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Bacterial Communities in Arctic Rivers Display Predictable Seasonal Patterns

Only in recent decades have biologists begun categorizing the vast diversity of bacteria in freshwater and marine ecosystems, known as bacterioplankton. The current understanding of freshwater bacterioplankton diversity and community dynamics comes mainly from studies of lakes. Relatively little is known about bacterioplankton communities in rivers, particularly in larger waterways. A new study helps fill that gap and provides evidence that bacterioplankton in the six largest rivers of the pan-Arctic watershed follow three predictable temporal patterns: seasonality, synchrony, and annual reassembly (25 November 2009 online edition of *Proceedings of the National Academy of Sciences*).

Byron C. Crump, of the University of Maryland's Center for Environmental Studies, and his colleagues investigated patterns of change in big-river bacterioplankton communities in the circumpolar region over a three-year period. They used a fingerprinting technique that analyzes bacterial 16S ribosomal RNA (rRNA) gene fragments to assess community composition in water samples collected near the river mouths. Of the 6 rivers studied (Ob', Yenisey, Lena, Kolyma, Yukon, and Mackenzie), 5 are among the world's 25 largest rivers.

In each river, Crump and coworkers observed three distinct seasonal communities of bacteria: winter/spring; spring freshet, when water from melting snow and ice flows into rivers; and summer/fall. Furthermore, the communities in all six rivers shifted synchronously from one type to another, correlating with seasonal shifts in hydrology and biogeochemistry. The researchers also found that the three seasonal communities reassembled each year in all six rivers. The communities remained relatively stable during each season and changed rapidly between seasons.

DNA sequencing of 16S rRNA genes from river samples collected during the spring freshet in June 2004 showed that each river contained bacteria from nine phylogenetic groups that are typical of freshwater systems around the world. However, the species composition in each river appears to vary, and Crump is now studying this in more detail.

Although seasonality, synchrony, and annual reassembly of bacterioplankton communities have been identified previously in a handful of small regional studies, Crump and colleagues say, this is the first report showing such shifts on global scales. The watersheds of the six rivers studied drain more than 11 million square kilometers and are distributed all around the northern hemisphere, many extending far into the temperate zone.

A range of environmental variables strongly predicted bacterial community composition in each of the six rivers, but individual variables differed from one river to another. Nevertheless, through statistical analyses Crump found that three categories of environmental variables explained most of the variability and diversity in community composition in all six rivers: the concentration and composition of dissolved organic matter, the concentration of nitrate, and the concentration of major ions. Because so many variables are at play, and because many of them change together (for example, river flow and dissolved organic matter are inversely related), Crump says, "It's a challenge…to tease out what the bacteria are responding to."

Adding to this challenge is the fact that the environmental variables change with the seasons. "One of my next goals," Crump says, "is to shift to working in temperate and tropical rivers, where the seasonal patterns are going to be different, and see if there's any commonality" in the environmental factors that explain bacterioplankton diversity around the globe.

Because bacterioplankton communities shift predictably and synchronously with seasonal changes in environmental conditions, Crump and colleagues conclude, these patterns may serve as sensitive indicators of climate change in the Arctic and elsewhere. "These temporal patterns of diversity [of bacterioplankton] are showing up in a lot of different systems," notes Crump. Arctic communities may be particularly sensitive indicators because that region of the globe tends to show early signs of climate change.

"The synchrony tells me there's something about the seasons that affects all the rivers the same way, and that effect has some control over the diversity of the bacteria," Crump says, noting that one would not necessarily expect such synchronous behavior. Similar synchronous phenological patterns, such as budding in plants and migration or mating in animal communities, are already being used to document long-term changes in climate. But bacterial communities may be more sensitive and rapid harbingers of change, because "with microbial communities, change can happen in a week," Crump says, whereas changes in plant or animal communities occur much more slowly. "You don't have to do much to a bacterial community to get it to change in composition. They grow quickly, and they often respond to environmental changes by changing species composition."

"Is this data set useful in a practical way [to monitor climate change]? Not yet," Crump says. "At this point we don't know that much about what controls the diversity of microbial communities…. A lot of effort is just being put into describing the diversity, let alone trying to understand the patterns of the diversity. But it seems like a very good, productive direction to go in."

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