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The Study of Genetic Diversity and Relationships on *Carica* sp. by Means of Random Amplified Polymorphic DNA (RAPD) Analysis

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ABSTRACT

The genus of *Carica* comprises 21 species, among them three species have been domesticated and cultivated. They are *Carica papaya, Carica candamarcencis* and *Carica monoica*. In Indonesia, two species have been cultivated viz. *Carica papaya* and *Carica candamarcencis*. In this study, four accessions of *Carica papaya* species and one accession of *Carica candamarcencis* species were analyzed using RAPD technique. We successfully amplified a total of 40 fragments from these DNA genome by using 6 random primers with GC bases content ≥ 60% of each primer. The number of fragments of each primer ranged from 5 to 8 averaged 6.7 fragments per primer. Out of total fragments, 90% showed as polymorphic ranged from 5 to 8 on average 6 fragments per primer. A dendogram based on the UPGMA-link method using Nei and Li similarity and Principal Component Analysis (PCA) plot separated the accessions into two main groups, the *Carica papaya* species on the one side and the *Carica candamarcencis* species on the other side. The result demonstrated that RAPD analysis was able to reveal genetic difference between *Carica papaya* and *Carica candamarcencis* species, as well as genetic diversity in *Carica papaya* species.

Key words: Carica papaya, Carica candamarcencis, Random Amplified Polymorphic DNA (RAPD), Genetic diversity

INTRODUCTION

The genus *Carica* comprise 21 species, and among them, three species have been domesticated and cultivated. Those are viz. *Carica papaya* L., *Carica candamarcensis* Hook and *Carica monoica* (Nakasone and Paull, 1999). Among the three species, only the common papaya, *Carica papaya* L. has high economic value.

Indonesia is very rich in *Carica* germplasm, spreading to almost all over Indonesian archipelago and cultivated as landraces (Pusat Kajian Buah-buahan Tropika, 2000), however, information on the characterization of *Carica* is lack behind. The characterization and quantification of genetic diversity have long been a major goal in evolutionary biology. In plant breeding programs, information on genetic diversity within and among closely related crops species is essential for rational use of genetic resources and particularly useful in characterizing individual accessions and cultivars, for detecting duplications of genetic materials in germplasm collections, and as a general guide in parent's assessment for crop improvement programs as well as developing informative mapping populations for genome mapping.

Molecular markers provide a quick and reliable method for estimating genetic relationships among genotypes of any organism (Thormann *et al.*, 1994). Random amplified polymorphic DNA (RAPD) analysis (Williams *et al.*, 1990) has been used for diversity analysis in a vast array of crops, widely used for the determination of genotypes (Hasizume *et al.*, 1993), gene mapping (Ohmori et al., 1996) and QTL analysis (Grandillo and Tanskley, 1996). This approach is based on the polymerase chain reaction (PCR) (Saiki *et al.*, 1988) amplification of template DNA genome using short, synthetic deoxyribonucleotides of random sequence as primers. Each primer can direct the amplification of several unrelated regions of the genome (Sondur *et al.*, 1996). The resolving power of RAPD technique is several folds higher than visual and protein markers and is much simpler and technically less demanding than RFLP and other similar techniques (Williams *et al.*, 1990).

In this study, we employed RAPD analysis to analyse genetic diversity and relationships between

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