



A single regulatory gene is sufficient to alter *Vibrio aestuarianus* pathogenicity in oysters

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Titre	A single regulatory gene is sufficient to alter <i>Vibrio aestuarianus</i> pathogenicity in oysters
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Résumé en anglais	<p>Oyster diseases caused by pathogenic vibrios pose a major challenge to the sustainability of oyster farming. In France, since 2012 a disease affecting specifically adult oysters has been associated with the presence of <i>Vibrio aestuarianus</i>. Here, by combining genome comparison, phylogenetic analyses and high-throughput infections of strains isolated before or during the recent outbreaks, we show that virulent strains cluster into two <i>V. aestuarianus</i> lineages independently of the sampling dates. The bacterial lethal dose was not different between strains isolated before or after 2012. Hence, the emergence of a new highly virulent clonal strain is unlikely. Each lineage comprises nearly identical strains, the majority of them being virulent, suggesting that within these phylogenetically coherent virulent lineages a few strains have lost their pathogenicity. Comparative genomics allowed the identification of a single frameshift in a non-virulent strain. This mutation affects the <i>varS</i> gene that codes for a signal transduction histidine-protein kinase. Genetic analyses confirmed that <i>varS</i> is necessary for infection of oysters and for a secreted metalloprotease expression. For the first time in a <i>Vibrio</i> species, we show here that <i>VarS</i> is a key factor of pathogenicity.</p>
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Liens

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- [2] <http://okina.univ-angers.fr/publications?f%5Bauthor%5D=35378>
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