

Altitude and host genetic identity shape the algal microbiome of congeneric hosts: a metabarcoding approach.

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Reshuffling symbiont-host combinations is a strategy used by symbiotic organisms to adapt to changing environments. Ecological contrasts are thus expected to drive changes in photobiont communities, but their reactions are not well understood. Here we used Illumina MiSeq sequencing of the ITS2 barcode to study altitudinal variation in photobiont diversity associated with two ecologically segregated, closely-related congeneric lichen-forming fungi, sympatric in the limit of their distribution. In particular, we examined the effects of macro-climatic variation and host genetic identity on intrathalline photobiont diversity, community structure, and strength of biotic interactions. Our results suggest that environmental changes on fungal–algal symbioses may be mediated by the population genetic processes of the fungal hosts and by the degree of specificity of the associations. Finally, we showed that the NGS approach provides superior power to interrogate photobiont genetic variation compared to the traditional Sanger sequencing technology.