

Optimization of Genomic Prediction of Hybrid Performance in Maize

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In maize hybrid breeding, inbreds from complementary heterotic groups are crossed to create hybrids with superior vigor and increased yield, exploiting a phenomenon known as heterosis. Although genetic and molecular underpinnings of heterosis are still elusive, it has been clear that the extent of heterosis depends on the pair of inbreds used as parents. Identification of pairs of inbreds with superior yield performance in single-cross combination is critical for the success of hybrid breeding. Unfortunately, performance per se of inbred does not provide good assessment of their value in hybrid combination because of strong dominance effect for grain yield in maize (Hallauer, 1990) making it necessary to evaluate the hybrids themselves in extensive yield trials. Maize breeders are unable to

evaluate all possible single cross combinations between inbreds from different heterotic groups because the number of possible single crosses increases exponentially as number of inbreds increases. If performance of all possible hybrids is estimated without generating and testing hundreds or thousands of crosses, it would bring paradigm shift in the efficiency of hybrid breeding (Reif *et al.* 2012).

In view of its potential to accelerate the hybrid breeding, hybrid performance prediction has been the major goal ever since the inception of maize hybrid breeding and numerous studies were carried out to identify reliable hybrid prediction method. Several approaches have been proposed that are described below. Davis (1932) suggested the use of top cross procedure to evaluate the inbreds for their performance in hybrids. In top cross testing, inbred is crossed with genetically broad based tester e.g. open pollinated variety and genetic worth of inbred is determined based on performance of test cross progeny. Although top cross testing has become established and economical approach to assess the genetic worth of inbred in hybrid combination, it has serious limitations. Topcross evaluation of a large number of inbreds is difficult (Albrecht *et al.* 2011) and selections based on single cross performances are performed in later stages which increases the time required for hybrid development. Bernardo. (1996) showed that pedigree-based BLUP is useful for prediction of untested single crosses. Pedigree based BLUP, however, is ineffective in comparing inbreds developed from single bi-parental population, as they possess the same pedigree (Bernardo. 2002), and maize breeders often work with large number of inbreds from same family (Riedelsheimer *et al.* 2013). Also, unavailability of deep pedigree information often limits its use. The relationship between genetic distance (GD) of parental inbreds, measured by

molecular markers, and heterosis has been extensively studied in maize. While it is possible to predict single cross performance using genetic distances for hybrid sets composed of both intra- and inter-heterotic pool crosses, correlations for predicting inter-heterotic group crosses only were reported to be very low (Melchinger. 1999).

Readily available genome-wide marker data and advances in statistical computing in recent years has led to the development of methods for genomic prediction of complex quantitative traits (Meuwissen *et al.* 2001). There is a resurgence of interest in prediction of hybrid performance with simulation and initial experimental studies demonstrating the usefulness of genomic prediction for hybrid performance in maize (Albrecht *et al.* 2011; Albrecht *et al.* 2014; Jacobson *et al.* 2014; Massman *et al.* 2013; Riedelsheimer *et al.* 2012; Technow *et al.* 2014; Windhausen *et al.* 2012). However, most of the experimental studies were focused on prediction of top cross performance of using single tester. Experimental studies on genomic prediction of single cross performance have been based on historical data consisting of established inbred parents with mixed and complex ancestry (Massman *et al.* 2013; Technow *et al.* 2014).

The potential of predicting single crosses made among random progenies derived from a series of bi-parental families, which resembles the structure of germplasm comprising the initial stages of a hybrid maize breeding pipeline, is remained to be investigated. Identification of superior single crosses early in the breeding pipeline would be beneficial to develop superior hybrids more quickly. Moreover, optimizing the application genomic prediction for hybrid performance with respect to the prediction model and training set composition is still an open question (Technow *et al.* 2014). With this background, three objectives have been decided for the present study: 1. Examine the potential of genomic hybrid prediction at early stages in hybrid development pipeline, 2. Investigate the effects of modelling specific combining ability (SCA), epistasis and genotype by environment interaction, and 3. Determine and find balance of important factors influencing success of genomic hybrid prediction.

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