**MODELING IN YEAST HOW rDNA INTRONS SLOW GROWTH AND INCREASE DESICCATION TOLERANCE IN LICHENS**

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Lichens are slow-growing and desiccation tolerant. In the face of climate change, understanding their tolerance mechanisms may have implications beyond lichens. We test whether slow growth and extreme desiccation tolerance in lichens are driven by the unusual introns present in the nuclear ribosomal DNA of their mycobionts. Self-splicing introns are found in the rDNA of several eukaryotic microorganisms, but most of those populating lichen rDNA are unable to self-splice, being either degenerate group I introns lacking the sequences needed for catalysis, or spliceosomal introns ectopically present in rDNA. Using CRISPR, we introduced a spliceosomal intron from the rDNA of the lichen fungus *Cladonia grayi* into all nuclear rDNA copies of the yeast *Saccharomyces cerevisiae*,which lacks rDNA introns. Three intron-bearing mutants were constructed with the intron inserted either in the SSU repeats, the LSU repeats, or in both. The mutants removed the introns correctly but had half the rDNA genes of the parent strain, grew 4.4 to 6 times slower, and were 40 to 1700 times more desiccation tolerant depending on intron position and number. Intracellular trehalose, a disaccharide implicated in desiccation tolerance, was detected but not at levels compatible with the observed resistance. Extrapolating from yeast to lichen mycobionts we propose that the unique requirement for a splicing machinery by lichen rDNA introns slows down intron splicing and ribosomal assembly. This effect, and the distinctive roles played by group I *vs.* spliceosomal rDNA introns, partly modify the regulatory patterns of the fungal Environmental Stress Response, leading to the twin lichen phenotypes of slow growth and desiccation tolerance.