**Articles of Significant Interest Selected from This Issue by the Editors**

**dcpA, a Novel Biomarker for 1,2-Dichloropropane-Reductive Dechlorination**

1,2-Dichloropropane (1,2-D) is a toxic groundwater pollutant. Pedilla-Crespo et al. (p. 808–818) identified the gene dcpa, encoding a 1,2-D-reductive dehalogenase, in *Dehalococcoides mccartyi* and *Dehalogenimonas* strains. DcpA catalyzes the dichloroelimination of 1,2-D, yielding environmentally benign propene and inorganic chloride. *Dehalococcoides mccartyi* strains lacking *dcpA* failed to dechlorinate 1,2-D. Using specific PCR tools, *dcpA* was detected in 1,2-D-dechlorinating microcosms but not in microcosms where 1,2-D persisted, indicating its utility as a 1,2-D detoxification biomarker.

**Antioxidant-Enzyme-Producing Streptococcus Strains**

To improve the intrinsic immunomodulatory/anti-inflammatory properties of *Streptococcus thermophilus*, a bacterium used in the production of yogurt and cheeses, constitutively expressed antioxidant enzyme genes have been introduced via recombinant DNA technology. del Carmen et al. (p. 869–877) developed recombinant *Streptococcus thermophilus* strains that produce catalase and/or superoxide dismutase in the mouse gastrointestinal tract. These novel engineered strains exhibit enhanced anti-inflammatory activities and have been proposed as part of medical treatments for inflammatory bowel diseases and intestinal cancers.

**Rethinking Electron Flow for Sulfate Respiration**

Confurcation of electrons, a newly recognized form of energy conversion, is the combination of electrons from two donors of different redox levels to generate a single reduced product. A paradoxical observation made by Keller and colleagues (p. 855–868) with a mutant of a sulfate-respiring *Desulfovibrio* strain provided genetic support for confurcation occurring during the first step of sulfate reduction to sulfide. Electrons for this reduction step were predicted to be derived from both the menaquinone pool and reduced ferredoxin, and reduction did not occur when either pathway was blocked.

**Adapting to the Feast**

While the human oral microbiota generally does little damage to the colonized tissues, an increase in the amount of carbohydrate ingested by the host induces compositional, genetic, and biochemical changes in the oral microbiota that lead to a substantial loss of tooth mineral, i.e., to dental caries. Moye et al. (p. 972–985) explore the effects of altering carbohydrate availability on the primary dental caries pathogen, *Streptococcus mutans*. A variety of physiological tests and transcription profiling of cells exposed to excess carbohydrate reveal a spectrum of adaptive strategies and highlight potential targets for novel anticaries therapeutics.

**Quantitative Investigation of Interactions between Bacteria and Insects**

Quantitative examination of the interactions between bacteria and their associated hosts/predators is extremely difficult. Chen and colleagues (p. 1150–1158) quantitatively analyzed interactions between the eastern tree hole mosquito, *Anopheles triseriatus*, and *Flavobacterium hibernum*, isolated from tree hole larval habitats, by using fluorescent protein markers and the next-generation reporter NanoLuc. The results showed that *F. hibernum* was ingested and digested by larvae, providing direct evidence that flavobacteria function as a food source for larval mosquitoes. Successful expression of larvicidal proteins demonstrated the possibility of developing novel bioinsecticides using flavobacteria as the delivery host.

**“Phenotype Clusters” Classifying Bacterial Effectors on the Basis of Host Cell Morphology**

Imaging the interaction of bacterial effectors with host cells is vital for understanding their function in infection processes. Dowling and Hodgson (p. 1185–1196) describe a novel analytical method to functionally classify bacterial effectors on a genomic scale. By using high-content cellular analysis and statistics, putative effectors in the genome of a bacterial pathogen are classified based on morphological alterations they induce in macrophages. These “phenotype clusters” are linked with infection-relevant functions, including modulation of phagocytosis. This method should prove useful for short-listing key candidate genes for directed investigation and predicting the function of unknown effectors from other microbial genomes.