Umbelopsis

Abstract

During a course at Uppsala university called "Diversity and evolution of microbial eucaryotes", soil samples were collected for fungal isolation, sequencing and identification. The sample was determined to be part of the *umbelopsis* genus.

Sampling

The soil sample was collected in a wooded area outside of Växjö Sweden, close to lake Torsjön, see figure 1.

Figure 1: Map of lake Torsjö, the red dot marks the sample site of the project (Google maps, 2023).

The sample site (figure 2) is a working forest consisting of mostly coniferous trees and birch, see figure. Some basidiomycete fungi such as funnel chanterelle and amanita were spotted close to the sample site at the time of the collection.

Figure 2: Sample site of the project. To the left the area is shown and the right shows the specific sample spot.

Methods and materials

The fungal isolation was done through several streakings of a fungal culture on agar plates treated with the growth enhancer PDA and antibiotic chloramphenicol. The isolated culture (figure 3) was then purified and sent for sequencing.

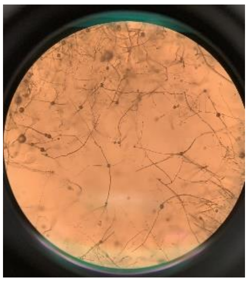

Figure 3: Microscope picture of the fungal structure of the isolated fungi.

Phylogeny of the fungi was determined with the help of digital tools, first examining chromatograms of the sequences in SnapGene (SnapGene). A BLAST® was then conducted on the gene sequence and the 25 best matches were collected (Altschul *et al.* 1990). The 25 matches, the sequence of the collected fungi and genetic code representing the biggest fungal groups were then examined using MAFFT (Rozewickii *et al*, 2019), compiled into a phylogenetic tree using iqTree (Minh *et al*, 2020) and shown through iTol (Letunic & Bork, 2021), part of which is shown in figure 4.

Discussion

While assessing the sequences in SnapGene it was noted that the sequence was not very good or clear. This led me to believe that the sample was contaminated in some way during the purification before the sample was sent for sequencing. This could have happened through accidentally forgetting to change pipette tips between samples, or through misconduct of the samples or vessels in which the purification was done.

Even so, the sequence seems clearly seem to be a *umbelopsis* fungi, part of the *Umbilopsidaceae* family of the *mucoromycota* order. *Umbelopsis ramanniana*, the species with the highest similarity to the sample, is important in biochemistry and biotechnology due to its capability to produce lipids. It is a common find in forests as it often lives in association with plants.(Wang *et al.* 2022)

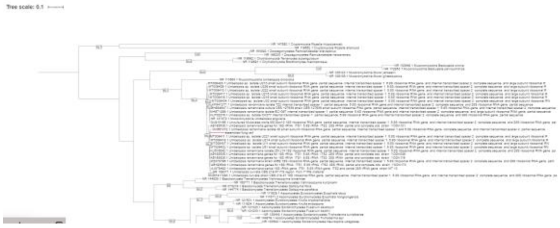

Figure 4: The phylogenetic tree achieved with iqTree and iTol. In red is the collected species.

References:

Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J. (1990) “Basic local alignment search tool.” J. Mol. Biol. 215:403-410. PubMed

B.Q. Minh, H.A. Schmidt, O. Chernomor, D. Schrempf, M.D. Woodhams, A. von Haeseler, R. Lanfear (2020) IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. Mol. Biol. Evol., 37:1530-1534. https://doi.org/10.1093/molbev/msaa015

Google Maps (2023) Torsjö 1:100. Available from: https://www.google.com/maps/@56.7593702,14.911947,5765m/data=!3m1!1e3?entry=ttu [Accessed 23 December 2023].

Letunic I and Bork P (2021) Nucleic Acids Res doi: 10.1093/nar/gkab301 Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation (full article)

SnapGene software, version 7.1 (www.snapgene.com)

Rozewicki, Li, Amada, Standley, Katoh 2019 (Nucleic Acids Research 47:W5-W10) MAFFT-DASH: integrated protein sequence and structural alignment (describes web interface for sequence and structural alignments)

Wang Y-N, Liu X-Y, Zheng R-Y. 2022. The Umbelopsis ramanniana Sensu Lato Consists of Five Cryptic Species. Journal of Fungi 8: 895.