

Towards a natural classification and backbone tree for Xylariaceae recognized from multigene phylogeny and taxonomy

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The family Xylariaceae, comprising over 1300 species, is considered as one of the largest families of the Ascomycota. Members of Xylariaceae exhibit a wide distribution and they are cosmopolitan. The objective of this study was to infer the evolutionary relationships among the species of the Xylariaceae based on multigene analysis including protein coding genes and to construct a backbone tree for the family. Combined analyses of ITS, LSU, RPB2 and β -tubulin sequence data were used to reconstruct the molecular phylogeny of Xylariaceae. Generic and familiar boundaries were revised and presented in an updated combined phylogenetic tree. A reliable phylogenetic and taxonomic relationship was utilized and a unified nomenclature for the genera by linking their asexual morphs with the respective sexual morphs was established. The generated phylogram was highly supported and showed well-resolute relationships within the Xylariaceae supported by morphology. This study confirmed the assumed separation of the genus *Anthostomella* and showed that the genus consists of six lineages, comprising several genera within Xylariaceae. This study provided an updated outline for the core Xylariaceae genera, which can easily be followed in the future applications. The morphological characters were redefined and limited only to include true Xylariaceae species. Based on the preliminary screening for secondary metabolites in micro-xylariaceous genera it was evident that they also contain several derivatives of secondary metabolites in their cultures. Even though the members of Xylariaceae studied, lack stromata, they are good source of secondary metabolite producers. Since these cultures were slow growing and the concentration of the crude extracts were comparatively lower than the stromatic Xylariaceae members, the analytical process take more time and more effort. As the final outcome, this study established a basis for the delimitation of the generic and familial boundaries of Xylariaceae and other related families and depicted a benchmark on DNA based multigene phylogeny within the Xylariaceae.

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