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Genetic variability among sugarcane lines/varieties and their response against whip smut

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Whip smut caused by *Ustilago scitaminea* is an economically important disease of sugarcane. In total, 103 promising sugarcane lines/varieties were screened to evaluate their performance against whip smut. All sugarcane lines were genotyped using simple sequence repeat (SSR) markers to find genetic diversity among them. Three hundred and fourteen (314) alleles were scored with an average of 10.46 alleles per marker. Ninety nine (99%) percent of the alleles were found polymorphic. High Polymorphism Information Content (PIC) values ranging 0.67 to 0.93 calculated for each marker determines the high potential of using these markers for genetic diversity studies. Similarly, the Resolving Power (RP) values which depends upon the distribution of alleles within the genotypes, were also found high ranging from 3.68 (SCC-89) to 16.54 (SMC 545 MS) with an average of 9.12 per marker. DNAMAN generated homology tree was constructed based upon the genotyping files of 103 sugarcane lines/varieties. The genetic similarity of 66% to 88% was found among all the sugarcane lines. Based upon the homology tree, the sugarcane lines were grouped into eighteen (18) clusters. Sugarcane lines under some clusters showed complete resistance to whip smut, whereas in others differential response to whip smut was observed. This indicated that whip smut resistance is neither restricted to particular sub-population nor governed by genes with widespread effect but is indeed a genuine quantitative trait. The markers mSSCIR-19 and mSSCIR-43 can be used to distinguish between whip smut resistant and susceptible sugarcane lines/varieties. These results may help cane breeders in designing crosses between more diverse whip smut resistant sugarcane line for the development of whip smut resistant sugarcane cultivars.

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