Distribution of bacterial genes driving dimethyl sulfide cycling in the polar oceans

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Video Byte

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Abstract

Dimethyl sulfide (DMS) is a gas produced by bacteria and algae that gives the ocean its distinctive scent. It also plays an important role in cloud formation, leading scientists to think its production may be instrumental in regulating climate change. But sea ice melt in the polar oceans under global warming has led to a reduction in DMS production, which may further intensify climate warming. To gain a better understanding of how bacteria contribute to DMS production, scientists recently investigated the distribution of bacterial genes involved in DMS cycling in seawater samples collected from around the world. They found evidence that intense DMS cycling facilitated predominantly by Alphaproteobacteria and Gammaproteobacteria occurs in the Arctic and Antarctic oceans, with high involvement of the enzymes DMSP demethylase, DMSP lyases, and trimethylamine monooxygenase. They also found that the microbial communities involved in DMS cycling in polar regions are shaped by water depth and a higher relative abundance of genes involved in DMS cycling were found in these oceans than in nonpolar regions. These findings provide critical insight into the microbial processes involved in DMS cycling in the polar oceans and their potential roles in future climate change.