Evaluation of the genetic variability in a sugarcane association mapping population for drought stress assessed through SSR and AFLP markers

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Drought is one of the major abiotic stresses that significantly affect sugarcane productivity. However, sugarcane has an extensive genetic variability to drought stress response. In the present work, the genetic variability of a group of 79 genotypes belonging to an association mapping population (including commercial varieties, breeding clones and Saccharum species) were assessed though molecular markers derived from microsatellites (SSRs) and Amplification Fragment Length Polymorphism (AFLP). Until now, 12 SSRs and 7 AFLP selective combinations were evaluated. The 12 SSRs produced a total of 196 alleles ranging from 7 (CIR74) to 31 (SCC01) with an average of 16.3 alleles per SSRs. The PIC values ranged from 0.770 to 0.942 with an average of 0.875. Two hundred and five scorable polymorphic markers were obtained for the 7 AFLP selective combinations with an average of 29.28 polymorphic scorable markers per combination. The EcoACT/MseCGT selective combination was the most polymorphic in terns of the number of scorable markers (41) whereas the EcoAGC/MseCGC was the less polymorphic with 17 scorable markers only. The PIC values ranged from 0.252 (EcoAGG/MseCGC) to 0.381 (EcoAAC/MseCGT) with an average of 0.299. This value is high as the maximum PIC value that can be achieved for each AFLP derived loci is 0.5. The estimation of the genetic similarity (GS) among the 79 genotypes was 0.41 with the maximum GS value (0.69) observed between the varieties RB855536 and RB845210 both derived from the cross between SP701143 and RB72454. In the other hand, the minimum GS value (0.17) was observed between an accession derived from S. robustum and IACSP96-7586. The high levels of polymorphism observed was encouraging as a relative small number of SSR primers (12 SSRs primers) and AFLP selective combinations (7 Eco/Mse) were evaluated until now.

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