

Characterizing the ectomycorrhizal fungal community of whitebark pine (*Pinus albicaulis*) in Mount Revelstoke and Glacier National parks

by Hanno Southam

Course: ENVR 449  
Instructor: Dr. Leah May Ver

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Department of Earth Ocean and Atmospheric Science  
University of British Columbia, Vancouver

Supervisors

Dr. Suzanne Simard, Department of Forest and Conservation Sciences (UBC)

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Natalie Stafli, Lead Ecologist Mount Revelstoke and Glacier National parks

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Committee

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## Abstract

Whitebark pine (WBP) (*Pinus albicaulis* Engelm.) is an endangered, high-elevation tree species and an obligate ectomycorrhizal mutualist. The ectomycorrhizal (ECM) fungal community with which it associates is central to its recovery. Previous efforts to describe this community have been focused in a single region of the species range (Greater Yellowstone Ecosystem) and relied on above ground sporocarp (mushroom) surveys. This project built upon that work by using NextGeneration sequencing of the ITS2 region to describe the WBP ECM fungal community in Mount Revelstoke and Glacier National parks of Canada. Samples were taken from root tips and adjacent soil of mature trees, naturally regenerated seedlings and planted seedlings. The major ECM lineages previously recorded with WBP were confirmed at our project site: generalist ascomycetes (*Cenococcum*, *Wilcoxina*), Agaricales (*Cortinarius*, *Inocybe*, *Tricholoma*, *Hygrophorus*), Atheliales (*Piloderma*, *Amphinema*, *Tylospora*), Suilloids (*Suillus*, *Rhizopogon*), Russuales (*Lactarius*, *Russula*) and Theleporales (*Pseudotomentella*, *Tomentella*). Twenty-one new species and two new genera were identified bringing the number of recorded WBP ECM associates to twenty-two genera and between fifty and fifty-five species. Compared with previous studies, a shift in the dominant ecological fungal guilds towards generalist associates was detected and attributed to the mixed conifer composition of the sites sampled. Distinct communities were detected on naturally regenerated and planted trees. Planted trees had lower colonization and diversity and lacked native ECM mycota. The ECM taxa identified here should be useful in the selection of planting sites, assessments of stand health and potential inoculation of planted seedlings. The assessment of planted seedlings reiterates the importance of selecting planting sites that support ECM development. This work makes a significant contribution to understanding the ECM fungal community and ecology of WBP.