



A COMPREHENSIVE REVIEW ON LICHEN: A POTENTIAL BIONT

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ABSTRACT

Organisms from two separate kingdoms come together to produce a structure with distinct morphology and anatomy. Lichens are not particularly attractive on the outside, but their inside structure is stunning. Individual couples' mutualistic affiliations are not shown by morphological investigations, but the beauty of their symbiotic relationship is revealed by anatomical studies. In addition to the major photobiont and mycobiont, current research on lichens and their symbiotic connection reveal that additional micro-communities such as algae, fungus, and bacterial bionts are connected with many lichens. Lichen's microbial connection aids in the development of a stable and effective symbiotic life that can adapt to its natural environment.

KEYWORDS: Lichen bionts, mycobionts, microbial community, bacterial bionts.

INTRODUCTION

Lichens are holobionts, meaning they have more than one member. They generally consist of a filamentous fungal partner known as a mycobiont and an algal partner known as a photobiont, which can be either a eukaryotic chlorobiont (green algae) or a prokaryotic cyanobiont (cyanobacteria), with a few exceptions from other algae groups. About 85% of lichens have chlorobionts as their photosynthetic partner, 10% have cyanobionts, and fewer than 5% have other photobionts.^[1,2] Bipartite lichens are defined by the presence of two partners, a fungus and an alga, and about 95 percent of lichens are bipartite. Lichens have a twofold nature, which is commonly understood. Chlorolichens (photobiont chlorobiont) and cyanolichens (photobiont cyanobacterium) are two types of bipartite lichens (cyanobiont as photobiont). More than 85% of bipartite lichens are chlorolichens, with just 13% having cyanobionts as their main photobiont.^[3]

Approximately 4% of lichens have more than two spouses. Tripartite lichens have a mycobiont and two photobionts (a green alga and cyanobacteria), and they are called co-primary photobionts if both photobionts contribute to photosynthesis.^[1] The principal photobiont in tripartite lichens is often a green alga, while cyanobacteria (secondary photobiont) is limited to specialized structures termed cephalodia, where they are more favored for nitrogen-fixing rather than photosynthesis.^[4,5] The majority of lichenized fungus belongs to the Ascomycetes class, with only a few belonging to Basidiomycetes and sterile species belonging to the artificial Deuteromycetes class.

Trebouxia, *Trentepohlia* (chlorobionts), and *Nostoc* (cyanobiont) are common photobiont partners.^[5-8]

Lichen is currently regarded as a conventional idea involving a mutualistic relationship between a fungal and an algal partner. In addition to the mycobiont and photobiont, lichens have a wide microbial community, both prokaryotic and eukaryotic, according to recent and sophisticated molecular level studies.^[9,10]

On big foliose cyanolichens in wet tropical woods, smaller biological entities such as heterotrophic bacteria, viruses, diatoms, green algae, free-living cyanobacteria, epiphytic algae, and epiphytic liverworts were discovered. With the lichen *Peltigera hymenina*,^[11] a total of 324 phyla were discovered, including 236 bacteria, 74 viruses, 8 eukaryotes, and 6 archaea.

Mycobionts

There isn't a single mycobiont connected with lichens, however, several lichenicolous fungi are present as parasites, saprobes, or commensals. They cause minimal harm to the host since they do not exchange nutrients directly with the major mycobiont, instead of relying on the photobiont of the host. Five distinct lichenicolous fungi were discovered in *Lecanora polytropa*. The majority of them were melanized fungi from the Dothideomycetes and Eurotiomycetes classes.^[12]

Photobionts

In a single lichen thallus, several green algal symbionts were discovered. In *Lecanora muralis*,^[13] many lineages of the green algae genus *Trebouxia* were discovered.

Different algae might be observed in the lobes or areoles of a single lichen thallus,^[14] because thallus outgrowths can interact with new algae. Several Nostoc genotypes have been identified from various cephalodia found on the same *Peltigera venosa* thallus. This might be due to its peculiar growth and lichenization patterns under a variety of environmental circumstances.^[15]

Cladonia and *Stereocaulon* species collected from metal (Copper) contaminated sites yielded around 50 internal transcribed spacer (ITS) algal (chlorobiont) sequences belonging to the *Asterochloris* and *Trebouxia* lineages.^[16] The lichen *Ramalina farinacea* has been shown to have a constant co-existence of *Trebouxia* species TR9 and *Trebouxia jamesii*. This lichen has a substantially greater chlorobiont diversity, with 31 OTUs representing distinct microalgal taxa, *Elliptochloris*, *Vulcanochloris*, and *Diplosphaera*, obtained using a 454-pyrosequencing approach.^[17] In *Ramalina farinacea*, the cohabitation of two *Trebouxia* species, TR9 and TR1,

was discovered to have a considerable impact on the lichen's growth and photosynthesis under diverse stressful situations. TR9 flourished in high temperatures and irradiances, whereas TR1 thrived in moderate and shaded conditions.^[18] *Ramalina fraxinea*.^[19] was discovered to be connected with seven distinct *Trebouxia* lineages belonging to two species, *T. decolorans* and *T. jamesii*.

The lichen connection with numerous bionts was more commonly reported in cooler temperatures than in warmer climates, according to studies on the genetic diversity of chlorobionts in different climates. Temperate regions had more variety than tropical regions. In the arctic, the mycobiont *Protopermella* was identified connected with many *Trebouxia* (chlorobiont) species, however, in the tropical environment, its affiliation was confined to a single species of *Trebouxia*. Algal selectivity was greater in tropical areas due to fewer multiple linkages.^[20]



Lichenicolous lichen bionts

Rikkinen claimed to have discovered lichenicolous lichens (2002). *Toninia* species have been discovered to begin their development on other cyanolichens before becoming self-sufficient. A cyanolichen called *Lichinodium sirosiphoideum* was discovered growing on parmelioid chlorolichens. For supplementary nitrogen supply, certain chlorolichens are connected with free-living cyanobacteria such as *Stigonema* and *Gloeocapsa*.

Bacterial bionts

Cladonia arbuscula, *Lecanora polytropa*, and *Umbilicaria cylindrica* samples from alpine locations were studied by Grube et al. (2009), who discovered bacterial communities in abundance as highly organized and biofilm-like assemblages on mycobiont surfaces. *Alphaproteobacteria* dominated the community, according to fluorescence in situ hybridization (FISH) study. Molecular fingerprints of the related microorganisms were created using PCR- single-strand conformation polymorphism with universal and group-specific primers, and each lichen species' fingerprints displayed different patterns. The presence of functional genes in cultivable bacterial strains revealed the participation of related bacteria in nutrient cycling. *Alphaproteobacteria* and *Firmicutes* displayed lytic action, antibiotic generation, vitamin and hormone production, particularly IAA (Indole-3-acetic acid), phosphate mobilization, and antagonistic activity against other microorganisms. The strains also had *nifH* genes, which are involved in symbiotic nitrogen fixation.

In addition to the chlorobiont and mycobiont, *Lobaria pulmonaria*, a lichenicolous fungus, and a complex prokaryotic community dominated by Rhizobiales were discovered in the lung lichen. A novel metaproteome analysis approach was used. Within lichen associations, multifaceted interactions were discovered, and the many activities of partners contributed to *L. pulmonaria*'s lifespan under particular ecological conditions.^[21] Rhizobiales were discovered to make up a third of the entire bacterial population of *L. pulmonaria*. Rhizobiales had endosymbiotic members from the *Methylobacteriaceae*, *Bradyrhizobiaceae*, and *Rhizobiaceae* families. Rhizobiales' roles in symbiosis were discovered by a metagenomics investigation (SEED-based functional analysis) that included vitamin and hormone synthesis, nitrogen fixation, and stress protection. FISH-CLSM used a unique probe to find rhizobiales. The presence of exo and endosymbiotic Rhizobiales members in *L. pulmonaria*,^[22] was verified. Along with the mycobiont and photobiont proteins, other bacterial proteins from members dominated by *Proteobacteria* and *Archaeobacteria* were discovered in *L. pulmonaria*.

Fungal proteins dominated with 75.4 percent of the total, whereas bacterial and green algal proteins were in the same 10% range. Bacterial proteins from *L. pulmonaria* were investigated and shown to be involved in post-translational modifications, protein turnover, and a variety of additional activities such as amino acid

transport, nucleotide transport, and co-enzyme transport.^[23]

From 35 lichen samples belonging to 22 genera,^[24] 213 Actinomycetes strains of the Actinobacteria phylum were isolated, including unique species belonging to 38 genera, 19 families, and 9 orders. Representatives of the extremophilic Acidobacteria are also found among the bacterial companions. *Acetobacteraceae*, *Brucellaceae*, multiple strains of *Methylobacterium*, and a novel lineage of Rhizobiales were also discovered, with the new lineage dominating the microbial community. To target such bacteria, 16s ribosomal oligonucleotide primers were created.^[25]

The bacterial community was dominated by *Alphaproteobacteria* in microbiota investigations of *Parmelia*, *Rhizoplaca*, and *Umbilicaria* species, and various phylotypes closely linked to *Rhizobiales* and other recognized nitrogen fixers including *Azospirillum*, *Bradyrhizobium*, and *Frankia* were also observed.^[27]

Bacterial communities were studied in relation to six *Cladonia* species, two *Hypogymnia* species, two *Roccella* species, and *Pseudevernia furfuraceae*. *Firmicutes*, *Actinobacteria*, *Proteobacteria*, *Paenibacillus*, *Burkholderia*, and *Luteibacter rhizovicina* species were discovered to be linked with thalli. Thirty-four bacterial isolates were purified and classified into phylotypes, with representative isolates from each phylotype being studied.^[28]

Biosca et al. (2016) discovered a link between ecto and endolichenic bacteria and three lichen species, *Pseudevernia furfuracea*, *Ramalina farinacea*, and *Parmotrema pseudotinctorium*, and found that extended thalli washing with a surfactant, using an antioxidant buffer to reduce endolichenic bacteria's oxidative stress during thalli disruption, and using minimal media enriched with lichen extract.

Diverse bionts

Heterotrophic eukaryotic protists (flagellates and non-flagellates) were discovered connected with lichens in another investigation. The *chrysophyte Ochromonas crenata* and the testate amoebae *Corythion dubium* were discovered in conjunction with the silica-rich lichens *Flavoparmelia carperata* and *Flavoparmelia baltimorensis*, which aid in nitrogen cycling and cell wall formation.^[30]

Bionts: Significant roles

Lichen heterotrophic microbial bionts play an important part in symbiosis. Symbiotic relationships between prokaryotic and eukaryotic organisms enabled them to thrive in harsh environments such as outer space and Mars.^[31] Secondary compounds produced by cyanobionts, mycobionts, and bacterial bionts play important functions in symbiosis. Mycobiont secretes lectins that detect certain ligands on suitable algal cells

and assess whether or not the interaction is successful. Arginase, a mycobiont-secreted algal binding protein, is bound to the cell wall of isolated phycobionts of *Xanthorina parietina*.^[32] *Sticta*, *Peltigera*, and *Nephroma* species from humid and temperate climates were shown to generate cyanobacterial hepatotoxins such as nodularin and microcystin, which aid in herbivore defence.^[33] The chlorobiont and mycobiont of the epiphytic lichen *Xanthorina parietina*,^[34] generated surface alkanes and fatty acids.

Varol et al. (2015) extracted usnic acid and atranorin, sunscreen lichen compounds generated by the mycobiont partners of *Cladonia foliacea* and *Pseudevernia furfuracea*, from their acetonetic extracts and investigated their photoprotective effects, but found them to be harmful to human skin. 3R-5-hydroxymellein, a secondary metabolite generated by the endolichenic fungus *Parmotrema austrosinense*, was discovered to exhibit UV protective properties, even on human skin, without causing any cytotoxicity.^[36]

According to Hauck et al. (2009), the presence of certain depsidones, depsides, fumarprotocetraric acid, perlatolic, and thamnolic acids is responsible for some lichens' exceptional resilience to acidic air pollution. In connection to their particular secondary metabolites, lichens display metal build-up and metal avoidance strategies. According to Paukov et al. (2015), various metal concentrations were discovered in four different species of *Aspicilia* that included different depsidones. Due to the penetration of its secondary compounds into the host tissue, dense development of the epiphytic lichen *Hypogymnia physodes* was observed to harm the host, *Picea abies*.^[39] Cultures of isolated mycobionts from lichen thalli of *Diorygma* species produced novel secondary metabolites.^[40]

CONCLUSION

Recent lichen symbiosis research has replaced the previous paradigm that "Lichens are symbiotic associations of a fungal and an algal partner" with the new paradigm that "Lichens are micro-ecosystems for numerous bionts including microspecies." Lichens and their bionts also produce new secondary metabolites that aid in effective association and survival in a variety of environments. Many other bacteria share a lichen association's shelter and food because there is an established mutualistic connection that is beneficial to them. As a result, lichen improves the microbial community's ability to thrive and benefit from one another. The study of lichen biota should receive a lot of attention, and extensive research on lichen bionts and their relevance should be carried out.

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