



Populations, not clones, are the unit of vibrio pathogenesis in naturally infected oysters

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Résumé en anglais	<p>Disease in oysters has been steadily rising over the past decade, threatening the long-term survival of commercial and natural stocks. Our understanding and management of such diseases are of critical importance as aquaculture is an important aspect of dealing with the approaching worldwide food shortage. Although some bacteria of the <i>Vibrio</i> genus isolated from diseased oysters have been demonstrated to be pathogenic by experimental infection, direct causality has not been established. Little is known about the dynamics of how the bacterial population hosted by oysters changes during disease progression. Combining experimental ecology, a high-throughput infection assay and genome sequencing, we show that the onset of disease in oysters is associated with progressive replacement of diverse benign colonizers by members of a phylogenetically coherent virulent population. Although the virulent population is genetically diverse, all members of that population can cause disease. Comparative genomics across virulent and nonvirulent populations identified candidate virulence factors that were clustered in population-specific genomic regions. Genetic analyses revealed that one gene for a candidate virulent factor, a putative outer membrane protein, is necessary for infection of oysters. Finally, analyses of oyster mortality following experimental infection suggest that disease onset can be facilitated by the presence of nonvirulent strains. This is a new form of polymicrobial disease, in which nonpathogenic strains contribute to increase mortality.</p>

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Liens

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