IMAGING BIOACTIVE PEPTIDES WITH MODEL MEMBRANES

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Membrane-active peptides like antimicrobial peptides (AMPs) interact with membranes by different mechanisms. Several models exist to explain their activity mechanisms [1]. Shared, decisive steps in these models seem to be the attachment of single peptides to the membrane lipids driven by electrostatic forces and the subsequent aggregation of several peptides sometimes leading to a pore formation.

To analyze peptide binding and mobility within biological model membranes we generated both giant unilamellar vesicles (GUVs) and planar supported lipid bilayers (SLBs) on glass surfaces. Translocation of peptides and tracer molecules was measured by optical sectioning microscopy in the GUV equatorial plane. Using high-speed, single-molecule fluorescence microscopy and tracking we determined the dynamics of fluorescently labelled molecules in bilayers [2]. Comparing the dynamics of fluorescently labelled lipid tracer molecules within membranes and fluorescently labelled peptides within and on model membranes allows conclusions about the interaction dynamics and peptide translocation mechanisms as demonstrated for the case of the TAT peptide [3,4].

We investigated two AMPs which possess diverse membrane interaction mechanisms. LL-37 is an antimicrobial peptide isolated from human. Differences in lipid structure and molecular topology were shown to have an influence on peptide-lipid interaction [5]. Here we present an analysis of LL-37 membrane activity as a function of the lipid composition. The lantibiotic nisin targets with high affinity a special component of the bacterial membrane in various gram-positive bacteria. This peptide-lipid interaction leads to the formation of a membrane spanning pore [6]. We visualize how this stimulating interaction factor influences nisin translocation.