

# Genomic and evolutionary features of nine AHPND positive *Vibrio parahaemolyticus* strains isolated from South American shrimp.

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## Abstract

*Vibrio parahaemolyticus* is a bacterial pathogen that when acquiring the pVA1-Type plasmid carrying the *pirAB*<sup>VP</sup> genes become lethal to *Penaeus* shrimps, causing Acute Hepatopancreatic Necrosis Disease (AHPND). This disease causes significant losses in the shrimp industry across the world, with outbreaks reported in Southeast Asia, Mexico and, more recently, South America. Virulence level and mortality differences have been reported in challenges tests with *V. parahaemolyticus* isolates from different locations, and whether this phenomenon is caused by plasmid related elements or genomic related elements from the bacteria remains unclear. In this project, nine genomes of South American *V. parahaemolyticus* isolates were assembled and analyzed using a comparative genomics approach, and then included for a phylogenomic analysis with another 87 strains. The results of these analyses indicated that all nine isolates contained plasmids with the characteristic Mexican-like origin, while phylogenomic analysis showed wide diversity clustering them with Asian and American isolates.. Furthermore, although all genomes were highly similar, two groups of genomes: (1) BA110 and BA37P5, (2) BA94C2, LH47-1, LH49 and LH53-1, could be clustered together by outstanding similarities that the members of the group presented between them with respect to the rest of the genomes. In depth analyses of these similarities were carried out at (i) whole-genome, (ii) secretion system oriented, and (iii) plasmid oriented level, and lead to the identification of genomic elements associated with the disease that varied among the different isolates in patterns that might be insightful for the understanding of the disease.

**Keywords:** AHPND, secretion systems, virulence factors, *V. parahaemolyticus*, shrimp