Conformation and Interaction of a d,l-Alternating Peptide with a Bilayer Membrane: X-ray Reflectivity, CD, and FTIR Spectroscopy

Abstract

Peptides with alternating amino acid configuration provide helical secondary structures that are especially known from the membrane channel and pore-forming gramicidin A. In analogy to this natural d,l-alternating pentadecapeptide, the potential of d,l-alternating peptides for membrane insertion is investigated using the model dodecamer peptide \( H-(\text{Phe-Tyr})_5-\text{Trp-Trp-OH} \). This aromatic peptide is introduced as a novel pore-forming synthetic analogue of gramicidin A. It forms a well-organized homodimer similar to one of the gramicidin A transmembrane motifs. X-ray reflectivity measurements are performed on solid-supported peptide–lipid complexes to obtain information about the influence of the artificial dodecamer peptide on the bilayer parameters. In addition, Fourier-transform infrared (FTIR) and circular dichroism (CD) spectroscopic studies determine the conformational state of \( H-(\text{Phe-Tyr})_5-\text{Trp-Trp-OH} \) within the model membrane. Site-specific iodine labeling assists in determining the topology of the membrane-embedded peptide by pinpointing the position of the iodine label within the bilayers.