



## New partner at the core of macrolichen diversity

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### A recommendation of

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It has long been known that most multicellular eukaryotes rely on microbial partners for a variety of functions including nutrition, immune reactions and defence against enemies. Lichens are probably the most popular example of a symbiosis involving a photosynthetic microorganism (an algae, a cyanobacteria or both) living embedded within the filaments of a fungus (usually an ascomycete). The latter is the backbone structure of the lichen, whereas the former provides photosynthetic products. Lichens are unique among symbioses because the structures the fungus and the photosynthetic microorganism form together do not resemble any of the two species living in isolation. Classic textbook examples like lichens are not often challenged and this is what Toby Spribille and his co-authors did with their paper published in July 2016 in *Science* [1]. This story started with the study of two species of macrolichens from the class of Lecanoromycetes that are commonly found in the mountains of Montana (US): *Bryoria fremontii* and *B. tortuosa*. For more than 90 years, these species have been known to differ in their chemical composition and colour, but studies performed so far failed in finding differences at the molecular level in both the mycobiont and the photobiont. These two species were therefore considered as nomenclatural synonyms, and the origin of their differences remained elusive. To solve this mystery, the authors of this work performed a transcriptome-wide analysis that, relative to previous studies, expanded the taxonomic range to all Fungi. This analysis revealed higher abundances of a previously unknown basidiomycete yeast from the genus *Cyphobasidium* in one of the lichen species, a pattern that was further confirmed by combining microscopy imaging and the fluorescent in situ hybridisation technique (FISH).

Finding out that a previously unknown micro-organism changes the colour and

the chemical composition of an organism is surprising but not new. For instance, bacterial symbionts are able to trigger colour changes in some insect species [2], and endophyte fungi are responsible for the production of defensive compounds in the leaves of several grasses [3]. The study by Spribille and his co-authors is fascinating because it demonstrates that *Cyphobasidium* yeasts have played a key role in the evolution and diversification of *Lecanoromycetes*, one of the most diverse classes of macrolichens. Indeed these basidiomycete yeasts were not only found in *Bryoria* but in 52 other lichen genera from all six continents, and these included 42 out of 56 genera in the family *Parmeliaceae*. Most of these sequences formed a highly supported monophyletic group, and a molecular clock revealed that the origin of many macrolichen groups occurred around the same time *Cyphobasidium* yeasts split from *Cystobasidium*, their nearest relatives. This newly discovered passenger is therefore an ancient inhabitant of lichens and has driven the evolution of this emblematic group of organisms.

This study raises an important question on the stability of complex symbiotic partnerships. In intimate obligatory symbioses the evolutionary interests of both partners are often identical and what is good for one is also good for the other. This is the case of several insects that feed on poor diets like phloem and xylem sap, and which carry vertically-transmitted symbionts that provide essential nutrients. Molecular phylogenetic studies have repeatedly shown that in several insect groups transition to phloem or xylem feeding occurred at the same time these nutritional symbionts were acquired [4]. In lichens, an outstanding question is to know what was the key feature *Cyphobasidium* yeasts brought to the symbiosis. As suggested by the authors, these yeasts are likely to be involved in the production of secondary defensive metabolites and architectural structures, but, are these services enough to explain the diversity found in macrolichens? This paper is an appealing example of a multipartite symbiosis where the different partners share an ancient evolutionary history.

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