

TAXONOMY & ECOLOGY

Beyond Classical Approaches

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RANDOMLY AMPLIFIED POLYMORPHIC DNA (RAPD) ANALYSIS OF SABAH AND SARAWAK TRADITIONAL RICE VARIETIES: A PRELIMINARY STUDY

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ABSTRACT

Traditional rice varieties in Sabah and Sarawak have a wide range of genetic diversity which is highly essential to be analysed for improvement and conservation works. The study aims to reveal the genetic diversity between a total of 23 traditional rice varieties from Sabah and Sarawak. The rice varieties were planted in greenhouse and the young leaves were extracted for its genomic DNA. All samples were subjected to RAPD analysis using 14 arbitrary 10-mer primers. PCR amplification of the DNA yielded 83 alleles of which 18.07 percent were monomorphic and 81.93 percent polymorphic. The size ranged of the amplified DNA was mostly between 0.3 kbp and 3 kbp. The cluster analysis of the RAPD data separated out the varieties into four distinct clusters. Relative genetic similarities between the varieties showed a range of 34.4 to 89.2 per cent of similarities. Four primers showed higher number of alleles and five primers showed least number of alleles generated. The study managed to reveal about the genetic diversity and relationships as for preliminary studies. More RAPD primers should be applied in further study to establish and assessing the diversity and relationship among the rice varieties.

Keywords: *Oryza sativa* L., RAPD, genetic diversity, genetic relationship, traditional rice

INTRODUCTION

Rice (*Oryza sativa* L.) is the main source of carbohydrates in Malaysia and it was consumed daily by the peoples. Throughout the year, demands for rice are increases and need to be fulfilled. Therefore, more research and development needs to be conducted on rice in order to release new variety which has improvement in production, shorter period of maturity and others. In order to achieve it, the research should focus on traditional rice varieties.

Traditional rice offers a wide range of genetic diversity and it was reported by Abdullah *et al.* (2003) about 75% of the 10, 730 rice accessions stored in Rice GeneBank at MARDI (Malaysian Agricultural Research and Development Institute) Seberang Perai are of local origin. Besides that, different localities in Malaysia also contribute to the diverse genetic diversity of rice. In Sabah and Sarawak, the rice varieties have its own special characteristics in terms of environmental conditions. Therefore, the release varieties from Peninsular Malaysia can not be planted in Sabah and Sarawak. Moreover, studies on the rice varieties are largely lacking compared to Peninsular

Malaysia. By assessing traditional rice varieties in Sabah and Sarawak, the genetic diversity and relationships can be revealed. These were valuable for breeding and variety improvements in local environments as traditional rice are easier to be manipulated compared to foreign varieties. According to Brondani *et al.* (2006) traditional varieties are more practical as they are more easily crossed with selected germplasm to accelerate the recovery of modern plant types in the breeding lines.

Advances in molecular biology had contributed to the development of new technology for analysing genetic diversity. Randomly Amplified Polymorphic DNA (RAPD) is mostly wide molecular marker used and proved to be useful in studying genetic diversity and variety documentation (Jalaluddin *et al.*, 2007; Virk *et al.*, 2000). As RAPD markers surveys numerous loci in the genome, it is particularly attractive for analysing genetic diversity in rice (Skaria *et al.*, 2011). The information can be utilized for genetic improvement and conservation. RAPD markers also offer a rapid and accurate detection of genetic variation in traditional rice compared to using phenotypic method which it needs longer