MINITOPIC
The April 2016 Set of Microbiota Studies Involving the Gut or Other Anatomic Sites

Here in brief is another set of findings from recent efforts to understand how microorganisms in the gut or elsewhere in the body interact with or affect the host:

- Vaginal microbial transfer—swabbing C-section newborns with fluids from the mother’s vagina—leads those children to develop gut microbiota resembling those of vaginally delivered babies, according to Maria Dominguez-Bello of New York University, Jose Clemente of Icahn School of Medicine at Mount Sinai, both in New York, N.Y., and their collaborators. Details appeared 1 February 2016 in *Nature Medicine* (doi:10.1038/nm.4039).
- After the age of nine months, the development of the infant gut microbiota is driven by the transition to family foods, not by maternal obesity, according to Tine Rask Licht of Technical University of Denmark, Soborg, and her collaborators. Details appeared 10 February 2016 in *mSphere* (doi:10.1128/mSphere.00069–15).
- The maternal diet influences the microbiome of breast milk, making it a “driver of the early infant microbiome, reinforcing the gestational dietary impact,” says Kristen Meyer of Baylor College of Medicine in Houston, Tex., who spoke during the Society for Maternal-Fetal Medicine annual meeting, the Pregnancy Meeting, last February in Atlanta, Ga.
- Low-fiber diets dramatically reduce the diversity of the gut microbiota in mice, and that diversity is not readily recovered without reintroducing the missing microbial taxa, according to Justin and Erica Sonnenburg of Stanford University in Stanford, Calif., and their collaborators. Details appeared 13 January 2016 in *Nature* (doi:10.1038/nature16504, 2016).
- Individual chimpanzees in Gombe National Park, Tanzania, carried roughly 25% more gut bacterial species during periods when they engage in social behaviors than when they spend time alone, according to Andrew Moeller at the University of California, Berkeley, and his collaborators. Moreover, the mix of bacteria in the animals’ bowels was just as similar between unrelated individuals as it was between mothers and offspring. Details appeared 15 January 2016 in *Science Advances* (doi:10.1126/sciadv.1500997).
- Before bears hibernate, their gut microbiota takes on more energy from their summer diet and then that microbiological diversity is reduced in diversity while they hibernate, according to Fredrik Bäckhed of the University of Gothenburg in Sweden and his collaborators. Details appeared 4 February 2016 in *Cell Reports* (doi.org/10.1016/j.celrep.2016.01.026).
- Neurons work with immune cells—specifically, muscularis macrophages—to help intestinal tissues respond to perturbations but without overreacting to them, according to Daniel Muuida of Rockefeller University in New York, N.Y., and his collaborators. “We now have a much better picture of how the communication between neurons and macrophages in the intestine helps to prevent potential damage from inflammation,” including from infections, he says. Details appeared 14 January 2016 in *Cell* (doi.org/10.1016/j.cell.2015.12.023).

Unsettling Case of Colistin-, Carbapenem-Resistant *P. aeruginosa* in Canada

David C. Holzman

The first North American instance of an individual infected with *Pseudomonas aeruginosa* that is resistant to colistin and also carries the resistance gene NDM-1 was documented last year, according to Johann Pitout of the Cumming School of Medicine at the University of Calgary in Calgary, Alberta, Canada, and his collaborators elsewhere in Canada and in South Africa. Importantly, that isolated case illustrates “the need for appropriate infection prevention and control measures and vigilant screening for carbapenem resistant gram-negative bacteria in patients with a history of travel to endemic areas, such as the Indian subcontinent,” they note. Details of appeared 11 January 2016 in *Antimi-

NDM-1 confers resistance to carbapenems, and pathogens carrying this trait are causing major public health problems because this group of antibiotics is considered “last line” for treating serious infections caused by gram-negative bacteria. Although this trait rarely is found in *P. aeruginosa*, this *P. aeruginosa* is considered a “high-risk” clone, meaning it readily acquires resistance genes and spreads rapidly among patients. The patient carrying this clone was transferred directly from a hospital in India, where he had acquired the infection, to a hospital in Calgary.

*P. aeruginosa* was only one of three NDM-producing microorganisms colonizing the man, the others being *Providencia rettgeri* and *Escherichia coli*, says Pitout. He and his collaborators expected the mobile genetic elements carrying the NDM-1 resistance gene to be the same, or similar, within this one patient. “To our surprise, we found that the underlying mobile genetic elements were totally different in the three organisms,” Pitout says. In *P. aeruginosa*, NDM was incorporated into the genome. In both *P. rettgeri* and *E. coli*, however, plasmids carried the NDMs. Moreover, the two types of microorganisms were carrying very different plasmids, with different sequences and sizes. “This is likely the first study to show such diversity of mobile genetic elements in antimicrobial-resistant organisms with the same carbapenemase from a single patient,” he says.

“That means that the NDM-1 gene did not transfer from organism to organism after the first NMD-1 carrying pathogen colonized the patient, but rather that the patient was colonized in three independent events,” says Patricia Bradford, of AstraZeneca Pharmaceuticals in Waltham, Mass. The case “highlights the need for obtaining a thorough patient history, including travel history, to be taken on every patient upon entry into a hospital, followed by adherence to infection control measures.”

“This *P. aeruginosa* is certainly extensively drug resistant, and would be pan-drug-resistant if it were not for susceptibility to aztreonam,” says Yoheil Doi of the University of Pittsburgh Medical Center in Pittsburgh, Pa. “It is even resistant to colistin, the last-resort agent for treatment of carbapenem-resistant *P. aeruginosa*. The fact that blaNDM-1 is located on the chromosome . . . [means] this strain is now permanently resistant to carbapenem. It is not comforting to realize that this kind of bacteria can suddenly appear at the doorstep of your hospital in this age of global travel.”

Doi notes that, as a matter of policy, the Canadian province of Alberta mandates hospitals to isolate patients preemptively when they are being transferred from areas where carbap-
enem-resistant, gram-negative bacteria are endemic. “In all likelihood this policy prevented these NDM-1 producing bacteria from spreading to other patients,” he says.

“With regard to the potential for treating these organisms, it is worrisome that two of the three isolates were also resistant to colistin, which is viewed as the last resort antibiotic to treat carbapenem-resistant organisms,” Bradford says. And, adds Doi, “I wish they had delved a bit into colistin resistance mechanism for *P. aeruginosa.*”

David Holzman, who writes from Lexington, Mass., is a contributing writer for Microbe.

## MINITOPIC

### Newly Identified Microbial Species

Several recent reports identify novel microbial species, including new Lyme and malarial parasites, a novel bacterial phylum, a newly identified photosynthetic bacteria found in the Gobi Desert and elsewhere, and newly identified algal species in waters near Hawaii:

- **A newly identified *Borrelia* species, candidatus *Borrelia mayonii,** found in the upper Midwestern United States, causes Lyme disease with unusually high spirochaetemia, according to Bobbi Pritt of Mayo Clinic in Rochester, Minn., and her collaborators. Details appeared 5 February 2016 in *Lancet Infectious Diseases* (doi:10.1016/S1473–3099(15)00464–8).

- **Plasmodium odocoilei** appears to be the first-ever malaria parasite known to infect white-tailed deer and the only native malaria parasite found so far in any wild-living mammal native to North or South America, according to Ellen Martinsen of the Smithsonian’s Conservation Biology Institute in Washington, D.C., and the University of Vermont, Burlington, and her collaborators. These same parasites are carried by the mosquito *Anopheles punctipennis.* Details appeared 5 February 2016 in *Science Advances* (doi:10.1126/sciadv.1501486).

- **Analysis of metagenomic datasets uncovered a novel bacterial phylum,** being called “Kryptonia,” whose members come from geothermal springs, according to Emiley Eloe-Fadrosh and Natalia N. Ivanova of the DOE Joint Genome Institute in Walnut Creek, Calif., and their collaborators there and at several other institutions. Details appeared 27 January 2016 in *Nature Communications* (doi:10.1038/ncomms10476).

- **A photosynthetic bacterium that was discovered several years ago in a lake within the Gobi Desert proves to be broadly distributed in nature,** according to Yonghui Zeng of the University of Southern Denmark in Odense and his collaborators. Also remarkable, the photosynthetic genes of this bacterial species, which belongs to the rare and understudied phylum Gemmatimonadetes, are found in a compact cluster, instead of being scattered throughout the genome. Details appeared 22 January 2016 in *Environmental Microbiology Reports* (doi:10.1111/1758–2229.12363).

- **Four new species of deep-water algae from Hawaii “resemble something you would see in a shallow-water lagoon, not at 400 feet,” says Heather Spalding at the University of Hawaii at Mānoa in Honolulu. These species are similar in appearance to limu palahalaha (*Ulva lactuca*), or sea lettuce, according to her and collaborators there and at Friday Harbor Laboratories of the University of Washington. Details appeared 12 January 2016 in *Phycology* (doi:10.1111/jpy.12375).

## RESEARCH ADVANCES

### Host microRNAs Help Regulate, Talk Back to the Gut Microbiome

**Carol Potera**

Epithelial cells lining the gastrointestinal tracts of mice secrete microRNA molecules that can enter and switch on genes that alter the growth of certain types of bacteria in the gut, according to Howard Weiner and Shirong Liu at Brigham and Women’s Hospital in Boston, Mass., and their collaborators.

“It’s a very basic finding, but it opens up an area of interaction between microRNAs and the gut microbiome that hasn’t been known before,” Weiner says. “Our findings highlight microRNAs as a strategy for manipulation of the microbiome that may affect the health of the host.” Details appeared 13 January 2016 in *Cell Host & Microbe* (doi.org/10.1016/j.chom.2015.12.005).

Weiner, Liu, and their collaborators wondered what mechanisms the host might use to regulate and manipulate its microbiome. They knew that microRNAs play a key role in controlling gene activity in species ranging from viruses to humans and also are implicated in colitis, colorectal cancer, and other intestinal disorders. Thus, they suspected that microRNAs could also act as host agents, exerting control over the microbiome.

They soon learned that intestinal epithelial cells produce microRNAs, and mice that are made deficient in gut microRNAs become more susceptible to colitis. When mice with colitis are treated with fecal transplants from normal mice, microRNA molecules within the gut are restored to their typical levels, while the signs of inflammation that are associated with colitis are reduced.

Moreover, when mice are made to be deficient in microRNAs, the gut bacteria undergo changes, including increases in *Bacteroides* and *Helicobacter.* Adding fecal microRNAs spurs the growth of cultures of *Fusobacterium*