

Characterization of the mitochondrial genome of *Phellinotus piptadeniae* (Basidiomycota, Hymenochaetales) and insights on the phylogeny of Agaricomycetes through comparative mitogenomics

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Abstract

The Fungi kingdom includes extremely diverse organisms and its taxonomy is constantly going through changes because of its diversity and discovery of new species. The elucidation of the phylogenetic relationships between fungi by analysis of mitogenomes is a common method, mainly because the mitochondrial genome is well conserved between different groups of fungi. In this work, the mitogenome of the wood-decaying fungus *Phellinotus piptadeniae*, a new species and genus of Agaricomycetes described by our group, was sequenced and assembled using the programs FastQC and SPAdes. The mitochondrial contig was identified with a BLASTn search against other mitogenomes, and the annotation was done using MITOS2, MFannot and RNAAweasel. Next, we used the available Agaricomycetes mitogenomes in NCBI and JGI to build a phylogenetic tree including *P. piptadeniae*. Available fungal mitogenomes were selected and annotated using aforementioned programs and an alignment was built using MAFFT program based on the 14 core mitochondrial genes, rps3 protein and two ribosomal RNA. The mitogenome of *P. piptadeniae* has a size of 137,790 bp with 24.1% GC content, 14 mitochondrial core-genes, 2 rRNAs, 30 tRNAs, 47 introns and 62 unidentified open reading frames. We also found coding domains for homing-endonucleases (HEs) (GIY or LAGLIDAGD) and dpo. For our comparative mitogenomics analysis, a total of 55 mitogenomes were retrieved from public databases and different genes, whose locations in the genome were conserved in the species of a same family or genus, were identified, such as: (i) atp6, cob, cox1, cox2, cox3, nad2, nad4, nad4l, nad5, rrnL and rrnS for *Ganoderma* genus; (ii) atp6, atp9, cob, cox1, cox2, cox3, nad1, nad2, nad3, nad4l, nad5 and nad6 for Hymenochaetaceae family; and (iii) also all the 17 genes for Russulaceae family. Deviations of these patterns may be explained by the presence of HEs in these mitogenomes: from all the mitogenomes used in our study, there were coding domains for HE in 50 of them. The phylogenetic tree was built by distance-based method on the genetic set comprised of the 14 core-genes, rrnL, rrnS and rps3. The use of the mitogenome as a tool for a better understanding of fungal phylogenetic relationships proved to be useful but the deficiency of enough mitogenomes of all different families in the Agaricomycetes class in public databases still is a problem to overcome since unbalanced sampling influences on the quality of the results.

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