

# Pathogenicity island region of clinical and environmental strains of *Vibrio parahaemolyticus*, isolated in Chile

## Isla de patogenicidad de *Vibrio parahaemolyticus* en cepas chilenas clínicas y ambientales

Núñez, Harold

Ulloa, María Teresa

Guerra, Fabiola

Osorio, Carlos G.

**Background:** Most clinical isolates of *Vibrio parahaemolyticus* produce a major virulence factor known as the thermostable direct hemolysin (TDH). TDH is encoded by the *tdh* gene which is located in a genomic pathogenicity island (PAI). Most environmental isolates are described as *tdh* negative. **Aim:** To assess if environmental strains lack the full pathogenicity island or if only the *tdh* gene is deleted. **Material and methods:** Thirty eight clinical and 66 environmental strains of *Vibrio parahaemolyticus* were studied. PAI was characterized by polymerase chain reaction (PCR). The presence of *tdhA* and *tdhS* genes, was determined by Southern blot. **Results:** Fifty three environmental strains (80%) lacked a full PAI when compared with clinical strains. In environmental strains, Southern blot and sequence analysis showed that a genetic region of 80 kilobase pairs including genes from VPA1310 to VPA1396 was missing. **Conclusions:** These results highlight the genetic dynamism of *Vibrio parahaemolyticus*