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MOLECULAR CHARACTERIZATION OF INTROGRESSED HYBRIDS OF SUGARCANE VARYING IN CELLULOSE CONTENT

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Sugarcane produces large lignocellulosic biomass and can be a highly potential alternative crop to fossil fuels. The recalcitrance of lignin reduces energy input/output ratio which necessitates gene identification, expression studies and marker identification of cellulose and lignin biosynthetic genes to diminish the effects of biomass recalcitrance and to improve the conversion efficiency. In the present study thirty-two introgressed hybrids: 17 genotypes representing high cellulose content of above 42.00% (fibre> 25.00%) and 15 genotypes with low cellulose content of < 35.00% (fibre< 17.00%) of different introgression groups [SSH (S. officinarum x S. spontaneum): 14 and SRH (S. robustum x S. officinarum): 18] were characterised using 14 SSR primers developed from cellulose synthase gene families of Populustomentosa. The study aims to test the amplification efficiency of SSR primers of CesA gene developed in Populusfor genetic diversity studies and marker identification in sugarcane. Primer pairs generated alleles ranging from 11 (PtCesA7-intron3) to 17 (PtCesA2-5' UTR) with an average of 12.43 alleles per primer and with a total of 94 polymorphic alleles. Polymorphism information content (PIC) varied from 0.46 to 0.82 with a mean value of 0.64. Dendrogram constructed from similarity matrices using UPGMA method with NTSYSpc v2.0 software grouped the 32 genotypes in to two major clusters with prominent discrimination between the hybrids with varied cellulose content. The similarity coefficient ranged from 0.53 to 0.71 with an average of 0.62. Primer, PtCesA6 (source: promoter region of CesA) amplified a marker PtCesA6200, which showed 92.11% correspondence between the marker and trait (high cellulose content) and also found to be associated with 88.24% of hybrids with high fibre %. The study further recommends the evaluation of marker, PtCesA620 in different Saccharum species and cultivars for effective application in MAS for improved biomass accumulation.