ENVIRONMENTAL CONTROLS ON VIBRIO VULNIFICUS AND OTHER PATHOGENIC VIBRIOS IN TROPICAL AND SUBTROPICAL COASTAL WATERS

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Abstract

The bacterial genus *Vibrio* comprises many species that are pathogens of invertebrate and vertebrate animals, including humans. The goal of this dissertation was to advance the understanding of the physical, chemical, and biological parameters that control the ecology and distribution of several pathogenic vibrio species that commonly cause disease in humans (*V. cholerae*, *V. parahaemolyticus* and *V. vulnificus*). Intensive year-long studies were conducted at two distinct sites where fatal vibrio infections have occurred, but for which data on vibrio ecology has been lacking. The first study was conducted in a subtropical estuarine lake (Lake Pontchartrain, Louisiana, USA) and the second in a tropical estuarine canal (Ala Wai Canal, Honolulu, HI). Correlation and regression analyses indicated that temperature explained most of the variability in vibrio abundance over a seasonal cycle in the subtropical system, but little of the variability in the tropical system. Conversely, salinity showed no correlation with vibrio abundance in the subtropical system, but had a variable effect (positive and negative) in the tropical system. Principle component analysis suggested that the variable influence of salinity is related to the source of freshwater, with slow-flowing groundwater supporting *V. vulnificus* growth better than the fast-flowing fresh water derived from overland runoff. This effect may be an indirect consequence of changing residence time in the canal. In both habitats investigated, more virulent strains of *V. vulnificus* tended to be lower in abundance than less virulent strains and differed in their response to environmental forcing. During the course of these intensive field projects, a novel approach to screening pathogenic vibrios on two selective media
was quantitatively evaluated and found to improve isolation efficiency. In addition, a bacteriophage (Vibrio phage VvAW1) that infects *V. vulnificus* was isolated and its genome was fully sequenced and annotated. The work presented here provides new insights into the physical and biological controls on pathogenic vibrios and lays the groundwork for future efforts to better predict their abundance using coupled biological-physical models. The data suggest that the prediction of the risks of vibrio infection may be improved by considering ecological differences among strains within the species.