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Elucidating the mode of action of antimicrobial peptides using small-angle X-ray and neutron scattering techniques: the lipids point of view

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It is generally believed that antimicrobial peptides, AMPs, are able to evade much of the bacterial resistance because they disturb the fundamental integrity of the entire cell by interfering with the life-defining cell membrane. However, there is no clear general consensus for the molecular basis by which AMPs act, although various structural modifications such as membrane deformation or pore formation have been suggested. [1,2] However, other factors may contribute such as changes in the lipid dynamics, changes in the lateral and transversal lipid composition and enhanced proton/ion transfer.

In order to fully understand the mechanism, we embarked on a study to investigate both the structural and dynamic effects on model membranes. To this end we employed state-of-the-art Small-angle X-ray and neutron scattering (SAXS/SANS) methods which are capable to probe the structure of both lipids and peptide on nanometer length scales[3]. In addition, by using H/D contrast variation scheme we could determine the lipid dynamics extracting both the transversal flip flop motion as well as lipid exchange.. The results further show that indolicidin inserts on the interface between lipid tail/head on the outer leaflet perturbing the lipid packing causing an acceleration in the dynamics. A similar acceleration is found for other AMPs although the structure differs. We speculate that the change in dynamics may cause effects that are detrimental to the bacterial cell.

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[3] J.E. Nielsen, J. E., V:A. Bjørnstad, & R. Lund, *Soft Matter*, 2018, 11, 37–14.

[4] Nielsen, J. E., Lind, T. K., Lone, A., Gerelli, Y., Hansen, P. R., Jenssen, H. M, Cárdenas and R. Lund *BBA - Biomembranes*, 1861(7), 1355–1364.

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