Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO₂ and tropospheric O₃

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Supplementary Material

1. Species accumulation curves (●), and the calculated ICE (■) and Chao 1 (triangle) estimates of fungal diversity under aspen and aspen birch at FACE II. Top panel; Ascomycetes. Bottom panel; Basidiomycetes

2. Neighbor Joining tree showing the phylogenetic relationship between Pezizomycotina operational taxonomic units and GenBank derived reference sequences. Bootstrap support > 75% is indicated above nodes, and strongly supported branches (> =90%) are indicated with bold type.

3. Maximum Likelihood Consensus tree of the Pezizomycotina from the FACE II site. Bootstrap support > 65% is indicated above nodes, and strongly supported branches (> =90%) are indicated with bold type.

4. Neighbor Joining tree showing the phylogenetic relationship between Basidiomycotina operational taxonomic units and GenBank derived reference sequences. Bootstrap support > 75% is indicated above nodes, and strongly supported branches (> =90%) are indicated with bold type.

5. Maximum Likelihood Consensus tree of the Basidiomycotina from the FACE II site. Bootstrap support > 65% is indicated above nodes, and strongly supported branches (> =90%) are indicated with bold type.
Suppl. Fig. 1

Number of genotypes vs. Number of ribosomal sequences

Number of genotypes vs. Number of ribosomal sequences
Suppl. Fig. 4.
Suppl. Fig. 5.