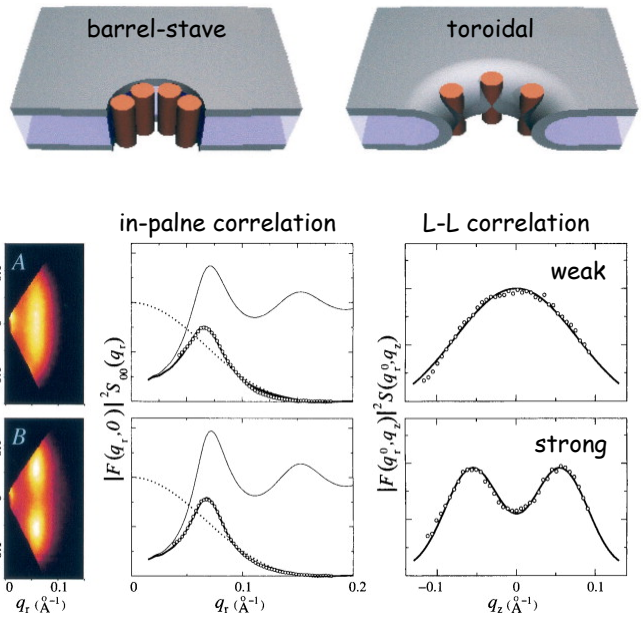
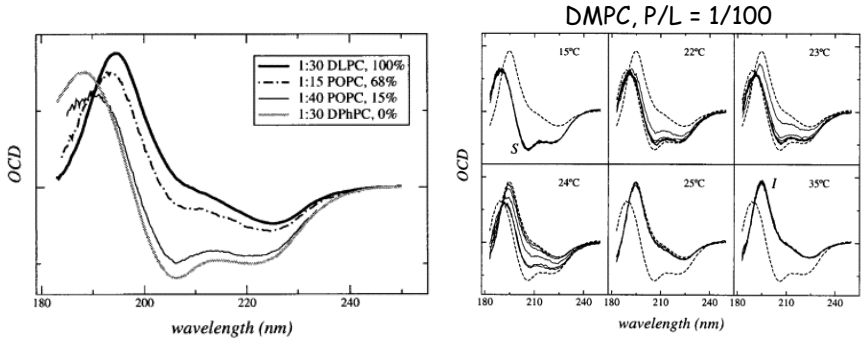
Trans-membrane pores formed by antimicrobial peptide melittin

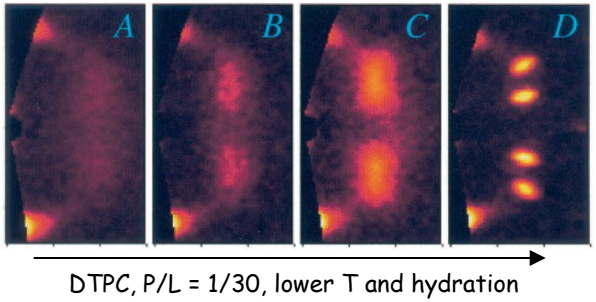
Motivation: Many naturally occurring antimicrobial peptides and toxins are believed to achieve their activity by forming pores in cellular membranes. But different peptides apparently form pores of different architectures (barrel-stave type vs. toroidal type). Oriented circular dichroism (OCD) and neutron scattering were used to characterize the structure of pores formed by melittin, a major component of bee venom.



Key result 2: Analysis of neutron scattering data showed the presence of in-plane density contrast (peptide pores) and different levels of layer-to-layer correlation between the pores in adjacent membranes.



Key result 1: OCD results show melittin insert in to membranes (perpendicular to membrane) at high peptide concentration (P/L). Peptide insertion also systematically depends on the type of lipid membrane, sample temperature and hydration. Pores are detected by neutron scattering when the peptides are dominantly in the inserted state.



Key result 3: Manipulation of sample temperature and hydration can lead to systematic increase in the correlation between pores in adjacent layers and the eventual formation of crystal-like structures, as indicated by the sharp diffraction peaks.

Conclusions and significance: This publication is a demonstration how OCD and neutron scattering can be used to provide a comprehensive characterization of the structure of pores formed by membrane active peptides. The general pore-forming behavior of melittin (orientation transition of peptides and pore size) suggest toroidal type pores rather than barrel-stave type. The possibility of producing crystal-like lattice of pores opens up the possibility to use X-ray diffraction to determine the pore structure.

Barrel-Stave Model or Toroidal Model? A Case Study on Melittin Pores L. Yang et.al. BIOPHYSICAL JOURNAL 2001