

Exploring the genomic traits of non-toxigenic *Vibrio parahaemolyticus* strains isolated in southern Chile

Castillo D.

Pérez-Reytor D.

Plaza N.

Ramírez-Araya S.

Blondel C.J.

Corsini G.

Bastías R.

Loyola D.E.

Jaña V.

Pavez L.

García K.

Vibrio parahaemolyticus is the leading cause of seafood-borne gastroenteritis worldwide. As reported in other countries, after the rise and fall of the pandemic strain in Chile, other post-pandemic strains have been associated with clinical cases, including strains lacking the major toxins TDH and TRH. Since the presence or absence of *tdh* and *trh* genes has been used for diagnostic purposes and as a proxy of the virulence of *V. parahaemolyticus* isolates, the understanding of virulence in *V. parahaemolyticus* strains lacking toxins is essential to detect these strains present in water and marine products to avoid possible food-borne infection. In this study, we characterized the genome of four environmental and two clinical non-toxigenic strains (*tdh*-, *trh*-, and T3SS2-). Using whole-genome sequencing, phylogenetic, and comparative genome analysis, we identified the core and pan-genome of *V. parahaemolyticus* of strains of southern Chile. The phylogenetic tree based on the core genome showed low genetic diversity but the analysis of the pan-genome revealed that all strains harbored genomic islands carrying diverse virulence and fitness factors or prophage-like elements that encode toxins like Zot and RTX. Interestingly, the

three strains carrying Zot-like toxin have a different sequence, although the alignment showed some conserved areas with the zot sequence found in *V. cholerae*. In addition, we identified an unexpected diversity in the genetic architecture of the T3SS1 gene cluster and the presence of the T3SS2 gene cluster in a non-pandemic environmental strain. Our study sheds light on the diversity of *V. parahaemolyticus* strains from the southern Pacific which increases our current knowledge regarding the global diversity of this organism. © 2018 Castillo, Pérez-Reytor, Plaza, Ramírez-Araya, Blondel, Corsini, Bastías, Loyola, Jaña, Pavez, and Garcia.

Accessory genome

Genomic island

Non-toxigenic

Prophage

RTX

Vibrio parahaemolyticus

Virulence

Zot

amino acid sequence

antibiotic resistance

Article

Caco-2 cell line

comparative genomic hybridization

cytotoxicity assay

DNA extraction

gastroenteritis

gene cluster

genetic variability

genome analysis

multiplex polymerase chain reaction

nonhuman

phylogenetic tree

phylogeny

sequence alignment

toxicity

Vibrio parahaemolyticus

whole genome sequencing