Bacterial Lipid Extracts as Advanced Model Membranes: Studying new Sample Architectures and Interactions with LL37

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Bacterial membranes exhibit significant compositional and structural complexity. Gram(-) bacteria like *E. coli* possess membranes with high contents of glycerophospholipids, whereas Gram(+) bacteria like *B. subtilis* possess membranes enriched in anionic lipids. Their membranes also differ in acyl chain composition, with *E. coli* lipids being dominated by linear fatty acid chains and *B. subtilis* lipids being rich in branched-chain fatty acids. Most biophysical studies of bacterial membranes have so-far involved model systems composed of only a few synthetic lipids [1, 2]. To overcome this limitation, we use lipid extracts obtained from both hydrogenated and deuterated *E. coli* and *B. subtilis* [3], enabling the development of more realistic model membranes compatible with characterization techniques such as X-ray and neutron scattering. In order to access these membranes also with surface-sensitive methods like grazing-incidence X-ray diffraction (GIXD, now applicable also to non-crystalline lipid layers [4]) and total-reflection X-ray fluorescence (TRXF), we aim to create sample architectures in which the membranes are loosely adsorbed to functionalized air/water interfaces, as was demonstrated earlier for synthetic bilayers [5, 6]. Moreover, we comprehensively investigate the interaction of bacterial lipid layers with the human antimicrobial peptide LL-37, using a combination of neutron reflectometry (NR), X-ray reflectometry (XRR), GIXD, and TRXF.

Keywords:
Bacterial membranes; Natural lipid extracts; Antimicrobial peptides; X-ray and neutron scattering.

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