STUDYING PLANTARICIN 149-MEMBRANE INTERACTIONS BY SPECTROSCOPIC METHODS

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Plantaricin 149 is an antimicrobial peptide from *Lactobacillus plantarum* described as bactericidal against Gram-positive food-borne pathogens. In order to shed light upon its structure and mechanism of action, synthetic C-terminal amidated peptide analog to Plantaricin 149 (Pln149a) and its membrane interaction were investigated by Surface Plasmon Resonance (SPR), Circular Dichroism and fluorescence spectroscopies. Synthetic Pln149a (SPPS-Fmoc chemistry), purified by reverse phase chromatography, presented a CD spectrum unordered structure-like in aqueous solution, however a helical structure spectrum and a blue shift of 20 nm in fluorescence maximum emission were observed after interaction with DPPG liposomes. No conformational change was observed when interacting with both zwitterionic and cationic liposomes (DPPC, DPPE, DLPC, DMPE, DSPE, and Asolecithin). The direct binding of Pln149a to DPPG was checked by SPR methodology on a BIACORE system using both liposomes reconstructed in monolayers, on a hydrophobic surface (HPA sensorchip), and liposome adsorption, on a dextran matrix modified with hydrophobic residues (L1 sensorchip). Sensorgrams were obtained to calculate the association/dissociation constants using a two-state binding model. Pln149a revealed high affinity for the anionic phospholipid on both chips. The results indicated that the cationic helical structure induced when binding to DPPG is compatible with the “carpet” mechanism proposed in literature.

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