

Structural and Dynamic Analysis of Phyllosphere Fungal Community of Walnut Leaves Infected by Leaf Spot Disease based Illumina High-Throughput Sequencing Technology

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Abstract

High-throughput sequencing technology was used to analyse the species diversity, richness and dynamics of fungal communities in healthy and infected walnut leaves. The dominant phyla included Ascomycota, Basidiomycota, and Glomeromycota; the dominant classes were Tremellomycetes, Dothideomycetes, and Leotiomycetes; the dominant orders were Tremelellas, Capnodiales, and Erysiphales; the dominant families were Bulleribasidiaceae, Mycosphaerellaceae, and Erysiphaceae; the dominant genera were Vishniacozyma, Cercospora, and Ramularia; and the dominant species were Vishniacozyma heimaeyensis, Cercospora asparagi, and Cladosporium chasmanthicola. The results of this study also provided a new understanding of the succession of the walnut phyllosphere fungal community, filling a void in the knowledge of the microbial diversity associated with walnut leaf spot disease. At the same time, these results provide a scientific basis for early intervention and micro-ecological regulation of walnut phyllosphere fungal communities to prevent and control leaf spot or anthracnose.

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