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.

**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.

**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 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 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.

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