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Title:	Current Perspective on the Membrane-Damaging Action of Thermostable Direct Hemolysin, an Atypical Bacterial Pore-forming Toxin
Authors:	Verma, Pratima (/jspui/browse?type=author&value=Verma%2C+Pratima) Chattopadhyay, Kausik (/jspui/browse?type=author&value=Chattopadhyay%2C+Kausik)
Keywords:	Perspective Membrane-Damaging Thermostable Direct Hemolysin
Issue Date:	2021
Publisher:	Frontiers
Citation:	Frontiers in Molecular Biosciences, 8.
Abstract:	Thermostable direct hemolysin (TDH) is the major virulence determinant of the gastroenteric bacterial pathogen <i>Vibrio parahaemolyticus</i> . TDH is a membrane-damaging pore-forming toxin (PFT). TDH shares remarkable structural similarity with the actinoporin family of eukaryotic PFTs produced by the sea anemones. Unlike most of the PFTs, it exists as tetramer in solution, and such assembly state is crucial for its functionality. Although the structure of the tetrameric assembly of TDH in solution is known, membrane pore structure is not available yet. Also, the specific membrane-interaction mechanisms of TDH, and the exact role of any receptor(s) in such process, still remain unclear. In this mini review, we discuss some of the unique structural and physicochemical properties of TDH, and their implications for the membrane-damaging action of the toxin. We also present our current understanding regarding the membrane pore-formation mechanism of this atypical bacterial PFT.
Description:	Only IISER Mohali authors are available in the record
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