

ABSTRACT

Lichens are a classic example of mutualistic symbiotic associations, yet the views on lichen symbiosis have changed considerably during the last fifty years. Nowadays, lichens are generally understood to be microecosystems consisting of several symbiotic partners which contribute in different ways to the prosperity of the whole system and which differ by the strength of their bond to other symbiotic partners. The level of knowledge of the individual partners (mycobionts vs. photobionts vs. bacteria) varies greatly in terms of their specificity, diversity and in the forces that shape this diversity.

The main aim of this work was to reveal the diversity of organisms participating in lichen symbiosis and to better understand the biological forces which shape this diversity. We worked with a relatively common lichen group, zeorin-containing red-fruited *Cladonia* species, and specifically, we focused on the mycobionts, photobionts and bacteria that participate in this association. During the course of the study, it became apparent that species delimitation, which is a fundamental requirement for accurate diversity estimates, is another topic that requires further research.

Our analyses revealed that species circumscription of most of recently recognized *Cladonia* mycobionts cannot be supported by molecular data. The genetic diversity of the mycobionts was relatively high and we detected several lineages that we were not able to characterize phenotypically, these probably correspond to cryptic species. These lineages are most likely a result of either hybridization or incomplete lineage sorting. The photobionts associated with these mycobionts also showed a relatively high level of diversity. Furthermore, in contrast to the mycobionts, the majority of photobiont lineages represent phenotypically distinguishable species.

We demonstrated that the reproductive and dispersal strategies of the mycobiont are the key factors influencing the diversity of the *Asterochloris* species in zeorin-containing red-fruited *Cladonia* species. We found that the sorediate *Cladonia* species were strongly selective towards their photobiont, whereas esorediate *Cladonia* species were photobiont generalists. In the case of bacteria, the age of the thallus was the main factor influencing the structure of the bacterial community. In the older thallus parts the bacterial community displayed a drastic change due both to the reduction of the otherwise dominant Alphaproteobacteria and to the increased abundance of other bacterial groups.