Title:	Skip Nav Destination Article|October 07 2021 Single-particle cryo-EM reveals conformational variability of the oligomeric VCC β-barrel pore in a lipid bilayer
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Abstract:	Vibrio cholerae cytolysin (VCC) is a water-soluble, membrane-damaging, pore-forming toxin (PFT) secreted by pathogenic V. cholerae, which causes eukaryotic cell death by altering the plasma membrane permeability. VCC self-assembles on the cell surface and undergoes a dramatic conformational change from prepore to heptameric pore structure. Over the past few years, several high-resolution structures of detergent-solubilized PFTs have been characterized. However, high-resolution structural characterization of small β-PFTs in a lipid environment is still rare. Therefore, we used single-particle cryo-EM to characterize the structure of the VCC oligomer in large unilamellar vesicles, which is the first atomic-resolution cryo-EM structure of VCC. From our study, we were able to provide the first documented visualization of the rim domain amino acid residues of VCC interacting with lipid membrane. Furthermore, cryo-EM characterization of lipid bilayer–embedded VCC suggests interesting conformational variabilities, especially in the transmembrane channel, which could have a potential impact on the pore architecture and assist us in understanding the pore formation mechanism.
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