



Articles of Significant Interest in This Issue

Diverse Array of Fungal Species and Enzymes Identified in Decayed Lodgepole Pine

The deconstruction of recalcitrant woody substrates is a central component of terrestrial carbon cycling and forest health. Laboratory investigations have contributed substantially toward understanding the mechanisms employed by model wood decay fungi, but few studies have examined the physiological processes in natural environments. Addressing this issue, Hori et al. (e01133-18) identified the functional genes present in field samples of extensively decayed lodgepole pine (*Pinus contorta*). Expression profiles revealed a wide range of oxidative and hydrolytic enzymes involved in lignocellulose degradation. The results suggest complex interactions among fungal species that employ different wood decay strategies.

A Quantitative Microbial Risk Assessment Perspective on Handling Data below Limits of Detection

Data below limits of detection, otherwise known as “left-censored” data, are common in microbiology. When these data are used to estimate human health risks, the methods for handling left-censored data become increasingly important, especially when detection limits are near infectious doses. Canales et al. (e01203-18) evaluated a variety of methods that have been used in other environmental contexts and utilized simulated data sets informed by real-world microbiological data to quantify and compare the errors in predicting doses and infection risks. Their study offers microbiologists and quantitative microbial risk assessment researchers useful method comparisons that can inform decisions regarding handling of left-censored data.

Revealing the Physiological Function of Cyanophycin in Nondiazotrophic Cyanobacteria

Cyanophycin is a granular nitrogen storage polymer [multi-L-arginyl-poly(L-aspartic acid)] produced by most cyanobacteria and a few heterotrophic bacteria. In diazotrophic cyanobacteria, cyanophycin serves as a buffer to store fixed nitrogen for a continuous intracellular nitrogen supply. However, in nondiazotrophic cyanobacteria, the physiological function of cyanophycin has remained unclear. Watzler and Forchhammer (e01298-18) revealed the cell biology of cyanophycin accumulation in the nondiazotrophic cyanobacterium *Synechocystis* sp. strain PCC 6803. They demonstrated that *Synechocystis* optimizes nitrogen assimilation through cyanophycin synthesis when exposed to limiting and fluctuating nitrogen sources or to day/night cycles.

Novel ABC Transporter for Compatible Solutes in *Bacillus* spp.

Importers for compatible solutes allow the energy-preserving scavenging of osmoprotective compounds from scarce external sources. Accumulation of these osmolytes is a cornerstone of stress responses to high environmental osmolarity by many microorganisms since this counteracts water efflux, drops in turgor to nonphysiological values, and undue increases in molecular crowding. Teichmann et al. (e01728-18) report the discovery, phylogenomics, and physiological characterization of a new transport system for compatible solutes (OpuF) that is widely found in members of the genus *Bacillus*. OpuF is a representative of a subgroup of ABC transporters in which the substrate-scavenging functions of an extracellular ligand-binding protein and the membrane-embedded substrate translocating subunit are functionally fused into a single polypeptide chain.

Structural Role for *Bacillus subtilis* Crust Proteins in the *Bacillus megaterium* Exosporium

Spores of certain *Bacillus* species are enveloped in an outermost layer termed the exosporium. Despite its significance as spores' point of contact with the environment, knowledge of exosporial composition, structure, and function is sparse compared with other aspects of spore biology. Manetsberger et al. (e01734-18) revealed that the composition of the distinctive walnut-shaped exosporium of *Bacillus megaterium* has more in common with the *Bacillus subtilis* crust—often considered to represent a vestigial exosporium—rather than the archetypal *Bacillus cereus* family exosporia. Collectively, the findings add to our understanding of the evolution of the outermost layers of bacterial spores.