RESEARCH ADVANCES

Wind-Blown Microbes Add only Modestly to Life in Greenland Glaciers

Barry E. DiGregorio

Aeolian, or wind-blown, microorganisms pelt the Greenland Ice Sheet all winter long but remain inactive until some of that ice melts to form metabolically active pools during the short summer growth season, according to Michaela Musilova from the University of Bristol in the United Kingdom and her collaborators from there and the Universities of Edinburgh and Leeds as well as the Woods Hole Oceanographic Institution in Woods Hole, Mass. Even then, however, those inputs to microbial communities that form in melt holes along these glaciers are “limited,” with the communities themselves being “stable and active” throughout the summer, “making them important contributors to biogeochemical nutrient cycling on glaciers,” the researchers note. Details appeared 20 March 2015 in *Frontiers in Microbiology* (6:193; doi:10.3389/fmicb.2015.00193).

During the summer, cylindrical holes in glaciers fill with water and debris, called cryoconite, forming small pools in which microbial communities can flourish. Stable communities within holes on the glacier contain mainly proteobacteria, cyanobacteria, and actinobacteria, according to Musilova and her collaborators. An open question was whether aeolian sources augment these established microbial mixtures, they note. “However, the dominant bacterial taxa in the aeolian samples—Firmicutes—did not establish themselves in local glacier surface communities.” As for the dust itself, it originates almost entirely from deserts and dry areas in eastern Asia, such as the Gobi desert.

“The evolution of the microbial community within cryoconite holes is very interesting,” says Andrew Fountain at Portland State University in Portland, Ore., who studies similar communities in Antarctica. “Seeded initially with aeolian biota in snow, then within a few weeks only a few were left, indicating a natural filtering of those who thrive in such a habitat. The fact that the microbial communities remained stable over time, once established, is useful to know for future investigations, saving time and energy sampling multiple holes over the season.”

These results raise questions as to how important it is for those established microbial communities to survive winters and then establish active communities during early spring melts, Fountain continues. A related question is how important input microbiota are for maintaining community structures in terms of adding different species versus bringing in new sources of nutrients, he says. “Perhaps indirect measures of water chemistry, such as electrical conductivity and partial pressure of gases in cryoconite waters, may be used as an index of microbial activity once the microbial community becomes established for the season.”

Little is yet known about the genes that collectively operate within these glacier surface microbial communities, according to Musilova, who plans metagenomics analyses to address such questions. “It would also be very interesting to learn more about the aeolian microbes to determine their origin, whether they are viable upon deposition on the glacier surface, and whether they are indeed out-competed by the local communities,” she says. “Here we determined the isotopic signatures of the organic carbon in the samples, but...
Host Signals Can Trigger Virulence in Candida albicans

Shannon Weiman

The virulence of Candida albicans changes in response to signals within and from the host, according to several researchers who spoke during the 28th Fungal Genetics Conference, held in Pacific Grove, Calif., last March. In some cases those host signals render this yeast innocuous. In other circumstances, however, C. albicans upregulates virulence factors in response to host signals, becoming an outright pathogen. A recent thrust of research is to reveal those signals that trigger such responses as well as the fungal regulatory pathways that respond to them, with a longer-term goal of combating infections not by killing this yeast, but by blocking virulence.

"C. albicans is the dominant [fungal] commensal of the human gastrointestinal tract, as well as the most common invasive fungal pathogen," says Suzanne Noble of the University of California, San Francisco. In its commensal state, gastrointestinal induced transition (GUT) cells of C. albicans are attenuated for mutualism. However, in its pathogenic invasive "white" form, metabolic and other adaptive changes enable these changed yeast cells to invade the host. This switch of C. albicans is triggered by gut environmental signals and mediated by the Wor1 transcription factor, she says. "The resulting GUT cells differ morphologically and functionally from previously defined cell types, and express a transcriptome that is optimized for the digestive tract ... exhibiting a striking reorientation of cellular metabolism towards nutrients available in the distal mammalian GI tract."

Carbon dioxide and N-acetylglucosamine are candidate signals from the host controlling this Wor1-induced transcription, Noble continues. "Our results indicate that the ability of a commensal organism to produce disease is not merely a consequence of impaired host immunity. The identification of specialized states for C. albicans commensalism and virulence offers opportunities for prevention as well as treatment of clinical diseases produced by this important human pathogen."

Meanwhile, temperature changes unambiguously can increase the virulence of C. albicans, according to Michelle Leach of the University of Aberdeen in the United Kingdom. When exposed to relatively higher tempera-