**PHYLOGEOGRAPHY OF *Bryoria fuscescens* (= *B. capillaris*) ACROSS THE EURO-MEDITERRANEAN REGION: PANMIXIA OR ANCESTRAL SHARED ALLELES?.**

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Lichenized fungal species are traditionally considered as panmictic at continental or worldwide scale. However population and phylogeographical studies are scarce and usually do not include extensive sampling on huge geographical areas. Here we investigate the phylogeography and dispersal capacities of the phenotypically variable species *Bryoria fuscescens* (=*B. capillaris*) along Europe and North Africa. For this, 1400 specimens from 64 populations were phenotypically characterized and genotyped with 18 microsatellites and eight highly variable DNA sequence markers. Results show Scandinavia as the genetically richest area followed by Iberian Peninsula, the Carpathians and the Alps. However, Carpathian populations seem originated from recent colonization from Western Europe. The high Scandinavian diversity may come from a mix of northern cryptic glacial refugia with recent immigration from southern populations. Three main genepools were detected, two of them widespread and displaying an overlapped distribution, comprising mainly *Bryoria fuscescens* and *B. capillaris* morphs, respectively. The third one, restricted to Scandinavia, was only composed by *B. capillaris* morphs and nested inside the American species *B. pseudofuscescens*. Genepool 1 lacks any type of diaspora apart of thallus fragmentation, whereas Genepool 2 produces soralia. The analyses however showed that both groups are panmictic at the continental scale, with similar levels of isolation by distance. Estimated migration routes show a pattern from Scandinavia to southern areas, lacking a correlation with the estimated glacial refugia. Thus, we hypothesize that the presence of ancestral alleles currently distributed among distant populations are producing a false sign of panmixia, biasing the phylogeographic reconstruction. This is supported by other results, among them, the high levels of incomplete lineage sorting in DNA sequences. As it is not possible to distinguish current migration from ancestral shared alleles, analyses can easily overestimate the dispersal capacities and distort the phylogeography of *Bryoria*. This phenomenon could be common in other lichens.