Multi-environment validation experiments to assess the accuracy of phenotypic and genomewide selection within biparental doubled haploid breeding populations

Genomewide selection (GS) was first proposed by Meuwissen et al. (2001) and is a promising breeding methodology in animal and plant breeding. While previous marker-assisted breeding strategies such as linkage and association mapping were using only significant markers, all markers are used in GS. In a first step a training population, which is genotyped and phenotyped, is used to estimate marker effects. In a second step these marker effects are used to predict performance of a candidate population, which is only genotyped. Selection then proceeds on the basis of predicted performance. Therefore, the objective of GS is to predict the breeding value of an individual instead of focusing on particular QTL. Several studies for evaluating the accuracy of genomic selection are available for maize (*Zea mays* L), oats (*Avena sativa* L.), wheat (*Triticum aestivum* L), and barley (*Hordeum vulgare* L.) suggesting that genomic selection might be a useful methodology in plant breeding (Albrecht et al., 2011; Lorenzana and Bernardo, 2009; Heffner et al., 2011).

In a commercial maize breeding program, the identification of superior hybrids is time consuming and costly. Because of dominance effects for yield, hybrid performance cannot be predicted from inbred lines per se. Thus, many lines must be evaluated for their testcross performance each year in extensive yield trials. A breeding methodology able to make selections based on predictions from genotypic data is therefore desirable. It has been shown that marker-assisted breeding methods can be more efficient than selecting individuals on the basis of phenotypic values (Cero´n-Rojas et al., 2008). GS is one form of a marker-assisted breeding strategy. Lande and Thompson (1990) proposed a different form of marker-assisted selection (MAS) which is based on the molecular selection index, which maximizes the response to selection by combining information on molecular markers linked to QTL and the phenotypic values of the traits of interest. Dekkers (2007) simulated pig breeding program and used selection index theory by adding marker derived breeding values as a separate correlated trait to the selection index. Greater accuracies were achieved when combining phenotypic values and genomic values.
There have been few large-scale empirical GS studies in crops. To our knowledge no empirical validation studies across multiple years and locations assessing the accuracy of genomewide selection within single biparental breeding populations have been published. The main goal of our experiment is to assess the efficiency of genomewide selection (GS) with respect to phenotypic selection (PS) through empirical validation experiments using commercial breeding material. In particular our objective is to compare the accuracy of different selection criteria (phenotypic selection alone, genomewide selection alone, and different indices for combined phenotypic and genomewide selection) for multiple traits based on multi-environment validation experiments.

Between 150 and 250 doubled haploid (DH) lines from three biparental elite breeding populations were evaluated for their testcross performance in 2008, 2011, and 2012. A total of 150 DH lines of a fourth DH population were evaluated in 2009, 2011, and 2012. The experiments in 2008 and 2009 correspond to a first stage of testcross evaluation of commercial breeding programs (TC1), whereas the experiments in the years 2011 and 2012 are special validation experiments using alpha designs with two replicates, 6 test locations, and partly two testers to evaluate the same set of lines evaluated in 2008 and 2009 at the TC1 level.

References:


