



Revealing cyanosphere microbial diversity of terrestrial cyanobacteria

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The cyanosphere contains heterotrophic microorganisms living within the exopolysaccharide sheath of cyanobacteria and serves as an interface between the cyanobacteria and their surrounding ecosystem. The symbiosis between the cyanobacterial host and its cyanosphere microbes spans the mutualistic-antagonistic spectrum. Understanding these relationships will predict the success of terrestrial cyanobacteria and the ecosystem services they provide including primary production in often oligotrophic environments. However, our understanding of the microbial diversity within the cyanosphere is limited. In this study, we used metagenomic sequencing to construct 528 metagenome-assembled genomes (MAGs) from the cyanosphere microbes associated with 50 unialgal terrestrial Cyanobacteria cultures, spanning 12 orders. We found that the composition of cyanosphere microbial communities was unique between Cyanobacteria hosts and was largely influenced by environmental (habitat, precipitation, and temperature) and phylogenetic variables (host order). Alphaproteobacteria was the most common cyanosphere microbial class and *Bosea*, *Devosia*, *Hyphomicrobium*, *Mesorhizobium*, and *Sphingomonas* were core genera found across all habitats. Interestingly, the nitrogen-fixing cyanobacterial order, Nostocales, contained the highest diversity of cyanosphere bacteria, many of which have the genomic potential also to fix atmospheric nitrogen. Given the observed variations in the cyanosphere microbial communities across different hosts, future considerations for ecological assessments and cyanobacterial restoration efforts must extend beyond the cyanobacteria to encompass their associated microbial communities.