenotypic diversity in the DH populations is of similar magnitude compared to the diversity in elite material. For several traits, the diversity is even lower within the DH populations, suggesting some fixation of these traits by selection or random drift within these landraces. Clustering based on phenotypic data partially corresponded to clustering obtained with marker data and allowed to differentiate the landraces. The difference in grain yield between DHs from landraces and the elite material shows the progress achieved by breeding in the last 60 years. Nevertheless, the best 5% lines in each DH population reach the level of the elite flint population and might therefore be directly used to widen the flint breeding pool.

Acknowledgments: *This study was financed by the German Research Foundation (DFG) (FK: RE2254/3-1). We thank KWS SAAT AG for providing the DH-lines.*

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Ihre Notizen

The landscape of recombination and variation in a European nested association mapping population

Eva Bauer

In the Plant-KBBE project CORNFED a large nested association mapping (NAM) population based on European flint and dent founder lines was established by the CORNFED consortium. The aim of the project is to identify genomic regions in European maize which influence target traits such as biomass production, flowering time and quality traits.

The NAM populations comprise more than 2000 doubled haploid (DH) lines. All populations were genotyped with the high-density MaizeSNP50 array. The genotyping data shed light on genetic relationship and linkage disequilibrium (LD) between the NAM parents. Genetic maps for 11 flint populations and 10 dent populations as well as consensus maps for flint and dent were constructed. The genetic maps reveal genomic regions with strong segregation distortion in the DH populations. Recombination rates uncover recombination hot spots within and across flint and dent populations. High-density genetic maps also allow the comparison of intact parental fragment length after recombination among populations and between flint and dent panels.

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Ihre Notizen

Chromosomal recombination and higher order linkage disequilibrium in four maize populations of double haploid lines

M. Stange¹, B. Stich², T. Schrag¹, E. Bauer³, C.C. Schön³ and A. E. Melchinger¹

Selection efficiency in plant breeding is greatly affected by variation in genetic recombination which can be characterized with a high-density single-nucleotide polymorphism (SNP) map. In order to assess the background levels of linkage disequilibrium (LD), multilocus LD measures can be used to detect simultaneous allele associations among multiple markers. In this study, the recombination landscape and multilocus LD was investigated through SNP linkage maps constructed for four populations of double haploid maize (*Zea mays* L.) lines, derived from four bi-parental crosses. A stepwise selection process was used to select a total of 1775 highly informative and high quality SNPs, with 786 to 1182 SNPs per population, which were used for the construction of linkage maps. High variation in recombination frequencies was observed between different chromosomal regions, ranging from 0 cM/Mbp for pericentromeric regions to values higher than 5 cM/Mbp for teleomeric regions. The investigation of recombination patterns across populations revealed similar trends on the one hand, but also high variation between populations on the other hand, depending on the population parents. In total, 20 out of the 40 investigated chromosomes of all populations showed significant deviation of the observed number of crossovers from the Poisson distribution. The identification and characterization of the re-

combination landscape in double haploid lines, as shown in this study, will facilitate the improvement of the probability to obtain desirable recombinants or to suppress undesirable crossovers.

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Ihre Notizen

Application of Genome Wide Approaches to Maize Breeding using Historical and de novo Data

Claude Lebreton

We examined, through data mining, the respective benefits and shortcomings of line panels, on the one hand, versus bi-parental populations or partial diallels, on the other hand, to estimate marker effects for subsequent Marker Assisted Breeding. Typical populations in a commercial breeding context were used. In the study, we distinguished oligogenic characters (or presumed so) from polygenic ones.

If it weren't for their potential statistical drawbacks, the breeder would naturally opt for line panels to estimate his marker effects for MAS because they only require mining (as opposed to producing on purpose) large sets of already existing (multi-year) data. Besides, marker-trait associations are potentially more durable.

It turns out from our study that line panels are mostly adapted to oligogenic characters. For polygenic traits such as yield, relevant models must be built on bi-parental or diallel populations. The latter populations also perform well for oligogenic traits, whether we used a QTL approach or a Genomic Selection one. Although, in a commercial breeder's context bi-parental populations mostly have one year's data only, first clues are here to demonstrate the portability of their allelic effect estimates over years.

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Ihre Notizen

Genome-based prediction of genetic values in highly structured maize populations

Chris-Carolin Schön

The assessment of quantitative traits in performance tests is time and resource consuming. Thus, prediction of the genetic potential of individuals from their DNA sequence is highly desirable. Advances in molecular high-throughput technologies allow the analysis of tens or hundreds of thousands of single nucleotide polymorphisms (SNPs), that are located at defined positions in the genome and vary between individuals with respect to the nucleotide they carry. Statistical models for prediction of genetic values from these genome-wide molecular marker data will be introduced. Experimental results on genome-based prediction of test-cross performance in different maize populations will be presented.

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Average predictive abilities based on genomic data were high when cross validation schemes allowed for a high degree of relatedness between the training and the validation set. Correlations between predicted and observed performance decreased substantially when training and validation sets were evaluated with different testers or in different years. For prediction of genetic values statistical models using variable selection and prior knowledge on genome structure did not outperform random regression genomic BLUP using the full set of markers.

Ihre Notizen

Whole-genome and metabolic prediction of testcross performance in maize

Christian Riedelsheimer¹, Angelika Czedik-Eysenberg², Christoph Grieder¹, Jan Lisec³, Frank Technow¹, Ronan Sulpice², Thomas Altmann⁴, Mark Stitt², Lothar Willmitzer³ and Albrecht E. Melchinger¹

Hybrid maize breeding has faced tremendous advancements in the fields of inbreeding, phenotyping and trait dissection. However, the production and evaluation of testcrosses remain a major bottleneck due to the inability to accurately predict testcross performance of highly polygenic heterotic traits using line per se performance data or QTL-based marker-assisted selection approaches. Here, we present experimental results of whole-genome and metabolic prediction which emerged as promising novel tools to alleviate this bottleneck. We crossed 285 diverse Dent inbred lines from worldwide sources with two European Flint F1 testers and predicted their general combining abilities (GCA) for seven biomass- and bioenergy related traits which were evaluated at three locations over two years. The lines were genotyped with 56,110 SNPs and 130 metabolites were measured in the fully developed third leaf in field-grown plants. In contrast to the agronomic traits, we found for 26 metabolites a relatively simple underlying genetic architecture. After correcting for population structure and cryptic relatedness, we detected on nine chromosomes 15 distinct SNP-metabolite associations each of which explained 15–32 % of the observed genetic variance. Using prediction models with normally distributed effects for either all SNPs or all metabolites, GCA prediction accuracies obtained from cross-validation ranged from 0.72 to 0.81 when using SNPs and from 0.60 to 0.80 when using metabolites. Although genetic distances only weakly corresponded to metabolic distances, a combination of both SNPs and metabolites did not lead to improved prediction for GCA. Limiting the population to a genetically unstructured core set of 124 unrelated lines led to an average drop in accuracy of only 3.6 % for SNPs and 6.0 % for metabolites suggesting that population structuring or pairwise relatedness affected the accuracies only marginally. We further observed a very moderate reduction in accuracy with declining marker density suggesting that effective population size is considerably smaller in elite breeding

germplasm than for maize in general leading to large haplotype blocks being transmitted intact across generations. In conclusion, our results provide empirical evidence that whole-genome and metabolic prediction using training populations of manageable sizes enable a reliable screening of large collections of diverse inbred lines for their potential to create superior hybrids.

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Genomic prediction of hybrid performance

F. Technow, C. Riedelsheimer, T.A. Schrag, A.E. Melchinger

Identifying high performing hybrids is an essential part of every maize breeding program. Genomic prediction of maize hybrid performance allows identifying promising hybrids, even when they themselves or other hybrids produced from their parents were not tested in field trials.

We used simulations to investigate the effects of marker density (10, 1, 0.3 marker per mega base pair, Mbp-1), convergence or divergence of parental populations, number of parents tested in other hybrid combinations (2, 1, 0), statistical model (including population specific and/or dominance marker effects or not) and estimation method (GB-LUP or BayesB) on the prediction accuracy. The simulations were based on marker genotypes of Central European flint and dent inbred lines, from the ongoing maize breeding program of the University of Hohenheim. To simulate convergent or divergent parent populations, phenotypes were generated by assigning QTL to markers with similar or very different allele frequencies in both pools, respectively.

Prediction accuracies increased with marker density and number of parents tested and were higher under divergent compared to convergent parental populations. Modeling marker effects as population specific, improved prediction accuracy under lower marker densities (1 and 0.3 Mbp-1) but

had almost no effect under the highest density of 0.1 Mbp-1. This indicated that modeling marker effects as population specific will be most beneficial under low linkage disequilibrium. Incorporating dominance effects improved prediction accuracies considerably for convergent parent populations, where dominance results in major contributions of SCA effects to the genetic variance among inter-population hybrids. The general trends regarding the effects of the above mentioned influence factors on prediction accuracy were similar for GB-LUP and BayesB. However, the latter method produced significantly higher accuracies for models incorporating dominance.

Reference: Technow F, Riedelsheimer C, Schrag TA, Melchinger AE (2012) Genomic Prediction of Hybrid Performance in Maize with Models Incorporating Dominance and Population Specific Marker Effects. Theor Appl Genet (accepted for publication)

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Ihre Notizen

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