**Genome-wide assessment of putative endemism and phylogeography of *Cladonia sandstedei* (Ascomycota: Cladoniaceae) in the Caribbean**

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*Cladonia sandstedei* is a cushion-forming lichen that colonizes open environments and is distributed throughout the Caribbean and southeastern United States. It co-occurs in parts of its range with *C. subtenuis*, a morphologically similar species that is distinguished from the former by the presence of usnic acid. Preliminary phylogenetic analysis with several barcoding loci revealed that these species were closely related, but relationships were inconsistent among markers. Here, we combined phylogenetic and population genomic analysis based on RADseq data to clarify evolutionary relationships and phylogeography of these species. Both approaches indicate strong geographic structure in genetic variation. Continental *C. sandstedei* was more closely related to continental C. *subtenuis* suggesting homoplasy of secondary chemistry as a trait for separating species. While phylogenetic analysis suggested that continental samples were separate from island-specific clades, population-level de-novo clustering merged populations from Cuba and Puerto Rico, and populations from Jamaica and the continent. These results yield contrasting phylogeographic and species delimitation scenarios which prevented us from confidently clarifying species boundaries and geographic ranges. However, analyses consistently separated Cuban and Puerto Rican samples as distinct genetic groups hinting that unrecognized cryptic species with a *C. sandstedei* phenotype might inhabit these islands. Better characterization of populations in Cuba, Jamaica and Hispaniola, and the southern tip of Florida is needed to assess the generality of our observations and determine potential taxonomic changes. Our work reaffirms the power of combining RADseq-based phylogenetics and population genetics to disentangle taxonomic and evolutionary histories in poorly understood, closely related and phenotypically similar lichen-forming fungal species.