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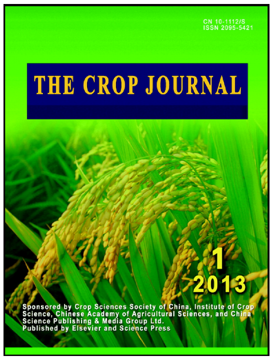

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# Use of genomic selection and breeding simulation in cross prediction for improvement of yield and quality in wheat (*Triticum aestivum* L.)

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**Abstract:** In wheat breeding, it is a difficult task to select the most suitable parents for making crosses aimed at the improvement of both grain yield and grain quality. By quantitative genetics theory, the best cross should have high progeny mean and large genetic variance, and ideally yield and quality should be less negatively or positively correlated. Usefulness is built on population mean and genetic variance, which can be used to select the best crosses or populations to achieve the breeding objective. In this study, we first compared five models (RR-BLUP, Bayes A, Bayes B, Bayes ridge regression, and Bayes LASSO) for genomic selection (GS) with respect to prediction of usefulness of a biparental cross and two criteria for parental selection, using simulation. The two parental selection criteria were usefulness and midparent genomic estimated breeding value (GEBV). Marginal differences were observed among GS models. Parental selection with usefulness resulted in higher genetic gain than midparent GEBV. In a population of 57 wheat fixed lines genotyped with 7588 selected markers, usefulness of each biparental cross was calculated to evaluate the cross performance, a key target of breeding programs aimed at developing pure lines. It was observed that progeny mean was a major determinant of usefulness, but the usefulness ratings of quality traits were more influenced by their genetic variances in the progeny population. Near-zero or positive correlations between yield and major quality traits were found in some crosses, although they were negatively correlated in the population of parents. A selection index incorporating yield, extensibility, and maximum resistance was formed as a new trait and its usefulness for selecting the crosses with the best potential to improve yield and quality simultaneously was calculated. It was shown that applying the selection index improved both yield and quality while retaining more genetic variance in the selected progenies than the individual trait selection. It was concluded that combining genomic selection with simulation allows the prediction of cross performance in simulated progenies and thereby identifies candidate parents before crosses are made in the field for pure-line breeding programs.

**Keywords:** Breeding simulation; Cross prediction; Genomic selection; Parental selection; Usefulness

## 1 Introduction

Breeding techniques have evolved rapidly in the last two decades. Historically, breeders used only phenotypic traits to make key progeny advance decisions, but the efficiency of this practice is reduced by genotype-by-environment (G × E) interaction, errors of measurement, and limitations of phenotyping methods. For example, wheat quality traits are normally tested in later breeding generations owing to (1) the lack of sufficient seeds in early generations and (2) the expense and time required by quality testing in the lab. For this reason, marker-assisted selection (MAS) was introduced in early generations to enable selection on such traits and increase selection efficiency [1–3]. MAS involves two major steps. First, a biparental population is developed to

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