therapeutic potential such as cyanobactins are made in a similar fashion,” he says.

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NEW IN ASM JOURNALS

Polymicrobial Infections Abound: Synergies and Greater Complexities

David C. Holzman

Polymicrobial infections exert a profound impact on both outcomes and responses to treatment, says W. Edward Swords of Wake Forest School of Medicine, Winston-Salem, N.C. Efforts to study such infections grew considerably during the last decade, due to “faster and more comprehensive [genomic] sequencing that makes it possible to identify every organism in a sample without having to grow anything in culture.” Three recent reports illustrate the breadth of this phenomenon, its importance for public health, and some of the practical challenges it poses.

Conventional culture-based diagnostic tests sometimes fail to uncover some of the culprits underlying infections in individual patients, according to Swords. “Lots of infections aren’t merely new colonization by an overt pathogen, but rather a shift in the population to a dysbiotic state, where the proportion of different species changes, resulting in disease,” he says.

For example, in periodontal disease, microbial community structures vary less from one case of disease to another than they do among healthy individuals, according to Gary Wang of the University of Florida, Gainesville, and his collaborators. “Samples from individuals with periodontal disease are characterized by high levels of Fusobacterium and Porphyromonas, while in healthy gums, subgingival bacterial communities have high levels of Rothia and Streptococcus,” he says. “Genes and functions related to bacterial motility, energy metabolism, lipopolysaccharide biosynthesis, flagellar assembly, methane metabolism, bacterial chemotaxis, and peptidase, are abundant in chronic periodontitis compared to healthy controls.” Details appeared 14 November 2014 in Applied and Environmental Microbiology (doi: 10.1128/AEM.02712-14).

“There is increasing appreciation that human indigenous microbial communities are a critical component of human biology,” Wang says. “In some disease states, we need to think of microbial communities, rather than specific bacteria, as pathogens.”

The effects of one pathogen can influence what happens with successor pathogens, according to Mary Ann Jabra-Rizk of the University of Maryland Dental School in Baltimore, and her collaborators. For instance, after...
**RESEARCH ADVANCES**

**In Wave Tanks, Microbial Fragments Wrangle Sands into Wrinkle Structures**

**Barry E. DiGregorio**

Wrinkle structures, found in ancient sedimentary environments along the surfaces of sandy beds, can be formed experimentally by adding microbial fragments to sand layers within wave tanks, according to Giulio Mariotti of the Massachusetts Institute of Technology (MIT) in Cambridge and his collaborators there and at Smith College in Northampton, Mass. They say that wrinkle structures in natural sediments are “morphological biosignatures” of microbial fragments—inscribed at the sediment–water interface.

**MINITOPIC**

**Another Set of Gut Microbiota Highlights from Microbe in 2015**

Efforts to understand how microorganisms in the gut affect the host continue to be part of the news. Microbe's second set of examples for 2015 include:

- The blood-brain barrier is “leaky” in newborn mice that were carried by germ-free mothers, but remains normal in those whose mothers’ gut microbiota was intact, according to Viorica Braniste and Sven Pettersson at Karolinska Institutet in Stockholm, Sweden, and their collaborators. Details appeared 19 November 2014 in *Science Translational Medicine* (doi:10.1126/scitranslmed.3009759).

- The ordinarily benign gut bacterium *Bacteroides thetaiotaomicron* can enhance virulence gene expression in enterohemorrhagic *Escherichia coli* cells and also change the metabolite environment at infection sites, perhaps explaining how resident microbiota can influence an individual’s susceptibility to pathogens, according to Vanessa Sperandio of the University of Texas Southwestern Medical Center in Dallas and her collaborators. Details appeared 10 December 2014 in *Cell Host Microbe* (doi:10.1016/j.chom.2014.11.005).

- Bacterial biofilms are associated with colorectal cancers, suggesting that the gut microbial community contributes to this type of cancer, according to Christine M. Dejea and Cynthia L. Sears of Johns Hopkins Medical Institutions in Baltimore, Md., and their collaborators there and at several other institutions. Details appeared 8 December 2014 in *Proceedings of the National Academy of Sciences* (doi:10.1073/pnas.1406199111).

- Consuming fiber increases the relative abundance of Bacteroidetes by about 12% compared to Firmicutes in the human gut and, along with that shift, the abundances of many microbial genes, including those associated with carbohydrate, amino acid, and lipid metabolism, according to Kelly Swanson of the University of Illinois, Urbana, and his collaborators. Those fiber-related changes in diet are associated with weight loss. Details appeared 12 November 2014 in the *American Journal of Clinical Nutrition* (doi:10.3945/ajcn.114.092064).

- Ingested nanosilver particles can upset the gut microbiome, shifting bacterial populations there and reducing their metabolic activity, according to Virginia Walker and Pranab Das at Queen’s University in Kingston, Ontario, Canada, and their collaborators. Details appeared October 18, 2014 in the *Journal of Nanomedicine and Nanotechnology* (doi:10.4172/2157-7439.1000235).

- Kissing, which strictly speaking is not about the gut microbiota, can lead to the exchange of some 80 million bacteria between two individuals, leading them to share “similar communities” of oral bacteria, according to Remco Kort of the Netherlands Organisation for Applied Scientific Research, or TNO, in Zeist, and his collaborators. However, because the “similarity does not clearly correlate to kissing,” there appears to be an “important role for specific selection mechanisms resulting from a shared lifestyle, environment, or genetic factors from the host.” Details appeared 17 November 2014 in *Microbiome* (doi:10.1186/2049-2618-2-41).