



Potential use of molecular markers for prediction of genotypic values in hybrid maize performance

M. Balestre¹, R.G. Von Pinho², J.C. Souza¹ and R.L. Oliveira¹

¹Departamento de Biologia, Universidade Federal de Lavras, Lavras, MG, Brasil

²Departamento de Agricultura, Universidade Federal de Lavras, Lavras, MG, Brasil

Corresponding author: M. Balestre
E-mail: marciobalestre@hotmail.com

Genet. Mol. Res. 8 (4): 1292-1306 (2009)
Received June 23, 2009
Accepted September 6, 2009
Published October 27, 2009

ABSTRACT. We evaluated the potential of genetic distances estimated by microsatellite markers for the prediction of the performance of single-cross maize hybrids. We also examined the potential of molecular markers for the prediction of genotypic values and the applicability of the Monte Carlo method for a correlation of genetic distances and grain yield. Ninety $S_{0.2}$ progenies derived from three single-cross hybrids were analyzed. All 90 progenies were genotyped with 25 microsatellite markers, including nine markers linked to quantitative trait loci for grain yield. The genetic similarity datasets were used for constructing additive genetic and dominance matrices that were subsequently used to obtain the best linear unbiased prediction of specific combining ability and general combining ability. The genetic similarities were also correlated with grain yield, specific combining ability and heterosis of the hybrids. Genetic distances had moderate predictive ability for grain yield (0.546), specific combining ability (0.567) and heterosis (0.661). The Monte Carlo simulation was found to be a viable alternative for a correlation of genetic distances and grain yield. The accuracy of genotypic values using molecular data information was slightly higher than if no such information was incorporated. The estimation of the

relationship using molecular markers proved to be a promising method for predicting genetic values using mixed linear models, especially when information about pedigree is unavailable.

Key words: BLUP; Relationship; Partial diallel; Genetic accuracy