

Ecological Shifts of Microbiota in Ginseng Disease Suppressive soil

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The phenomenon in which the damage of plant diseases is suppressed by continuous cropping is defined as "suppressiveness" and the development of suppressive soils and key beneficial microorganisms have been identified through various previous studies. However, no studies have been conducted on microbial communities related to disease occurrence before the initial occurrence of diseases in crop monoculture. Here we aimed to investigate the ecological modifications of pathogen population density in soil, disease occurrence rate, and microbiota community shifting during ginseng monoculture better to understand the tripartite social relationships in the monoculture system. To achieve the study's objectives, a long-term monoculture of ginseng was established. The microbial diversity and community structure were analyzed using high-throughput sequencing, and the pathogen population density and disease occurrence rate were determined using qPCR and observation. The results showed that the initial rhizosphere bacterial community of ginseng had already collapsed before the development of the root rot disease. The study also identified the crucial role of soil-borne pathogens in causing disease and the loss of initial keystone taxa populations in the early stages of monoculture. Our study revealed a novel aspect of soil microbiota dynamics during ginseng monoculture, with seven distinct microbes (Beijerinckiaceae, Comamonadaceae, Devosiaceae, Rhizobiaceae, Sphingobacteriaceae, Sphingomonadaceae, and Xanthomonadaceae) participating in soil nitrogen metabolism as an 'initial community' that regulates root rot disease through nutritional competition. The findings contribute to ecological research on disease-suppressiveness soil, disease management, and sustainable agriculture.

Keywords: Influencer taxa, Ginseng, Keystone taxa, Root rot disease, Suppressiveness soil