## Abstract

In the present day scenario, tackling multi-drug resistant organisms has become quite challenging. Escalating rate of resistance and slow discovery of antibiotics has brought us back to pre-antibiotic period. Therefore, it has become utmost important to design new antimicrobials that can efficiently kill microbes and has less chances of acquiring resistance. Antimicrobial peptides (AMPs) hold promise to be one such molecules that can ward-off a broad range of invading microrganisms without instigating any toxic effect to the host cells. AMPs possess distinctive characteristics such as amphipathicity and cationicity, which helps them to interact with the microbial membrane. We explored the shorter peptide fragments from membrane-binding stretches of bacterial proteins. Studies were conducted on peptides derived from *E. coli* membrane binding protein MreB, and FtsA. In addition to that, we investigated the activity of another shorter peptide $LCI_{22\text{-}47}$ from the C-terminal region of *B. subtilis* AMP LCI. All the peptides were found to be very effective against both Gram-positive bacteria, Gram-negative bacteria, *M. smegmatis*, and fungus as well. Moreover, membrane binding studies have also shown peptides ability to interact and permeabilize the bacterial outer and inner membranes. Majority of the peptides retained their activity in the presence of salts and divalent cations without instigating any toxicity to mammalian erythrocytes. Therefore, development of membrane-perturbing AMPs from the membrane-binding stretches of microbial proteins, could be an excellent strategy to combat microbes. Smaller peptide fragment from bacterial antimicrobial peptide could be developed into potent antimicrobial agent without loss in its activity. Moreover, self-like sequence may elude the possibility of enzymatic degradation by the bacteria.