

Secondary Structure of the Ribosomal PreRNA ITS2 region as a Tool in Studies of Fungal Diversity and Phylogeny

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The ribosomal RNA gene, and particularly its 18S and 25S sequences, have proven valuable in large-scale phylogenetic analyses. The ITS region of the ribosomal RNA gene, instead, has not been regarded so useful in this respect. The main problem has been that these sequences show significant sequence and length variation and that they have been more or less unalignable beyond small closely related groups.

We have determined the common secondary structure of the ITS2 region and used it to align the sequences over the whole fungal kingdom. Significant properties of this structure include a central ring structure and three or four conserved loops – the presence of the ring being the most conserved feature. The core structure has also revealed the most conserved sites that are usable in kingdom-wide phylogenetic analyses. Surprisingly, the tree that is calculated with only the 5.8S ribosomal RNA and the conserved ITS2 sites has a very high correlation with the Fungal Tree of Life that has been calculated with four markers and much longer sequences. Furthermore, finding of the ITS2 secondary structure has revealed a number of group specific sequence signatures and structural RNA elements that can be used for more detailed analyses of different subgroups and their phylogeny.

Currently we are (mainly) examining the variation of the loop structures among the basidiomycetes and linking that to the taxonomy of fungi. Some examples of current findings will be shown.