DNA BARCODES FOR IDENTIFICATION OF *PHYTOPHTHORA* SPP. INFECTING NATURAL RUBBER TREES IN INDIA

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Abnormal leaf fall (ALF) disease caused by *Phytophthora* spp. is one of the most destructive diseases of rubber causing extensive defoliation leading to a reduction in the yield of natural rubber. Shoot rot and die back occur on young rubber plants due to infection with *Phytophthora* spp. Panel diseases *viz.* black stripe and patch canker are also caused by *Phytophthora* spp. on mature rubber trees. As a molecular tool for species identification, DNA barcodes offer significant potential using a short, unique, standardized portion of the DNA. This study aimed at presenting a molecular phylogeny of the four major *Phytophthora* species *viz. P. meadii, P. botryosa, P. colocasiae* and *P. citrophthora* predominantly infecting rubber trees in India. Two nuclear DNA regions: Internal Transcribed Spacer region of the nuclear ribosomal DNA and the microtubule constituent protein β-tubulin, and the mitochondrial gene cytochrome c oxidase subunit II were used in this study to get a more resolved phylogeny of the four *Phytophthora* species of rubber, providing better interpretation of the overall evolutionary history of the genus. Sequence information suggests that *P. meadii* has a hybrid origin with *P. colocasiae* as a parent and it is also possible that *P. citrophthora* is an asexual derivative of *P. colocasiae.* The study also demonstrates significant diversity in the population of *Phytophthora* spp. isolated from rubber plantations in India.

Key words: β-tubulin, Cytochrome c oxidase, DNA barcoding, Internal Transcribed Spacer, Molecular phylogeny, *Phytophthora* spp., Species identification.

INTRODUCTION

DNA sequences are a major source of information for understanding any species. DNA barcoding is an important species identification technique, holding promise for reliable, quick and accurate identification of fungal pathogens. As a unique and standard species identification tool, it offers a great potential by using various conserved universally accepted DNA barcode regions. DNA barcoding was first proposed by Hebert *et al*. (2003a) who used standardized 500 to 800 bp cytochrome c oxidase I sequences to identify species of all eukaryotic kingdoms with primers applicable for the broadest possible taxonomic group. DNA barcoding is being used for accurate, efficient and high-throughput assignment and discrimination of numerous animal, plant and fungal taxa (Kress and Erickson, 2007; Seifert *et al*., 2007; Chen *et al*., 2010; Massimiliano *et al*., 2010).

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