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POS-27 - ^{2}H NMR studies of bacterial membrane perturbation by antimicrobial polypeptides

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Small amphipathic polypeptides that can reduce the viability of bacterial cells are known as antimicrobial polypeptides (AMPs). Permeabilization of lipid bilayers by AMPs has been previously investigated in model lipid systems that mimic aspects of bacterial membrane composition. Model studies, however, do not address the possibility that polypeptide antimicrobial activity might also involve the disruption of non-membrane targets or might be enhanced by interaction with non-membrane cell components. In order to learn how AMPs interact with more complex structures within real bacterial cell envelopes, we have deuterium-labeled membranes of the gram positive bacteria *Bacillus subtilis* and have used ^{2}H NMR to study how lipid acyl chain orientational order in the membranes of these bacteria is affected by the presence of specific AMPs. In the absence of AMP, the ^{2}H NMR spectrum of the labeled bacterial membrane is a superposition of doublets characteristic of fast axially symmetric chain reorientation. Prominent shoulders, at +/-12 kHz, reflect an order parameter profile having a plateau near the headgroup end of the chain. In the presence of CAME (a hybrid of cecropin and melattin), intensity shifts from the plateau spectral region to smaller quadrupole splittings suggesting a peptide-induced disordering of the bacterial membrane. Spectra have also been obtained from deuterated *B. subtilis* in which the peptidoglycan layer has been disrupted using lysozyme. The capacity to observe such spectra will facilitate studies of how the bacterial peptidoglycan layer affects AMP perturbation of the *B. subtilis* membrane. Supported by NSERC and Colciencias-Colfuturo.

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