

FLUCTUATING MEMBRANE PORES - A POSSIBLE MECHANISM FOR THE ACTION OF THE ANTIBIOTIC PEPTIDE KLA1

D. KIM¹, M. DATHE², S. BEZRUKOV³, TH. HAUSS⁴, S. DANTE⁴
and BEATE KLÖSGEN¹

¹University of Southern Denmark, Phys Dept. and MEMPHYS – Center for Biomembrane Physics, Odense, Denmark, ²Institute of Molecular Pharmacology, Berlin, Germany, ³Section on Molecular Transport (LPSB-SMT), NICHD, Bethesda, MD, USA, ⁴Hahn-Meitner Institute, Berlin, Germany

Antimicrobial peptides constitute the first natural line of defense against pathogens in animals and plants. During the last decade, thousands of these AMPs have been isolated from their natural sources or designed *de novo* with the goal of creating another generation of antibiotics to counter increasingly resistant bacteria. The effect of a synthetic antimicrobial peptide, KLA1, on a lipid model bilayer was studied by a combination of methods including cryo-TEM, SANS, conductivity experiments, and micromechanical deformation studies by micropipet aspiration. Experiments were done on small unilamellar vesicles (SUVs), planar membrane stacks, black lipid membranes (BLMs), and giant unilamellar vesicles (GUVs). Results are presented and discussed with respect of different models for membrane lysis induction. Our system seems to represent an example for the toroidal pore model that involves the spontaneous formation of transitory membrane holes. Such pores fluctuate, and their formation and stability are governed by local defect induced modulations of the elsewhere continuous bending elastic properties of the membrane. Neutron diffraction studies with deuterated peptides will hopefully report on the detailed position of the peptide in its target membrane.