

Pathophysiology and transcriptomic responses of *Pinus armandii* defenses to ophiostomatoid fungi

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Abstract: **【Objective】** *Pinus armandii* Franch. is an ecologically and economically important evergreen tree species native to western China. *Dendroctonus armandi* and pathogenic ophiostomatoid fungi pose substantial threats to *P. armandii*. With the interplay between species, the defense mechanisms of *P. armandii* have evolved to withstand external biotic stressors. However, the interactions between *P. armandii* and pathogenic ophiostomatoid fungal species/strains remain poorly understood. We aimed to analyze the pathophysiological and molecular changes in *P. armandii* following artificial inoculation with ophiostomatoid species. **【Method】** Four representative ophiostomatoid species (*L. qinlingense* and *O. shennongense* two dominant and widespread species in the ophiostomatoid community and *G. parakesiyea* and *Ophiostoma* sp. 1 two less frequently obtained but widely distributed ophiostomatoid fungal species across the sampling area) associated with *D. armandi* on *P. armandii* were selected for pathogenicity analysis. Chemical analyses were performed to assess changes in monoterpene content during host responses to pathogens to clarify the differences in virulence among different ophiostomatoid fungal species/strains. Additionally, a transcriptome assay was used to analyze differential gene expression between co-/single inoculation of *P. armandii* with fungal species. **【Result】** The study revealed that *L. qinlingense* produced the longest necrotic lesions, and *G. parakesiyea* produced the shortest. All strains induced monoterpene release, and monoterpene levels of *P. armandii* were positively correlated with fungal virulence ($R^2=0.93$, $P<0.01$). Co-inoculation of two dominant highly (*L. qinlingense*) and weakly virulent (*O. shennongense*) pathogens reduced the pathogenicity of the highly virulent fungi. Transcriptomic analysis of *P. armandii* (LQ: *L. qinlingense* treatments, QS: co-inoculation treatments, and OS: *O. shennongense* treatments) showed that the expression pattern of differentially expressed genes (DEGs) between QS and OS was similar, but different from that of LQ. The DEGs (LQ vs. QS) involved in flavonoid biosynthesis and phenylpropanoid biosynthesis were downregulated. Notably, compared with LQ, QS significantly decreased the expression of host defense-related genes. **【Conclusion】** This study provides a valuable theoretical basis for managing infestations of *D. armandi* and associated ophiostomatoid fungi.