



Microbial diversity in *Paris polyphylla* var. *yunnanensis* rhizomes of varying ages

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ABSTRACT. Endophyte microorganisms live inside plants without causing them any apparent damage. Recently, endophytic microorganisms have attracted attention because they can produce bioactive compounds of biotechnological interest. The endophytic microorganisms in *Paris polyphylla* var. *yunnanensis* (Liliaceae) - a species used since antiquity in traditional Chinese medicine - are under scrutiny because they may be responsible for producing the bioactive metabolites associated with the plant. The levels of bioactive metabolites in the rhizomes of *P. polyphylla* increase with rhizome age. To elucidate the roles played by endophytes in the accumulation of bioactive metabolites, we investigated the community structure and diversity of the endophytic microorganisms in *P. polyphylla* rhizomes of different ages (4, 6, and 8 years) using 16S rRNA and internal transcribed spacer (ITS) sequence analysis. 16S rDNA amplicon pyrosequencing revealed that the number of operational taxonomic units was lower in the 8-year-old samples than in the other samples. A total of 28 phyla were observed in the *P. polyphylla* samples and the predominant

bacteria were of the Cyanobacteria and Proteobacteria phyla. Moreover, the percentage of Cyanobacteria increased with rhizome age. Similarly, ITS1 amplicon pyrosequencing identified developmental changes in the most abundant fungal classes; some classes were more prevalent in the 8-year-old rhizomes than in younger rhizomes, indicating the importance in secondary metabolism in older rhizomes. Our study showed that endophyte microorganism diversity and prevalence depend on *P. polyphylla* rhizome age. There was also an indication that some endophyte microorganisms contribute to the higher saponin content in older *P. polyphylla* specimens.

Key words: Endophytic microorganism; *Paris polyphylla*; HiSeq 2000 sequencing