Potential of maize single-cross hybrids for extraction of inbred lines using the mean components and mixed models with microsatellite marker information

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ABSTRACT. The present study examined the importance of mean (m+a'
and d) components in the performance of single-cross hybrids for the
formation of new populations and determined the contribution of the mixed
model (best linear unbiased predictor of random effects, BLUP) method
associated with molecular markers for the choice of crosses to obtain
interpopulation hybrids. Ten single-cross commercial hybrids of different
companies were used for this purpose, producing all possible double-
cross hybrids through a complete diallel. The hybrids were evaluated
in 15 locations in the agricultural year 2005/2006, using randomized
complete block design with three repetitions. In three of these locations,
estimates of m+a' and d were obtained. DNA was extracted from the
single-cross hybrids and 20 SSR primers were used, nine of which were
linked to QTL for yield. There was no correlation between m+a' of the
single-cross hybrids with general combining ability (r = -0.15) inferring
that populations with lines with high means do not always produce good
hybrids. Also, it was observed that the correlation between the genetic
distances with specific combining ability varied from 0.31 to 0.80 in
the inter-group hybrids, while in the intra-group hybrids these estimates
were low and non-significant. The heritability value obtained by BLUP

was high and greater than that obtained by ordinary least squares (h^2 = 0.95 and 0.86), confirming the greater selection accuracy by the BLUP method. There were no differences between the accuracy values obtained with microsatellite information and without this information, inferring that there was no advantage of progenitor information on balanced data. It can be concluded that the estimate m+a' should not be used as a deciding parameter about the potential for extracting lines from a given population. The heritability and accuracy values obtained by BLUP allow the inference that it is possible to predict success in the choice of progenitors to obtain interpopulation hybrids.

Key words: m+a'; Specific combining ability; BLUP; Molecular markers; Interpopulation hybrids