Phylogenetic placement of the genus *Tricholosporum* by DNA sequencing.

**Introduction**

In 1975, *Tricholosporum* was placed into the family *Tricholomataceae* by Mexican mycologist Gaston Guzman based on its morphological characters (Guzmán, 1975). However, *Tricholosporum* has characters that are quite different from most other family members. The unique cruciate-shaped spores and the purplish pigments in the pileus and basidocarp may point to an error in the taxonomic placement of *Tricholosporum*. By comparing LSU and ITS sequence data from *Tricholosporum* with DNA sequences from other genera in the family *Tricholomataceae* and from different families in the *Tricholomatoid clade* (Matheny et al. 2006), we gained a better understanding of the phylogeny of *Tricholosporum*.

**Results/Methods**

*Tricholosporum pseudosordidum* specimens from Belize were obtained and the DNA was extracted (Kropp et al. 1997). After extraction, the target DNA was amplified using standard polymerase chain reaction (PCR) protocols. LR0R and LR0S primers along with ITS4 and ITS5 primers were used to attain DNA sequences of the nuclear large subunit (nLSU) and both internal transcribed spacers (ITS1 & ITS5). Gel electrophoresis was used to confirm the presence of DNA from the extractions. After the DNA sequences were purified using the QIAquick PCR purification kit from Qiagen, they were sequenced. The new sequences generated for this study will be deposited in Genbank. Initial BLAST searches of the LSU sequences indicated relation to *Tricholomataceae*, while ITS sequences indicated relation to *Entolomataceae*. Taxon sampling for the ITS and LSU phylogenies included species from the *Cortinariaceae*, *Lyophyllaceae*, *Marasmiaceae*, *Entolomataceae*, *Tricholomataceae*, *Agaricaceae*, and *Mycenaecae*. Genbank was utilized to find the ITS and LSU sequences. Clustal was used to align the DNA sequences, while Bioedit was used to edit the aligned sequences. The phylogenetic trees were generated using Mr. Bayes. Members of *Mycenaecae* rooted the ITS tree, and members of the *Marasmiaceae* rooted the LSU tree.

**Conclusions**

The trees generated from LSU and ITS sequences are incongruent. The ITS tree supports *Tricholosporum* belonging in the *Entolomataceae* family, while the LSU tree supports *Tricholosporum* belonging in the *Tricholomataceae* family. Further analyses should be conducted. Examining RNA polymerase using RPBI primers would likely lead to a better understanding of the phylogenetic placement of *Tricholosporum*.

**References**


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