Environmental reservoirs and mechanisms of persistence of *Vibrio cholerae*

Carla Lutz 1, Martina Erken 1,2, Parisa Noorian 1, Shuyang Sun 1 and Diane McDougald 1,2 *

1 Centre for Marine Bio-Innovation, School of Biotechnology and Biomolecular Science, University of New South Wales, Sydney, NSW, Australia
2 Advanced Environmental Biotechnology Centre, Nanyang Environment and Water Research Institute, School of Biological Sciences, Nanyang Technological University, Singapore, Singapore
3 The Singapore Centre on Environmental Life Sciences Engineering, Nanyang Technological University, Singapore, Singapore

Edited by:
Rita P. Colwell, University of Maryland, USA

Reviewed by:
Barbara J. Campbell, Clemson University, USA

*Correspondence:
Diane McDougald, Centre for Marine Bio-Innovation, School of Biotechnology and Biomolecular Science, University of New South Wales, Sydney, NSW 2052, Australia

E-mail: d.mcdougald@unsw.edu.au

INTRODUCTION

While it is likely to have been responsible for human infections and mortality throughout human history, cholera outbreaks have only been formally known to science since 1817 (Pollitzer, 1954). Sir John Snow was credited in 1849 as being the first person to connect contaminated water with cholera outbreaks and to use that information as an infection control strategy (Snow, 1855).

In addition to being the genesis of modern epidemiology, his observation may also be the first study on the ecology of *Vibrio cholerae*. However, it took another 120 years for *V. cholerae* to be recognized as an autochthonous aquatic bacterium rather than a human pathogen that is a transient resident of the aquatic environment (Colwell et al., 1977). *V. cholerae* has over 200 serogroups, with O1 and O139 being the causative agents of cholera, due to their carriage of the genes encoding cholera toxin (CT) and the toxin co-regulated pilus (TCP; Chatterjee et al., 2007). Surveys of serogroups associated with the human host are only one small aspect of the *V. cholerae* life cycle and is not necessary for environmental persistence.

*Vibrio cholerae* inhabits a vast geographical range from the tropics (e.g., the Bay of Bengal where pandemics still occur, e.g., Albert et al., 1995; Huq et al., 2005; de Magney et al., 2011) to temperate waters worldwide (e.g., USA, South America, Australia, Sweden, and Italy, e.g., Vezzulli et al., 2009; Collin and Robins-Browne, 2011; Schuster et al., 2011; Islam et al., 2013; Tall et al., 2013, Figure 1). An increasing understanding of the ecology of *V. cholerae*, along with advances in molecular detection has demonstrated that this bacterium is a cosmopolitan aquatic species that is capable of causing illness in humans (Sack et al., 2004).

The capability to survive in many different environmental niches is largely due to the evolution of a range of adaptive responses that allow *V. cholerae* to survive stressors such as nutrient deprivation, fluctuations in salinity and temperature and to resist predation by heterotrophic protists and bacteriophage. One such strategy is the conversion into a viable but non-culturable (VBNC) state during unfavorable conditions (Colwell, 2000, Thomas et al., 2006). Additionally, *V. cholerae* attaches to abiotic and biotic surfaces (chitinous as well as gelatinous zoo- and phytoplankton) as biofilms (e.g., Huq et al., 1996; Akselman et al., 2010; Shikuma and Hadfield, 2010). Biofilm formation is associated with increased stress resistance, increased access to nutrients and as a means of dispersal when attached to living, mobile hosts (Costerton et al., 1995; Hall-Stoodley et al., 2004). Here, the current understanding of how *V. cholerae* is able to adapt to, and persist in the aquatic environment is summarized.

SURFACE COLONIZATION AND BIOFILM FORMATION

ENHANCE *V. cholerae* PERSISTENCE

For aquatic bacteria, surface attachment provides a selective advantage through access to nutrients that accumulate at the liquid–surface interface (Dawson et al., 1981). Therefore, surface adhesion may be a survival strategy that allows bacteria to persist in nutrient-limited natural environments (Dawson et al., 1981; Figure 2). Additionally, some biotic surfaces may provide nutrients for attached bacteria (e.g., chitin; Nalin et al., 1979). Thus, it is not surprising that *V. cholerae* has been detected on many abiotic
FIGURE 1 | Global distribution of *Vibrio cholerae*. Triangles indicate where *V. cholerae* was detected by molecular and/or culture-based methods. Red indicates O1/O139 detection, light blue non-O1/non-O139 detection, and dark blue did not specify. Referenced studies here are only a small fraction of the studies published for certain areas and should guide as an example. North – and Middle America: (Colwell et al., 1981; Ogg et al., 1989; Blackwell and Oliver, 2009; Lizárraga-Partida et al., 2009; Hill et al., 2011; Dickinson et al., 2013), South America: (Franco et al., 2010; Lipp et al., 2010; Led et al., 2009; Martínez-Fité et al., 2010; Sa et al., 2012; Africa: (Ewanari et al., 2008; Europe: (Andersson and Ekdahl, 2006; Cowzin Harrague et al., 2008; Kindtner et al., 2008; Vezzulli et al., 2008; Vezzulli et al., 2011; Bier et al., 2013; Canteti et al., 2013; Tai et al., 2013)), Middle East: (Balin et al., 2009; Grimm et al., 2010; Sultamov et al., 2011; Rashid et al., 2013; Asia Pacific: (Eslam et al., 1994; 2013; De Schacht et al., 1995; Miyagi et al., 2010; Alam et al., 2006; Vimala et al., 2010; de Magra et al., 2011; Singh et al., 2012).

FIGURE 2 | Biofilm formation enhances *Vibrio cholerae* persistence. *V. cholerae* uses chemotaxis to detect suitable surfaces for attachment. Substrate components, such as sugar concentrations of the conditioning film, play a role in the reversibly attached cells “decision” to become permanently attached. Permanent attachment is mediated by pili (ChiRP and MSHA) and outer membrane proteins such as GbpA. Biofilm formation is reinforced through the production of VPS, which is controlled by QS (yellow star) and c-di-GMP. Anti-protozoal mechanisms such as T6SS protect surface attached bacteria. *V. cholerae* within biofilms undergoes horizontal gene transfer (HGT), which may aid in survival.

and biotic surfaces, including ship hulls (Shikuma and Hadfield, 2010), zooplankton (Tampin et al., 1999; Epstein, 1993; Huq et al., 2005; Turner et al., 2009), macroalgaee (Hood and Winter, 1997), and as floating aggregates (Alam et al., 2006).

*Vibrio cholerae* attachment is mediated by pili, which are surface expressed proteins, comprised of pilin subunits that promote surface attachment and subsequent biofilm formation. The ability of *V. cholerae* to attach to a range of surfaces is reflected in the variation in pilin subunits, and hence variation in pili, expressed by *V. cholerae* (Boyd and Waldor, 2002; Aagesen and Häse, 2012).

One ecologically important substratum is chitin, and *V. cholerae*, as are most Vibrionaceae, is chitinolytic and possesses multiple conserved genes to attach to and degrade chitin (McBoon et al., 2004; Hunt et al., 2008). This organic polymer of *N*-acetylglicosamine (GlcNAc/NAG) is the second most abundant organic polymer in nature and is an excellent carbon source for bacteria (Rinaudo, 2006; Martínez et al., 2009). The binding of *V. cholerae* to chitin involves the GlcNAc binding protein, GbpA (Kirn et al., 2005;
Stauder et al., 2010), as well as the mannose sensitive hemagglutinin (MSHA), which is a type IV pilus (Chavelli et al., 2001; Figure 2). Furthermore, the TCP which is a colonization factor of human intestinal epithelia, has a duel role in association with chitin. TCP is required for differentiation of attached biofilms, and undifferentiated biofilms lacking TCP have reduced ecological fitness, as they are less efficient at degrading chitin (Rogers and Kolter, 1999).

After initial surface attachment, *V. cholerae* forms “matrix-enclosed, surface-associated communities” or biofilms (Yildiz and Visick, 2009). *V. cholerae* biofilm formation is enhanced through the actions of type IV pili, flagella and production of the biofilm matrix, Vibrio polysaccharide (VPS; Watnick and Kolter, 1999). VPS is involved in cell immobilization, microcolony formation, and biofilm maturation (Watnick and Kolter, 1999; Watnick et al., 2001). High and low VPS producing *V. cholerae* colony types are referred to as “rugose” and “smooth,” respectively, with the rugose having a higher protective effect toward a variety of stresses, including chlorine (Rice et al., 1992; Morris et al., 1996; Yildiz and Schoolnik, 1999), low pH (Zhu and Mekalanos, 2003), osmotic and oxidative stress (Wai et al., 1998), anti-bacterial serum (Morris et al., 1996), SDS (Fong et al., 2006), phage (Neper et al., 2001), and heterotrophic protists (Sun et al., 2013). The importance of VPS for protection in the environment is still unknown as there are few published reports on the occurrence of rugose *V. cholerae* in the environment (Ali et al., 2002; Ibarbar et al., 2012).

The structural genes for VPS production are encoded on two carbohydrate biosynthesis operons located on the large chromosome, which encodes many essential housekeeping genes (Yildiz and Schoolnik, 1999; Fong et al., 2010). The *vps* operon contains the genes *vpsA* to *vpsH* and the *vps* operon contains the genes *vpsI* to *vpsQ*. The six genes located between the two vps operons (rbmA-F) are also involved in biofilm formation (Fong and Yildiz, 2007; Abelson et al., 2011; Berk et al., 2012). The requirement for sugars in the synthesis of VPS is an important determinant for the control of biofilm formation (discussed in Section “V. cholerae Responses to Environmental Stresses – Biotypes are not Cell Denaturable”). In addition to sugars, multiple regulators control the expression of VPS. For example VPS biosynthesis is positively regulated by VpsR (Yildiz et al., 2001) and VpsP (Casper-Lindley and Yildiz, 2004) in a c-di-GMP-dependent manner (Krsteva et al., 2010; Srivastava et al., 2013). C-di-GMP is an intracellular secondary messenger that controls the surface association of bacteria in response to environmental conditions (Yildiz, 2008).

Bacterial cell–cell communication, or quorum sensing (QS), is critical for biofilm maturation and subsequent dispersal (Liu et al., 2007; Muller et al., 2007). At high *V. cholerae* cell densities, the QS response regulator, HapR, positively regulates the transcription of *hapA* encoding the hemagglutinin protease (HAP; Jobling and Holmes, 1997; Zhu et al., 2001), cyaR, a repressor of biofilm development, flagellum biosynthesis genes (Yildiz et al., 2004), and represses VPS production and toxR, the regulator of virulence (Jobling and Holmes, 1997; Zhu et al., 2002; Hammer and Bassler, 2003; Zhu and Mekalanos, 2003; Yildiz et al., 2004). It has been proposed that the coordination of QS and c-di-GMP controlled traits allows for survival through rapid adaptation to environmental conditions. For example, the switch from a free-swimming to an attached lifestyle (Yildiz and Visick, 2009; Srivastava and Waters, 2012) enables natural competency and horizontal gene transfer (HGT; Lo Scrudato and Blokesch, 2012) as well as protection against predation (Matz et al., 2005). Mechanisms such as biofilm formation enable the persistence of *V. cholerae* and are not limited to interactions with nutritious biotic factors. Indeed, as described in the following sections, many abiotic factors including temperature, salinity, and pH influence the expression of adaptive traits.

"Viable but non-culturable" *V. cholerae* in plankton

In contrast to starved cells, VBNC cells fail to grow on culture media normally used to grow them, and are often reduced in size but remain metabolically active (Nilsson et al., 1991; McDougald et al., 1999; Oliver, 2003, 2010). Factors known to induce VBNC formation in *V. cholerae* include extremes in temperature and salinity as well as nutrient deprivation (Colwell et al., 1985; Ravel et al., 1995; Carroll et al., 2001; Gonzalez-Escalona et al., 2006; Thomas et al., 2006; Mishra et al., 2012). VBNC cells of *V. cholerae* have been detected on the surface of higher organisms, such as crustaceans and algae in the plankton and benthos, attached to chironomid egg masses, as well as suspended in bacterioplankton (e.g., Louis et al., 2003; Binsstein et al., 2004; Alam et al., 2007; Halpern et al., 2007). Interestingly, *V. cholerae* appears predominately as VBNC cells within the bacterioplankton and as culturable cells in biofilm consortia, either as aggregates or attached to biotic and abiotic surfaces (Alam et al., 2006). The importance of the VBNC state in cholera epidemiology was demonstrated by Mishra et al. (2012), where virulence and colonization traits were actively expressed in *V. cholerae* VBNC incubated in freshwater microcosms.

For the VBNC response to impart protection allowing for persistence during unfavorable conditions, the cells must be able to resuscitate and divide when conditions become favorable (McDougald et al., 1998). For example, Vibrio vulnificus enters the VBNC state and can be resuscitated when incubated in environmental diffusion chambers in the marine environment (Oliver et al., 1995). Just as there are numerous conditions that induce VBNC formation in different species, there are numerous factors that induce resuscitation, including temperature upshift (Nilsson et al., 1991; Mishra et al., 2012) or an increase in nutrients (Binsstein et al., 2004; Srsno et al., 2010). VBNC *V. cholerae* cells have also been shown to regain culturability by passage through animal digestive tracts (Colwell et al., 1985; Alam et al., 2007; Asakura et al., 2007). Furthermore, the ingestion by human volunteers of *V. cholerae* cells that had been VBNC for as long as 7 weeks resulted in colonization of the intestine and excretion of culturable cells (Colwell et al., 1996). Thus, VBNC cells represent an important environmental reservoir of *V. cholerae* as an agent of disease. However, VBNC cells remain capable of resuscitation for a limited time, and eventually,
these cells lose the ability to resuscitate (Weichart et al., 1997). For example, VBNC cells can be resuscitated after co-incubation with eukaryotic cell lines, but resuscitation does not occur for cells that have been VBNC for a prolonged time (more than 91 days; Senoh et al., 2010).

Recently, QS has been implicated in the regulation of the VBNC state. For example, transition of cultivable \textit{V. cholerae} to the VBNC state involves biofilm formation and was shown to be dependent on QS (Kamruzzaman et al., 2010). In accordance with these results, VBNC cells from surface waters in Bangladesh have been resuscitated by natural or chemically synthesized QS autoinducers, as high colony forming unit (CFU) counts were detected after 4–5 h of exposure to two different autoinducers (Bari et al., 2013).

One hypothesis for the non-culturability of viable cells on common agar plates is that accumulation of reactive oxygen species (ROS) in the non-growing VBNC cells is detrimental when growth is initiated after nutrient addition. Thus, increased nutrient could lead to an imbalance in metabolism resulting in the production of ROS and cell death (Bloomfield et al., 1998). In fact, treatment of VBNC \textit{Escherichia coli} with catalase or peroxide-degrading compounds can restore culturability (Mintun et al., 1998) and elimination of hydrogen peroxide from starved cultures of \textit{E. coli} can prevent VBNC formation (Arana et al., 1992). Furthermore, loss of culturability of \textit{V. vulnificus} under low temperature incubation has been correlated with loss of catalase activity, making the cells ROS sensitive (Kong et al., 2004).

It was recently hypothesized that VBNC cells resuscitate in a stochastic manner rather than in response to environmental parameters (Epstein, 2009). The authors argue that some cells of a dormant community will randomly revive from dormancy and if conditions are favorable, they will grow. Thus, these revived cells can be likened to “scouts” inspecting environmental conditions (Buerger et al., 2012a,b). If conditions are not permissive for growth, the scouts will die, resulting in the loss of only a small fraction of the population. However, if conditions are favorable, then the genetic pool is amplified and maintained. The authors demonstrated that sampled marine and soil bacteria randomly became cultivable during long term incubation in the wells of microtiter plates containing single cells. Furthermore, strains that were slow growing initially, with a cultivation time of 3–4 weeks could be sub-cultured within 48–72 h (Buerger et al., 2012b). In this way, the VBNC state represents a low cost population-based strategy that allows bacteria to remain dormant in the environment for extended periods, and to potentially either revive when an appropriate cue is present, e.g., an inducer signal, or to randomly test their environment to subsequently grow when conditions are favorable. Although stochastic VBNC resuscitation was not tested with \textit{V. cholerae}, it has implications for identifying resuscitation cues and for understanding triggers of \textit{V. cholerae} growth and cholera outbreaks.

\textbf{\textit{Vibrio} cholerae RESPONSES TO ENVIRONMENTAL STRESSES – BOTTOM-UP CONTROL OF \textit{V. cholerae}}

The occurrence of \textit{Vibrio} spp. in the environment is correlated with temperature, salinity, and phyto- as well as zooplankton (Turner et al., 2009, 2013; Johnson et al., 2010; Asplund et al., 2011). High water temperature is a strong predictor for the presence of \textit{Vibrio} spp. (Blackwell and Oliver, 2008; Lama et al., 2011; Johnson et al., 2012), as they are mainly detected in warmer waters (above 15°C). Many studies have demonstrated that the abundance of \textit{Vibrio} spp. follows a seasonal pattern that is dictated to a large extent by temperature (e.g., Louis et al., 2003; Binzstein et al., 2004). Increased temperature can influence the attachment of \textit{V. cholerae} to chitin-rich zooplankton. At temperatures above 15°C, attachment of \textit{V. cholerae} to chitin increases significantly due to an increase in the expression of the MSHA pilus and the colonization factor, GbpA (Castronou and Escartin, 2005; Turner et al., 2009; Stauder et al., 2010).

In contrast, despite the water temperatures in the Chesapeake Bay being above 19°C, \textit{V. cholerae} was found more often in the water column, as planktonic cells, than attached to plankton (Louis et al., 2003). Thus, in addition to elevated temperature, other factors must influence biofilm formation or dispersal, demonstrating the importance of environmental surveying, collecting, and interpreting metadata to determine those factors that influence cholera epidemics.

Temperature fluctuations due to seasonal changes, as well as freshwater influx can strongly influence the salinity of marine water bodies. Open ocean waters have an average salinity of 35 ppt. However, near coastal and estuarine areas the salinity can drop due to freshwater input from rivers or rain run-off (Sinha et al., 2011), and can increase in areas with higher solar evaporation, especially in the tropics. \textit{Vibrio} spp. grow preferably at salinities <25 ppt (e.g., Jiang, 2001; Thomas et al., 2006; Baker-Austin et al., 2010). In high salinity environments \textit{V. cholerae} increases the production of the protective pigment, melamin (Coyne and al-Harthi, 1992), which provides UV resistance (Valera et al., 2009). The relationship between \textit{V. cholerae} occurrence and salinity appears to be variable, with some studies reporting a significant correlation (Singleton et al., 1982; Johnson et al., 2010), while others demonstrate a lack of correlation between the occurrence of the organism and salinity (Johnson et al., 2012). For example, Stauder et al. (2010) showed that different salinities had no effect on attachment to surfaces, which is important for environmental persistence (as discussed in Section “Association with Other Organisms”).

Seasonal fluctuations are often correlated with changing nutrient concentrations, as rain-run off is generally higher in spring/autumn and in coastal and estuarine areas. This can lead to higher phytoplankton abundance, followed by zooplankton blooms (e.g., Lobitz et al., 2000; Huq et al., 2005), which provide the chitinous surfaces that harbor bacteria such as \textit{V. cholerae}. This may enable overall numbers of the organism to increase in the environment even though bacteriovorous predators are also more abundant.

Nutrient sources in the environment are not uniformly distributed but occur as microscale patches, influenced by localized events such as cell lysis and waste excretion (Blackburn et al., 1998). Planktonic bacteria use motility and chemotaxis to take advantage of such nutrient patches (for a review of see, Stocker and Seymour, 2012). \textit{V. cholerae} possesses a single sheathed polar flagella (Hrantzy et al., 1980) powered by sodium motive force (Kojima et al., 1999). The number of duplicated chemotaxis-related genes possessed by \textit{V. cholerae} indicates the importance of this response for environmental survival (Heidelberg et al., 2000). \textit{V. cholerae}
have multiple chemotaxis genes, however not all are required for chemotaxis under standard laboratory conditions, suggesting that the other genes act as accessory chemotactic genes or have as yet undiscovered functions in the environment (Gosink et al., 2002). *V. cholerae* has been shown to be chemotactic toward all amino acids (Fever and O’Brien, 1981), suggesting that proteins, peptides, or amino acids may be important nutrient sources in the aquatic environment. In addition, *V. cholerae* upregulates chemotaxis genes in response to chitin oligosaccharides, facilitating detection and attachment to chitinous organisms (Meibom et al., 2004).

The ability of *V. cholerae* to persist in the environment is intrinsically linked to biofilm formation and VPS synthesis, both of which allow for the exploitation of nutrients available at the surface. Concentrations of sugars, phosphorus, and nitrogen influence attachment and biofilm formation *V. cholerae* cells. The presence of glucose and mannose induce VPS synthesis during biofilm development (Kierck and Watnick, 2003; Moorthy and Watnick, 2004). The phosphoenolpyruvate phosphotransferase system (PTS) is one of the major sugar transport systems in *V. cholerae* and activation of PTS results in derepression of VPS gene transcription and thus increased biofilm formation (Houot and Watnick, 2008; Houot et al., 2010). In addition, a *V. cholerae* PTS that responds to intracellular nitrogen concentrations, is believed to repress VPS production, however the receptor molecule and signaling pathway are still unknown (Houot et al., 2010).

Phosphorous also affects surface colonization. In phosphorus depleted environments, *V. cholerae* adopts a free-swimming planktonic lifestyle that is mediated by a two-component system, PhoBR. The histidine kinase, PhoR, phosphorylates the response regulator, PhoH, resulting in further repression of VPS production (Pratt et al., 2009; Sultan et al., 2010).

Planktonic *V. cholerae* cells have been shown to settle in response to extracellular DNA (eDNA), which is a component of the pre-established biofilm matrix (Hasuo and Watnick, 2002). This occurs by repression of CytR, which in turn represses VPS and formation (Houot and Watnick, 2008). Since nutrient availability fluctuates in the aquatic environment, planktonic bacteria that live a “feast-to-famine lifestyle.” In bacteria, glycogen is stored in granules and can serve as a carbon source during periods of starvation (Press and Romeo, 1994). Under nutrient rich conditions *V. cholerae* increases glycogen storage precursors (Kan et al., 2004). In addition, glycogen granules are present in nutrient poor rice water stools shed by patients with cholera (Bourassa and Cassilli, 2009), indicating that glycogen storage may provide nutrients to *V. cholerae* as it passes from the human host into the aquatic environment. In addition to glycogen storage, the ability to store inorganic phosphorus (Pi) facilitates protection against environmental stresses such as acidity, salinity fluctuations, and the damaging effects of hydrogen peroxide, as it is required for activity of the general stress response regulator, RpoS (Jahid et al., 2004). *V. cholerae* is also able to store Pi within membrane bound granules at 100 times the concentrations achieved by E. coli (Ogawa et al., 2000). *V. cholerae* mutants deficient in Pi storage displayed reduced attachment to abiotic surfaces, decreased motility and a delayed adaptation to high calcium media (200 mM) (Ogawa et al., 2006).

In addition to carbon and phosphorous, iron is also a growth limiting factor required for cellular metabolism as it is a component of many cofactors (Wacke et al., 1989) and has low solubility in aquatic environments (Martin, 1992). Iron concentrations in the aquatic environment are highly variable and are generally correlated with water depth (Martin and Michael Gordon, 1988). *V. cholerae* has evolved several iron transport systems and receptors that enable persistence in low iron environments (Heidelberg et al., 2000; Wyckoff et al., 2006, 2007). These iron acquisition systems include a catechol siderophore, vibriobactin (Griffiths et al., 1984), and a transport system, Fev, that can take up ferrous iron (Wyckoff et al., 2006). Most iron acquisition genes, such as irgA (Goldberg et al., 1991), are repressed by the ferric uptake regulator (Fur) in environments with sufficient iron, as Fe(II)-Fur binds to the promoter of iron-regulated genes, preventing their expression (Bagg and Neilands, 1987). *V. cholerae* can also make use of siderophores secreted by other microorganisms, such as fluorides synthesized by Vibrio fluvialis, as it possesses the required receptors and uptake systems (Yamamoto et al., 1993).

In nutrient limited environments, *V. cholerae* can enter a starvation state, in which the cells are non-growing but culturable. In a recent laboratory study, Jubair et al. (2012) described the long-term starvation survival of *V. cholerae* (700 days). The authors suggest the term “persister phenotype” to differentiate starved cells from the VBNC state. The growth of persister cells was enhanced in the presence of phosphate and chitin, both important nutrients, which further highlights their importance for *V. cholerae* survival. An earlier study on the behavior of *V. cholerae* starved for 40 days showed that chitin attachment ligands were maintained (Pruzzo et al., 2003). These findings demonstrate the importance of association with chitinous organisms with details of specific interactions discussed in the Section “Association with Other Organisms.”

**TOP-DOWN CONTROL BY PREDATORY MICROGRASERS**

While availability of nutrients exerts “bottom-up” control of *V. cholerae*, predation by heterotrophic protists is one of the major mortality factors faced by bacteria in the environment (Hahn and Höfle, 2001; Matz and Kyllenberg, 2005). As part of the bacterioplankton, *V. cholerae* is under constant predation pressure by phagotrophic protists and other bacterivorous members of the zooplankton community. The long-term persistence and seasonal accumulation of *V. cholerae* is dependent on how it responds to this stress. Microcosm studies of natural bacterioplankton communities from the Gulf of Mexico showed that ciliates and heterotrophic nanoflagellates (HNFs) efficiently eliminate *V. cholerae* from environmental water samples (Martinez Pérez et al., 2004). In addition, ciliates as well as flagellates can feed on *V. cholerae*, with grazing rates of up to 600–2,000 bacteria cell$^{-1}$ h$^{-1}$ (Marcik et al., 1997). Control of *V. cholerae* numbers by heterotrophic protists was also demonstrated by Woden et al. (2006), where *V. cholerae* growth rates of up to 2.5 doublings per day were countered by heavy grazing mortality by HNFs. During intense phytoplankton blooms, these growth rates increased to more than four doublings per day, allowing...
V. cholerae to overcome grazing pressure, potentially attaining sufficient numbers in the environment to reach an infectious dose.

Vibrio cholerae cells encased in a biofilm matrix are protected from predation by HNFs, while planktonic cells are rapidly eliminated (Matz et al., 2005). Predation induces biofilm formation and a smooth to rugose morphological shift, due to an increase in VPS production (Matz et al., 2005). VPS has subsequently been confirmed to be partly responsible for biofilm grazing resistance, whereas the V. cholerae cells encased in VPS were protected from predators (Sun et al., 2013). In addition to physical protection provided by biofilms, the high cell density in V. cholerae biofilms provides a sufficient quorum to promote expression of several QS-regulated anti-protozoal factors that cannot accumulate in the planktonic phase.

The importance of QS for protection from protozoal predation is supported by field tests demonstrating that QS-deficient V. cholerae was more susceptible to grazing than the wild type. However, the QS mutant strain did not lose all grazing resistance, suggesting that V. cholerae regulates anti-protozoal activities by a combination of QS and other regulatory systems (Eiken et al., 2011). VPS mutants were less resistant than the wild type strain to surface grazing by the amoeba, Acanthamoeba castellanii and the HNF, Rhynchomonas nasuta, but were more resistant than the hopR mutant strain, indicating that QS is more protective than VPS against predators (Sun et al., 2013). QS has been shown to regulate secreted compounds that provide resistance from functionally different predators such as Tetrahymena pyriformis, Caenorhabditis elegans, and Acanthamoeba castellanii, e.g., an uncharacterized anti-protozoal factor (Matz et al., 2015) and the PrtV protease (Vintkenius et al., 2006).

The type VI secretion system (T6SS) also functions as an anti-predation mechanism that is inhibitory against Dictyostelium discoideum, mammalian macrophages, and E. coli (Pukatzki et al., 2006; Machtay et al., 2010). Three proteins (VgrG-1, -2, and -3) secreted by the T6SS form syringe-like structures, puncturing the cell membrane and delivering a virulence factor, VaaK, into D. discoideum (Pukatzki et al., 2007; Miyata et al., 2011). The expression of another major component of T6SS, Hcp, is positively regulated by QS in V. cholerae (Ishikawa et al., 2009). Although all V. cholerae strains have this system, expression differs between them (Unterweger et al., 2012). For example, pandemic El Tor strains do not express T6SS under laboratory conditions while in regions where cholera outbreaks have occurred, such as Peru (Talledo et al., 2003), Kolkata (Sen and Ghosh, 2005), and Kenya (Maina et al., 2013). Control of V. cholerae populations may be influenced by phage to a larger extent than by nutrient limitation (Wei et al., 2011). Phage predation has shaped cholera epidemics in Bangladesh, where high concentrations of phage are detected after an initial peak in cholera cases and numbers of V. cholerae cells in the aquatic environment (Farsique et al., 2005). Following the increase in phage numbers, the number of cholera cases decreases. An increase in phage numbers in the environment was also correlated with an increase in V. cholerae fitness traits is required to understand the persistence and spread of the pathogen in the environment.

In addition to aforementioned predation pressure by phagotrophic protists, phage, and predatory bacteria also affect the abundance and serogroup prevalence of V. cholerae in the environment. For example, the CTXφ phage carries the genes encoding CT and is required for conversion of non-toxigenic to toxigenic strains (Miller and Mekalanos, 1988; Pearson et al., 1993; Waldor and Mekalanos, 1996). Phage predation has shaped cholera epidemics in Bangladesh, where high concentrations of phage are detected after an initial peak in cholera cases and numbers of V. cholerae cells in the aquatic environment (Farsique et al., 2005). Following the increase in phage numbers, the number of cholera cases decreases. An increase in phage numbers in the environment was also correlated with an increase in V. cholerae lytic bacteriophage in patient stool samples, with one of the predominant bacteriophage species belonging to the Myoviridae family (Seed et al., 2011). Environmental surveys have detected Myoviridae in regions where cholera outbreaks have occurred, such as Pera (Talledo et al., 2003), Kolkata (Sen and Ghosh, 2005), and Kenya (Maina et al., 2013). Control of V. cholerae by phage is supported by a continuous culture experiment, which suggests that V. cholerae populations may be influenced by phage to a larger extent than by nutrient limitation (Weitz et al., 2011). Predatory bacteria such as Bdellovibrio sp. also prey on V. cholerae (Chen et al., 2012) and might also shape V. cholerae occurrence in the environment. However, there is limited information on the interactions between predatory bacteria and V. cholerae.
ASSOCIATION WITH OTHER ORGANISMS

*Vibrio cholerae* is an integral part of the aquatic environment and in addition to heterotrophic protists, interacts with a wide range of organisms. It has been demonstrated to interact with waterfowl (Halpern et al., 2008), fish (Kiyukai et al., 1992; Senderovich et al., 2010), chironomids (Broza and Halpern, 2001; Halpern et al., 2006), mussels (Deriu et al., 2002; Collins et al., 2012), cyanobacteria (Islam et al., 1999), diatoms (Binsztein et al., 2004; Seeligmann et al., 2008), and dinoflagellates (Binsztein et al., 2004; Akselman et al., 2010; Figure 3). The association of *V. cholerae* with zooplankton has been a topic of study since the discovery of cells attached to the surface of copepods in the early 1980s (Huq et al., 1983; Tamplin et al., 1990). Zooplankton are an important part of the aquatic food web, grazing on autotrophic and heterotrophic bacterio-, nano-, and micro-plankton and are in turn preyed upon by larger plankton, such as insect and crustacean larvae and fish. One well-studied interaction is that between *V. cholerae* and chitinous zooplankton, e.g., copepods and cladocerans (Nalin et al., 1979; Huq et al., 1983; Rawlings et al., 2007). For example, pivotal experiments link the transmission of cholera with zooplankton (Huq et al., 1996, 2005; Colwell et al., 2003). In a now classic experiment, the filtration of water through readily available sari cloth reduced *V. cholerae* numbers by 99% (Huq et al., 1996). This method proved to be effective in field trials in reducing the incidence of cholera cases and was continued by villagers as a treatment for drinking water (Colwell et al., 2003; Huq et al., 2010). de Magny et al. (2011) suggested the use of different zooplankter to predict cholera epidemics as they demonstrated that the cladocerans, *Moina* spp. and *Daphnopsis* spp. as well as the rotifer *Brachionus angularis*, were significantly correlated with the presence of *V. cholerae* and with cholera outbreaks. *V. cholerae* has repeatedly been found to be associated with the copepod *Acartia tonsa*, which appears to harbor higher numbers of *V. cholerae* than co-occurring copepods (e.g., Huq et al., 1995; Binsztein et al., 2004; Rawlings et al., 2007; Lizná-Furga et al., 2009, for further information, see Pruzzo et al., 2006).

The predominately attached lifestyle of *V. cholerae* enables it to use many different biotic surfaces as nutrient sources. In addition to degrading chitin, *V. cholerae* has the ability to degrade the egg masses of chironomids (Broza and Halpern, 2001; Halpern et al., 2004). The production of the QS-regulated HAP is necessary for the degradation of the gelatinous matrix of the egg masses (Halpern et al., 2003). Although high numbers of *V. cholerae* were found attached to the egg masses (3.9 × 10⁴ per egg mass; Halpern et al., 2007) 99.5% of the attached cells were other species, e.g., *Acinetobacter*, *Aeromonas*, *Klebsiella*, *Shewanella*, and *Pseudomonas*. These species may benefit from the nutrients that are released by *V. cholerae* as it degrades the egg mass. Alternatively, these species may have a negative impact on *V. cholerae* by expressing bacteriocins or competing for nutrients and space, which may in part explain why the majority of *V. cholerae* on the egg masses, 99.7%, were VBNC (Halpern, 2011). *V. cholerae* has been shown to be associated with chironomids in all four stages of development, from egg to adult (Broza and Halpern, 2001; Halpern et al., 2003; Broza et al., 2005), suggesting these insect eggs and larvae can serve as vectors for the transmission of cholera. Indeed, chironomids that were collected in air 3 km away from a water source...
were found to harbor \textit{V. cholerae} and thus, these midges can carry
the pathogen from one body of water to another (Brouza et al., 2005).
Although no toxigenic serogroups of \textit{V. cholerae} have been
detected in association with chironomids to date, it remains possible
that these could also be associated with chironomids (Halpern, 2011).

The association between \textit{V. cholerae} and phytoplankton has
been well studied (e.g., Tamplin et al., 1990; Lobitz et al., 2000;
Turner et al., 2009). Autotrophic protists, such as diatoms and
dinoflagellates (Binszttein et al., 2004; Eiler et al., 2006), cyanobac-
teria (Islam et al., 1999; Eiler et al., 2007) as well as macroalgae
(Vágia et al., 1997; Haley et al., 2012) support \textit{V. cholerae} growth
(e.g., Vezzulli et al., 2010). Various laboratory and environmen-
tal studies have shown that \textit{V. cholerae} cells attach to microalgae
cells. In a study off the coast of Argentina, Seeligmann et al. (2008)
detected 1–10 VBNC \textit{V. cholerae} cells attached to a single algal cell.
It was suggested that attachment to phytoplankton might enable
\textit{V. cholerae} to survive prolonged exposure in freshwater environ-
ments due to the nutrients and salts excreted by the phytoplankton
cells (Islam et al., 1989; Tamplin et al., 1990; Binsztlein et al., 2004).
Nutrients supplied by phytoplankton, e.g., due to a massive bloom,
can also support explosive growth of \textit{V. cholerae} (Mourino-Pérez
et al., 2003). In fact, remote sensing of chlorophyll a has been
proposed as a method to predict cholera outbreaks (Lobitz et al.,
2000).

Attachment of \textit{V. cholerae} to macroalgae is induced by the
plant-derived polyamine, norspermidine (Hamana and Mas-
suzaki, 1982). Norspermidine is bound by NspS, a periplasmic
2000).

Interestingly \textit{V. cholerae} spp. in their tissue and are
an important niche for these bacteria (e.g., Olafsen et al., 1993;
Mauger et al., 2001; Kirs et al., 2011). Food poisoning resulting
from the ingestion of contaminated raw or undercooked seafood
is a major threat to human health. While infection by \textit{V. vulni-
fera} and \textit{Vibrio parahaemolyticus} from ingestion of seafood are
the most common (Green and Hartwood, 2013), mussels can also
harbor high numbers of \textit{V. cholerae} and thus are a potential health
threat (e.g., Murphee and Tamplin, 1995; Bauer et al., 2006; Haley
et al., 2012).

The bivalve immune system consists of hemocytes (phagocytic
cells) and the hemolymph (i.e., lysozomal enzymes and antimicro-
bial peptides; Motta et al., 2000; Prauszn et al., 2005). In order
to reside in bivalve tissues, bacteria need to survive the antimicro-
bial activity of the hemolymph and engulfment by the hemocytes.
Vibrios are resistant to derapation treatments (Murphee and
Tamplin, 1995) and show resistance toward the hemocytes of the
blue mussel \textit{Mytilus edulis} (Hernroth et al., 2010). Some Vibrios
were able to inhibit filtration in adult \textit{M. edulis}, which was not cor-
related with the binding of the bacteria to the gills of the mussels
(Halpern et al., 2007), suggesting another mechanism is involved.
Interestingly \textit{V. cholerae} strains of different origin have different
retention times in mussels (Collin et al., 2012). An environmental
\textit{V. cholerae} strain isolated from the blue mussel was both taken up
and eliminated much faster than a clinical non-O1/O139 strain.
The clinical strain had a much longer retention time, implying that
pathogenic strains have better fitness in the mussel than environ-
mental strains. This has implications for control measures such as
depuration, as they will be less effective at removing clinical strains
than environmental strains. In addition, Collin et al. (2012) iden-
tified a highly virulent El Tor strain that was not ingested at all,
indicating that Vibrios did not eliminate this pathogenic strain
from the water column. These results highlight the importance of
interaction of \textit{V. cholerae} with other organisms in its environment
and the evolution and selection for virulent strains.

In addition to being incorporated into the benthos by filter
feeders, \textit{V. cholerae} can be isolated from sediments in numbers that
are much higher than in the planktonic phase (Covazzi Harriague
et al., 2008; Vezzulli et al., 2009). Sediments may therefore also
act as a reservoir for cholera, especially in colder months, seeding
the water column when temperatures rise (Vezzulli et al., 2009).
Interestingly, in this study nematodes accounted for the high-
est abundance of the meiofauna, and bacteriivorous nematodes
accounted for 50% of the total. This suggests that Vibrio spp. are
under high grazing pressure and top-down control by these nema-
todes (Vezzulli et al., 2009). In a laboratory study with \textit{C. elegans},
Vitičevcius et al. (2006) showed that \textit{V. cholerae} kills the nematode
after ingestion by secreting the extracellular protease PrtV. Neither
C. elegans nor TCP were required for the killing. Interestingly, PrtV
was also required to prevent grazing by the flagellate \textit{C. neoformen-
sis} and the ciliate \textit{T. pyriformis}. In a \textit{Daphia} strain, the ability to
kill the nematode was strongly diminished. This is in accordance with the role of the QS response regulator, hpR, which is important for grazing resistance in the laboratory (Matz et al., 2005) as well as in the environment (Erken et al., 2011). Thus, V. cholerae has evolved or acquired a number of genetic systems that facilitate its ability to resist top-down control exerted by predatory eukaryotes.

CONCLUSIONS

Vibrio cholerae is a significant pathogen that has played an important role in human history. Its role in the spread of disease and in epidemics has been reported for more than 150 years and the organism has even played an important role in establishing modern epidemiology. While the mechanisms leading to infection and epidemics have been well studied, the ecology and mechanisms that underpin environmental persistence have been less well documented. Interestingly, environmental V. cholerae strains are largely represented by non-toxigenic strains and indeed, environmental strains display a high degree of genetic variability which has been suggested to aid in V. cholerae environmental stress resistance and subsequent persistence. The bacterium has an array of genetic systems involved in stress resistance, when faced with nutrient starvation, iron limitation, or changes in salinity and temperature. One such adaptation is the ability to grow as a biofilm on a range of abiotic and biotic surfaces. This not only increases resistance to stress, but may also directly provide access to nutrients, such as when attached to chitinous surfaces. Biofilm formation has also been directly linked to avoidance of predation by microeukaryotes. Predation resistance can be provided either by physical protection offered by the biofilm, the production of anti-predator compounds or defensive molecules or both. Perhaps not surprisingly, some of the gene systems involved in anti-predator defenses are the same as those associated with virulence during human infection. This may support the co-occidental virulence hypothesis that suggests that virulence factors evolve, at least in part, from the competition between predator and prey rather than against a human host. V. cholerae is a common inhabitant of many marine and freshwater habitats and this is most likely because it has evolved a range of strategies to enable its persistence in the natural environment. The identification and elucidation of these mechanisms, from ecological, evolutionary and molecular perspectives are likely to deliver exciting discoveries for the next 150 years.

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