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Fungal community associated with different stages of pathogenesis of Rough Bark Disease of cinnamon in major cultivation regions of Sri Lanka

H.D.A. Tharangani^{1,2*}, D.M. De Costa¹ and G.G. Jayasinghe³

¹ Department of Agricultural Biology, Faculty of Agriculture, University of Peradeniya, Sri Lanka

² Post Graduate Institute of Agriculture, University of Peradeniya, Sri Lanka

³ National Cinnamon Research and Training Center, Department of Export Agriculture, Palolpitiya, Thihagoda, Matara, Sri Lanka

Abstract

Rough bark disease (RBD) is an economically important disease in cinnamon grown in Sri Lanka. The aim of the present study was to determine the fungal genera/species consistently associated with the RBD-infected stems and their relative abundance at different stages of the pathogenesis. Cinnamon stems showing typical RBD symptoms of initial, moderate, and severe stages of the disease development were collected from a total of 41 fields in Galle, Matara, Ratnapura, Kalutara and Matale districts. Fungi were isolated using PDA medium and identified based on their colony and spore morphology. Morphologically different fungal isolates which were consistent to different locations of a selected district and different disease developmental stages were proved for pathogenicity by standard Koch's rules under field conditions. Data collected was used to calculate colony forming unit (CFU) richness, fungal colony abundance, relative abundance of morphologically identified fungi and Shannon-Wiener diversity index. A total of 2407 different fungal isolates were obtained as pure cultures and based on the colony and spore morphology, they were grouped as Pestalotia-like (1909), Colletotrichum-like (150), Botryodiplodia-like (213), Phomopsis spp.-like (110), Trichoderma spp. (2) and unidentified fungi (23). A representative set of fungi of the above categories were identified by molecular methods as Pestalotia spp., Colletotrichum spp., Botryodiplodia spp., Phomopsis spp. and Trichoderma spp. Fungal CFU richness did not differ significantly among the districts but differed among the disease developmental stages. Fungal abundance significantly varied among the districts from where the samples were collected ($P < 0.05$). Fungal diversity index differed significantly among disease developmental stages ($P < 0.05$) having the highest at the severe stage. Relative abundance of Botryodiplodia, Colletotrichum and Pestalotia spp. differ significantly ($P < 0.05$) among the disease developmental stages. No significant difference for the relative abundance of Botryodiplodia spp., Colletotrichum spp., Pestalotia spp., Phomopsis spp. and Trichoderma spp. among the districts ($P > 0.05$). Findings confirmed that consistent association of Pestalotiopsis, Colletotrichum, Botryodiplodia and Phomopsis spp. (which were proven to be pathogenic) with RBD infected stems with a shift of their relative abundance among the disease developmental stages.

Keywords: Abundance, Fungal diversity index, Molecular identification, Morphological, Richness

*Corresponding Author: achz1991@gmail.com