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IDENTIFICATION OF DNA POLYMORPHISM AMONG CLONES OF *HEVEA BRASILIENSIS* MUELL. ARG. USING RAPD ANALYSIS

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RAPD (Random amplified polymorphic DNAs) were used to study the DNA polymorphism in 37 *Hevea* clones representing variability for several morphological, physiological and other characters. Eighty random sequences 10-mer primers were used of which nine produced clear and scorable bands while eight produced polymorphic amplification products between 300 to 4000 base pairs in size, sufficient to distinguish between the clones. Of bands from the 8 primers 51.5% were polymorphic in the *Hevea* clones studied. A dendrogram developed using Jaccard's coefficients indicated genetic relationships among these clones. Most of the primary clones were clustered together in the dendogram. UPGMA cluster analysis indicated that some of the clones are genetically close although they have been developed from different breeding programmes. The presence of polymorphic bands in the genomic DNA was further confirmed by Southern blot analysis. Detection of DNA polymorphism in the *Hevea* clones opens up the possibility of development of molecular map. This molecular approach will be useful for developing marker-assisted selection tools for genetic improvement of *Hevea*.

Key words: DNA polymorphism, *Hevea brasiliensis*, RAPD, Random oligonucleotide.

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INTRODUCTION

Crop improvement has been achieved in rubber tree (*Hevea brasiliensis*) by incorporating new sources of genetic variability for high rubber production and disease resistance (Costa *et al.*, 2000). If selection is only for certain desirable traits, it may lead to inbreeding depression in an advanced generation. Therefore, genetic variability in a breeding population needs to be preserved to sustain long-term breeding programmes. However, information on genetic relationships among clones is rather limited. The perennial nature, the long breeding and selection cycle and difficulties in raising F_2 population make conventional genetic analysis in *Hevea* difficult (Varghese *et al.*, 1997; Lespinasse *et al.*, 2000).

The DNA based marker procedures lead to a greater understanding of genetic relationships among clones or cultivars. These techniques are used by the breeders to identify genetic variability among the species and clones / cultivars by means other than morphological characteristics (Graham and McNicol, 1995). Morphological traits do not provide good estimates of genetic distance because they are influenced by the environment and are not variable enough to adequately characterize genetic differences among elite genotypes. Biochemical methods, such as isozyme analysis, have been used to determine the degree of variability within plant population. Isozyme analysis is limited by the small number of marker loci available, a general lack of polymorphism for these loci in elite breeding materials and variability in the banding patterns due to the stage of plant development (Bai *et al.*, 1998). Isozyme loci