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RESUMO

The genetic breeding of *Coffea canephora* is held back by several factors, such as it being a perennial species and bienniality of culture. It is important to apply techniques that enable the selection of superior genotypes while easing the process. Therefore, genome wide association studies (GWAS) have been used in order to identify genetic variations that may be associated with phenotypic traits of interest. The success of this approach depends on the use of a sized population. The objective of the present study was to analyze the influence of the size of the population in detecting significant associations through GWAS. A total of 165 genotypes of coffee plants were genotyped for 17,885 SNPs markers. The data was provided by the Empresa Brasileira de Pesquisa Agropecuária and Empresa de Pesquisa Agropecuária de Minas Gerais in collaboration with the Universidade Federal de Viçosa. The incidence of cercosporiosis was assessed under field conditions. The effect of each marker was estimated by the multiple regressions method through single-SNP. The detection of significant markers was carried through single-SNP method for the application by multiple t-tests with the significance level corrected for the false discovery rate (FDR). Different populations of 165, 149, 133 and 117 individuals were tested. The R *software* was used for carrying out the analyses. Reducing the size of the population reduced the power of detection for the analyzed trait, resulting in a lower number of significant markers when compared to the analysis that considered 165 genotypes. When 165 genotypes were considered, 157 significant markers were found, while when 149, 133 and 117 genotypes were considered, six, 23 and 17 significant markers were found, respectively. These results indicate that reducing the number of genotypes considered also reduces the number of detected significant markers that are linked to the phenotypic trait of interest.

PALAVRAS-CHAVE: GWAS, SNPs, Cercosporiosis

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