**Eco-evolutionary dynamics of Nitrogen fixation by lichenized *Nostoc* revealed by metagenomics**

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Biological Nitrogen Fixation (BNF) by cyanobacteria can contribute significantly to Nitrogen (N) inputs in terrestrial ecosystems, especially in N-poor environments. Within cyanolichens, lichenized cyanobacteria can fix N2 and contribute to BNF. Cyanolichens often form large, conspicuous thalli with high cyanobacteria content per volume, and involve a high diversity of partners. Hence, they are ideal models to study how BNF is influenced by the evolutionary history of the symbionts. Lichenized cyanobacteria can fix nitrogen by using two nitrogenases, coded by distinct genes. The most common nitrogenase uses Molybdenum (Mo) as cofactor, whereas an alternative, complementary nitrogenase uses Vanadium (V). It was recently shown that the V-nitrogenase contributes significantly to BNF in cold and Mo-poor environments. Here, we explored the eco-evolutionary dynamics of BNF by lichenized cyanobacteria. To achieve this, we sequenced the metagenomes of ca. 80 *Peltigera* thalli representing the phylogenetic and geographic diversity of the genus. We developed a bioinformatic pipeline to correctly assign DNA sequences to each symbiont. We also developed a synteny-based approach to select genes (for both partners) and intergenic spacers (for the mycobiont) to generate phylogenomic datasets. We inferred the evolutionary histories of *Peltigera* and their N2-fixing cyanobionts of the genus *Nostoc*. These synteny-based phylogenomic approaches greatly improved the confidence levels of the resulting evolutionary trees for both partners, and more prominently for *Nostoc*. We will discuss the patterns of N2-fixation by *Peltigera* thalli within the phylogenetic context of the two main partners, as well as the presence/absence of nitrogenase genes within genomes of lichenized *Nostoc*. Genes coding for the V-nitrogenase seems to be very important in the *Peltigera-Nostoc* lichens, as they are found in almost all lichenized *Nostoc* strains sampled so far, and some are even present in two copies in the genomes of the most common *Nostoc* strains associated with *Peltigera* in boreal forests.