



## Evolutionary compatibility in lichen symbiosis

<sup>1</sup>Camelia Oroian, <sup>2</sup>Claudia Balint, <sup>3</sup>Maria Popescu, <sup>4</sup>Florin D. Bora, <sup>2,5,6</sup>I. Valentin Petrescu-Mag, <sup>7</sup>Teodor Rusu, <sup>8</sup>Diana Voicu

<sup>1</sup> Faculty of Horticulture and Business for Rural Development, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania; <sup>2</sup> Department of Environmental Engineering and Protection, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania; <sup>3</sup> Equine Clinic, Faculty of Veterinary Medicine, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania; <sup>4</sup> Viticulture and Oenology Department, Advanced Horticultural Research Institute of Transylvania, Faculty of Horticulture and Business for Rural Development, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania; <sup>5</sup> Bioflux SRL, Cluj-Napoca, Romania; <sup>6</sup> University of Oradea, Oradea, Romania; <sup>7</sup> Department of Technical and Soil Sciences, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania; <sup>8</sup> Institute of Biology, Romanian Academy, Bucharest, Romania. Corresponding author: C. Balint, claudia.balint@usamvcluj.ro

**Abstract.** Lichens represent one of the most successful and evolutionarily stable forms of symbiosis, arising from intimate associations between specialized fungi (mycobionts) and photosynthetic partners (photobionts), primarily green algae or cyanobacteria. Their compatibility reflects a complex evolutionary process involving genomic remodeling, metabolic integration, coordinated signaling, and ecological filtering. Comparative genomic and phylogenomic studies demonstrate that lichenization evolved multiple times independently, supported by convergent gene loss, gene gain, and regulatory innovation in both partners. Fungal genomes show reductions in plant cell wall-degrading enzymes and expansions of lineage-specific genes encoding symbiosis-related secreted proteins, while photobionts exhibit adaptations related to carbohydrate metabolism, stress tolerance, and cellular interface formation. Compatibility is expressed ecologically through patterns of specificity and selectivity, where fungal identity strongly constrains realized associations despite the broad availability of potential photobionts. Molecular and developmental studies reveal that symbiosis formation involves sequential stages of recognition, adhesion, and differentiation, mediated by coordinated gene expression and specialized symbiotic interfaces enabling bidirectional nutrient exchange. Increasing evidence also highlights the role of additional microbial partners and environmental factors in shaping symbiotic stability and functional performance. Furthermore, experimental systems and intermediate associations, such as alcobioses, semilichens, and laboratory-induced symbioses, demonstrate that compatibility can emerge between previously unrelated partners under appropriate conditions. These findings support a reconceptualization of lichens as dynamic, multi-partner systems occupying a broader evolutionary compatibility space. Overall, evolutionary compatibility in lichen symbiosis emerges from distributed genetic adaptations, ecological constraints, and regulatory integration, allowing both stability and flexibility in symbiotic associations across diverse environments.

**Key Words:** coevolution, evolutionary compatibility, experimental symbiosis, lichen symbiosis, lichenization, metabolic integration, multi-partner symbiosis, mycobiont, photobiont, photobiont diversity, phylogenomics, symbiotic interfaces, symbiotic selectivity, symbiotic signaling, symbiotic specificity.

**Introduction.** Lichens arise from long-term, intimate associations between specialized fungi (mycobionts) and photosynthetic partners (photobionts), mostly green algae (Trebouxiophyceae) or cyanobacteria. Their global success reflects a deep evolutionary tuning of compatibility between partners, at the levels of genomes, metabolism, signaling and ecology, which constrains but also diversifies possible pairings (Armaleo et al 2019; Song et al 2022; Spribille et al 2022; Pichler et al 2023). Recent phylogenomic and comparative studies show that lichenization has evolved multiple times and that both fungal and algal lineages have acquired specific traits enabling stable mutualistic integration, while

retaining a surprising degree of flexibility that allows for novel or experimental symbioses in nature and in the laboratory (Leavitt et al 2015; Armaleo et al 2019; Spribille et al 2022; Puginier et al 2024).

The aim of this study is to synthesize current genomic, phylogenomic, ecological, and experimental evidence in order to elucidate the evolutionary mechanisms and biological processes that determine compatibility between fungal and photosynthetic partners in lichen symbiosis.

**Evolutionary acquisition of compatibility in lichen partners.** Parallel genomic analyses reveal that lichen-forming fungi have undergone characteristic genome remodeling consistent with a transition to a symbiotic lifestyle. Comparative genomics of Eurotiomycete and Lecanoromycete mycobionts shows widespread loss of genes for plant cell-wall-degrading enzymes, many sugar transporters and numerous transcription factors, reflecting reduced reliance on complex external polysaccharides and specialization on a narrow set of carbon sources provided by photobionts (Song et al 2022). At the same time, lichen fungi gained many lineage- and species-specific genes encoding small secreted proteins that are strongly induced during the early stages of symbiosis, indicating a central role in partner recognition, interface construction and modulation of photobiont physiology (Song et al 2022).

Genomics of the photobiont *Asterochloris glomerata* and its partner *Cladonia grayi* likewise shows expansions in carbohydrate-active enzymes and stress-response pathways, including carbonic anhydrases and desiccation-related proteins, and horizontally acquired archaeal ATPases, all consistent with adaptation to life within increasingly desiccation-tolerant, stratified thalli (Armaleo et al 2019). Together, these data suggest that compatibility is not the product of a single “lichen gene” but of distributed evolutionary changes in membrane transport, signaling, cell-wall architecture and stress tolerance in both partners (Armaleo et al 2019; Song et al 2022; Spribille et al 2022).

Phylogenomic reconstruction across Chlorophyte algae demonstrates that the capacity for lichenization originated multiple times independently, with at least three gains of lichen-forming ability: one in Trebouxiophyceae and two in Ulvophyceae (Puginier et al 2024). In Trebouxiophyceae, the acquisition via horizontal gene transfer of a glycoside hydrolase 8 (GH8) enzyme capable of degrading fungal cell-wall polysaccharides coincided with the origin of lichenization, suggesting that controlled modification of the fungal cell surface was a key innovation enabling intracellular compatibility and stable appression of algal cells to hyphae (Puginier et al 2024). This evolutionary mosaic of gene loss, gain and co-option in both partners underpins their capacity to form persistent symbioses.

**Specificity, selectivity and macroevolutionary patterns of compatibility.** Compatibility in lichens is manifested ecologically as patterns of specificity (range of partners actually used) and selectivity (preference among available partners). Large-scale studies of *Trebouxia* and other green photobionts show extensive, often undescribed diversity, with many algal operational taxonomic units having broad geographic ranges and the capacity to associate with multiple fungal genera (Leavitt et al 2015; De Carolis et al 2022). At the same time, individual fungal species or lineages often display strong selectivity for particular algal OTUs, indicating that fungal identity is a major determinant of realized partnerships (Leavitt et al 2015; Zuo et al 2023). In the globally distributed family Parmeliaceae, fungal specificity and selectivity for *Trebouxia* photobionts are more important than broad ecogeographic context in determining observed pairings, suggesting that co-evolved recognition and compatibility traits limit partner swapping even where multiple algae co-occur (Leavitt et al 2015).

Cophylogenetic analyses in different systems typically detect significant, though incomplete, congruence between fungal and algal phylogenies, consistent with a mixture of codiversification, host switches and “failure to diverge” of algae relative to their fungal hosts (Singh et al 2017; Zuo et al 2023). In *Trebouxia*-associated lichens spanning four biomes, both fungal and algal identities strongly structure association networks, and partner combinations deviate from random expectation, again indicating evolutionary constraints on compatibility (Zuo et al 2023). Macroclimatic factors modulate these

patterns: in some genera, fungi and algae tend to be more specific in warmer climates, while cooler climates favor interactions with multiple partners, possibly because fluctuating conditions select for more flexible photobiont use (Singh et al 2017; Zuo et al 2023). Such context-dependent specificity shows that compatibility is not absolute, but is channeled by historical and ecological filters.

At the organismal level, compatibility is also reflected in tightly coordinated metabolic exchanges. Photobionts export sugar alcohols that are converted by the fungus into polyols with dual roles as carbon sources and protectants against desiccation, enabling mycobiont persistence in habitats otherwise hostile to free-living filamentous fungi (Spribille et al 2022). In return, fungi supply fixed nitrogen and phosphorus and provide structural and photoprotective benefits, but photobionts can exert leverage over fungal reproduction and morphogenesis, indicating that compatibility involves an evolving balance of mutual control rather than unilateral fungal dominance (Spribille 2018; Spribille et al 2022).

**Developmental and molecular basis of symbiotic compatibility.** The transition from free-living fungus and alga to a differentiated lichen thallus (“lichenization”) requires a cascade of developmental events whose success depends on fine-tuned recognition and signaling. A recent synthesis of experimental and molecular data divides lichenization into five stages: pre-contact, contact, envelopment, incorporation and thallus differentiation, each dominated by distinct suites of extracellular metabolites and signaling processes (Pichler et al 2023). Early stages involve fungal lectins and algal cyclic peptides that promote adhesion and alignment of compatible partners, followed by remodeling of fungal and algal cell walls, including formation of hydrophobic sheaths and symbiotic interfaces akin to plant–microbe interfaces (Kono et al 2020; Pichler et al 2023).

*In vitro* resynthesis of the fruticose lichen *Usnea hakonensis* has enabled dissection of symbiosis-specific transcriptional programs. Comparative transcriptomics between isolated cultures and both natural and resynthesized thalli identified sets of fungal and algal genes up-regulated specifically in the symbiotic state, including genes for modified fungal cell walls at contact sites, formation of a hydrophobic layer encasing both partners, algal sugar export, and fungal nitrogen and phosphorus transporters (Kono et al 2020). These results show that compatibility is implemented through coordinated, reversible shifts in gene expression that build and maintain a specialized interface for bidirectional nutrient flow. Similar stages and molecular functions appear widespread among lichens, suggesting that convergent regulatory architectures underlie compatible mycobiont–photobiont interactions across taxa (Armaleo et al 2019; Kono et al 2020; Pichler et al 2023).

At the same time, microbiome research has revealed that lichen thalli are complex, multi-species biofilms. Many macrolichens harbor basidiomycete yeasts in their cortices, as well as diverse bacteria with roles in nitrogen cycling, vitamin provisioning and secondary metabolism (Du et al 2019; Spribille et al 2022). These additional partners likely contribute to structural integrity and stress tolerance, and they may modulate compatibility by influencing signaling environments or resource flows among the canonical symbionts (Spribille 2018; Du et al 2019; Spribille et al 2022). The cortex itself has been proposed to function as a three-dimensional biofilm matrix held together by specific polysaccharides, raising the possibility that compatibility extends beyond binary fungus–alga interactions to emergent properties of multi-partner consortia (Du et al 2019; Spribille et al 2022).

**Photobiont diversity, environmental filters and adaptive compatibility.** The compatibility spectrum is further shaped by the diversity and ecological breadth of photobionts. Many lichen-forming algal genera, such as *Trebouxia* and *Asterochloris*, comprise numerous cryptic species-level lineages that occupy distinct climatic and altitudinal niches (De Carolis et al 2022; Zuo et al 2023). Surveys of extreme environments, including high mountains and polar regions, show that a given fungal species complex can associate with multiple photobiont lineages along environmental gradients, and that photobiont turnover often tracks altitude and microclimate (De Carolis et al 2022; Valim et al 2025). This pattern suggests that compatible pairings are filtered

not only by historical co-evolution but also by local performance trade-offs in photosynthesis, desiccation tolerance and light capture.

Transcriptomic comparisons of fungal and algal partners from contrasting climate zones reveal that different partner combinations adjust their gene expression to match local conditions. In a Mediterranean lichen system, high- and low-elevation thalli exhibit distinct fungal expression profiles for circadian and temperature-associated genes, while algae show climate-specific expression of light-responsive genes and sugar transporters (Valim et al 2025). Both partners differentially regulate sugar transport in a climate-dependent manner, implying that compatibility involves adjustable metabolic interfaces tuned to ambient temperature and light regimes (Valim et al 2025). Such plasticity allows a given symbiotic species to maintain functional compatibility across environments, but only within the bounds set by the inherent physiological capacities of its partner repertoire.

From an evolutionary perspective, partner switching and flexible photobiont use can facilitate range expansion and ecological diversification, while high specificity may promote co-speciation and niche specialization (Leavitt et al 2015; Singh et al 2017; Zuo et al 2023). However, photobiont pools are not unconstrained: lichen-associated algae show their own phylogenetic structure, with repeated evolution of lichen-forming capabilities in certain clades and widespread, but not universal, tendencies for association with fungi (De Carolis et al 2022; Puginier et al 2024). Thus, the set of experimentally or naturally realizable mycobiont–photobiont pairings is limited by the intersection of these independently evolved compatibilities.

**Experimental and “incipient” algal-fungal symbioses.** Beyond classical lichens, recent discoveries highlight a continuum of algal–fungal associations that illuminate how compatibility can emerge evolutionarily and be probed experimentally. Alcobioses are loose symbioses between corticioid basidiomycete fungi and green algae on bark or wood, where algae form a layer in or under the fungal basidioma reminiscent of a photobiont layer but without full lichen dependence (Vondrák et al 2023). Physiological experiments demonstrate substantial photosynthetic activity of the algae, and in at least one *Lyomyces–Desmococcus* pairing, carbon fixed by the alga is transferred to fungal polyols, indicating incipient trophic mutualism (Vondrák et al 2023). Yet the fungal partners in alcobioses can live independently, and their thalli lack the complex stratification and desiccation tolerance of true lichens, suggesting these systems represent early or partial stages on the path to full lichenization (Vondrák et al 2023).

Semilichens, recently described intermediary systems between “green biofilms” and lichens, further illustrate minimal but functionally significant compatibility. Here, a single dominant fungus intimately associates with green algal biofilms from Trebouxiophyceae or Ulvophyceae lineages. Algae remain alive and perform substantial photosynthesis, and stable carbon transfer to fungal polyols has been demonstrated, yet biomass production is extremely low and morphological differentiation is minimal (Vondrák et al 2025). Semilichens thrive in environments where “true” lichens are largely absent, implying that even basic compatibility (adhesion, limited carbon flow, shared stress tolerance) can provide selective advantages under harsh, frequently desiccating conditions (Vondrák et al 2025).

*In vitro* resynthesis experiments provide a more controlled view of experimental compatibility. The *U. hakonensis* system, where axenic cultures of fungus and alga are recombined to form visible thalli, shows that fully lichen-like morphogenesis is possible in the lab when genetically matched partners are used (Kono et al 2020). Transcriptomic signatures clearly distinguish symbiotic from non-symbiotic states, and many of the up-regulated symbiosis genes correspond to those identified as expanded or conserved in comparative lichen genomes, reinforcing the idea that experimentally realized compatibility draws upon evolutionarily entrenched molecular toolkits (Armaleo et al 2019; Kono et al 2020; Song et al 2022). At the same time, a broad review of 150 years of resynthesis studies indicates that “*in vitro* lichens” rarely recapitulate natural morphology, and that contaminant microbes or non-axenic tissue cultures often yield the most lichen-like results, suggesting that full compatibility in thallus construction may require additional, non-canonical symbionts or environmental cues (Du et al 2019; Belosokhov & Spribille 2025).

A striking experimental example of novel algal–fungal symbiosis outside the traditional lichen framework is the recently described photosynthetic mycelium formed by co-cultivation of the filamentous fungus *Mortierella elongata* and the green alga *Nannochloropsis oceanica* (Du et al 2019). In this association, algal cells first attach to fungal hyphae, then become internalized, remaining photosynthetically active, growing and dividing within the hyphae over months of co-culture. Stable bidirectional exchange of carbon and nitrogen has been demonstrated using isotope tracers (Du et al 2019). This endosymbiotic interaction, achieved between partners with no history of lichenization, underscores how basic compatibility - adhesion, nutrient exchange, immune moderation - can arise experimentally from free-living lineages given appropriate conditions, and it offers a model to study early steps toward endosymbiosis.

Finally, newly discovered thallus-forming nitrogen-fixing symbioses, such as a leaf-like “phyllosymbia” composed of interwoven cyanobacterial filaments with hyphae nested inside their sheaths, reveal that morphologically complex, lichen-like structures can evolve independently in lineages not previously recognized as lichenized (Chen et al 2025). Here, the fungus resides entirely within cyanobacterial structures, and the symbiosis shows distinct nitrogen-fixation rates and phylogenetic placements from known cyanolichens, representing a novel, experimentally tractable configuration of algal–fungal compatibility (Chen et al 2025).

**Reconceptualizing lichen symbiosis and its compatibility space.** These diverse observations have fueled calls to reconceptualize lichens as multi-species, dynamic systems rather than static dualisms (Spribille 2018; Du et al 2019; Allen & Lendemer 2022; Spribille et al 2022). Compatibility, in this view, is not merely a binary property of particular fungus–alga pairs but a multidimensional trait shaped by relative contributions of all partners, by environmental context and by the developmental stage of the symbiosis. Recent theoretical work emphasizes that understanding lichen phenotypes and evolutionary trajectories will require integrating microbial community composition, host genomic architecture, ecological gradients and evolutionary history into a single framework (Spribille 2018; Du et al 2019; Allen & Lendemer 2022; Spribille et al 2022).

Within this broadened perspective, classical lichens represent one region of a larger “compatibility space” of algal–fungal interactions, bounded by the need to maintain balanced nutrient exchange, structural coherence and joint stress tolerance. Alcobioses, semilichens, experimentally resynthesized thalli and novel laboratory consortia such as photosynthetic mycelia and phyllosymbia occupy adjacent regions of this space, illustrating how new configurations of compatibility can emerge from lineages that share core traits such as desiccation tolerance, cell-wall plasticity and responsive signaling networks (Du et al 2019; Vondrák et al 2023; Puginier et al 2024; Belosokhov & Spribille 2025; Chen et al 2025; Vondrák et al 2025).

From an evolutionary standpoint, the repeated origin of lichenization in fungal and algal lineages, the convergent acquisition of functional gene sets, the phylogenetically structured yet flexible partner associations, and the ease with which partial symbioses arise in extreme environments all suggest that compatibility for lichen-like symbiosis is both emergent and contingent: emergent from shared ancestral capacities for stress tolerance and metabolic exchange, and contingent on specific historical events of gene gain, loss and regulatory rewiring. Experimental symbioses between non-lichenized partners provide powerful systems to dissect the minimal requirements for compatibility and to test how far evolutionarily derived lichen toolkits can be generalized across the algal–fungal interface.

**Conflict of interest.** The authors declare that there is no conflict of interest.

## References

Allen J. L., Lendemer J. C., 2022 A call to reconceptualize lichen symbioses. *Trends in Ecology and Evolution* 37(7):582-589.

- Armaleo D., Müller O., Lutzoni F., Andrésón Ó. S., Blanc G., Bode H. B., Collart F. R., Grande F. D., Dietrich F., Grigoriev I. V., Joneson S., Kuo A., Larsen P. E., Logsdon Jr. J. M., López D., Martin F., May S. P., McDonald T. R., Merchant S. S., Miao V., Morin E., Oono R., Pellegrini M., Rubinstein N., Sanchez-Puerta M. V., Savelkoul E., Schmitt I., Slot J. C., Soanes D., Szövényi P., Talbot N. J., Veneault-Fourrey C., Xavier B. B., 2019 The lichen symbiosis re-viewed through the genomes of *Cladonia grayi* and its algal partner *Asterochloris glomerata*. *BMC Genomics* 20:605.
- Belosokhov A., Spribille T., 2025 Making fungal-photobiont symbioses in the lab: past, present, and future of the elusive *in vitro* lichen. *Annual Review of Microbiology* 79: 713-730.
- Chen C. C., Xie Q. Y., Chuang P. S., Darnajoux R., Chien Y. Y., Wang W. H., Tian X. J., Tu C. H., Chen B. C., Tang S. L., Chen K. H., 2025 A thallus-forming N-fixing fungus-cyanobacterium symbiosis from subtropical forests. *Science Advances* 11(7):4093.
- De Carolis R., Cometto A., Moya P., Barreno E., Grube M., Tretiach M., Leavitt S. D., Muggia L., 2022 Photobiont diversity in lichen symbioses from extreme environments. *Frontiers in Microbiology* 13:809804.
- Du Z. Y., Zienkiewicz K., Pol N. V., Ostrom N. E., Benning C., Bonito G. M., 2019 Algal-fungal symbiosis leads to photosynthetic mycelium. *eLife* 8:e47815.
- Kono M., Kon Y., Ohmura Y., Satta Y., Terai Y., 2020 *In vitro* resynthesis of lichenization reveals the genetic background of symbiosis-specific fungal-algal interaction in *Usnea hakonensis*. *BMC Genomics* 21:671.
- Leavitt S. D., Kraichak E., Nelsen M. P., Altermann S., Divakar P. K., Alors D., Esslinger T. L., Crespo A., Lumbsch T., 2015 Fungal specificity and selectivity for algae play a major role in determining lichen partnerships across diverse ecogeographic regions in the lichen-forming family Parmeliaceae (Ascomycota). *Molecular Ecology* 24(14): 3779-3797.
- Pichler G., Muggia L., Carniel F. C., Grube M., Kranner I., 2023 How to build a lichen: from metabolite release to symbiotic interplay. *New Phytologist* 238(4):1362-1378.
- Puginier C., Libourel C., Otte J., Škaloud P., Haon M., Grisel S., Petersen M., Berrin J. G., Delaux P. M., Grande F. D., Keller J., 2024 Phylogenomics reveals the evolutionary origins of lichenization in chlorophyte algae. *Nature Communications* 15:4452.
- Singh G., Grande F. D., Divakar P. K., Otte J., Crespo A., Schmitt I., 2017 Fungal-algal association patterns in lichen symbiosis linked to macroclimate. *New Phytologist* 214(1):317-329.
- Song H., Kim K. T., Park S. Y., Lee G. W., Choi J., Jeon J., Cheong K., Choi G., Hur J. S., Lee Y. H., 2022 A comparative genomic analysis of lichen-forming fungi reveals new insights into fungal lifestyles. *Scientific Reports* 12:10724.
- Spribille T., 2018 Relative symbiont input and the lichen symbiotic outcome. *Current Opinion in Plant Biology* 44:57-63.
- Spribille T., Resl P., Stanton D. E., Tagirdzhanova G., 2022 Evolutionary biology of lichen symbioses. *New Phytologist* 234(5):1566-1582.
- Valim H. F., Otte J., Schmitt I., 2025 Fungal and algal lichen symbionts show different transcriptional expression patterns in two climate zones. *Proceedings of the Royal Society B: Biological Sciences* 292(2050):20242962.
- Vondrák J., Svoboda S., Zíbarová L., Štenclová L., Mareš J., Pouska V., Košnar J., Kubásek J., 2023 Alcobiosis, an algal-fungal association on the threshold of lichenisation. *Scientific Reports* 13:2957.
- Vondrák J., Svoboda S., Říha P., Hauser T., Kantnerová V., Škaloud P., Kubásek J., 2025 Semilichen, an unjustly neglected symbiotic system between green biofilms and true lichens. *Scientific Reports* 16:927.
- Zuo Y. B., Han D. Y., Wang Y. Y., Yang Q. X., Ren Q., Liu X. Z., Wei X. L., 2023 Fungal-algal association drives lichens' mutualistic symbiosis: a case study with *Trebouxia*-related lichens. *Plants* 12(17):3172.

Received: 20 October 2025. Accepted: 30 November 2025. Published online: 30 December 2025.

Authors:

Camelia Oroian, Department of Economic Sciences, Faculty of Horticulture and Business in Rural Development, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăştur, 400372 Cluj-Napoca, Romania, e-mail: [camelia.oroian@usamvcluj.ro](mailto:camelia.oroian@usamvcluj.ro)

Claudia Balint, Department of Environmental Engineering and Protection, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăştur Street, 400372 Cluj-Napoca, Romania, e-mail: [claudia.balint@usamvcluj.ro](mailto:claudia.balint@usamvcluj.ro)

Maria Popescu, Equine Clinic, Faculty of Veterinary Medicine, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Mănăştur Street, 400372 Cluj-Napoca, Romania, e-mail: [maria.popescu@usamvcluj.ro](mailto:maria.popescu@usamvcluj.ro)

Florin Dumitru Bora, Viticulture and Oenology Department, Advanced Horticultural Research Institute of Transylvania, Faculty of Horticulture and Business in Rural Development, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăştur Street, 400372 Cluj-Napoca, Romania, e-mail: [florindumitru.bora@usamvcluj.ro](mailto:florindumitru.bora@usamvcluj.ro)

Ioan Valentin Petrescu-Mag, Department of Environmental Engineering and Protection, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăştur Street, 400372 Cluj-Napoca, Romania, e-mail: [zoobiomag2004@yahoo.com](mailto:zoobiomag2004@yahoo.com)

Teodor Rusu, Department of Technical and Soil Sciences, Faculty of Agriculture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, 3-5 Calea Mănăştur Street, 400372 Cluj-Napoca, Romania, e-mail: [teodor.rusu@usamvcluj.ro](mailto:teodor.rusu@usamvcluj.ro)

Diana Voicu, Institute of Biology Romanian Academy, Spl. Independentei street, no. 296, 060031 Bucharest, Romania, e-mail: [diana.voicu@ibiol.ro](mailto:diana.voicu@ibiol.ro)

This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

How to cite this article:

Oroian C., Balint C., Popescu M., Bora F. D., Petrescu-Mag I. V., Rusu T., Voicu D., 2025 Evolutionary compatibility in lichen symbiosis. *ELBA Bioflux* 17(1):41-47.