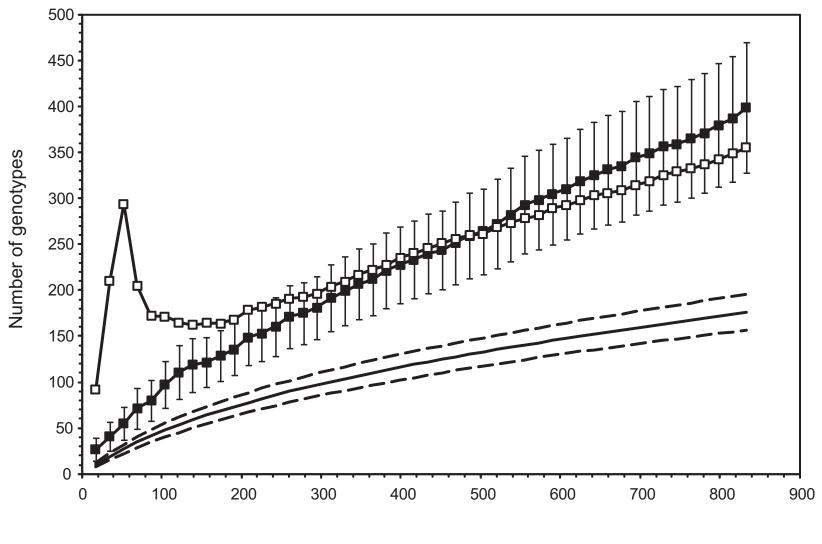
Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO_2 and tropospheric O_3

Ivan P. Edwards^{1*} and Donald R. Zak^{1,2}

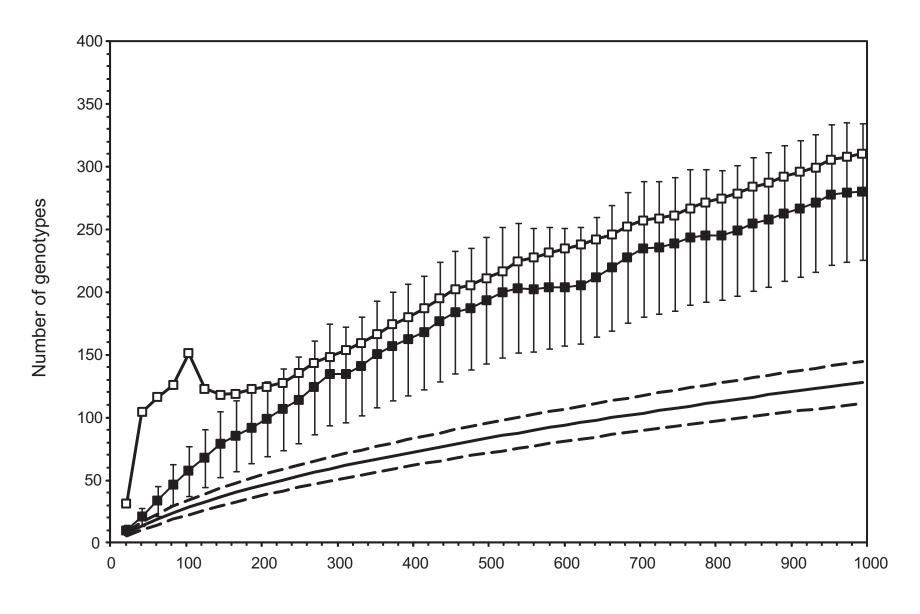
Supplementary Material

- 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.

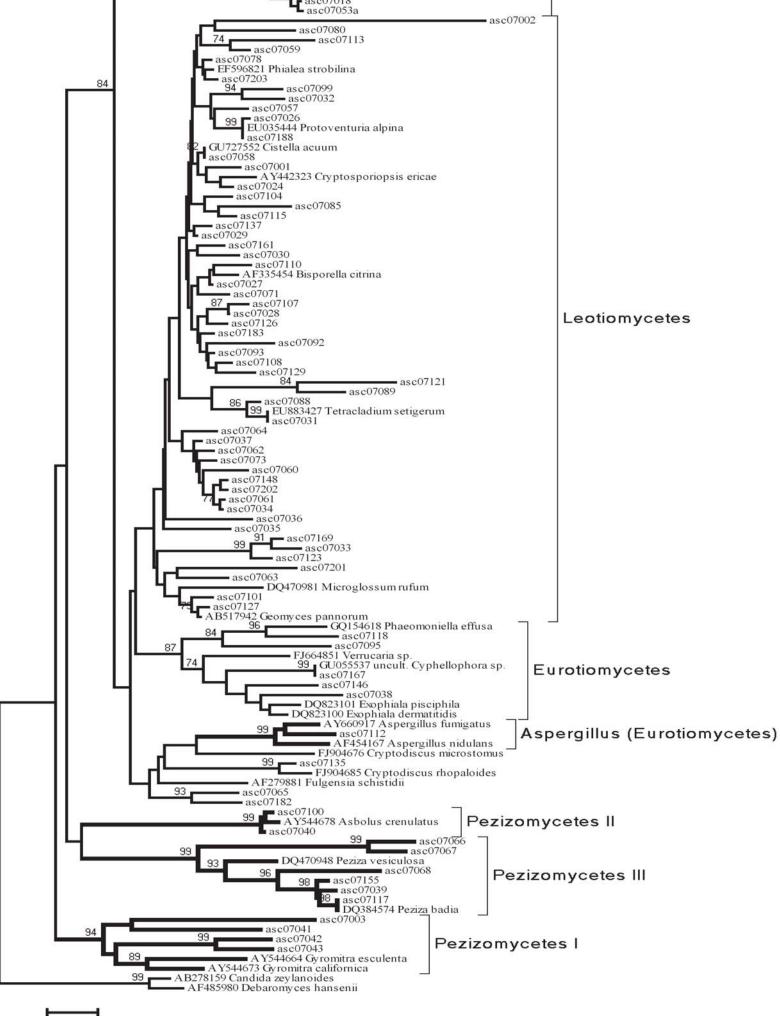
 Bootstrap support > 65% is indicated above nodes, and strongly supported branches (> =90%) are indicated with bold type.



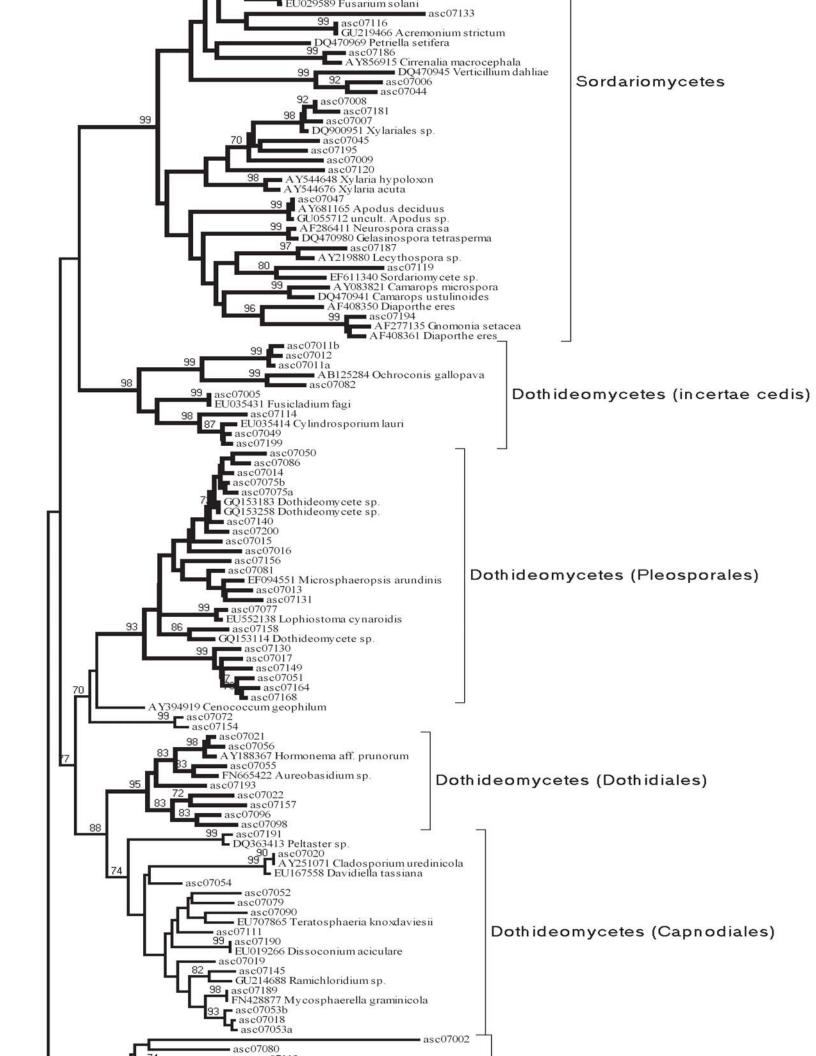
Number of ribosomal sequences

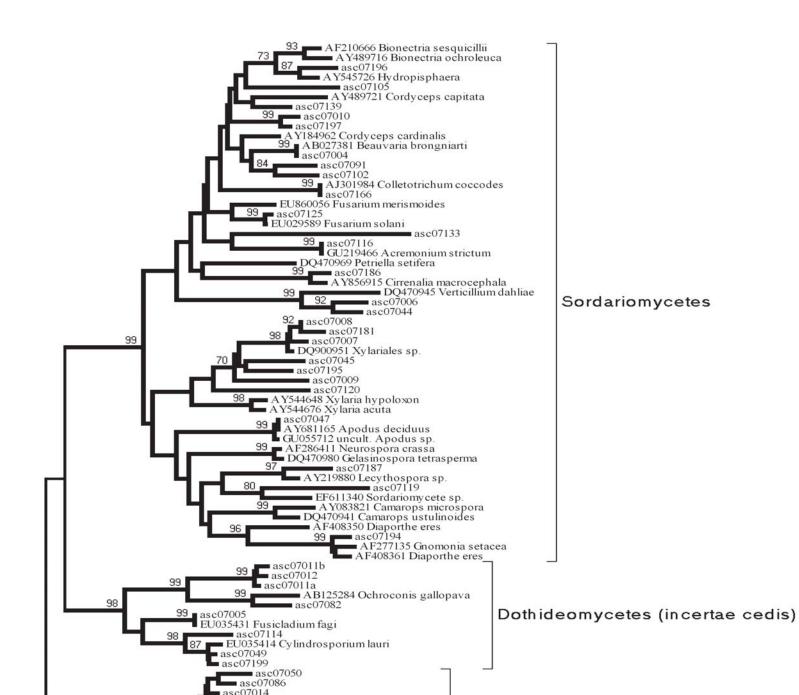


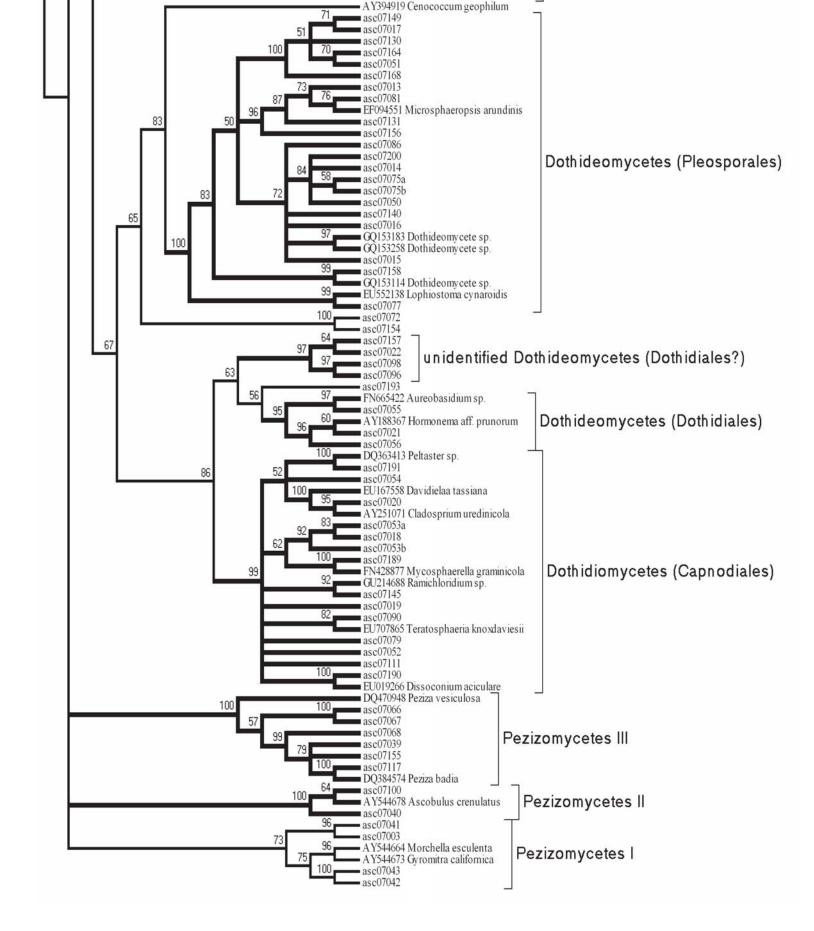
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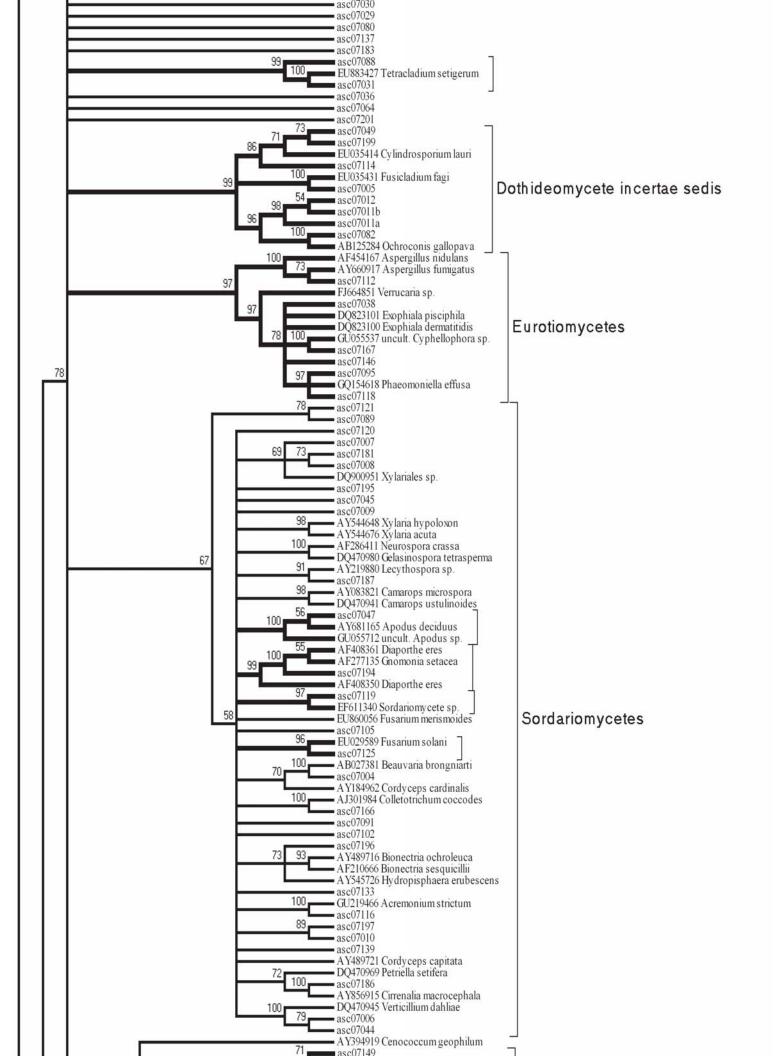
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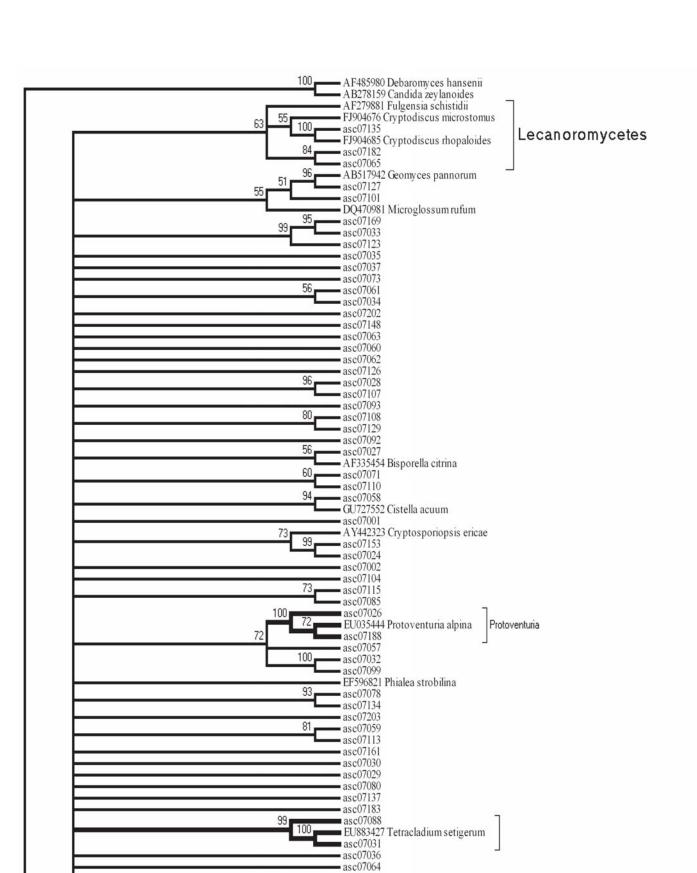


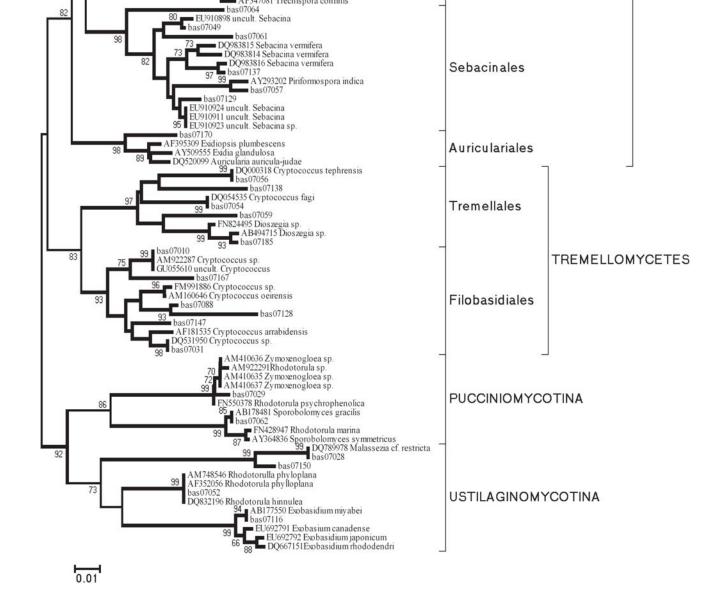




Suppl. Fig. 3.







Suppl. Fig. 4.

