

Discovery of Mycovirus Community in White Pine Blister Rust Ecosystems by Rust Transcriptome Profiling

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In North America, the nonnative rust fungus *Cronartium ribicola* kills immature native five-needle pine trees and indirectly predisposes maturing trees to secondary attack by insects and other fungi, which may result in severe mortality. Since the early 1900s when *C. ribicola* arrived, environmental factors, individual trees, the rust fungus, and insects (for example, mountain pine beetle [*Dendroctonus ponderosae*]) have all interacted to dramatically change forested ecosystems across North America. To date our white pine blister rust (WPBR) research has generated genomics data from the WPBR ecosystem, including transcriptomes and single nucleotide polymorphisms (SNPs) from healthy western white pines (WWPs, *Pinus monticola*), whitebark pines (WBPs, *P. albicaulis*), and infected white pines (down to 60 percent of transcripts from tree tissues, up to 40 percent of transcripts from *C. ribicola*), and from *C. ribicola* strains at different stages of its life cycle by RNA-sequencing technology. Transcriptome analyses have identified many expressed genes derived from mycoviruses. Even though the genomic information from organisms other than white pine and *C. ribicola* accounted for about 1 percent of the total sequence data, this eco-genomics strategy showed complex interactions of multiple

organisms in the WPBR ecosystem. Bioinformatics analysis indicates that there are multiple mycoviral double-stranded RNAs (ds-RNAs) in *C. ribicola*, the presence of which was further supported by ds-RNA extraction and gel electrophoresis analysis. We observed variation in mycoviral sequences (including presence and absence) across *C. ribicola* strains collected from British Columbia (Canada) and Oregon (USA). Kinloch et al. (2004) provided evidence and suggested cytoplasmic inheritance of *C. ribicola* virulence (both *vcr1* and *vcr2*), so our discovery of novel mycoviral ds-RNAs as cytoplasmic genetic factors in *C. ribicola* may open new avenues for WPBR management. We are investigating rust mycoviruses to develop cytoplasmic markers for epidemiological diagnosis and study of biodiversity. Progress on this and our related work will be further discussed.

REFERENCES

Kinloch, Bohun B., Jr.; Sniezko, Richard A.; Dupper, Gayle E. 2004. Virulence gene distribution and dynamics of the white pine blister rust pathogen in western North America. *Phytopathology*. 94(7): 751–758.

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