

Equatorial to Polar genomic variability of the picoalga *Bathycoccus prasinos*

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Abstract

Phytoplankton plays a fundamental role in the ecology of ocean systems and is the key player in the global carbon cycle. At a time of global warming, understanding the mechanisms of its adaptation to temperature is therefore of paramount importance. Cosmopolitan planktonic species abundant in different marine environments provide both a unique opportunity and an efficient methodological tool to study the genomic bases of their adaptation. This is the case for the eukaryotic picoalga *Bathycoccus prasinos*, whose genomic variability we chose to study in temperate and polar oceanic waters. Using multiple metagenomic datasets, we found that ~5% of *B. prasinos* genomic positions are variable, with an overwhelming majority of biallelic motifs. Cold and temperate waters are clearly associated with changes in variant frequencies, whereas in transitional waters we found more balanced polymorphism at most of these positions. Mesophilic and psychrophilic gene variants are distinguished by only a few amino acid changes located at positions critical for physical and functional protein properties. These results provide new information on the genomic diversity of a cosmopolitan eukaryotic planktonic species and suggest “minimal mutational strategies” related to the properties of specific proteins at different temperatures.

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