420

ANTARCTIC MARINE BACTERIAL GENOME SEQUENCE ANALYSIS SUGGESTS WIDESPREAD COLD ADAPTATION

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One of the key questions in the study of Antarctic marine microbial evolution involves understanding adaptation to cold temperature. In the marine environment temperatures are persistently below 0 degrees C and don't deviate more than a few degrees over the annual cycle, even in surface waters. Recent DNA sequencing efforts have provided data from both environmentally-derived partial microbial genome sequence data from Antarctic libraries and several draft-level Antarctic microbial genome sequences. Following gene-finding and sequence annotation, we have analyzed properties of the coding regions from a large number of predicted proteins. Analysis has included comparing amino acid composition, identified substitutions and bias in composition as well as regions of disorder in genome sequences representing diverse Antarctic marine bacteria spanning more than four phyla (Proteobacteria, Actinobacteria, Bacteriodetes, and Gemmatimonadetes) in comparison to homologous proteins from mesophilic bacteria.

The most significant changes in these Antarctic bacterial protein sequences include a reduction in salt-bridge forming residues like arginine, glutamic acid and aspartic acid, reduced proline content and a reduction in stabilizing, hydrophobic clusters. Stretches of disordered amino acids were significantly longer in the Antarctic sequences than in the mesophile sequences. These characteristics could be grouped into COG role categories that were particularly cold adapted, though the adaptations do not appear to be specific to any one phylum, or the result of genome G+C content. Overall our results suggest that underlying genotypic and biochemical adaptations to the cold are inherent to life in the permanently subzero waters of the Antarctic.