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Vibrios – from genes to ecosystems

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Editorial

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This special edition of Environmental Microbiology “*Vibrios – from Genes to Ecosystems*” brings together and captures the sheer breadth of research across this fascinating genus of microorganisms, through a variety of research, opinion and review articles. Perhaps one of the most captivating aspects related to vibrios is the duality that they represent in microbiology. On one hand they are important autochthonous constituents of marine and coastal waters throughout the world, playing critical ecological roles through a myriad of phylogenetically and functionally diverse representatives; on the other, unfortunately, vibrios constitute a uniquely potent group of human and animal pathogens capable of causing an array of diseases such as gastroenteritis, sepsis, and wound infections. Through the most famous (or *infamous*) member of this genus - *V. cholerae*, cholera has remained a global scourge, and alongside the seafood pathogen *V. parahaemolyticus*, the only pathogens that have emerged from aquatic and marine sources to cause bona fide global pandemics. Certainly, the research studies presented in this special edition draw on many aspects of this duality and provide critical insights regarding the growing importance of these bacteria, perhaps in the process highlighting that vibrios constitute a separate field of study in and of itself.

Several review articles in this special edition highlight why these bacteria are a critically important topic to study in microbiology. Vezzulli *et al.* (2020) outlines the growing

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importance of non-cholera *V. cholerae* (non O1/O139) using a variety of epidemiological, microbiological and public health data, and asks the pertinent question if this member of the *Vibrionaceae* family deserves greater research emphasis, particularly given the impact of climate change on this important human pathogen. Similarly, Daines and Froelich (2020) outline how and why a warming climatic system may place humans in greater contact – and consequently risk, of pathogenic vibrios. The risk of contamination is also explored by Canty *et al.* (2020) who study the effect of farming practices on the prevalence of the human pathogen *V. vulnificus* in oysters. Moreover, the review article by Hernández-Cabanyero and Amaro (2020) provides insights into the evolution and life strategies of this pathogen in response to selected environmental parameters. This article also contributes to fill an important gap in the existing knowledge on the biology of *V. vulnificus* and stresses its importance as a zoonotic pathogen linked to fish farms and climate change.

Several aspects related to the fascinating biology and genomics of vibrios are described here too. Sozhamman and Waldminghaus (2020) outline the importance of dual chromosomes in vibrios – focussing on the pathogen *V. cholerae*. Single-chromosome *V. cholerae* have been previously identified, and these particular strains are essential to study fundamental questions on chromosome biology in general, and DNA replication in particular. Furthering our understanding of the biology of these organisms, Crisan and Hammer (2020) provide a cogent overview of the importance of the type 6 secretions system (T6SS) as proteinaceous weapons used by a variety of Gram-negative bacteria. Utilizing *V. cholerae* as an exemplar model organism for T6SS they reveal the broad yet growing importance of these secretion

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systems as intrinsic mechanisms to evade phagocytic eukaryotes, cause intestinal inflammation, and compete against other bacteria with toxins that disrupt lipid membranes, cell walls and actin cytoskeletons.

Recently, *Vibrio* bacteria have also garnered attention as host for molecular biology and biotechnology applications. As outlined in the review article by Hoff *et al.* (2020), this is the case with *V. natrieigens*, the fastest-growing non-pathogenic bacterium known to date. Spanning all the way from its initial isolation to its latest applications, the article focuses on *V. natrieigens* successful applications in synthetic biology and biotechnology in recent years, and examines missing methods and tools which need to be established in order to exploit the full potential of this fascinating bacterium.

Identifying the mechanisms underpinning virulence traits and understanding the drivers of their selection is key for the prevention of human and animal diseases caused by vibrios. Here are a series of articles that study virulence determinants in environmental and clinical strains. The article by Piel *et al.* (2019) reveals the importance of a plasmid highly prevalent in oyster farms, which encodes a T6SS involved in virulence in the oyster pathogen, *V. crassostreae*. While the T6SS contributes to dampen the immune defenses of the oyster, Drebes Dörr and Blokesch (2020) show that T6SSs in environmental isolates of *V. cholerae* are major players of interbacterial competition while others, which harbor an actin cross-linking domain on the VgrG protein, and confer resistance to amoeba grazing. Seibt *et al.* (2020) explore the role of the σ^{54} -dependent transcriptional regulator VasH in the expression of such secretion

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system in pandemic cholera causing El Tor strain A1552, which requires specialized growth signals of low temperature and high osmolarity for T6SS expression. A study presented here by Stutzmann *et al.* (2020) compared the chitin-induced competence and transformation behavior in a variety of pandemic O1 El Tor *V. cholerae* isolates as well as an O139 isolate. Using a variety of methodologies, including molecular microbiological approaches, sequencing and comparative bioinformatics they demonstrate both the integral role of the competence regulon as well as conserved nature of this system in pathogenic *V. cholerae*, further outlining the role of chitin and HGT in this context.

Two articles show that the multiple host and environmental stressors acting on the selection of *Vibrio* virulence factors may lead to cases of conflicting or coincidental selection. In *V. splendidus*, Oyanedel *et al.* (2020) show that the structure of the O-antigen is detrimental for virulence but essential for resistance to amoeba grazing, which likely explains its hypervariability in environmental isolates. In contrast, the article by Robino *et al.* (2019) shows that resistance to copper and toxic factors (metalloproteases) in *V. tasmaniensis* are beneficial in the interaction with both oysters and marine amoeba. How the interactions of vibrios with environmental predators and metazoan hosts may be beneficial or costly for *Vibrio* virulence is discussed in Destoumieux-Garzón *et al.* (2020), who review the current knowledge on *Vibrio*–bivalve interactions. Critically important to understand how and why these bacteria can cause infections in humans and animals is the need for reliable, tractable and repeatable model systems, and especially those that constitute and reflect real exposure hazards. Hubert and Michell (2020) outline an approach to generate ‘artificial’ marine snow,

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into which bacteria such as *V. vulnificus* can be incorporated to facilitate extensive uptake by oysters. This represents a highly promising and adaptable model for bacterial study within filter-feeding shellfish – the major route through which many of these species cause disease in humans. This study also outlines the growing importance of the T6SS in terms of potentially modulating numbers of these pathogens in the environment, critically important information to more fully understand the ecology of *V. vulnificus*.

Other articles of this special edition tackle the vast complexity of *Vibrio* biology and ecology highlighting how science is moving on fast in this fascinating research field. The opinion paper by Baker-Austin *et al.* (2020) outlines some of the most exciting, innovative and translational scientific advances that are currently being applied to these ecologically, environmentally and clinically important bacteria. From this paper, as well as from the other contributions of the special edition, it is evident that the coordinated use of different experimental approaches across various disciplines, not just microbiological, is the most fruitful strategy to decipher structures and mechanisms underlying the duality of life style of *Vibrio* bacteria, and to clarify the still obscure aspects of their interactions with both the environment and their host. We feel that the enormous breadth of research captured in this special edition - encompassing microbiology, molecular biology, genetics, and bioinformatics, among others - outline the true interdisciplinary nature of vibrios, and underline why they continue to represent such a fascinating and rewarding group of microorganisms to study.

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