

Diversity of phototrophic bacteria in terrestrial samples from the Sør Rondane Mountains, East Antarctica

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Although Cyanobacteria are generally considered the most important phototrophic primary producers and diazotrophs in Antarctic ecosystems, they appear to be scarce in some high-altitude Antarctic locations. Other organisms can therefore be hypothesized to take over their role in these systems. Furthermore, given the limited supply of organic matter, in oligotrophic surface samples, bacteria may use sunlight as an alternative energy source. To test these hypotheses, we investigated the diversity of phototrophs and nitrogen fixing microorganisms in exposed soils from the Sør Rondane Mountains, East Antarctica. An Illumina sequencing approach was used to analyze the bacterial community composition and the diversity and abundance of key genes involved in phototrophy and nitrogen fixation.

Analysis of *pufM* genes, encoding a subunit of photoreaction center 2 found in anoxygenic phototrophic bacteria, revealed a broad diversity, dominated by *Roseobacter*- and *Loktanella*-like sequences. *BchL* and *chlL* genes, involved in (bacterio)chlorophyll synthesis, showed a high relative abundance of either cyanobacterial or green algal trebouxiophyceael *chlL* reads, depending on the sample, while most *bchX* sequences belonged to previously unidentified phylotypes. Rhodopsin-containing phototrophic bacteria could not be detected in the samples. Our results, while suggesting that Cyanobacteria and green algae are the main phototrophic groups, show that light-harvesting bacteria including aerobic anoxygenic photoheterotrophs are nevertheless very diverse in microbial communities in Antarctic soils.

Nostocales Cyanobacteria, present in greatly varying numbers as assessed by Illumina sequencing of 16S rRNA and *nifH* gene fragments, appear to be the main nitrogen fixers in these habitats.

We also set up a cultivation campaign for culturable aerobic phototrophic bacteria present in the same samples collected in the proximity of the Belgian Princess Elisabeth Station. Approximately 1,000 isolates were obtained and identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and partial 16S rRNA gene sequence analysis. Over half of the isolates grouped among known aerobic anoxygenic phototrophic taxa, particularly with Sphingomonadaceae, *Methylobacterium* and *Brevundimonas*. A total of 330 isolates were tested for presence of key phototrophy genes. While rhodopsin genes were not detected, multiple isolates possessed key genes of the bacteriochlorophyll synthesis pathway. Laboratory growth experiments revealed that light indeed benefits the growth of several of these isolates, whereas others demonstrated better growth in the dark.