

Tracheophyte genomes keep track of the deep evolution of the *Caulimoviridae*

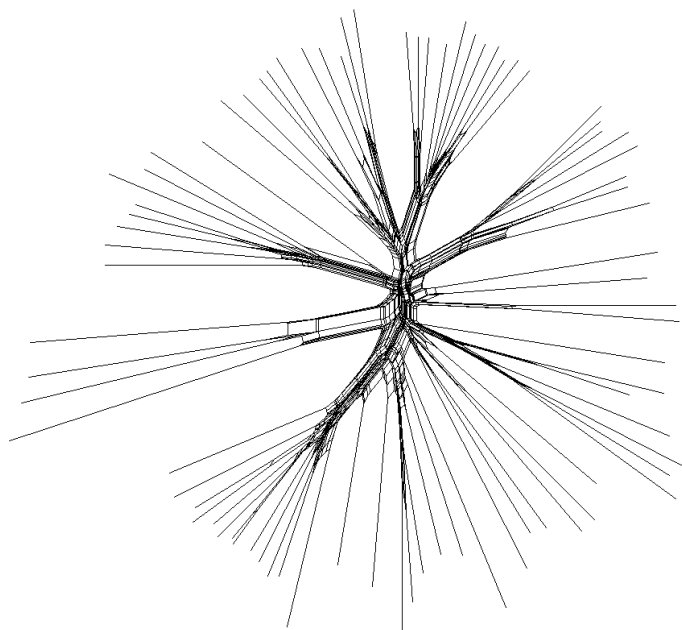
Authors

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Supplementary figures

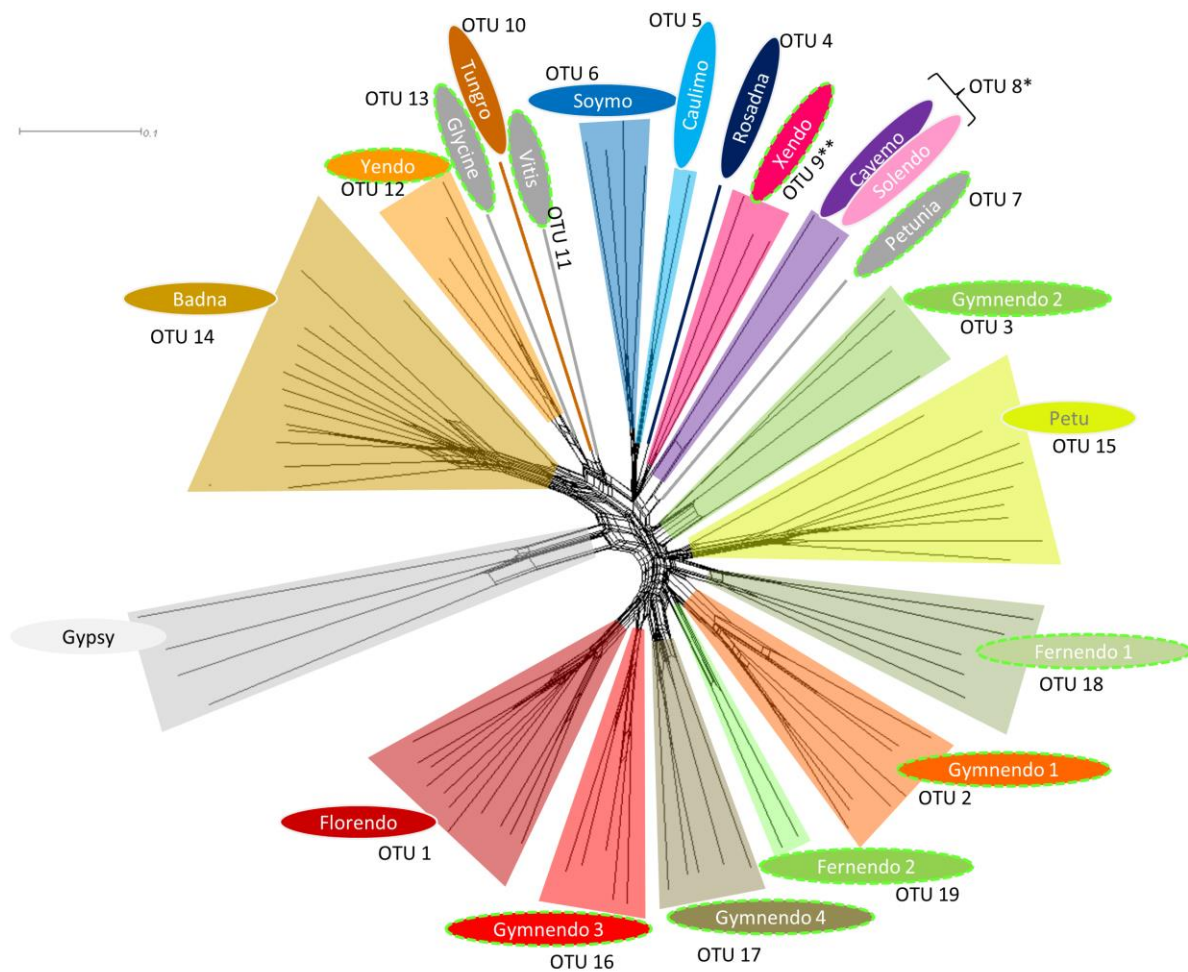
Supplementary figure 1

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Supplementary Figure 1: Overview of the phylogenetic network used to build Figure 1.

Supplementary figure 2



Supplementary Figure 2: ECRT ORFs collected from ferns cluster as two novel OTUs. Representative sequences identified in fern genomes were appended to the collection of sequences represented in Figure 1. The resulting library has been re-aligned with MUSCLE and phylogenetic network was built using SplitsTree. The branches containing fern sequences have been empirically grouped into two novel OTUs (OTU 18 and OTU 19).