

## AN APPROACH TO IDENTIFY DISEASE RESISTANCE GENE ANALOGUES IN *HEVEA*

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A preliminary attempt was made to identify possible disease resistance gene analogues in rubber. A procedure was developed for the extraction of high quality DNA from rubber leaves, which can be used for the polymerase chain reaction (PCR) amplification of DNA. Eighteen primers, designed based on homologies between known resistance genes, were used in various combinations to amplify sequences from rubber cultivar FX 516, which is resistant to *Phytophthora* leaf fall disease and cultivar RRTI 105, which is tolerant. The PCR products were cloned into plasmid vectors and the cloned inserts were sequenced. Although none of the clones obtained had high homology to resistance gene sequences, the putative protein encoded by one sequence had some homology to hem N gene.

**Key words :** Cloning, *Hevea*, *Phytophthora* leaf fall, Polymerase chain reaction, Resistance genes.

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### INTRODUCTION

Exploitation of genetic resistance is one of the main approaches for controlling stresses in plants. Breeding for resistance to both biotic and abiotic stresses requires the development of suitable and reliable screening techniques and identification of heritable resistance characters. Considerable efforts have recently been made to utilize molecular methods to combat diseases caused by fungi, bacteria and viruses. Abnormal leaf fall disease caused by *Phytophthora* spp. leading to serious crop loss is a major biotic stress in rubber (Jacob *et al.*, 1989). Rubber being a perennial tree

crop, any attempt to breed and evolve clones takes a long period of 25 to 30 years. It is therefore important to develop techniques to speed up the process. Low and Gale (1991) have discussed the potential usefulness of RFLP markers in *Hevea* breeding programme. More recently, a number of genes that confer resistance against a diverse range of diseases have been cloned from a range of plant species (Hammond-Kosack and Jones, 1996). Many of these genes contain conserved domains that are postulated to encode functional features such as kinase activity, nucleotide binding