Comparison of methods used to identify superior individuals in genomic selection in plant breeding

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ABSTRACT. The aim of this study was to evaluate different methods used in genomic selection, and to verify those that select a higher proportion of individuals with superior genotypes. Thus, F2 populations of different sizes were simulated (100, 200, 500, and 1000 individuals) with 10 replications each. These consisted of 10 linkage groups (LG) of 100 cM each, containing 100 equally spaced markers per linkage group, of which 200 controlled the characteristics, defined as the 20 initials of each LG. Genetic and phenotypic values were simulated assuming binomial distribution of effects for each LG, and the absence of dominance. For phenotypic values, heritabilities of 20, 50, and 80% were considered. To compare methodologies, the analysis processing time, coefficient of coincidence (selection of 5, 10, and 20% of superior individuals), and Spearman correlation between true genetic values, and the genomic values predicted by each methodology were determined. Considering the processing time, the three methodologies were statistically different, rrBLUP was the fastest, and Bayesian LASSO was the slowest. Spearman correlation revealed that the rrBLUP and GBLUP methodologies were equivalent, and Bayesian LASSO provided the lowest correlation values.

Similar results were obtained in coincidence variables among the individuals selected, in which Bayesian LASSO differed statistically and presented a lower value than the other methodologies. Therefore, for the scenarios evaluated, rrBLUP is the best methodology for the selection of genetically superior individuals.

Key words: Statistics; Biometric; SNPs; Selection