Articles of Significant Interest in This Issue

Glutaredoxins and Purine Metabolism Cooperate To Regulate the Integrated Stress Response

Mechoud and colleagues (e00221-20) reveal a novel and evolutionary conservation, from the yeast *Saccharomyces cerevisiae* to humans, of the interaction between monothiol glutaredoxins (Glr3, Grx3, and Grx4) and purine metabolism (GMP synthase). A functional connection between the Grx/GMP complex and the integrated stress response (GCN2/ISR) with the participation of iron metabolism was deciphered for *S. cerevisiae*. Tight regulation of ISR would avoid exhaustion of GTP in the cells, in a context of general limitation of nutrients. *S. cerevisiae* is presented as a suitable model to contribute to the understanding of the mechanisms underlying cancer and Alzheimer's disease in which human Glrx3 and GCN2 are involved.

Ergot Alkaloids Accumulate during Insect Colonization by Certain Biocontrol Fungi

Ergot alkaloids are fungal metabolites infamous for causing human and animal toxicoses. They also may be modified to produce prescription pharmaceuticals or the psychedelic drug lysergic acid diethylamide (LSD). Leadmon et al. (e00373-20) observed ergot alkaloids accumulating in several fungi of the genus *Metarhizium*, a previously undocumented source. These fungi symbiotically colonize the roots of many plants and are applied as biocontrol agents to combat insect pests. High concentrations of the compounds accumulated in *Metarhizium*-infected insects, whereas they were not detected in colonized plants and were rarely observed in cultures of the fungi, indicating a potential role for ergot alkaloids in insect colonization.

Sea Cucumber Evisceration and Regeneration Shed Light on Gut Microbiome Assembly

Understanding the processes that mediate microbial community assembly in the animal gut is paramount, as the gut microbiome is closely linked to host health. Weigel (e00489-20) used the rapidly regenerating sea cucumber *Sclerodactyla briareus* as a novel experimental system to study microbial colonization of the gut. By inducing evisceration, or expulsion of digestive organs, and tracking the microbiome of regenerating gut tissues over 20 days, Weigel discovered that different individuals developed highly similar gut microbiomes, providing evidence for deterministic gut microbiome assembly. Further, some gut microbiome members likely conferred energetic and immune advantages to the sea cucumber host.

How Bacteria Respond to Biocide Exposure

Antiseptics and disinfectants are ubiquitous and essential in our quest to control and eliminate pathogens. The mechanisms by which bacteria tolerate residual concentrations of such everyday products are mostly unknown. Transcriptomic analysis by Pereira et al. (e00708-20) showed that *Escherichia coli* switches from early upregulation of chaperones to late downregulation of motility and chemotaxis and to induction of biofilm regulators when exposed to biocides. Zinc homeostasis was determined to be a key factor in bacterial survival of exposure to conventional biocides. These discoveries provide a window to the rich repertoire that bacteria employ to survive and potential targets for controlling them more effectively.

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Directed Evolution of Mesozoic Fungal Laccases

The reconstruction and resurrection of ancestral enzymes is arising as a potent biotechnology tool, and its synergy with directed evolution methods may render “reprogrammed” biocatalysts for novel functions. In a study by Gomez-Fernandez et al. ([e00778-20](#)), fungal Mesozoic laccases up to 250 million years old were resurrected and further subjected to laboratory evolution aimed at producing vinyl polymers. While the ancestral laccase was rapidly evolved for the new activity, it showed a stronger expression level and a broader pH stability than its modern counterpart, a footprint of its ancestral origin.