Articles of Significant Interest in This Issue

Allopatric Divergence of a Plant Pathogen following Its Introduction into the United States

The reduced genetic diversity of monoculture agricultural crops has been associated with adaptation of plant pathogens to local environments. This is of concern on a global scale for emerging plant pathogens such as the bacterium *Xylella fastidiosa*. Castillo et al. (e02095-20) show that following its establishment in the U.S., grapevine-infecting strains of *X. fastidiosa* split into populations on the East and West Coasts. Subsequently, population diversification occurred via nucleotide changes in the core genome sequences and gene gain/loss. This finding shows that *X. fastidiosa* populations can quickly become differentiated, which may lead to local pathogen specialization in newly introduced landscapes.

Microbiomes of Ticks Collected from Small Mammals Are Predictable across Neotropical Forest Fragments

Blood-sucking ticks are a persistent pest of neotropical mammal species, and if you spend some time hiking, you may find this out firsthand. Remarkably, little is known about the naturally occurring bacterial species that are found inside these stealthy creatures. Kueneman et al. (e02668-20) studied the microbial community compositions and richness among 11 tick species collected from eight species of small mammals across 18 tropical forest fragments. The data show a consistent consortium of genera, including *Francisella*, *Coxiella*, and *Rickettsia*. While the similarities across tick microbiomes should not be ignored, compositional differences were strongest across tick life stages and several taxa were differentially abundant across sites. Their analyses inform how tick microbiomes are structured and can help anchor our understanding of tick microbiomes from tropical environments more broadly.

Evolution of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Sewage during a COVID-19 Pandemic Wave

A 6-month SARS-CoV-2 wastewater-based epidemiology (WBE) study by Chavarria-Miró et al. (e02750-20), covering 2.7 million inhabitants, anticipated the original COVID-19 pandemic wave by several weeks and the onset of the second wave. WBE evidenced the efficacy of the adopted lockdown measures with regard to the circulation of SARS-CoV-2. Health authorities profited from this information, which allowed them to locate COVID-19 hot spots and conduct massive reverse transcription-PCR tests among the population. A model developed for the estimation of the total number of shedders showed an infection prevalence of 2.0 to 6.5%, evidencing the high proportion of asymptomatic infections.

Dynamic Polyphosphate Metabolism Coordinating with Manganese Ions in a Radioresistant Bacterium

Polyphosphate (PolyP) is unique in its likely role in the origin and survival of life. PolyP can effectively chelate manganese ions and donate phosphate. Dai and colleagues (e02785-20) demonstrate that dynamic PolyP metabolism coordinating with Mn ions is a defense strategy of *Deinococcus radiodurans* in response to oxidative stress. A novel exopolyphosphatase, PPX\textsubscript{Dr}, with a cofactor preference for Mn\textsuperscript{2+} mediated effective PolyP-Mn degradation to Pi and Mn ions, which formed Mn-Pi complexes to protect proteins. The findings provide insight into the functions of PolyP metabolism in organisms under oxidative stress.
Stringent Starvation Protein Regulates Prodiginine Production

The regulation of prodiginine biosynthesis has been extensively studied in Serratia and Streptomyces species; however, the process in the marine bacterium Pseudoalteromonas remains a mystery. Studies by Yin et al. (e02949-20) demonstrate that prodiginine biosynthesis in Pseudoalteromonas sp. strain R3 is positively regulated by stringent starvation protein A (SspA), an RNA polymerase-associated regulatory protein. SspA-regulated prodiginine biosynthesis is mediated by the siderophore-dependent iron uptake pathway. This discovery establishes connections among the stringent response, iron homeostasis, and prodiginine biosynthesis. The study uncovers a novel regulatory mechanism for prodigiosin biosynthesis.