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| Title: | Exploring unique structural motifs in Vibrio parahaemolyticus Thermostable Direct Hemolysin |
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| Abstract: | Seafood borne bacterial gastroenteritis is majorly caused by PFT secreted by Vibrio parahaemolyticus. Pore-forming Toxins (PFTs) are predominantly water-soluble monomers, which oligomerize upon interacting with target cells whereas thermostable direct hemolysin (TDH) is an atypical PFT secreted by V.parahaemolyticus which oligomerizes and forms tetramer in solution before interacting with target cells. This protein also manifest an inconsistent phenomenon to heat treatment known as Arrhenius effect as it denatures and then starts renaturing to its tertiary structure as we go to higher temperature. TDH shows core β- sandwich structural similarities with eukaryotic actinoporin family of PFTs. With high structural similarities and very low sequence similarities there are some conserved residues within these eukaryotic actinoporins and TDH. These residues in TDH plays a critical functional role by interacting with neighboring residues and forming bonds. Our studies show how mutating these residues caused no structural changes however compromises the hemolytic activity as well as reduce binding to the membrane. Thus showing the importance of these residues at those particular sites. By this study we can find out critical residues involved in binding and insertion of TDH on and into the membrane. All these results will give us a critical insights into the pore formation mechanism of TDH. |
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