

Molecular identification of the causal agent of horse hair blight *Marasmius crinis-equi* in tea (*Camellia sinensis*)

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Horse hair blight (HHB) prevails in tea plantations of Sri Lanka below 1200 m altitude, and it has been reported from a wide range of host plants including tea. HHB forms black, horse hair-like network on the canopy of the affected tea bush. Although there are no records supporting HHB as a pathogen in tea plants, its fungal network directly interferes plucking, pruning and other agronomic practices during tea cultivation. The causal agent of HHB in tea had been previously identified as *Marasmius crinis-equi* (Basidiomycetes) by using morphological characters. However, identification of HHB fungus under *in-vitro* conditions is always difficult as the fungus does not produce conidia or any other distinctive structures in culture. Therefore, the aim of the present study was to confirm the identity of HHB fungus by DNA sequencing. DNA was extracted both from pure cultures of HHB established from rhizomorphs (strands) as well as fruit bodies collected from the field. Polymerase chain reaction was conducted for four samples using universal primers, ITS1 and ITS4-B which amplifies internal transcribed spacer (ITS) region of the 18S-26S nuclear ribosomal DNA. During the BLAST search, DNA sequences of the resultant ITS amplicons (approximately 850 bp) showed 96-97% identity to *Marasmius crinis-equi* at nucleotide level. Thus, the ITS sequence-based identification confirmed the phenotypic identity of HHB causal agent as *Marasmius crinis-equi*. Further, the identity of pure cultures of HHB was possible only by adopting sequence based identification approach.

Keywords: Horse Hair Blight, Sequence-based identification, *Marasmius-crinis equi*, Tea

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