

Shift in the Rhizosphere Soil Fungal Community Associated with Root Rot Infection of *Plukenetia Volubilis* Linneo Caused by *Fusarium* and *Rhizopus* Species

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Abstract : Background: *Plukenetia volubilis* Linneo is an oleaginous plant belonging to the family Euphorbiaceae. Due to its seeds containing a high content of edible oil and rich in vitamins, *P. volubilis* is cultivated as an economical plant worldwide. However, the cultivation and growth of *P. volubilis* is challenged by phytopathogen invasion leading to production loss. Methods: In the current study, we tested the pathogenicity of fungal pathogens isolated from root rot infected *P. volubilis* plant tissues by inoculating them into healthy *P. volubilis* seedlings. Metagenomic sequencing was used to assess the shift in the fungal community of *P. volubilis* rhizosphere soil after root rot infection. Results: Four *Fusarium* isolates and two *Rhizopus* isolates were found to be root rot causative agents of *P. volubilis* as they induced typical root rot symptoms in healthy seedlings. The metagenomic sequencing data showed that root rot infection altered the rhizosphere fungal community. In root rot infected soil, the richness and diversity indices increased or decreased depending on pathogens. The four most abundant phyla across all samples were Ascomycota, Glomeromycota, Basidiomycota, and Mortierellomycota. In infected soil, the relative abundance of each phylum increased or decreased depending on the pathogen and functional taxonomic classification. Conclusions: Based on our results, we concluded that *Fusarium* and *Rhizopus* species cause root rot infection of *P. volubilis*. In root rot infected *P. volubilis*, the shift in the rhizosphere fungal community was pathogen-dependent. These findings may serve as a key point for a future study on the biocontrol of root rot of *P. volubilis*.

Keywords : *fusarium* spp., *plukenetia volubilis* l., *rhizopus* spp., rhizosphere fungal community, root rot

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