**A UNIVERSAL PROBE SET FOR TARGET ENRICHMENT SEQUENCING TO RECONSTRUCT THE PHYLOGENY OF FILAMENTOUS ASCOMYCETES (PEZIZOMYCOTINA)**

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The sub-phylum Pezizomycotina is the largest clade within Ascomycota and includes most lichenized fungi. Despite its importance, with members that are pathogenic, parasitic, or producers of relevant molecules, our understanding of the evolution of this group of fungi is still limited by insufficient taxon sampling. Although next-generation sequencing technology allows us to obtain complete genomes for phylogenetic analyses, generating complete genomes of fungal species can be challenging when the fungi occur in symbiotic relationships and/or when the DNA of rare herbarium specimens is degraded. In addition, assembly, annotation, and gene extraction of whole-genome sequencing data requires elevated bioinformatics skills and computational power. To overcome these obstacles, we designed a universal target enrichment probe set to reconstruct phylogenetic relationships of all filamentous ascomycetes. From a pool of orthologous genes extracted from available Pezizomycotina genomes, we identified the smallest subset of genetic markers which can reliably reconstruct a robust phylogeny. Based on the selected markers we used a machine learning approach to identify a sequences set able to provide a good trade-off between missing data, and the probe set cost. We designed the probe set and tested the effectiveness and universality of the markers bothon existing phylogenomic datasets and on fresh material and herbarium specimens. The probe set and a user-friendly wrapper script named Universal Filamentous Ascomycete Target Enrichment (UnFATE) are available to the public and will allow phylogenomic inferences, without expert bioinformatics knowledge. In addition, our software solution will integrate a periodically updated database of available Pezizomycotina genomes, already processed to extract the markers of interest. This way, we aim at providing a framework for a collaborative approach to build robust, conclusive phylogenies of this important fungal clade.