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An ecological clade-based genomic approach for the study of symbiotic pairing mechanisms between lichen-forming fungi and their cyanobacterial partners

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Abstract:

The evolution of eukaryotes is largely symbiotic. Yet, symbiotic networks have been predominantly studied within an ecological framework, where all interacting species of a functional group are examined simultaneously at a specific time and place.

An alternative approach involves studying ecological networks using closely related species (e.g., within a genus) that are interacting with species from another genus across spatial scales ranging from local to global. The latter enables robust comparative genomic analyses that are fully integrated within an eco-evolutionary framework. We developed a model system to investigate the pairing mechanisms between two genera, the lichen-forming genus *Peltigera* and its cyanobacterial partner *Nostoc*, across different spatial scales. This is a powerful symbiotic system because *Peltigera* individuals form large distinct thalli that include only one main *Nostoc* strain per thallus, both genera are cosmopolitan, and *Peltigera* thalli are often abundant and diverse locally, facilitating the implementation of complex and stratified sampling designs to address questions at the junction of evolutionary biology, ecology, and genomics. We systematically determined *Peltigera-Nostoc* pairings at the species level for over 5000 thalli worldwide and conducted dense regional sampling to assess the biotic and abiotic factors shaping pairing frequencies.

To better understand the transmission of *Nostoc* cyanobionts (vertical vs horizontal) from one lichen generation to the next, we compared *Nostoc* living in *Peltigera* thalli with *Nostoc* communities in their surrounding environment using amplicon sequencing. Also, we used a dataset of 151 genomes, including 124 newly generated *Nostoc* MAGs from cyanolichens sampled globally, and obtained metatranscriptomic data to compare gene expression of *Nostoc* living in *Peltigera* thalli versus *Nostoc* living in the surrounding mossy substrates of these lichen thalli. We found that the central metabolism and development are rewired in lichenized *Nostoc*.

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