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Biology of *Vibrio cholerae* Editorial overview

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In this monographic issue, we have the pleasure to present contributions from six of the leading laboratories at the forefront of *Vibrio cholerae* genetics, ecology and evolution, together with a brief tribute by Diego Romero to Doctor Jaime Ferrán y Clua, a pioneering Spanish bacteriologist who developed the first vaccine against this pathogen.

V. cholerae is a free-living aquatic bacterium that interacts with and infects a variety of organisms. In humans it causes cholera, the deadly diarrhoea that was responsible for millions of deaths during seven pandemics since 1817, and still thousands every year. The Boucher lab presents a study of the ecology, evolution and dispersal of pandemic *V. cholerae* biotypes in relation to environmental reservoirs. They show how both species-specific and lineage-specific genetic determinants play a role in the ability of *V. cholerae* strains to cause pandemics, having evolved gradually over centuries.

One of the key aspects that makes a particularly successful pathogen is its genomic plasticity. The *V. cholerae* genome contains a superintegron (SI) that is involved in development and dissemination of antibiotic resistance genes among diverse bacterial species, permitting population expansion in challenging conditions. Escudero and Mazel review the SI as a true hotspot of *V. cholerae's* genomic diversity and low-cost memory of adaptive functions in its complex lifestyle and ecology. Another remarkable aspect of *V. cholerae*'s genetics is the presence of two chromosomes. Segregation and division in multi-chromosomal becteria is relatively complex, and *V. cholerae* remains the paradigm. Espinosa and colleagues review the cell cycle of *V. cholerae*, comparing and contrasting with that of *E. coli*.

In addition to genome plasticity, *V. cholerae* uses a variety of attack/defence strategies to compete and thrive in different niches, through interaction with bacteriophages, bacteria and eukaryotes. The role of phages in the life cycle of *V. cholerae* has been increasingly recognized and investigated over the past decade. Andrew Camilli and colleagues take us through the exciting evolutionary arms race between *V. cholerae* and virulent bacteriophages, based both on mechanisms of phage resistance in the bacterium and a unique phage-encoded CRISPR-Cas system used to counteract this resistance. Finally, the authors discuss the impact of these predator-prey dynamics in the context of infection, and their use as a strategy to limit cholera transmission within a community.

In regards to its ability to coexist with other microbes, *V. cholerae* can produce effectors that are either released to the extracellular media, or delivered via intimate cell-to-cell contact such as those injected via the type VI secretion system (T6SS). The Pukatzki lab reviews the versatility of the T6SS to produce different combinations of such effectors, which establishes the strains of *V. cholerae* that can co-exist in the environment. After killing a cell, its DNA is released and incorporated by natural competence into other living cells, thereby being a potential source of diversification for *V. cholerae's* T6SS effectors.

Finally, I revisisit the discovery of non-canonical D-amino acids, recently identified effectors secreted by *V. cholerae* which have increasingly been shown to be important in enhancing the ability of the bacterium to colonize and persist in a particular niche. I focus on recent observations that suggest different D-amino acids influence distinct cellular processes in bacteria, and discuss their role in modulating environmental bacterial biodiversity.

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