Articles of Significant Interest in This Issue

Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Groups

Ribosomes of almost all bacteria contain the same set of 54 ribosomal proteins, 33 in the 50S subunit and 21 in the 30S subunit. However, some ribosomal protein genes are absent in parasites and symbionts with dramatically reduced genomes. Galperin et al. (e00058-21) compiled a list of ribosomal proteins that were missing in representative bacterial and archaeal genomes and compared this list with experimental data on the deletion of ribosomal protein genes. They concluded that proteins that are located at the surface of the ribosome are more likely to be lost in the course of microbial evolution.

Sensor Domain of Histidine Kinase VxrA of *Vibrio cholerae*—a Hairpin-Swapped Dimer and Its Conformational Change

The VxrAB two-component system (TCS) positively regulates a number of important *V. cholerae* phenotypes. Tan et al. (e00643-20) determined several crystal structures of the VxrA histidine kinase (HK) sensing domain (SD) and its mutants. These structures reveal a novel structural fold forming an unusual β hairpin-swapped dimer and demonstrate a large conformational change between two VxrA-SD dimers, supporting a putative scissor-like closing regulation mechanism for the VxrA HK. Given that VxrA lacks a signal amplifier linker domain, this work provides insight into a potentially unique TCS signal sensing and transmission mechanism.

Streptococcus pyogenes Peptide SpoV Regulates Streptolysin O and Enhances Survival in Murine Blood

Peptide-mediated signaling plays an important role in the adaptation of Gram-positive bacteria to changing environments. Herrera et al. (e00586-20) used peptidomics to discover signaling peptides produced by the human pathogen *Streptococcus pyogenes*. One peptide, designated SpoV, increases the expression of known virulence factors, including streptolysins O and S, and enhances virulence. The authors also show that expression of *spoV* varies among clinical isolates due to allelic variation in the *rocA* gene. The *spoV* gene is present only in the genomes of *S. pyogenes*, suggesting that it may be a candidate for highly targeted therapeutic intervention.

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