Analysis of the Zonula occludens Toxin Found in the Genome of the Chilean Non-toxigenic Vibrio parahaemolyticus Strain PMC53.7

Pérez-Reytor, D.
Pavón, A.
Lopez-Joven, C.
Ramírez-Araya, S.
Peña-Varas, C.
Plaza, N.
Alegría-Arcos, M.
Corsini, G.
Jaña, V.
Pavez, L.
del Pozo, T.
Bastías, R.
Blondel, C.J.
Ramírez, D.
García, K.

Abstract
Vibrio parahaemolyticus non-toxigenic strains are responsible for about 10% of acute gastroenteritis associated with this species, suggesting they harbor unique virulence factors. Zonula occludens toxin (Zot), firstly described in Vibrio cholerae, is a secreted toxin that increases intestinal permeability. Recently, we identified Zot-encoding genes in the genomes of highly cytotoxic Chilean V. parahaemolyticus strains, including the non-toxigenic clinical strain PMC53.7. To gain insights into a possible role of Zot in V. parahaemolyticus, we analyzed whether it could be responsible for cytotoxicity. However, we observed a barely positive correlation between Caco-2 cell membrane damage and Zot mRNA expression during PMC53.7 infection and non-cytotoxicity induction in response to purified PMC53.7-Zot. Unusually, we observed a particular actin disturbance on cells infected with PMC53.7. Based on this observation, we decided to compare the sequence of PMC53.7-Zot with Zot of human pathogenic species such as V. cholerae, Campylobacter concisus, Neisseria meningitidis, and other V. parahaemolyticus strains, using computational tools. The PMC53.7-Zot was compared with other toxins and identified as an endotoxin with conserved motifs in the N-terminus and a variable C-terminal region and without FCIGRL peptide. Notably, the C-terminal diversity among Zots meant that not all of them could be identified as toxins. Structurally, PMC53.7-Zot was modeled as a transmembrane protein. Our results suggested that it has partial 3D structure similarity with V. cholerae-Zot. Probably, the PMC53.7-Zot would affect the actin cytoskeletal, but, in the absence of FCIGRL, the mechanisms of actions must be elucidated.

Author keywords
Campylobacter concisus
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