A decade (and a half) of microbial ecology research in the McMurdo Dry Valleys

Cowan Don A.

Centre for Microbial Ecology and Genomics, University of Pretoria, Pretoria, South Africa

don.cowan@up.ac.za

The McMurdo Dry Valley of eastern Antarctica represent a substantial proportion of the continent's ice-free land. Dry Valley mineral soils are widely considered to represent one of the most hostile environments on Earth. Although once considered to be effectively sterile, these soils are now known to host substantial populations of bacteria (> 10^6 cells g⁻¹: [1]) and a wide species diversity [2]. The Dry Valleys are also characterised by specialised cryptolithic niche habitats (particular endoliths and hypoliths [3]) which play important roles in regional ecosystem services [4]. Over the past 15 years, we have contributed to an increasingly comprehensive understanding of the structures [5-8], drivers [9], assembly processes [10] and adaptations [11,12] of microbial communities in Antarctic cold desert soils. The use of modern molecular phylogenetic survey methods, coupled with in situ and ex situ analyses of community function and adaptation, have led to the concept that despite the extreme abiotic properties of this desert ecosystem, these depauperate soils support a wide microbial [2], viral [8] and microeukaryote [7] species diversity. With our entry into the field of full metagenome sequence analysis and comparative metagenomics, we have obtained some insight into the metabolic capacity of Dry Valley microbial communities [13, 14], including the degree of metabolic redundancy and the breadth of molecular adaptation strategies employed by these organisms.

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