Current Topics

RESEARCH ADVANCES

Samples of Airborne Microbes, Active Communities or Not?

Barry E. DiGregorio

Microorganisms in the middle to upper troposphere might belong to an active community, one that could be playing a critically active role in the biochemistry and hydrological cycle of the atmosphere, according to Kostas Konstantinidis from the Georgia Institute of Technology (GIT) in Atlanta and his collaborators there and at the National Aeronautics and Space Administration (NASA) Langley Research Center in Hampton, Va. Their view challenges others who see microbes as likely playing more passive roles while aloft in the atmosphere. Details appear in the February 12, 2013 Proceedings of the National Academy of Sciences (doi: 10.1073/pnas.1212089110).

Using a specially equipped aircraft, Konstantinidis and his collaborators collected air samples over the Caribbean Sea before, during, and after two tropical hurricanes, Earl and Karl, in 2010 from altitudes ranging from 8–10 km. Members of the research team determined that viable bacterial cells account for about 20% of total particles in the 0.25- to 1-μm diameter range and are 10-fold more abundant than fungal cells, suggesting that bacteria are an important but underestimated fraction of atmospheric aerosols.

Samples from the two hurricanes carried different bacterial communities. Further, they “could remain metabolically active in clouds,” the researchers note in their report. “Microbiome implies that microbes are metabolically active and alter their environment,” Konstantinidis adds. “Whether or not this happens in the atmosphere, nobody really knows for sure. Our study indicates that this is plausible but is not a direct proof.”

“I think that the atmosphere as a whole can be considered a microbial habitat,” says Athanasios Nenes, a collaborator of Konstantinidis, who is also from GIT. “The big question is where the bacteria are metabolically active while at low temperature, low relative humidity and substrate, and high UV conditions. . . . Once in the upper troposphere, bacteria get transported over large distances [and], upon descent, can resume their metabolic activities.”

“It will be challenging to demonstrate activity in situ,” says microbiologist David A. Pearce from the British Antarctic Survey in Cambridge, United Kingdom, who was not involved in the GIT-NASA atmospheric research effort.

Meanwhile, other microbiologists resist calling the atmosphere a microbial habitat and doubt whether microorganisms are metabolically active while aloft. In this case, David J. Smith from the NASA Surface Systems Office at the Kennedy Space Center in Florida raises specific questions about the methods that were used to collect samples. “Publishing air-pump specifications is absolutely critical for standardizing aerobiology methods,” he points out, referring to the report from Konstantinidis and his collaborators. “The authors do not describe how the system prevents contamination . . . How was sterility within the intake-plumbing
lines and filters maintained from take-off until sampling altitudes?”

“If there were contamination of the line or a systematic sampling artifact, we would have detected the corresponding microbes in high abundances in all flights/samples, since most of our flights began from the same airport,” Konstantinidis replies. “No such patterns were observed.”

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RESEARCH ADVANCES
Resilience of Bifidobacteria Suggests Potential as a Probiotic

David C. Holzman

Two broad-spectrum antibiotics, ampicillin and metronidazole, have little impact on bifidobacteria growing in cultures containing mixed bacterial populations, suggesting that probiotics containing those bacteria might stabilize the gut microbiota during and following antibiotic treatments of the host, according to George and Sandra MacFarlane and their collaborators at the University of Dundee in Dundee, United Kingdom (UK). Their article was published ahead of print in Antimicrobial Agents and Chemotherapy on February 12, 2013 (doi: 10.1128/AAC.00079-13).

Both of those antibiotics reduce levels of Bacteroides bacteria in mixed cultures that resemble but greatly simplify those involving the gut microbiota. However, ampicillin affected only some of the bifidobacterial species, and only while they were being grown with low nutrients, according to Sandra MacFarlane. Although antibiotics disrupt many species within mixed microbial populations and alter their metabolic products, the resilience of the bifidobacteria component within such culture-grown populations points to their potential as probiotic therapy for patients undergoing antibiotic treatments, she says.

These bacterial growth studies involved a “continuous culture colonic model,” MacFarlane says. Compared to experiments with animals, this in vitro system simplifies efforts to test the effects of antibiotics and other environmental agents on mixed microbial populations and their metabolism, she points out. Nutrients are fed into one end of a vessel containing in this case 14 bacterial species, and waste materials are removed from the other end of the vessel. Those 14 species were chosen “to represent different microbial communities occupying diverse nutritional niches within the intestinal microbiota,” she and her collaborators note.

“The approach used is a refreshing change from studies that attempt to characterize microbial complexity, which is often very challenging, even with modern analytical techniques,” says Andrew McBain of the University of Manchester in Manchester, UK. “By complexity I mean microbial composition, metabolic activities at the cellular and community level, physical and metabolic relationships between organisms, growth on surfaces, and metabolic interaction between bacterium and host.”

The model was “not intended to simulate the human colon but was employed to investigate ecological and physiological interactions between specific groups of bacteria under strict, environmentally controlled conditions,” note the members of the Dundee research group. The sheer complexity of the colonic microbiota can stymie efforts to determine exactly what is causing changes in physiology and metabolism of individual bacterial species when antibiotics are applied, in relation to other environmental influences, such as availability of nutrients and gut transit times.

“Realistically, this work is several steps away from a direct impact on society,” McBain says. “Ultimately, any therapies that could reduce the incidence or severity of antibiotic-associated diarrhea would save many lives and reduce a great deal of suffering.”

David C. Holzman is the Microbe Journal Highlights Editor.

MINITOPIC
Outbreak of H7N9 Influenza in China under Close Scrutiny

Chinese health officials confirm a slow but continuing outbreak of H7N9 influenza viral infections, affecting more than 131 patients by early May with at least 32 deaths, according to the World Health Organization (WHO). “There is no evidence of ongoing human-to-human transmission,” WHO officials note. The first human cases were reported at the end of March. An early genetic analysis indicates that the “human isolates, but not the avian and environmental ones, have a protein mutation that allows for efficient growth in human cells and that also allows them to grow at a temperature that corresponds to the upper respiratory tract of humans, which is lower than you find in birds,” report Masato Tashiro of the Influenza Virus Research Center at the National Institute of Infectious Diseases in Tokyo, Japan, Yoshihiro Kawaoka of the University of Wisconsin-Madison and the University of Tokyo, and their collaborators. Details appear April 11, 2013 in Eurosurveillance (http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20453).

RESEARCH ADVANCES
Way-Different Ways of Predicting, Tracking Infectious “Trends”

Jeffrey L. Fox

“We saw the Twitter trend spike a week sooner than CDC [Centers for Disease Control and Prevention (CDC) in Atlanta, Ga.] . . . and that means conversations in social media can give insights