Linking genomic and physiological traits of cold-loving microbes to metagenomic data

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Video Byte

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Abstract

Microorganisms are critical drivers of biogeochemical cycles and are the most abundant organisms in frigid regions. Identifying the genomic traits of cold-loving microbes may help explain their physiology and adaptation, but recognizing which genomic traits are important for environmental adaptation is challenging. A new study compared the genomes of *Arthrobacter* bacteria isolated from the Tibetan Plateau with published genomes of related bacteria and defined a new group of *Arthrobacter* that live in polar and alpine environments. In the laboratory, the bacteria in this group grew comparatively rapidly at 0 °C. Compared to bacteria from warmer environments, the polar/alpine bacteria had different genomic and amino acid compositions, and their predicted proteins had different stability levels and functions. However, according to genomic marker analysis, the polar/alpine bacteria were rare in other cold environments except specific permafrost communities, indicating that the observed growth and genomic traits did not translate to general cold adaptation but rather contributed to niche adaptation. Although the exact niche of the polar/alpine bacteria needs to be defined, the findings suggest that genomic markers of these unique bacteria could be used to monitor environmental change and illustrate that environmental situations cannot always be extrapolated from genomic and physiological data.