

# Microbial diversity within the vicinity of the Antarctic Concordia Station - an analog for human exploration sites on Mars or the icy moons of Jupiter or Saturn

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## **Abstract:**

The extreme terrestrial environment of the Antarctic ice sheet serves as an excellent probing ground for the adaptation of extremotolerant microorganisms. To inhabit this hostile environment, microorganisms resist sub-zero temperatures, wide temperature fluctuations, high incidence of solar UV radiation, desiccation, and very low nutrient availability. Located on a 3200 meter-high plateau in Antarctica, the Concordia Station is a remote, isolated habitat, providing an ideal location to monitor the indigenous microbial diversity and human-associated bacterial dispersal on the surface snow. In this study, (ESA project No. AO-13-Concordia-23) surface snow was sampled monthly at three areas varying in proximity (10 m, 500 m, and 1 km) to the Concordia Station across two years (March 2015 to December 2016). Snow samples from the months January, March, May, July, September, and November of both years (n=33) were phylogenetically profiled via sequencing of the 16S rRNA gene to identify microbial presence and abundance with respect to seasonal changes and human activity. While harboring low microbial diversity, the surface snow samples were characterized by heterogeneous microbiomes. Interestingly, snow samples were found to have a core microbiome consisting of the genera *Acinetobacter*, *Micrococcus*, *Delftia*, *Bacillus*, *Enhydrobacter*, *Cutibacterium*, and *Alcanivorax*, which persisted regardless of the measured environmental factors and level of human activity. Ultimately, this study will further inform improvements or modifications to the existing techniques to interrogate the microbial ecology in extreme (sub-zero) environments as well as provide suggestions for future life-detection driven space missions.