

Biogeography of aquatic fungi: preliminary conclusions

## **Biodiversity and Biogeography**

### **Oral presentation**

**(MÁX title. 110 characters)**

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Aquatic hyphomycetes occur worldwide on a wide range of plant substrates decomposing in freshwaters, and are known to play a key role in organic matter turnover. However, the presumed worldwide distribution of many species is based on morphology-based taxonomy and identification, which may overlook cryptic species, and therefore hide global-scale biogeographical patterns. This might be circumvented by using DNA sequence data. The internal transcribed spacer (ITS) region from rDNA has been claimed to be the most suitable barcode for fungal identification [1, 2]. We used this approach to elucidate biogeographical patterns of aquatic hyphomycetes. We generated ITS barcodes of 130 isolates belonging to 6 common aquatic hyphomycete species (*Anguillospora filiformis*, *Flagellospora penicillioides*, *Geniculospora grandis*, *Lunulospora curvula*, *Tetrachaetum elegans* and *Tricladium chaetocladium*), collected from streams of Southwest Europe (86 isolates) and East Australia (44 isolates). European and Australian populations of 4 species (*A. filiformis*, *F. penicillioides*, *G. grandis* and *T. elegans*) grouped into different phylogenetic clades, and molecular diversity indices supported significant differentiation between those populations. Continents did not share haplotypes except for *T. chaetocladium*. Overall our study indicates considerable population diversity for all tested species and suggests that the biogeography of aquatic hyphomycetes may be species-specific.

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1. Letourneau A, Seena S, Marvanová L, Bärlocher F. 2010. Potential use of barcoding to identify aquatic hyphomycetes. *Fungal Diversity* 40: 51-64.
2. Seena S, Pascoal C, Marvanová L, Cássio F. 2010. DNA barcoding of fungi: a case study using ITS sequences for identifying aquatic hyphomycete species. *Fungal Diversity* 44: 77-87.