
THE RECONSTRUCTION OF 269 NEW DRAFT BACTERIAL GENOMES FROM ANTARCTIC CRYPTOENDOLITHIC COMMUNITIES IN THE CLOSEST MARS TERRESTRIAL ANALOGUE.

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Abstract

Antarctica is one of the driest, coldest, and most remote places on Earth (Cary et al., 2010). While most of the continent is covered with ice and snow, a small portion (< 2%) is ice-free and mostly composed of exposed rocks and oligotrophic mineral soils (Ugolini and Bockheim, 2018). Victoria Land (Continental Antarctica) includes McMurdo Dry Valleys, the widest ice-free regions and considered among the best terrestrial analogues of Martian environment (Wynn-Williams, 1990; Wierchos and Ascaso, 2002). The region, considered life-free until few decades ago (Friedmann, 1982), is exposed to severe environmental stressors such as low temperature, high UV radiation and low water availability (Cowan and Tow, 2004). There, the highly specialized and adapted Antarctic cryptoendolithic communities are microbial ecosystems dwelling inside rocks, representing excellent models to investigate the limit of the habitability of edge environments, relevant for future exploration of extraterrestrial life (Cockell et al., 2016).

Recent efforts have attempted to characterize these border ecosystems (Selbmann et al., 2017; Coleine et al., 2018a, b), but the community composition and functionality remain still scarcely understood. With the project "Metagenomic reconstruction of endolithic communities from Victoria Land, Antarctica" funded by the JGI (PI: L. Selbmann, Co-PI: J.E. Stajich), we used the culture-free recovery metagenomics tool to identify and characterize the composition of these communities in order to gain insight into their biodiversity, functionality and stress-adaptation strategies. We sequenced eighteen differently sun-exposed rocks collected during the XXXI Italian Antarctic Expedition (Dec. 2015- Jan.16) along an altitudinal transect from 834 up to 3100 m a.s.l.

A total of 3,817,654,184 high-quality filtered reads were generated by a Novaseq Illumina into

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more than 10 million of scaffolds. We classified the shotgun reads and the most frequently bacterial reads were dominated by Cyanobacteria, Actinobacteria and Proteobacteria, while very few archaeal reads were obtained, represented by Thaumarchaeota only. Green algae and either lichenized (Lecanoromycetes, Ascomycota) and dothideomycetous fungi were largely predominant among the Eukaryotes.

We also created a set of draft bacterial bins (completeness: $\geq 50\%$; contamination: $\leq 10\%$) and 269 dereplicated new genomes were generated. Phylogenetic assignment, based on 120 universal marker genes, showed that all reconstructed genomes represented previously unrecovered strains and new families, genera and species and they clustered apart from other genome references.

By reconstructing the genomes of environmental organisms through metagenomics, we will be able to study the functional potential of these microbes allowing for the exploration of novel metabolisms.

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