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Pathogenic mechanism and life cycle of a marine bacterium *Vibrio parahaemolyticus*

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Vibrio parahaemolyticus, a Gram-negative marine bacterium, is a worldwide cause of food-borne gastroenteritis. Our genome sequencing of a clinical *V. parahaemolyticus* strain RIMD2210633 (Lancet 361: 743-749, 2003) identified two sets of genes for the Type III secretion system (TTSS), TTSS1 and TTSS2. Construction of a series of mutant strains and comparative genomic hybridization with a microarray revealed that both the TTSSs function as secretion systems, and may have a role in pathogenicity of the organism. The presence of TTSS1 apparatus gene homologues was demonstrated in non-pathogenic *V. parahaemolyticus* and other vibrios such as *V. alginolyticus*, *V. harveyi* and *V. tubiashii*. Since the TTSS is a bacterial tool to intimately interact with eukaryotic cells, the results suggest that those vibrios may have a stage/phase in which they intimately interact with certain (but unknown) eukaryotic cells in their life cycle in natural environment.

