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Genetic diversity among aerobic rice accessions using RAPD markers

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Investigation was carried out to evaluate genetic diversity between 103 aerobic rice (Oryza sativa L.) accessions using RAPD markers. Eighty random primers were used to generate the RAPD profiles of 103 aerobic rice accessions. Fourteen markers that showed reproducibility were used to detect polymorphism. Of the 94 bands obtained, 74 (78.72%) were polymorphic. The pair wise similarity ranged from 0.62 to 0.94 with a mean of 0.78. The PIC (polymorphic information content) ranged from 0.01 (OPE7) to 0.36 (OPC14 and OPD9) with an average PIC 0.26. The genotypes were grouped into clusters and sub-clusters. The genotype 109 (DGI 155) was found distinct from all other accessions. A group of RAPD primers showing 100% polymorphism can be used in genetic diversity studies of rice germplasm.

Key words: Genetic diversity, RAPD, Rice.

INTRODUCTION

Rice is a staple food for more than 2.5 billion people around the world (IRRI, 2004). Growing rice is the largest single use of land for producing food, covering 9% of the earth's arable land (IRRI, 2002). Asia itself accounts for over 90% of the world's production of rice. About half the total world rice area is rain fed, where drought is a major constraint (Fukai Cooper *et al*., 1998), so cultivation of drought tolerant rice varieties under such conditions is the only alternative. One of the major future challenges for agriculture is to produce more food with less water. Rice is mainly grown in the submerged conditions but there is a need to find out the strategy for growing rice under aerobic conditions to decrease water use in rice production.

In rice, molecular markers have been used to identify accessions (Olufowote *et al*., 1997; Virk *et al*., 1995) to determine the genetic structure and pattern of diversity for cultivars of interest (Akagi, *et al*., 1996). Compared to morphological analysis, molecular markers reveal differences among accessions at the DNA level and thus provide a more direct, reliable and efficient tool for germplasm conservation and management. Molecular markers are useful tools for evaluating genetic diversity and determining cultivar identity (Ni *et al.*, 2002).

Agriculture relies heavily on the genetic diversity of crop plants, during the process of domestication and cultivation of crop plants, a wealth of genetic diversity has been utilized and partly preserved. Thousands of valuable allelic variations of traits of economic significance remain unutilized in nearly all crop plants. Approximately 15 per cent of the potential diversity in crop plants has been utilized for developing new varieties or hybrids. These can be discovered and effectively used to meet the existing and emerging challenges that threaten world food security. The objective of the present study was to evaluate the genetic variation within a collection of aerobic rice accessions and to reveal genetic relationships among them using RAPD markers.

MATERIALS AND METHODS

Plant Materials :

103 Aerobic rice accessions used in the present study were obtained from International Rice Research Institute (IRRI) Philippines. Details of genotypes are shown in Table 1.

Plant DNA extraction :

The genotypes were grown in an experimental field of University of Agricultural Sciences, GKVK, Bangalore. The genotypes were grown in aerobic conditions without water stagnation and irrigation was given at an interval of five days. The leaves were collected at maturity and dried properly in an oven at 55^0C. Dried leaves were then powdered in a mixer, and the fine powder was used for the DNA extraction. DNA was extracted by following the Porebski *et al*. (1997) method with certain modifications. 100mg of leaf powder in 2.0ml of pre-warmed extraction buffer (100mM Tris pH 8.0 containing

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