# Is El Niño a long distance corridor of waterborne disease?

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*A striking observation is the apparent emergence of new and devastating Vibrio diseases into Latin America during significant El Niño events. New advances in microbiological, genomic and bioinformatic tools provides us with the first evidence that El Niño may represent a long-distance corridor of waterborne diseases into the Americas.*

## El Niño and waterborne disease

Many infectious diseases are driven by the subtle interplay between environment, climate and pathogen. Waterborne bacterial pathogens such as vibrios are an excellent example of a group of bacteria that are both restricted and also driven by the physio-chemical limitations placed on their lifestyle by the natural environment. Because this group of bacteria grow in warm (>15ºC), low salinity waters, their presence and subsequent abundance in the environment uncannily mirrors ambient water temperatures. They represent the perfect sentinel species to study the interface between climate and waterborne disease emergence.

El Niño Southern Oscillation (ENSO) is a climate pattern that describes the unusual warming of surface waters along the tropical west coast of South America that causes an extraordinary impact on ocean temperatures, the speed and strength of ocean currents, the health of coastal fisheries, and local weather patterns as well as global climate. El Niño events occur irregularly and are not strictly predictable, but tend to take place every 2–7 years. The role of El Niño in disease emergence has been hotly debated over the last 2 decades. Until recently, however, a paucity of microbiological, genomic and bioinformatic tools coupled to oceanographic and climatic data has prevented a clear evaluation between these events and the emergence of *Vibrio* diseases. We argue here that El Niño events may represent a long distance "biological corridor" for disease emergence between Asia and the Americas, with global ramifications for the study and understanding of waterborne diseases.

## *Vibrio parahaemolyticus* and El Niño events

In 1997, a *Vibrio parahaemolyticus* epidemic emerged in Peru and spread down the Chilean coast, leading to 10,000 cases of enteritis and the decimation of the shellfish industry in the space of a few months[1]. *V. parahaemolyticus* was historically a sporadic pathogen in Peru and Chile, comprised of a variety of different strains and serovars[2], but this outbreak represented a single strain termed the “Pandemic complex” that had arisen in Calcutta in 1996[3]. While the route through which this pandemic complex spread to Peru remains unclear, it is striking that a major El Niño episode coincided with the emergence of this variant into Latin America. Furthermore, the movement of El Niño waters spatiotemporally tracked with the spread of infections along the Western coastline of South America[2] (Figure 1).

In collaboration with the National Institute of Health (Instituto Nacional de Salud, INS) in Peru, we have been systematically characterizing over the last 10 years *Vibrio* strains obtained from clinical and environmental sources in Peru using whole genome sequencing with the aim of identifying new evidence to potentially link populations in Asia and the Pacific coast of South America. High resolution genomic analyses have identified several instances in Peru where new and distinct genetic variants of *Vibrio* have emerged, which had been previously only been identified in Asia. More importantly, these variants have also been identified in environmental sources, which supports not only the arrival of these variants into Latin America, but also their introduction in natural settings where they remained as part of the domestic microbial community. Furthermore, we have been able to identify in a strain from Peru a particular and unique genetic signature only found in strains previously isolated in South East Asia[4], further supporting the role of long-distance translocation as a key factor in disease transmission. Further (yet anecdotal) strands of evidence that support the theory of El Niño and disease emergence include the emergence of shrimp diseases in Latin America following El Niño events in the 1980s and 1990s[5].

## El Niño – A route of transmission for *Vibrio cholerae*?

Cholera had regularly struck Latin America in several discernible waves since the early 1800s; however, it disappeared from the Americas by turn of the 20th century. In 1961, the seventh and still active-cholera pandemic caused by the O1 biotype El Tor began in Indonesia and was confined to Asia until 1970 when it reached Africa and Europe. After almost a century cholera free, the disease re-emerged in the American Continent without warning in the early 1990s. The first case was identified in northern Peru[6], and within weeks had disseminated across South and Central America, eventually causing more than 1,000,000 cases and 10,000 deaths through 1994s[7]. After a resurging of cases during the 1997-98 El Niño even, the epidemic was eradicated from Peru in 2002.

To this day the route of cholera into South America in the early 1990s has been hotly debated, with ballast water introducing strains into surrounding waters, or human sources being two possible explanations[8,9]. And although recent studies have suggested that the introduction of *V. cholerae* into South America may have occurred from Africa by 1981[9], it is still unclear how these strains could have reached Peru and remained undetected for a decade. As the emergence of *V. cholerae* coincided in both time and space with a significant El Niño event in late 1990 and early 1991, we and others have also suggested El Niño may have served as a possible route of this pathogen into the region[10,11], with the unusually heavy rainfall and serious flooding from this even playing a contributory factor in disease transmission.

## Hitching a ride

How might El Niño serve to facilitate such long cross continent transmission? El Niño manifests as a zonal displacement of warm water from the Western to Eastern side of the Pacific Ocean, which has been shown to transport foreign zooplankton populations into Peru and Chile[12]. As the survival and spread of vibrios in the marine environment under adverse conditions has been linked to the ability of these bacteria to attach to plankton[13,14], which form a major component of biomass in the open ocean, it is possible that zooplankton provide a source of nutrients and protection, enabling vibrios to potentially "piggyback." As El Niño can translocate larger organisms, notably exotic Asiatic marine mammals, fish, crustacean and snake species into the Americas, microbial transmission seem also likely. Further studies are clearly needed to elucidate a relationship between El Niño and long-distance transmission.

## The open question of El Niño in disease transmission

There is almost unanimous consensus that the 2015 El Niño may be the most powerful since records started in the early 1950s. An event of this magnitude may offer a valuable opportunity to study the potential introduction of another wave of pathogenic *Vibrio* populations into South America. The use of WGS has been instrumental in using human clinical samples to track the introduction and human spread of *V. cholerae* epidemics[15], but it remains difficult to use only these samples to assess human vs. environmental transmission. For example, sequencing of the recent cholera outbreak in Haiti, suggests that the infection originated from Asia and may have been transmitted through humans, rather than purely environmental in origin. To unambiguously show the connection between El Niño and waterborne disease emergence into Latin America, extensive sampling and sequencing of environmental samples (e.g., in both South American and Asian marine environments, in the open ocean as have been done in the recent TARA study of microbial diversity[16]), with a particular focus on the analysis of zooplankton is required. Furthermore, the selection of *V. parahaemlyticus* as a model organism for assessing the potential role of El Niño in the oceanic dispersion of pathogenic vibrios could provide some advantages over other species. One of the main difficulties for an effective tracking of pathogenic *V. cholerae* is the explosive nature of the outbreaks, and the rapid spread of infections due to the contribution of human transmission through drinking water. However, *V. parahaemolyticus* would offer a more pertinent model for tracing the dispersion of strains across the ocean: *V. parahaemolyticus* is a strictly halophilic organism with a habitat limited to the marine environment and infections are exclusively linked to environmental sources ruling out the confounding role human transmission inherent with cholera. Finally, infections caused by *V. parahaemolyticus* are endemic in Peru, which provides a stable source of strains to identify the introduction of novel genetic variants in the region. The ability to identify pathogenic strains in intermediate sources, such as zooplankton as a potential vehicle for dissemination, or shellfish, that represent a direct route into the human population, at both sides of the El Niño track coupled to phylogenetic reconstructions[9] would provide an even more persuasive strand of evidence that this link exists, and drives waterborne disease emergence.

In conclusion, the positive identification of Asiatic strains of vibrios in South America suggest that regional oceanography conditions provide both a periodic and unique source of new pathogens into Latin America with serious implications for the spread of waterborne infections. While more work will be necessary to validate El Niño’s role in *Vibrio* transmission, it is interesting to speculate that it may also could play roles in other diseases such as waterborne disease of Crustacea. In addition to physical translocation of disease agents, El Niño could mediate other climactic effects on temperature and chemical distribution that intersect with other disease parameters such as vector and host redistribution, physio-chemical stress or availability of nutrients. For example, there is some evidence that increased sea surface temperatures may reduce salinity and aid in *Vibrio* fitness in the Bay of Bengal[9]. These avenues of investigation would be particularly interesting to study in the general context of climate change, as environmental factors are emerging as major contributing factors in the emergence and spread of infectious disease.

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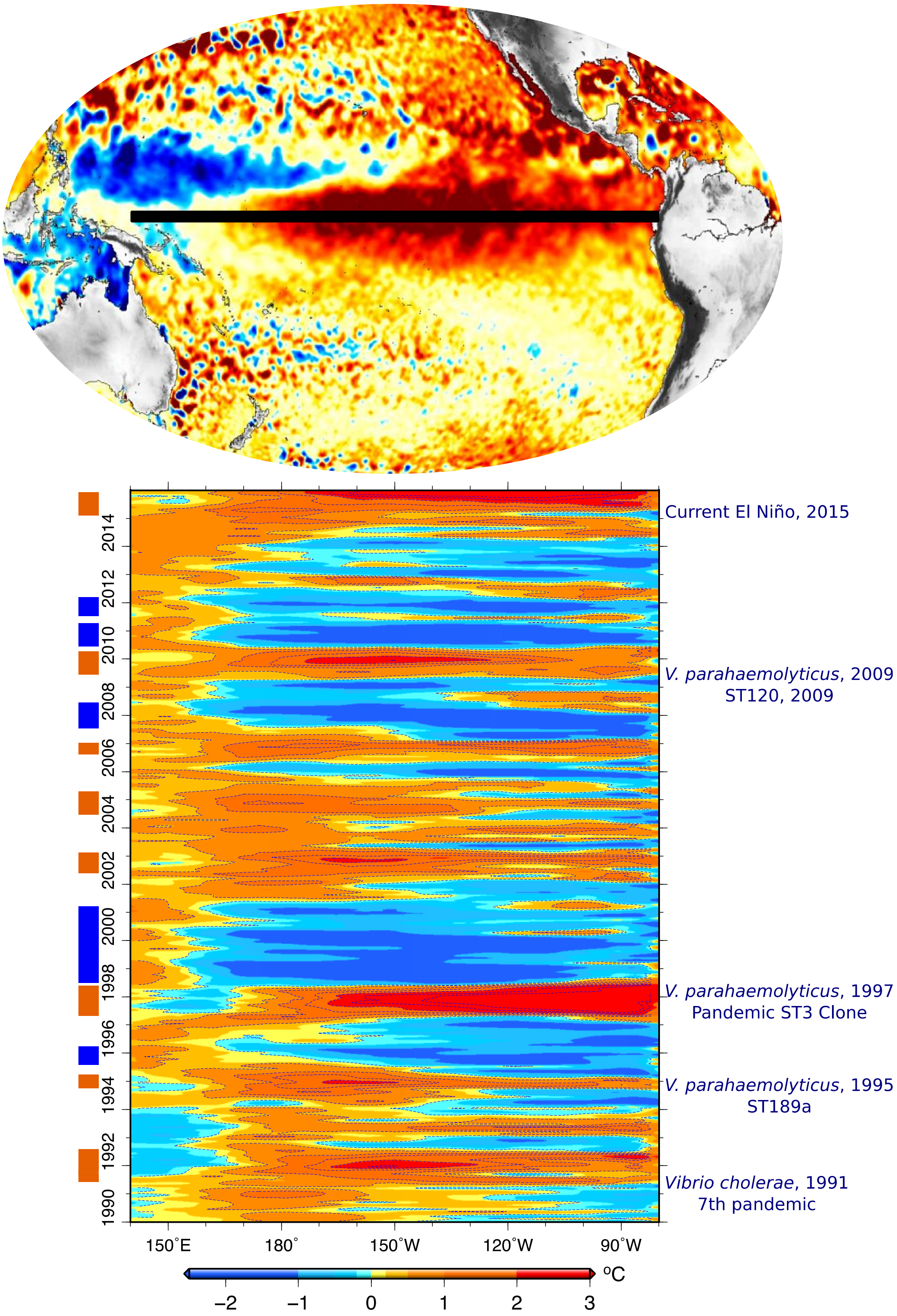

**Figure 1.** El Niño events correlate with water surface temperature rises and emergence of new vibrio infections in South America.