

Articles of Significant Interest Selected from This Issue by the Editors

New Insights into Fe(II) Toxicity under Anoxic Conditions

Bird et al. (p. 3619–3627) determined that ferrous iron interacts synergistically with copper at environmentally relevant concentrations to delay the anaerobic growth of several bacterial species. Preliminary evidence suggests that ferrous iron may interfere with one or more copper efflux systems, at least in *Escherichia coli*. This work not only suggests a mechanism for iron toxicity under anoxic conditions but demonstrates that trace iron and copper levels should be considered when studying bacterial behavior in natural and anthropogenic environments; this may be particularly important in the context of mixed waste bioremediation.

Microbial Life in a High-Arctic Hypersaline Subzero Spring

The Lost Hammer spring in the Canadian high Arctic is the coldest (-5°C) and saltiest ($\sim 24\%$) terrestrial spring known, a place where microbes must overcome subzero temperatures, low water activity, and high solute concentrations to sustain their viability. Using metagenome sequencing and 16S ribosomal cDNA pyrosequencing analyses, Lay et al. (p. 3637–3648) reconstructed metabolic pathways responsible for C, N, and S biogeochemical cycling and identified active community members, including ammonia oxidizers, denitrifiers, sulfate reducers, and sulfur oxidizers, highlighting their involvement in nitrogen and sulfur cycling. This study expands our knowledge of microbial life in extreme cryoenvironments on Earth and provides evidence of how microbial life could inhabit the subzero briny environments thought to exist on Mars and Enceladus.

Mixed Cultures Respond to Excess Energy by Storing It and Burning It Off as Heat

Some pure cultures of microbes respond to excess energy by storing it, but others dissipate energy entirely as heat (“energy spilling”). The response by mixed communities from natural environments has received little attention. Hackmann et al. (p. 3786–3795) used calorimetry coupled with chemical and thermodynamic analysis to quantify responses by mixed microbial communities from the rumen. Under conditions of a modest excess of glucose, microbes stored energy as reserve carbohydrate. With higher glucose excesses, up to 39% of the energy was spilled. Spilling is thus not restricted to pure cultures, and future research can adapt this quantitative approach to clarify its evolutionary purpose in natural environments.

Electron Beam Pasteurization of Raw Oysters Can Reduce Virus Infection Risks

Noroviruses and hepatitis A virus are major threats to those who consume raw oysters. Virus infection risks associated with consumption of raw oysters are estimated to cost around \$200 million a year. A nonthermal food processing technology is needed to reduce these infection risks. Praveen et al. (p. 3796–3801) demonstrate that electron beam (e-beam) irradiation-based pasteurization can indeed achieve significant reductions in infection risks. They employed a human norovirus surrogate, namely murine norovirus, as well as hepatitis A virus in a quantitative microbial risk assessment. They report that if the virus loads in oysters are kept low to begin with, norovirus and hepatitis A virus infection risks can be reduced by as much as 26% and 91%, respectively. Their study highlights the importance of adopting novel technologies to address contemporary public health risks.

Metagenomic Analysis Reveals the Genetic Basis for Intestinal Colonization by Gut Microbes

A molecular genetic basis for the formation of an adhesive microbial community by gut commensal microbes remains unexplored. Using a murine large-bowel microbiota metagenome library, Yoon and colleagues (p. 3829–3838) identified two novel operons responsible for enhanced intestinal colonization by gut commensals. These operons, predicted to be derived from *Bacteroides* species, include genes encoding membrane-associated proteins with either lysozyme-like function or a complement domain. This work, a successful application of a functional metagenomic approach, reveals novel genetic determinants that help elucidate potential mechanisms by which gut microbes form biofilms in mammalian intestines and establish mutual commensalism.