**AN EXCEPTION TO THE RULE? CAN PHOTOBIONT IDENTITY BETTER PREDICT THE LICHEN PHENOTYPE THAN MYCOBIONT?**

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With rare exceptions, the shape and appearance of the lichen thallus are determined by the fungal partner, and therefore, mycobiont identity is used for lichen identification. In the last two decades, DNA-barcoding approaches, which usually rely on the use of a single mycobiont molecular marker, underwent rapid development and started to be commonly used for lichen diversity assessments. Due to their wide geographic and ecological ranges, *Cladonia* lichens (comprising approximately 500 species worldwide) are often included in these studies. During our previous work, it turned out that two *Cladonia* species that differ morphologically, chemically, ecologically, and by their distribution ranges (*Cladonia bellidiflora* and *C. polydactyla*) cannot be successfully distinguished by their fungal ITS rDNA sequences (i.e., recent mycobiont barcoding marker). Therefore, we applied four additional highly variable molecular markers previously successfully used to distinguish *Cladonia* species, specifically the second largest subunit of RNA polymerase II gene (RPB2), mitochondrial cytochrome c oxidase I (cox1), elongation factor‐1α (EF-1α), and mitochondrial ribosomal DNA (mtSSU) along with the photobiont ITS rDNA region. A third species, very close to *C. polydactyla* but having a distinctly narrower ecological amplitude (*C. umbricola*), was included in the dataset to provide a complete picture. Material for this study was collected in different parts of Europe. All mycobiont markers studied showed very low variability and failed to separate the species. However, photobiont identity better corresponded to the lichen phenotype and separated esorediate *C. bellidiflora* from the other two sorediate taxa. These results can be interpreted either by photobiont determining lichen phenotype or by recent speciation of mycobionts, not yet mirrored in molecular markers studied. A second scenario would have serious consequences for DNA-barcoding approaches.