*Vibrio* bacteria are Gram negative, motile organisms that occur naturally in most coastal and estuarine ecosystems. Some vibrios are important human pathogens, including *Vibrio parahaemolyticus* and *Vibrio vulnificus*. The CDC estimates that these two species cause 80,000 cases of disease (vibriosis) each year in the United States. Most cases are caused by *V. parahaemolyticus*, which infects humans after the consumption of contaminated raw or undercooked seafood, primarily oysters. *V. parahaemolyticus* causes mild gastroenteritis that is self-limiting unless the patient is immunocompromised. *V. vulnificus* has a much lower incidence of disease (100 cases in the USA yr\(^{-1}\)); however, this organism causes much more severe infections, including necrotizing fasciitis (flesh eating disease) and sepsis when introduced into an open wound. With global climate change, *Vibrio* outbreaks are expanding in size, frequency, and latitude. This investigation examined the reliability of using “species specific” marker genes to identify a *Vibrio* strain, the distribution of pathogenicity islands (PAIs) within *Vibrio* genomes, and the distributions of potential pathogenic *V. parahaemolyticus* within oysters and oyster tissues. We determined that some oysters, designated as “hot” oysters, can harbor significantly more vibrios than surrounding oysters. These “hot” oysters, which occur at low frequency, may explain the sporadic (and difficult to predict) nature of *V. parahaemolyticus* infections. The cytotoxic effects of environmental *Vibrio* strains and the interactions of vibrios with various marine microalgae were also studied.