

Evolution of mitochondrial genomes in three closely-related *Armillaria* species

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Motivation and Aim: Comparative analysis of mitochondrial genomes of closely related organisms allows obtaining new information about their phylogenetic and evolutionary relationships. Plant and fungi mitochondrial genomes are especially interesting due to their large mtDNA size.

Methods and Algorithms: In this study we analyzed mitochondrial genomes of *Armillaria borealis* (116443 bp) and *A. sinapina* (103563 bp) sequenced and annotated in Laboratory of Forest Genomics of the Siberian Federal University. The complete sequence of the *A. solidipes* (122167 bp) mitochondrial genome was retrieved for annotation and comparative analysis as a single scaffold from the JGI Genome portal. Genome rearrangements were detected using the MAUVE 2.0 program. Duplicated sequences were identified by local BLASTn searches of mtDNAs against themselves with a cut-off e-value of 10^{-3} . Intronic nucleotide sequences of three species were compared with each other and NCBI GenBank database using BLAST.

Results: Despite conserved gene content, there were significant genome rearrangements in a region between *rps3* and *atp9* genes. We found gene duplications in all species. There was an 87 bp long truncated duplication of *atp9* located on the minus strand together within *rnl* in *A. solidipes* and *A. sinapina*. We also found a 42 bp long duplication of *atp9* in *A. borealis*, which was located next to *atp9* after mobile element of the LAGLIDADG family.

Conclusion: Our study revealed active intronic and mobile genetic elements acquisition during evolution. Some introns have homology with rather distant species. We consider that horizontal DNA transfer has played a significant role in size variation and genome structure of the *Armillaria* mitochondrial genomes.

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