

Diversity and biogeography of symbiotic microalgae of the lichen genus *Psoroma*

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The specific relationship between a mycobiont and a photobiont in lichens has been challenged recently. One species of mycobiont can make symbiotic partnerships with various photobiont species when they grow in geographically distant locations. In some cases, several different algal genotypes were observed in a single thallus with NGS technology. In these cases, the microalgal community was usually composed of one major species and several minor species. To investigate the genetic diversity and geographical distribution of major and minor microalgal species in the lichen genus *Psoroma*, LSU rRNA gene sequences, which were obtained with NGS sequencing, were analyzed for samples from Australia, Chile, King George Island, Falkland Islands, and Norway. The results revealed that lots of thalli contained diverse microalgal OTUs as the previous studies. Most *Psoroma* mycobionts showed preference for *Trebouxia arboricola* lineages as a major and minor microalgal partners. Some mycobiont phylogenetic lineages formed symbiotic relationship with specific microalgal OTU as a major partner unlike the other mycobiont lineages. Lichens from Norway had simpler microalgal communities than those from other geographical areas. Although some microalgal OTUs were detected from several geographical regions including Southern and Northern hemisphere, most microalgal OTUs were recovered from specific geographical regions and climates.

Global, continental, and local genetic structure in *Lobaria pulmonaria* and its photobiont *Dictyochochloropsis reticulata*

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Lobaria pulmonaria is a widespread, though regionally rare and threatened old-growth forest dependent epiphyte that is exclusively associated with the asexual green-algal photobiont *Dictyochochloropsis reticulata*. The lichen symbionts regularly co-disperse by symbiotic propagules but sexual reproduction of the fungal symbiont and photobiont switch during early stages of the thallus development may lead to new mycobiont-photobiont combinations in populations. Populations of *L. pulmonaria* were analysed from four continents and a model-based clustering method for inferring population structure using genotype data revealed a complex distribution pattern of fungal and algal gene pools and their associations at the local, continental and global level. We test how climatic and geographic variation co-vary with associations of mycobiont and photobiont gene pools.