Genome-level characterization of environmental and clinical *Vibrio parahaemolyticus* strains from the U. S. Pacific Northwest

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Vibrio parahaemolyticus (Vp) is a gram-negative bacterium indigenous to coastal marine waters worldwide and the leading cause of seafood-borne bacterial gastroenteritis in the United States, Japan and Taiwan. Infections are commonly associated with the consumption of raw or undercooked seafood; and while illness is typically self-limited, life-threatening septic infections can result in patients with underlying immune disorders. The control and prevention of *V. parahaemolyticus* infections is largely based on the screening of water and seafood for the presence or absence of virulence-associated genes such as the thermostable direct hemolysin (*tdh*) and the thermostable-related hemolysin (*trh*). Unfortunately, virulent strains are periodically discovered that elaborate neither hemolysin, suggesting that additional and yet undiscovered virulence factors may play a role in human pathogenesis. Given the importance of *V. parahaemolyticus* to human health and the seafood industry, a more comprehensive suite of virulence factors is needed to safeguard the public from this pathogen. For this purpose, we are using genome-level comparisons (suppressive subtractive hybridization [SSH], virulence locus sequence typing [VLST] and SOLiD pyrosequencing) to assay genetic variation between environmental and clinical Vp strains (originating from the Pacific Northwest, U. S.).

Once the specific genes and allelic variants of pathogenesis are determined, new virulence gene-specific assays will be developed for the improved detection of virulent Vp strains in environmental samples. Further, these new virulence gene assays will be integrated on *in situ* biosensor platforms for the development of improved disease forecasting and risk assessment. Additionally, knowledge of genome-level variations among environmental and clinical strains will be used to examine the hypothesis that physio chemical parameters (unique to the Pacific Northwest) have selected for the emergence of an endemic and highly virulent Vp clonal complex.