

Návrh témy doktorandského štúdia v odbore Botanika so začiatkom štúdia v školskom roku 2024/2025

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Téma dizertačnej práce: Diversity and interactions of bionts in lichen thalli of the genus *Solenopsora* (Leprocaulaceae)

Traditional view of lichen thallus as a consortium of fungus and photosynthesizing alga, or cyanobacteria has changed substantially over the recent years. We know, that the holobiont system of lichen symbiosis is complex. Besides stabile, majoritarian lichen partners – mycobiont and photobiont, it includes other associated components. In particular additional fungi associated to the lichen thalli have been found to be diverse and represented by both symptomatic and asymptomatic taxa, which all constitute the lichen mycobiome. European Mediterranean and other regions with Mediterranean climate belong to one of the most important biodiversity centres of the world. Distribution of *Solenopsora* A. Massal. (Leprocaulaceae) species has been intensively studied within their species ranges since 2010 and we gained a clear overview enabling us to evaluate their biogeography and link it to the Mediterranean climate type. We identified mycobionts of the European taxa, which interestingly indicate polyphyly and infrageneric taxonomy. This topic remains unresolved. Another point associated with photosynthesizing partners includes open questions – disclosed photobiont lineages are so far undescribed and the issue, whether the pattern correlates eventually with ecological guilds is still open. At last but not least, it is necessary to zoom on overall diversity of bionts of selected species from both macro- and microecological aspect. Thus the aim of the thesis is to address the following points:

- resolving taxonomical issues related to polyphyletic nature of *Solenopsora* mycobionts
- revealing whether photobiont lineages of selected *Solenopsora* species fit to ecological guilds
- zoom on overall diversity of *Solenopsora* bionts across micro- and macro-ecological gradients

Proposed methods:

- Most of the material was already collected for previous studies, additional field work is expected if necessary
- Genetic data: Sanger sequencing – DNA isolation (for majority of samples DNA already isolated), amplification of selected regions, sequence analyses; Metagenomic profiling/metabarcoding – Isolation of environmental DNA from lichen thallus (holobiont) with high quality and necessary concentration of the product for metagenomic profiling (for part of the samples already done): regions ITS1 and ITS2; preparation of libraries, Illumina MiSeq sequencing at commercial provider of the service; processing of amplicons through relevant pipeline implemented in SEED2

Financial resources:

- VEGA 2/0054/21; expected fundrasing in 2024
- Erasmus stay, Lab of Lucia Muggia – Department of Life Sciences, Università degli studi di Trieste
- DoktoGrant

Expected papers:

High quality WOS papers (preferably Q1): 3