

SUPPLEMENTARY DISCUSSION

Sequences were unevenly distributed among AM fungal lineages; 84% of all OTUs belonged to the order Glomerales (93.6% of the sequences), 15% to the Diversisporales (6.4% of the sequences), and 1.3% to the Archeosporales (< 0.01% of the sequences). The 20 most frequently observed taxa accounted for 88% of all sequences. Across all samples, *Sclerocystis_VTX00126* was the most abundant OTU, representing 41% of the total number of assigned sequences.

We used the copy number of DNA sequences as a measure of relative abundance of OTUs. Although sequence abundance may reflect biases introduced through PCR and sequencing protocols [1], the NS31-AM1 primer set has very low levels of PCR bias when used to amplify artificial community templates of known composition [2], possibly due to the consistent length (*c.* 1.5% variation) and GC content (*c.* 3% variation) of the amplified region across different AM fungal taxa ([3] ; variation in amplicon length and GC content are known to cause biases in PCR reactions [4], and may cause biases in the 454-sequencing process as well [5]).

1. Nguyen, N. H., Smith, D., Peay, K. & Kennedy, P. 2015 Parsing ecological signal from noise in next generation amplicon sequencing. *New Phytol.* **205**, 1389–1393. (doi:10.1111/nph.12923)
2. Cotton, T. E. A., Dumbrell, A. J. & Helgason, T. 2014 What Goes in Must Come out: Testing for Biases in Molecular Analysis of Arbuscular Mycorrhizal Fungal Communities. *PLoS ONE* **9**, e109234–7. (doi:10.1371/journal.pone.0109234)
3. Helgason, T., Fitter, A. H. & Young, J. P. W. 1999 Molecular diversity of arbuscular mycorrhizal fungi colonising *Hyacinthoides non-scripta* (bluebell) in a seminatural woodland. *Mol. Ecol.* **8**, 659–666. (doi:10.1046/j.1365-294x.1999.00604.x)
4. Ihrmark, K. et al. 2012 New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. *FEMS Microbiology Ecology* **82**, 666–677. (doi:10.1111/j.1574-6941.2012.01437.x)
5. Kauserud, H., Kumar, S., Brysting, A. K., Nordén, J. & Carlsen, T. 2011 High consistency between replicate 454 pyrosequencing analyses of ectomycorrhizal plant root samples. *Mycorrhiza* **22**, 309–315. (doi:10.1007/s00572-011-0403-1)