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ectomycorrhizal fungus *Cenococcum geophilum*
from *Populus trichocarpa* soils in the Pacific
Northwest and comparison to globally distributed
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ABSTRACTS - Oral Presentations

Phylogenetic relationships of 200+ isolates of the ectomycorrhizal fungus *Cenococcum geophilum* from *Populus trichocarpa* soils in the Pacific Northwest and comparison to globally distributed representatives

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The ubiquitous ectomycorrhizal fungus *Cenococcum geophilum* has been proposed as a model organism for fungal genetics and ecological studies due to several factors, including its wide-spread association with both gymno- and angiosperm plant species, straightforward *in vitro* cultivation, and species hardiness in response to a number of soil stressors. *Cenococcum geophilum* is likely a complex of cryptic species due to extreme phylogenetic divergence within same site-associated populations among morphologically identical members. To further understand the phylogenetic relationships within *C. geophilum*, we performed a maximum likelihood analysis using the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene on a newly isolated population of 231 *C. geophilum* isolates collected from soils under *Populus trichocarpa* in the United States Pacific Northwest (PNW). We also performed an additional GAPDH phylogenetic analysis of 790 total isolates, including the PNW isolates introduced in this study and populations gathered within the United States, Europe, Japan, and other sites accessed from either GenBank or MycoCosm. Phylogenetic analyses of the PNW isolates revealed 16 clades strongly resolved at >80% bootstrap support based on a GAPDH phylogeny, and 31 clades strongly resolved at >80% bootstrap support in the global population (GP) phylogeny. Nine of the PNW clades persisted in the GP analysis with relatively similar bootstrap support values, and an additional PNW clade was resolved due to persistence between the two phylogenies. Previous GAPDH studies were also compared in this GP analysis and are indicated on the ML analysis, but do not directly reflect the previous GAPDH ML phylogenies due to the inclusion of additional worldwide isolates which were not previously identified. As a result, this study introduces >200 newly isolated *C. geophilum* and presents the most inclusive phylogenetic analysis of the global *C. geophilum* population to date.