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Program and Abstracts



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Genetic distance in relation with specific combining abilities and heterosis for vegetative traits in maize

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Prediction of maize hybrids performances based on the genetic distance between their parents has long been an important path in the implementation of molecular marker technology in maize breeding programs. In this study genetic distance assessment of six maize inbred lines was done using 21 SSR primers. In the analysis, 92 alleles were detected with a mean of 4.38 per locus. Genetic distance (GD) determined using Simple matching coefficient (SM) between inbred lines ranged from 0.11 to 0.549. Using UPGMA clustering method a dendrogram was constructed in which inbred lines were separated into two main clusters, one containing 2 inbred lines, and the other one with 4 inbreds. The bigger cluster furthermore was divided into two smaller subclusters. This classification was in accordance with known pedigree data of analysed genotypes. Six investigated inbred lines were furthermore crossed according to an incomplete diallel design forming 15 hybrid combinations. These genotypes were tested in field trials on 3 locations together with inbred lines per se. In this study maize vegetative traits: plant height and leaf number per plant were analyzed. Statistically significant specific combining abilities (SCA) and high parent heterosis (HPH) were calculated for both traits. Spearman's rank correlation coefficient between genetic distance and SCA for plant height and leaf number was positive and statistically significant while the correlation between high parent heterosis and genetic distance although positive was not significant.

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Genetic variation for early development and cold tolerance in DH libraries from maize landraces

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Due to the high sensitivity of current maize varieties to cold stress in early development, farmers bear the risk of yield losses because of cold periods in late spring. Improving cold tolerance in maize could reduce this risk and would allow earlier sowing dates. The European maize landraces are considered as “gold reserve” of genetic variation for many quantitative traits. Strategies for efficiently utilizing this resource are currently evolving. In our study, we aim to detect relevant regions for the expression of cold tolerance through genome-wide association studies (GWAS). Further, we examine the practicability of whole-genome based prediction of genotypic values in material derived from landraces with a focus on cold tolerance related traits. We applied in-vivo doubled-haploid (DH) induction to three selected landrace populations and produced libraries of about 1000 DH lines. The complete set of DH lines was genotyped using the 600k Affymetrix® Axiom® Maize array. In 2017, all lines were phenotyped for early vigor, early plant height, flowering time, final plant height and other agronomic traits in six diverse environments in Germany and Spain.

In GWAS, we identified genomic regions significantly associated with cold tolerance related traits on chromosomes 1 and 10, respectively. Cross-validated genomic predictions yielded intermediate to high predictive abilities for cold tolerance traits within landrace populations (0.48 to 0.60). In predictions across landrace populations, predictive abilities were close to zero. We will use these resources to identify novel candidate genes and to assist breeding for cold tolerance in elite germplasm.

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