GENOME-WIDE SELECTION FOR APOMIXIS IN *Panicum maximum*

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Guinea grass cultivars occupy 20% of 120 million hectares of cultivated pastures in Brazil. Breeding program of this species involves crosses between sexual and apomictic individuals andthe resultant progenies have to be phenotype daccording the reproductive mode, which is of late expression and laborious to perform. Aiming to evaluate the potential association among microsatellite markers and apomixis trait, 317 accessions were screened for 30 microsatellite (SSR) loci in which markers were treated as binary. Of those accessions, 15 were supposedly of sexual reproduction and the remainder apomictic. Accessions were first grouped using Structure 2.3.4 analysis to consider population structure effects, and four genetic clusters were formed. Compressed mixed linear model (MLM) module with Q + K of the Tassel 5.0 software package was employed for genome wide-association of mode of reproduction.MLM association analysis revealed three markers with significant association signals at a threshold of $P<0.05$ and Bonferroni correction. Genomic selection based on Ridge-Regression method was also performed on the data. Accessions of sexual reproduction ranked separately of apomictic ones, except for accession S22 that was in fact apomictic after phenotypic re-evaluation. This result reinforces the power of genomic selection even considering the lack of molecular information in *P. maximum*, mostly on genetic mapping of SSR markers and linkage disequilibrium. Validation of the results is under way on hybrid population from the *P. maximum* breeding program.

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