Supporting Information

Lipid-controlled peptide-topology and -interactions in bilayers: Structural insights into the synergistic enhancement of the antimicrobial activities of PGLa and magainin 2

Evgeniy S. Salnikov and Burkhard Bechinger Université de Strasbourg / CNRS, UMR7177, Institut de Chimie, 4, rue Blaise Pascal, 67070 Strasbourg, France

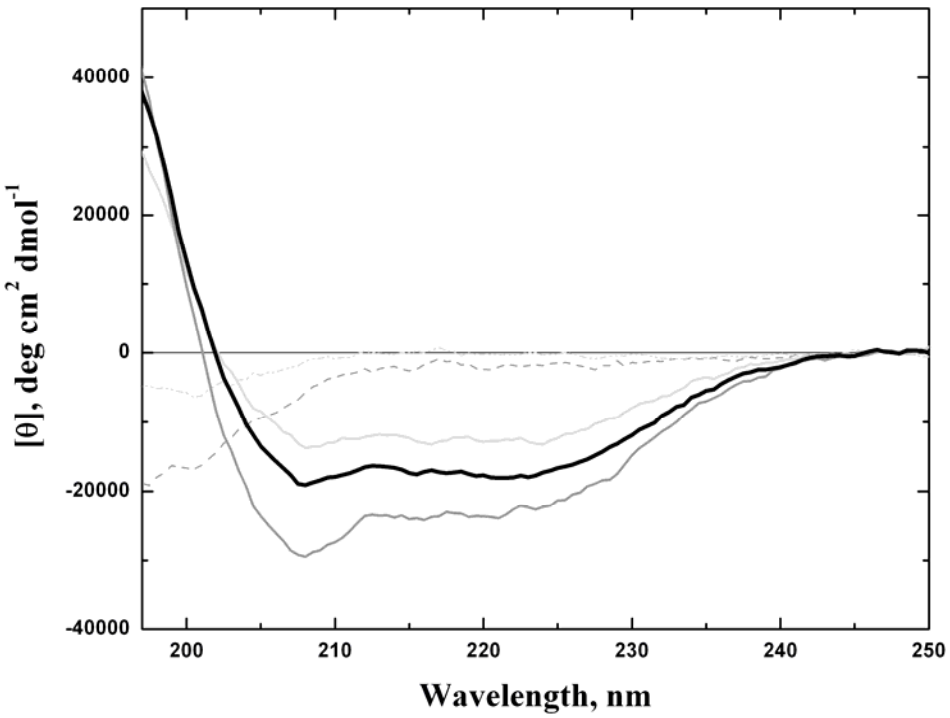

Figure S1. CD spectra of PGLa, magainin 2, and their 1:1 mixture were measured at 37 ºC ([peptide] = 20 μM). The spectra of PGLa and magainin 2 in a 10 mM Tris buffer (pH 7.5) are shown by gray dashed and light gray dotted lines, respectively. The CD spectra of peptides in the presence of 1 mM diC10:0-PC SUVs are shown by solid lines. Gray is for PGLa, light gray for magainin 2, and the thick black line for a PGLa / magainin 2 equimolar mixture.

CD spectra were measured on a Jasco J-810 apparatus using a 1-mm path length quartz cell to minimize the absorbance due to buffer components. The instrumental outputs were calibrated with nonhygroscopic ammonium d-camphor-10-sulfonate. Three scans were averaged for each sample, and the averaged blank spectra (the vesicle suspension) were subtracted. The total peptide concentration was 20 μM.

Figure S1 shows that PGLa and magainin 2 adopt random coil conformations in aqueous buffer (dashed and dotted curves, respectively). In contrast, the peptides-associated to diC10:0-PC bilayers (P/L = 50) show double minima at 208 and 222 nm characteristic of a high content of α-helical secondary structure. The CD spectrum of the PGLa / magainin 2 1/1 (mole/mole) mixture is close to the numerical average of those of magainin 2 (light gray) and PGLa (dark gray), indicating that there are no marked conformational changes in perfect agreement with the previous study of these peptides in the presence of egg PC (Matsuzaki et al. Biochemistry 1998,

37, 15144-15153). Simulating the latter spectrum with CDPro program gives helix contents of 70% - 82% depending on the sub-routine and protein basis set used for the calculations.