**LICHEN SYMBIOSES THROUGH THE GENOMIC LENS: WHAT CAN WE LEARN ABOUT LICHEN EVOLUTION FROM THE GENOMES OF LICHEN-FORMING FUNGI?**

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Lichens exhibit a plethora of unique features, which manifest only in symbiosis. The remarkable tolerance to harsh environmental conditions, colonization of extreme niches and their unique biochemical capabilities are only a few examples of how lichens innovate through symbiosis. All of this is achieved through persistent and intimate interactions of fungi and algae in complex interaction networks resulting in unique body plans. It is highly likely that these long-lasting symbiotic relationships also shape the genomes of the symbiotic partners. With the aim to identify and characterize potential genomic changes unique to lichen-forming fungi we present results from a comprehensive comparative analysis of more than 80 fungal genomes from six classes of *Ascomycota*. Our phylogenomic analyses show that using more data does not necessarily increase support for previously uncertain phylogenetic relationships. By applying phylogenetic comparative methods, we highlight several characteristics lichen-forming fungi share with closely related free-living fungal groups, despite their long-lasting association with algae. We identified dynamics of gene family evolution preceding the emergence of *Lecanoromycetes* and especially the evolution of Carbohydrate active enzymes. Genes found in rapidly evolving *Lecanoromycete* gene-families exhibit a wide array of different functions, potentially related to the formation of lichen-symbiotic interactions.