**Genomic CONSEQUENCES OF HYBRIDIZATION IN an open species complex. The saxicolous *Pyrenodesmia* (Teloschistaceae) in Eurasia**

Fernando Fernandez-Mendoza1\*; Eva Strasser1; Jan Vondrak2; Ivan Frolov2; Lucia Muggia3; Ester Gaya4; Helmut Mayrhofer1; Martin Grube1

1 Institute of Biology, Karl-Franzens-University of Graz, Austria; 2 Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice, Czech Republic; 3 Universita degli Studi de Trieste, Italy; 4 Royal Botanic gardens, Kew, Surrey, UK; \*E-mail:fernadf@uni-graz.at

The idea that species constitute a natural unit of biological organization has remained a central dogma in evolutionary biology. While speciation is a major outcome of evolution, it does not necessarily result in the segmentation of life into discrete categories, but in a more continuous landscape of diversification. Extrinsic reproductive boundaries between species may fluctuate as their ranges develop, and in the absence of intrinsic boundaries, species may remain reproductively compatible.

In this survey, we hypothesize that maintaining open reproductive boundaries is an evolutionary strategy common in lichen fungi, and that it may be enabled by the strong fungal DNA-repair pathways.

The genus *Pyrenodesmia* comprises a morphologically diverse clade of Caloplacoid species. Its taxonomic treatment is hampered by the instability of diagnostic characters, and by its high genetic diversity, which has been used to coin new *binomina*, with little evidence beyond phylogenetic trees. The study of a broad phylogenetic dataset, rendered contrasting results. While species delimitation methods identified ca. 100 species in western Eurasia, analyses of population stratification only identify 10 strongly admixed demographic entities. Pairing of MAT loci, shows that most European morphospecies form a single interbred network, in which individual species retain their ecological uniqueness, but are connected through gene flow.

To understand pangenomic signatures of an open species complex, we assembled a comparative dataset, consisting of 23 genomes of saxicolous *Pyrenodesmia* specimens. We compared the genomes in terms of gene content and functional structure, identified candidate genes under positive selection. We focused on MAT and HET loci implicated in sexual and self-recognition and in genes implicated in DNA repair pathways. Orthologous genes were used to understand overall genomic tendencies, and to trace a phylogenomic baseline. Intergenic spacers were identified within syntenic blocks, and used to estimate the interference of DNA repair mechanisms across different parts of the genome.