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| | Sommario/riassunto | Vibrio parahaemolyticus is a gram negative, halophilic bacterium that occurs in the coastal and estuarine environments worldwide and is implicated in several cases of seafood-born gastroenteritis around the globe. However, not all strains of V. parahaemolyticus are pathogenic. Clinical isolates of V. parahaemolyticus most often produce either the thermostable direct haemolysin (TDH) or TDH-related haemolysin (TRH) encoded by tdh and trh genes, respectively. A pandemic clone of O3:K6 which was first detected in Kolkata (India), has been responsible for many outbreaks in Asia and the USA. With the emergence of pandemic clone of V. parahaemolyticus, this organism has assumed significance. Although most of the V. parahaemolyticus outbreaks are invariably related to seafood consumption, pathogenic strains are rarely isolated from seafood. Virulent strains producing TDH or TRH and the pandemic clone, which is responsible for most of the outbreaks (that have occurred after 1996) have been rarely isolated from seafood and other environmental samples. This could be due to the occurrence of pathogenic strains in the estuarine environment at a lower level compared to non-pathogenic strains. Another reason can be that the pathogenic stains are more sensitive to dystropic conditions in the aquatic environment and rapidly become non-culturable. Similarity in growth kinetics between virulent and non-virulent strains also made the isolation of virulent strains from the aquatic environment difficult. Several studies were done to determine the factors responsible for an |

increased virulence and persistance of pandemic clone. However, none of those studies were conclusive. Several researchers have proposed various genetic markers for specific detection of pandemic clone of V. parahaemolyticus. But many of those genetic markers were found to be unreliable. Recently, seven genomic islands (VPaI-1 to VPaI-7) unique to pandemic clone were identified. This Research Topic is dedicated to improve our current understanding of ecology, pathogenesis and detection of pathogenic and pandemic clone of V. parahaemolyticus, and will also strive to identify areas of future development.