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THE ECOLOGY OF DRY VALLEY MICROBIAL COMMUNITIES ASSOCIATED WITH MUMMIFIED SEAL CARCASSES

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The Antarctic continent offers access to one of the most physically and chemically demanding environments on earth inhabited by bacteria. Antarctic Dry Valley ecosystems, in particular, experience large fluctuations in temperature and light regimes, along with steep chemical gradients, which greatly impact physiological adaptations and life cycle strategies. These ecosystems provide an extraordinary opportunity to examine metabolic adaptations that allow microbial communities to function in extreme environments. The presence of mummified seal carcasses in the Antarctic Dry Valleys is a natural phenomenon that provides a unique opportunity to study the effects of a localized nutrient supplement on the bacterial population in an otherwise harsh and nutrient (carbon and nitrogen) deprived environment. During two recent field season (2005/6) to the Meirs Valley we discovered a remote area (approx. 1000m^2) containing over 50 mummified seals (95% Crab-eater and 5% Weddell), equivalent to over 2 metric tons of organic input). Environmental samples were collected from cross-sectional transects in the vicinity of the carcasses of 13 mummified seals and from a vertical transect distant from any apparent seal remains in Miers Valley. Three of the seal transects and the vertical transect as a control were used in this study. Total carbon and nitrogen were found to be higher in those samples in close proximity to the carcasses and the source was considered to be from gradual disintegration of the cellular material. Using a suite of molecular approaches phylogenetic analysis conducted on bacterial 16S rDNA amplified from directly beneath one of the seal carcasses, and from a control that showed no obvious signs of organic contamination, revealed that the structure and composition of the microbial community under the seal appears entirely unique to the amended environment. The bacterial communities sampled from directly beneath the mummified seal were predominantly gram positive, with 70% of the sequences identified belonging to either the *Actinobacteria* or *Firmicutes* phyla. The mummified seal microbial community appeared to be significantly less phylogentically diverse than that of the control site.