Competition and cooperation between microbial species in foods contribute to growth and persistence of human pathogens, according to several researchers who presented recent findings during the 2015 ASM General Meeting, held last May in New Orleans. Examining microbial communities on foods from vegetables to cheeses, these researchers are unraveling the phylogenetic and molecular nature of these interactions, with the longer-term goals of better predicting, identifying, and preventing food contamination to improve food safety.

“During their interactions with plants, human enteric pathogens, such as *Salmonella enterica*, are known to benefit from interactions with phytopathogens,” says Andrée George of the University of Florida, Gainesville. *S. enterica* gains a better foothold in host plants through metabolic interactions with *Pectobacterium carotovorum*, which causes soft rot in tomatoes, he says. *P. carotovorum* carries enzymes that break down the oligosaccharide pectin in plant cell walls, releasing nutrients that *S. enterica* feeds on but cannot access itself because it lacks genes encoding such enzymes.

*S. enterica* thrives within soft-rot lesions of plant tissues, upregulating genes for transporters and enzymes encoded in its KdgR regulon that metabolize plant tissue breakdown products. “Bioinformatic, phenotypic, and gene expression analyses demonstrated that the KdgR regulon included genes involved not only in uptake and metabolism of molecules resulting from pectin degradation, but also those central to utilization of a number of other carbon sources,” says George. These regulatory changes enable *S. enterica* populations to become 10–1,000 times larger in soft rot lesions than on intact plants, he notes. These principles may also apply to pathogenic strains of *Escherichia coli*, which similarly thrive in soft-rot lesions and possess KdgR regulons.

However, some bacterial species protect plants against colonization by human pathogens, according to Maria Marco of the University of California, Davis. For example, the epiphyte *Erwinia* could help to stop *E. coli* O157:H7 from colonizing lettuce by outcompeting this human pathogen, she says. “These bacteria, *Erwinia*, might compete for nutritional resources available on the leaf surface.” *E. coli* O157:H7 tends to persist on plants that harbor fewer of these protective epiphytes, she adds.

Interactions between fungi and bacteria within cheese can promote the growth and dispersal of some bacterial species, including the human pathogen *Listeria*, says Benjamin Wolfe of Tufts University in Medford, Mass. Mucor fungi, a common component of microbial communities within cheeses, form hyphae that serve as superhighways for specific bacterial species, including proteobacteria and *Listeria*, to spread across the cheese blocks, he says.

Metabolic changes, rather than motility mechanisms, enable those bacte-
ria to interact with the fungi and thus spread across the surfaces of the cheeses, Wolfe points out. For instance, proteobacteria within cheeses alter their nitrogen metabolism, while downregulating chitinases, suggesting a symbiotic relationship to protect their fungal partners. “Several bacteria grew poorly without the presence of a fungal partner, demonstrating that the cheese environment may be unable to support the growth of some bacteria,” he says. However, this seeming deficiency is “rectified by the presence of several different genera of fungi.”

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RESEARCH ADVANCES

Simulating Microbiome Activities in Silico—with Robots as Hosts

Barry E. DiGregorio

Because the interactions and influences between host and microbiome sometimes prove too complex to analyze directly, one simplifying alternative is to model them in silico, according to Warren C. Ruder of Virginia Polytechnic Institute and State University (Virginia Tech) in Blacksburg, Va., and his collaborators. Their approach “computationally simulates a hybrid robot-bacteria system,” and this virtual host-and-microbiome duet appears to “replicate a range of different biological ‘host’ behaviors,” they report. Details appeared in the July 2015 Scientific Reports (doi:10.1038/srep11988.)

In other words, the model incorporates an engineered bacterial population to stand in for the microbiome, while the robot stands in for an animal host, according to Ruder. “In our simulations, we borrowed Escherichia coli signaling machinery that drives the bacteria’s desire to acquire lactose or arabinose, but we modeled the system with normal culture media,” he says. The “host”—that is, the computer-simulated robot—was equipped with sensors and a miniature microscope.

This model system allows its users to make simple changes to engineered gene networks in the bacteria that are part of the virtual microbiome or to the host robot’s programming, and then watch complex behaviors emerge within the overall model, Ruder says. Such computer simulations belong to the growing field of synthetic biology, whose virtual birth traces more or less to the year 2000.

“In most simulations, the robot was passive and simply took commands,” Ruder says. “When we programmed it with a single additional subroutine whereby it detected when it got close to a fuel depot and injected a biochemical into the bioreactor, we saw a new behavior. The result was a system that exhibited stalk-pause-strike behavior. This showed that simple additions to the genetic circuitry and robot programming caused relatively complex behavior to emerge.”

“By integrating an engineered microbiome, a microfluidic chemostat mimicking the microbiome’s environment within an organism, and a robotic conveyance, we have designed, modeled, and simulated a biomimetic system that allows us to explore natural phenomena through both synthetic biological and robotic programming,” note Ruder and his collaborators. “We expect this model system will have implications in fields ranging from synthetic biology and ecology to mobile robotics.”

“The work will serve as a good foundation for other researchers in the fields of computational systems biology or synthetic biology,” says Rahul Sarpeshkar at Dartmouth College in Hanover, N.H. “Such control systems are very important in enabling these fields to engineer and to understand the noisy, analog, and complex feedback dynamical systems actually seen in living cells.” And adds Vikas Berry at the University of Illinois, Chicago, “I believe that a prototype of the proposed model can be built in a year or two. However, the complete development of this ‘biotechnology’ and the realization of the vast variety of functions and operations that can be possible will take a few decades of work.”

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SCIENCE AWARDS

Lasker, National Academy “Convergence” 2015 Awards Recognize Microbiology

Jeffrey L. Fox

The 2015 Lasker Awards in several categories recognize microbiologists and...