

**MORPHOLOGICAL AND GENETIC VARIATION OF *Rigidoporus microporus* ISOLATES FROM *Hevea brasiliensis***

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*Rigidoporus microporus* is one of the most destructive root pathogenic fungi. This pathogen infects a wide range of hosts in tropics and subtropics among which *Hevea brasiliensis* is notable with its white root disease. The variation among 11 isolates of *R. microporus*, collected from different rubber growing agro-climatic regions of Sri Lanka were assessed on growth rate, colony characteristics and pH sensitivity. The molecular analysis was performed using 15 random primers by RAPD-PCR. Different isolates varied significantly in growth rate and pH sensitivity. Isolate, Rm 9 showed the highest growth rate, while the isolate Rm 2 showed the lowest growth rate on Malt Extract Agar (MEA). A notable maximum dry weight occurred when pH of the medium was 7. Of the 15 primers, six (OPM 5, OPB17, OPL 8, OPN 14, OPN 13 and OPL 10) showed reproducibility with 80 bands, and with an average of 13.33 bands per primer. Molecular cluster analysis indicated two distinct clusters and many sub clusters. Rm 4, Rm 7 and Rm 10 were clustered into one group, based on pH sensitivity and molecular analysis and those isolates had comparatively higher dry weight at pH 7. The results indicated that there is no correlation between genetic variation of *R. microporus* isolates and their geographical origin. Therefore, *R. microporus* has a greater potential to spread across plantations of different agro-climatic regions in Sri Lanka, with the possibility of reaching epidemic levels of the disease.

**Keywords:** Genetic variability, *Hevea brasiliensis*, RAPD-PCR, *Rigidoporus microporus*