**COMPARATIVE GENOMICS OF THREE FUNGI IN A LICHEN SYMBIOSIS**

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The “one fungus – one lichen” paradigm has recently been challenged by the discovery of additional, stably associated fungi in many macrolichens. Two distantly related groups of basidiomycete yeast, Cyphobasidium and Tremella, have been found to be ubiquitous in some macrolichens formed by ascomycetes from the Parmeliaceae. However, their role in the lichen system and their relationship with the two dominant members of the lichen symbiosis remain unclear. Answering these questions is complicated by the difficulty lichens pose as an experiment model. The fact that neither of the basidiomycete yeasts has been cultured effectively means that currently the only option to study the biology of this lineage is indirectly through genomics and associated shotgun techniques. We present a combination of wet lab techniques and bioinformatics analyses to reconstruct genomes of low-abundance cortical symbionts with high estimated completeness. These metagenome-derived assemblies allow us for the first time to infer secondary metabolism, carbohydrate activities, and secretome and narrow down their contributions to the lichen symbiotic outcome.