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Mechanism of bacterial membrane poration by Antimicrobial Peptides ANKITA ARORA, ABHIJIT MISHRA, Materials Science & Engineering, Indian Institute of Technology, Gandhinagar, India — Bacterial resistance to conventional antibiotics is a major health concern. Antimicrobial peptides (AMPs), an important component of mammalian immune system, are thought to utilize non-specific interactions to target common features on the outer membranes of pathogens; hence development of resistance to such AMPs may be less pronounced. Most AMPs are amphiphilic and cationic in nature. Most AMPs form pores in the bacterial membranes causing them to lyse, however, the exact mechanism is unknown. Here, we study the AMP CHRG01 (KSSTRGRKSSRRKK), derived from human β defensin 3 (hBD3) with all Cysteine residues substituted with Serine. Circular Dichorism studies indicate that CHRG01 shows helicity and there is change in helicity as it interacts with the lipid membrane. The AMP was effective against different species of bacteria. Leakage of cellular components from bacterial cells observed by SEM and AFM indicates AMP action by pore formation. Confocal microscopy studies on giant vesicles incubated with AMP confirm poration. The effect of this AMP on model bacterial membranes is characterized using Small Angle X-ray scattering and Fluorescence spectroscopy to elucidate the mechanism behind antimicrobial activity.

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