The binding of designed short α-helix peptides with model lipid monolayers at the air/water interface

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Abstract

Increase of antibacterial resistance to antibiotics has led to huge demand for developing new antibacterial agents with different mechanisms of action. Many natural antimicrobial peptides (AMPs) can disrupt bacterial membranes and kill them without causing resistance. Extensive studies have been undertaken to search for novel AMPs from various origins and sources (from plants, insects, mammals and extremophiles from deep seas), develop biomimetic versions and evolve their membrane selective actions and targeting [1,2]. Over the past 10 years or so, we have developed a series of rationally designed peptides. Their general sequence of peptides is $G(IIKK)_nI\text{-}NH_2$, with n- the number of coils of α-helix (n=2-4, denoted as G2, G3 and G4)[3]. These peptides show better efficacies than most known peptides. In addition, they are benign to mammalian cell hosts, exhibiting high mildness or biocompatibility. To help understand their membrane lytic actions and selective responses, we have developed lipid monolayer models using Langmuir film technique and characterized how our peptides interact with model G+, G- and red blood cell monolayer models consisting of 1, 2 and 3 membrane components.

Hence in the first part of the project we recorded pressure-area isotherms for the model monolayers with 1, 2 and 3 components. So far we observed that the peptide induces an increase in the surface pressure of the model monolayer, and that the extent of pressure increase was affected by the initial pressure, and the lipid composition of the monolayer. The exact molecular mechanism of interaction is not known yet, but from preliminary results, i.e. pressure recordings as well as Brewster angle microscopy images, we noticed that the peptide exhibited a clear preference to the negatively charged DPPG and DOPG; and that it also had more influence on the unsaturated DOPC and DOPG monolayers.

References:

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