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Ribosomal DNA Polymorphisms of *Trametes versicolor*

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The sequences of *Trametes versicolor* placed in the 'core polyporoid clade' showed polymorphism. In spite of the rDNA homogenization by concerted evolution, 51 nucleotide substitutions with one indel were found in 72 clonal sequences of the ITS region. The low genetic distance, the evolutionary speed of clonal sequences on the phylogenetic tree, GC ratio, and short life cycle of the target organism (*T. versicolor*) implied that the occurrence of ITS polymorphisms in a strain could be caused by the relaxation of concerted evolution on nonhomologous rDNA locations. No recombination was observed in within-strain level while one and five events were found in ITS1 and ITS2 regions, respectively, among strains, indicating that ITS variation among individuals could be generated by the recombination based on gene conversion during their mono- and dikaryotic states. The neutrality tests on the secondary structures of ITS1 and ITS2 showed that the most structural elements of two regions have been neutrally evolved according to the Kimura's neutral hypothesis. However, the similarity tests on the secondary structures proved that the helices I of ITS1 and ITS2 might have been controlled under the selection through the neutrality. The coexistence of G•U pairs and their canonical pairs on the stems of the rRNA secondary structures and the absence of coupled compensatory mutations make it possible to infer that all G•U pairs are not advantageous but completely deleterious in ITS sequences of *T. versicolor*. In conclusion, the evolutionary mechanisms of ITS polymorphisms of *T. versicolor* were explained by nearly neutral theory.

In aligned IGS1 sequences of *T. versicolor*, *T. pubescens* and *T. velutina*, three polymorphic regions consisting of six types (Type 1 and 1-1, Type 2 and 2-1, and Type 3 and 3-1) were observed. The results of IGS1 sequences, polymorphism-specific PCR, and the maximum-likelihood trees make it possible to infer that Type 1 and 1-1, and Type 3 and 3-1 have been occurred in the common ancestral states of *T. versicolor* and *T. velutina*, and that the occurrence of Type 2 and 2-1 could be the most plausibly explained by the evolutionary scenario that the generation of a polymorphism after the speciation of *T. versicolor* from the recent common ancestor. The polymorphism referred to Type 2 and

2-1 was discovered to be caused by the expansion of microsatellites based on replication slippage while Type 3 and 3-1 have been probably occurred by intramolecular recombination and replication slippage.

Key words:

concerted evolution, neutral evolution, polymorphism, *Trametes versicolor*