

秦岭蕙兰根系微生境真菌群落结构与土壤环境因子的 时空动态及相互关系

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摘要:【背景】野生兰花在植物多样性、植物进化和植物与环境关系等研究领域有非常重要的地位。由于兰花非常漂亮,野生兰花的盗采和非法交易是一个世界性的问题,联合国《濒危野生动植物种国际贸易公约》把所有的野生兰花都被纳入了保护范畴。蕙兰是典型的菌根共生植物,共生真菌在蕙兰的各个生长阶段发挥着重要的生态作用,而我们对蕙兰共生真菌群落结构与土壤环境因子的时空动态却知之甚少。【目的】为了掌握不同生长阶段蕙兰根系微生境以及真菌群落特征,【方法】本文以秦岭野生蕙兰为研究对象,采用高通量测序技术研究了原生态下蕙兰微生境真菌的群落组成与土壤环境因子的时空变化及其相互关系。【结果】研究表明蕙兰根内真菌群落和土壤优势真菌群落存在季节性变化。蕙兰根内、根际、非根际优势真菌群落易受季节变化影响的程度依次为根际土>非根际土>根内。3者真菌群落的 Shannon 和 Chao1 指数变化趋势几乎相同,Shannoneven 指数不存在季节差异。根内真菌的 Shannon 和 Chao1 指数显著低于土壤真菌,但 Shannoneven 指数最高。根据 β 多样性分析,春季与秋季的真菌群落结构差异最大,根内真菌与土壤真菌的群落结构存在显著差异。总的来说,蕙兰根系微生境中真菌群落的空间变异大于时间变异。对土壤环境因子的分析表明真菌在冬春季节的分解过程中易受到 C 的限制,在所有阶段受到 P 而不是 N 的限制。春夏季节的真菌相对丰度与土壤元素含量呈正相关,秋冬季节的真菌与土壤元素呈负相关,土壤 pH 对真菌的影响与土壤元素相反。【结论】了解微生境真菌群落变化规律对蕙兰保护而言无疑是重要的,我们推测这种变化可能来自于蕙兰根系平衡和调整微生物群落结构的“招募”功能,而这个过程很可能发生在春季。由于我们目前的研究仅限于同一生境的真菌群落状态,因此无法在更大范围内评估这种动态模式的适用性,可能需要在宏观空间上选择多个地点进行更长时间和更精细时间的深入研究。

关键词: 蕙兰; 根系微生境; 根际; 真菌群落; 时空动态; 秦岭

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Spatiotemporal dynamics and interrelationships between fungal composition and soil environmental factors in the root microhabitat of *Cymbidium faberi* in Qinling Mountains, China

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Abstract: 【Background】 Wild orchids hold a significant position in research fields such as plant diversity, plant evolution, and the relationship between plants and the environment. Due to their aesthetic appeal, the illegal

harvesting and trade of wild orchids pose a global issue, leading the United Nations to include all wild orchids under protection in the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES). Wild orchids like *Cymbidium faberi* are pivotal components of plant diversity and evolution but face threats from illegal harvesting, necessitating protective measures such as inclusion in CITES. Understanding the spatiotemporal dynamics of its mycorrhizal fungal communities is crucial for devising effective conservation strategies. **【Objective】** To address this, we investigated the seasonal variations in fungal communities within roots, rhizosphere soil, and bulk soil across different growth stages of *C. faberi*. **【Method】** High-throughput sequencing technology was employed to analyze the fungal community composition and its correlation with soil environmental factors in the Qinling Mountains in their native habitat. **【Result】** Our findings revealed that rhizosphere soil exerts the most substantial influence on fungal communities, followed by bulk soil and roots. Notably, significant differences were observed between spring and autumn communities, particularly between root and soil fungi. Spatial variation within root microhabitats was found to surpass temporal variation. Furthermore, our study elucidated the role of soil environmental factors, indicating carbon (C) constraints on fungal decomposition during winter and spring, while phosphorus (P) limitations persist throughout growth stages. Fungal abundance correlates positively with soil element content in spring and summer but negatively in autumn and winter, with soil pH exhibiting contrasting effects. **【Conclusion】** These insights underscore the importance of understanding spatiotemporal dynamics for *C. faberi* conservation and suggest avenues for future research to generalize these findings across broader spatial and temporal scales.

Keywords: *Cymbidium faberi*; microhabitat; rhizosphere; fungal community; spatiotemporal dynamics.