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Quality assessment and molecular characterization of rice genotypes using DNA markers

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ABSTRACT : Genetic relatedness among rice varieties were assessed using ten RAPD, two SSR and two STS markers. The 56 rice genotypes studied included improved varieties and landraces collected from different parts of India. The number of alleles per RAPD locus ranged from 3 to 7, averaging 4.7 alleles per locus. Polymorphism information content (PIC) values ranged from 0.474 to 0.811, with an average of 0.665. The number of alleles per SSR locus ranged from 2 to 4, averaging 2 alleles per locus and PIC values ranged from 0.069 to 0.278, with an average of 0.017. The band size for a given SSR locus varied between 170 bp and 180 bp and for STS markers the band size varied between 175bp to 180bp with an average pic value of 0.299. Characterization of the genotypes was also done for important quality parameters including amylose content, gel consistancyn and gelatinization temperature. Cluster analyses were used to group cultivars by constructing dendrograms based on DNA marker analysis and physicochemical characterization of grains. The dendrogram based on molecular marker analysis grouped the 56 rice cultivars into different diverse groups. Clustering of these varieties according to their genotypes as well as phenotypes revealed the possible linkage or pleiotropic effects of the genomic regions associated with some grain quality traits. Information generated through cluster analysis based on phenotypic and genotypic data could be efficiently used in breeding rice varieties harboring grain quality traits. Pure-line selection can be made using farmer varieties that are characterized morphologically and phenotypically in the study.

KEY WORDS : Rice genotypes, DNA markers, Molecular characterization,

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