Opportunistic bacteria with reduced genomes have a competitive edge in phytoplankton blooms

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Abstract

Phytoplankton blooms are a common event in coastal areas and represent a dramatic increase in available nutrients for opportunistic heterotrophic bacteria. The interaction between these two groups plays a key role in oceanic carbon cycles, but little is known about the specific responses of the bacterial community during a bloom. A recent study examined the bacterial community from a coastal Akashiwo sanguinea bloom. They characterized the dissolved organic matter found in the bloom and the dominant bacterial groups. Then they isolated a representative species from each of the three dominant groups to analyze in more detail. The researchers found that these species exhibited "genome streamlining", which is defined by a small genome size, low density of non-coding sections, and low GC content. These representatives also had fewer transporter and protein breakdown genes than related species. Each also had a unique metabolic signature when exposed to multiple dissolved organic nitrogen compounds. While further work examining the metabolism of bacteria present during a bloom is warranted, these results suggest that bloom conditions select for streamlined, specialized genomes, and this allows bacteria to maintain nutrient cycling by exploiting their preferred nitrogen-containing compounds.