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

## An Abundant Salivary Enzyme's "Love Affair" with Oral Streptococci

α-Amylase is the most abundant enzyme in saliva, and commensal oral streptococci are very prevalent in developing dental plaque biofilms. Salivary α-amylase binds to the surface of selected oral streptococcal species via specific surface-exposed α-amylase-binding proteins. This interaction may be important for the colonization of teeth by these bacteria. Nikitkova et al. (p. 416–423) describe the structural basis and functional significance of this interaction as related to oral colonization by streptococci. Recent studies that suggest the possibility of a novel signaling pathway involving this interaction are discussed.

## Genetic Structure of Cyanobacterial Populations

How bacteria disperse and the mechanisms that cause them to genetically differentiate are not well understood. Sogge et al. (p. 508–515) show that cyanobacterial populations have a subpopulation structure shaped by frequent gene flow between populations and by recombination events within and between populations. This study demonstrated that subpopulation composition is a determinant of population properties, including toxicity to humans. These findings improve our understanding of aquatic bacterial populations and have implications for our view of toxic cyanobacterial blooms.

## Host Cholesterol Secretion Likely To Influence Hamster Gut Microbiota

The gut microbiota impacts cholesterol metabolism by the mammalian host with consequences for health. Martínez et al. (p. 516–524) now provide evidence that the links between the gut microbiota and cholesterol metabolism are bidirectional. Dietary intake of plant sterol esters by hamsters induced parallel changes in host cholesterol metabolism and gut microbiota composition that were highly interconnected. Some of these associations followed a sigmoidal model of bacterial inhibition, suggesting an antibacterial role for cholesterol in the gut. This work has implications for our understanding of gut microbiota-host lipid metabolism interactions and the directionality within these relationships.

## Geospatial Algorithm To Predict the Presence of Food-Borne Pathogens on Produce Farms

Maintaining the microbiological safety of fresh fruits and vegetables is challenging, in part because effective surveillance methods in the preharvest environment must account for unique combinations of topography, land use interactions, and climate on each farm. Strawn and colleagues (p. 588–600) used classification tree models to discover which remotely sensed geographic data could partially predict the presence of pathogens in produce fields. They demonstrated an algorithm that makes spatially explicit predictions regarding the prevalence of *Listeria monocytogenes* in crop lands. This work advances our understanding of the environmental microbiology of food-borne pathogens and permits tailored solutions to predict contamination of produce commodities during cultivation.

## Rapid, Automated Detection of Infected Cells by Using TAT Peptide-Delivered Molecular Beacons

Rapid detection of viral infection is crucial in preventing the spread of disease and in timely clinical treatment. Sivaraman et al. (p. 696–700) show that using a Tat-modified molecular beacon detection scheme coupled with flow cytometry resulted in an automated, high-throughput method for the identification of poliovirus-infected cells. Rapid intracellular delivery enabled the detection of infected cells within 30 seconds. The authors envision that this technique will be useful for clinical detection of epidemiologically important viruses, such as influenza virus.