Population genetic structure of *Vibrio parahaemolyticus* in New Hampshire's Great Bay Estuary

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Abstract (extended ASM format, to be expanded)

Vibrio parahaemolyticus (Vp) is a natural resident of estuaries that is commonly associated with shellfish but whose ecological role remains poorly understood. A subset of this species causes severe inflammatory gastroenteritis and wound infections and is one of the leading causes of foodborne illness worldwide. Reports of such disease are growing in part because of increased human contact with Vp, but a potentially greater contributor is environmental change (increased temperature and rainfall) that could favor greater prevalence of pathogenic strains in coastal waters. In warmer waters, most infections in have been linked to the O3:K6 pandemic lineage, but infections in colder waters have been caused by distinct bacteria of unique genetic composition. To characterize these northern populations we collected >200 isolates of Vp from 2007-2009 from oysters, sediment, and overlying waters from the Great Bay Estuary near Durham, NH. Collection occurred at two sites known to vary in salinity and water quality. We subjected each isolate to a novel two-phase multi-locus sequence typing (MLST) scheme involving seven well-characterized housekeeping genes (*dnaE, dtdS, gyrB, pntA, pyrH, recA,* and *tnaA*) and three genes known to be associated with pathogenicity (*varA*, *toxR*, and *vppC*). We hypothesized that the latter genes would be more diverse owing to more variable selection on their functions and the former genes would be less diverse because they are essential for survival. Surprisingly, we found the opposite: housekeeping genes were more diverse (nucleotide diversity, π, ranging from 0.011 to 0.022) and yielded more unique sequence types (>85% of isolates were unique). In contrast, alleles of virulence genes were less diverse (π: 0.005 to 0.009) and defined fewer unique sequence types (63%). These patterns may reflect a legacy of past recombination associated with directional or purifying selection that homogenized virulence-associated genes amidst a diverse backdrop of distinct Vp lineages. The exceptional diversity of these isolates did not associate with any particular physical variable but nevertheless revealed a continuing history of genetic exchange that could facilitate the emergence of novel lineages in response to changing environmental conditions.