Articles of Significant Interest in This Issue

Nature versus Nurture: Survival and Growth of Foodborne Pathogens on Produce

Inoculation studies that evaluate population dynamics of pathogens on foods are essential for accurate and robust microbial risk assessment. Harrand et al. (e01925-20) found that different pregrowth conditions (“nurture”) yielded a wider range of Salmonella enterica and Escherichia coli growth and survival patterns on produce than did genetic diversity alone (“nature”). For Listeria, neither pregrowth condition nor genetic diversity showed a substantial effect on growth. These findings suggest that studies on bacterial growth and survival in foods or other matrices should use strains grown under different conditions, particularly if the likely pregrowth conditions expected in the “real world” are not known.

A Matter of Context: Alkylquinolone Monoxygenases in Synthesis and Degradation of Pseudomonas aeruginosa Signals and Antibiotics

2-Alkylquinolones (AQs) and their N-oxides (AQNOs) act as quorum sensing signals or antibiotics and greatly increase competitiveness of Pseudomonas aeruginosa. AQ 3-monoxygenases amplify signaling but are also used by competitors as defense against toxic AQ/AQNO compounds. Ritzmann et al. (e02241-20) demonstrate that phylogenetically distant AQ 3-monoxygenases exhibit similar catalytic properties and substrate preferences, even though organisms suppressed by AQNO toxicity would benefit from AQNO hydroxylation. For P. aeruginosa, this reaction is unfavorable and minimized by efflux. The authors conclude that catalytic constraints likely restrict evolutionary adaptation of AQ 3-monoxygenases and reveal that compartmentalization mediates substrate preference on organismic level.

Potential Selection of Initial Mother-Child Shared Gut Bacteria by Mucins

Factors driving mother-child sharing of gut bacteria are important for human health and disease. Understanding of these factors has been limited by technological challenges in resolution and sensitivity of the sequencing approaches used. Nilsen et al. (e02201-20) solved these issues by using a new reduced metagenome sequencing (RMS) approach, analyzing a large mother-child longitudinal cohort including the first stool sample of the infant. Most of the mother-child shared bacteria were found to belong to potential mucin-utilizing species within the genus Bacteroides. This knowledge will be important in future understanding and securing mother-child transmission of beneficial gut bacteria.

Formate Is the Preferred Electron Donor for Methanogenesis in the Order Methanomicrobiales

Most methanogens are capable of reducing CO₂ to CH₄. H₂ is the preferred electron donor for this reaction in all methanogens tested to date; however, many methanogens from the order Methanomicrobiales lack hydrogenases essential for H₂-dependent methanogenesis. Using a genetic and biochemical approach, Abdul Halim et al. (e02698-20) show that formate is the sole electron donor for two of the four reductive steps in methanogenesis in Methanoculleus thermophilus. These results highlight the importance of formate in methanogenesis and force a reevaluation of methane metabolism in this globally distributed group.
**Aspergillus niger Enzymes for the Production of the Platform Chemical cis,cis-Muconic Acid from Salicylic Acid**

The biobased economy requires alternative methods to produce platform chemicals from renewable sources, to replace chemical processes. Lubbers et al. (e02701-20) studied the salicylic acid metabolic pathway of the fungus *Aspergillus niger* using whole-genome transcriptomic data for *A. niger* grown on salicylic acid. Two genes were identified and were recombinantly expressed, and the enzymes were characterized. The enzymes can convert salicylic acid to the platform chemical cis,cis-muconic acid. This compound can be used for synthesis of the polymers nylon, polyurethane, and polyethylene terephthalate. This work contributes to the creation of alternative methods for the production of platform chemicals.

**Modulation of the Gut Microbiota by Using Plant Glycans**

The community of microbes inhabiting the colon (the gut microbiota) is considered essential to the well-being of humans. Perturbations of the community associated with diseases and medical conditions may exacerbate illness. Tannock (e02757-20) considers the research options that would make modulation of the gut microbiota to correct these perturbations a valid proposition. Differential modulation might be achieved by modification of the intake of plant polysaccharides (i.e., glycans and dietary fiber) in the daily diet by using knowledge of the metabolic abilities of bacterial consortia within the microbiota and their contribution to functional resilience of the bowel ecosystem.