Genetic parameters and prediction of genotypic values for root quality traits in cassava using REML/BLUP

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ABSTRACT. The aim of this study was to estimate the genetic parameters and predict the genotypic values of root quality traits in cassava (Manihot esculenta Crantz) using restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP). A total of 471 cassava accessions were evaluated over two years of cultivation. The evaluated traits included amylose content (AML), root dry matter (DMC), cyanogenic compounds (CyC), and starch yield (StYi). Estimates of the individual broad-sense heritability of AML were low ($h^2 = 0.07 \pm 0.02$), medium for StYi and DMC, and high for CyC. The heritability of AML was substantially improved based on mean of accessions ($h^2_m = 0.28$), indicating that some strategies such as increasing the number of repetitions can be used to increase the selective efficiency. In general, the observed genotypic values were very close to the predicted average of the improved population, most likely due to the high accuracy (>0.90), especially for DMC, CyC, and StYi. Gains via selection of the 30 best genotypes for each trait were 4.8 and 3.2% for an increase and decrease for AML, respectively, an
increase of 10.75 and 74.62% for DMC for StYi, respectively, and a decrease of 89.60% for CyC in relation to the overall mean of the genotypic values. Genotypic correlations between the quality traits of the cassava roots collected were generally favorable, although they were low in magnitude. The REML/BLUP method was adequate for estimating genetic parameters and predicting the genotypic values, making it useful for cassava breeding.

**Key words:** Breeding; Germplasm; *Manihot esculenta* Crantz; Selection; Genotypic value; Mixed models