**The evolutionary significance of mitochondrial genomes in *Pyrenodesmia* (Teloschistaceae)**

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The mitochondrial genomes of lichen fungi have received significant attention during the last couple of years. Most surveys have encountered that mitochondrial genomes show highly conserved gene content, and to a lesser extent, gene order. On the other hand, the unique properties and ease of use of mitochondrial genes, especially ribosomal mtSSU and mtLSU, made them frequent candidates to be used in combination with nuclear loci in phylogenetic surveys.

For the present survey we focused on the assembly and annotation of 23 genomes of species belonging to the genus Pyrenodesmia s.s., within the family Teloschistaceae. In addition to describing the patterns of synteny and gene content, we used phylogenetic methods to explore the usability of mitochondrial genes in low level phylogenetic surveys, and the signal of mitochondrial exchange within an open species complex. For this purpose, we compared inferences drawn using mitochondrial genes and nuclear genes.