**EARLY-DIVERGING LINEAGES OF LICHEN-FORMING ASCOMYCOTA: NEW PHYLOGENOMIC EVIDENCE**

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While shotgun DNA sequencing technology has proven useful for resolving some of the deepest relationships of the tree of life, the relationships of many mid-range to lower nodes within the fungal tree of life remain unresolved. Currently, nearly all Ascomycota-wide topologies rely on fewer than 10 genetic markers and are driven largely by ribosomal DNA data. Here we present phylogenomic evidence for the positions of several of the early diverging lineages of lichen-forming Ascomycota based on proteomes derived from over 40 culture-derived and metagenome-derived fungal genomes. We stress-tested the topologies by iterative sampling and assessing internode certainties. The resulting topology provides a new baseline on which to assess the origin of lichen symbiosis within the Ascomycota and likely secondary delichenization events.