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Articles of Significant Interest in This Issue

Staphylococcus aureus Toxin-Antitoxin Systems (TA): a Promising Approach To Study Novel TA Systems

Toxin-antitoxin (TA) systems are widely conserved in bacteria and consist of a toxin that inhibits essential cellular functions (e.g., DNA replication, transcription, translation, or ATP synthesis) and an antitoxin that neutralizes its cognate toxin. Kato et al. (e00915-19) found novel TA systems on the *Staphylococcus aureus* chromosome, using a combination of manual base-by-base screening and functional assignments in *Escherichia coli* and *S. aureus*. The newly discovered TA systems exhibited no sequence similarities with known TA systems and were unique to staphylococci. These findings provide a promising approach for discovering unannotated TA systems in various bacterial species.

Non-Energy-Limited Near-Zero Growth of *Saccharomyces cerevisiae*

Achievement of near-zero growth of *Saccharomyces cerevisiae* through limited supply of nonenergy substrates, relevant in both natural and industrial environments, remains largely unexplored. Liu and coauthors (e01161-19) established near-zero-growth retentostat cultures of *S. cerevisiae* through restricted supply of the nitrogen or phosphorus source. For both conditions *S. cerevisiae* was kept in a virtually nongrowing state, while maintaining a high-viability, adequate energy status and metabolic active state. The possibility to achieve near-zero growth *S. cerevisiae* cultures through limited supply of a nonenergy nutrient may offer interesting prospects to develop novel fermentation processes for high-yield production of biobased chemicals.

Harnessing an Endogenous CRISPR-Cas System for Genome Editing in the Human Pathogen *Clostridium difficile*

Clostridium difficile is the leading cause of diarrhea associated with health care worldwide. Despite continuous efforts, efficient genetic tools are still needed to accelerate the research on this emerging enteropathogen. Maikova et al. (e01416-19) have developed an efficient method harnessing CRISPR-Cas, one of the endogenous defense systems against foreign DNA invaders, for *C. difficile* genome editing. They also show that this CRISPR-Cas system could be easily redirected towards self-targeting for development of new therapeutic strategies to limit *C. difficile* infections.

Fine-Tuning Dietary Fiber Metabolism in the Human Gut

The xyloglucans are a family of complex plant polysaccharides, which vary subtly in their side chain compositions. As predominant matrix glycans in the cell walls of common fruits and vegetables, xyloglucans are ubiquitous in well-balanced human diets. Déjean et al. (e01491-19) used a cross-genome analysis together with detailed enzymology to reveal how individual *Bacteroidetes* from the human gut microbiota (HGM) address distinct xyloglucan branches through variation in the cohorts of glycosides and carbohydrate-binding proteins encoded by homologous polysaccharide utilization loci (PUL). This study refines our understanding of complex carbohydrate metabolism by the HGM and outlines specific molecular markers to predict xyloglucan utilization across bacterial taxa.

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Exploiting Spheroplast Formation as a Pretreatment for Enhanced Viability Detection of Bacterial Cells by Propidium Monoazide and Quantitative PCR

The combination of propidium monoazide (PMA) with quantitative PCR (qPCR) assays is promising for viability detection, though challenged by false-positive signals by dead cells and the lack of an internal control addressing them. Spheroplast formation combined with a mild osmotic shock has been exploited by Lazou et al. (e01499-19) as a pretreatment for enhancing the subsequent selective entrance of PMA into dead *Campylobacter coli* cells without compromising their viable counterparts. Moreover, an internal sample process control (ISPC) has been developed resulting in reliable viability quantification in both pure cultures and inoculated meat. The proposed methodology could be combined with qPCR assays targeting other Gram-negative bacteria.