Anti-microbial protein/membrane interactions – nature's super-drugs?

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Abstract

The rapid adaptation of bacteria to traditional antibiotics means that a number of drug-resistant strains exist which pose as serious public health concerns. Antimicrobial proteins (AMPs) exist widely throughout nature, and protect organisms from microbial infection by destroying a broad range of pathogens. Consequently they provide potential for the development of new antibiotics. However, although it is known that AMPs destroy pathogens by permeabilising the microbial membrane, very few details of this membrane-protein interaction exist.

Two potent antimicrobial proteins, amoebapore-A and Hydramacin-1 (shown in their putative active forms, below), are exemplars of AMPS that are thought to work through different membrane disruption methods, A powerful combination of neutron and X-ray scattering and NMR spectroscopy has been applied to AMP-model membrane complexes to elucidate the . The molecular sensitivity of these two methods, not otherwise accessible, provides information on the changes in membrane structure and function driven by protein association. These measurements enable the validity of competing proposed models for AMP activity to be assessed, and lay the groundwork for understanding how AMPs function generally.