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Molecular phylogenetics and anti-Pythium activity of endophytes from rhizomes of wild ginger congener, Zingiber zerumbet Smith

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Abstract

Zingiber zerumbet, a perennial rhizomatous herb exhibits remarkable disease resistance as well as a wide range of pharmacological activities. Towards characterizing the endophytic population of Z. zerumbet rhizomes, experiments were carried out during two different growing seasons viz., early-June of 2013 and late-July of 2014. A total of 34 endophytes were isolated and categorized into 11 morphologically distinct groups. Fungi were observed to predominate bacterial species with colonization frequency values ranging from 12.5 to 50%. Among the 11 endophyte groups isolated, molecular analyses based on ITS/16S rRNA gene sequences identified seven isolate groups as Fusarium solani, two as F. oxysporum and one as the bacterium Rhizobium spp. Phylogenetic tree clustered the ITS sequences from Z. zerumbet endophytes into distinct clades consistent with morphological and sequence analysis. Dual culture assays were carried out to determine antagonistic activity of the isolated endophytes against Pythium myriotylum, an economically significant soil-borne phytopathogen of cultivated ginger. Experiments revealed significant P. myriotylum growth inhibition by F. solani and F. oxysporum isolates with percentage of inhibition (PoI) ranging from 45.17 ± 0.29 to 62.2 ± 2.58 with F. oxysporum exhibiting higher PoI values against P. myriotylum. Using ZzEF8 metabolite extract, concentration-dependent P. myriotylum hyphal growth inhibition was observed following radial diffusion assays. These observations were confirmed by scanning electron microscopy analysis wherein exposure to ZzEF8 metabolite extract induced hyphal deformities. Results indicate Z. zerumbet endophytes as promising resources for biologically active compounds and as biocontrol agents for soft rot disease management caused by Pythium spp.

Keywords: Bioactivity; Endophyte; Fusarium spp.; Soft-rot disease; Zingiber zerumbet.