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Interaction Mechanism between the Antimicrobial Peptide Magainin2 and Lipid Membrane Revealed by Synchrotron-Radiation Circular- and Linear-Dichroism Spectroscopy

Ryoga Tsuji[a], Munehiro Kumashiro[b], Koichi Matsuo[c]

[a]*Physics Program, Graduate School of Advanced Science and Engineering, Hiroshima University, 1-3-1 Kagamiyama, Higashi-Hiroshima, Hiroshima 739-8526, Japan*
[b] *Institute of Advanced Medical Sciences, Tokushima University, 3-18, Kuramoto-cho, Tokushima 770-8503, Japan*
[c]*Hiroshima Synchrotron Radiation Center, Hiroshima University, 2-313 Kagamiyama, Higashi-Hiroshima, Hiroshima 739-0046, Japan*

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Magainin2 (M2), is one of the antimicrobial peptides and composed of 23 amino acids, induces the permeabilization of membranes for numerous gram-negative and gram-positive bacteria, by interacting with membrane followed by forming an amphipathic helix. We have investigated the effects of some physical characteristics of membranes such as spontaneous curvature [1] and fluidity [2] etc. on the membrane interaction of M2 using four types of lipid molecules and found that in the membrane with the positive spontaneous curvature (dilauroyl phosphatidylcholine, dimyristoyl phosphatidylcholine, and dipalmitoyl phosphatidylcholine), M2 could adsorb onto the membrane surface when its fluidity was increased and decreased (annealing), forming the helical structure, while in the membrane with the negative spontaneous curvature (distearoyl phosphatidylcholine), M2 could not access the membrane surface even after annealing procedure, retaining its random coil structure. In this study, to further confirm the effects of the spontaneous curvature and fluidity on the membrane interaction, we analyzed the membrane-bound conformation of M2 in the presence of the lipid membrane composed of dipentadecanoyl phosphatidylcholine (15:0PC), which has positive spontaneous curvature and phase transition temperature of 35ºC, using a synchrotron-radiation circular-dichroism (CD) and linear-dichroism (LD) spectroscopy. The results showed that M2 mostly retained a random coil structure in the presence of 15:0PC membrane at 25ºC but the CD spectrum of M2 showed the formation of helical structure after the annealing. These are very similar phenomena to those observed in the presence of DPPC membrane, suggesting that as mentioned above, M2 could clearly adsorb onto the membrane surface with the positive spontaneous curvature and the change of fluidity due to phase transition is necessary for M2-membrane interaction. The LD spectrum of M2 in the presence of 15:0PC lipid membrane showed the positive sign around 200 nm. The analytical results indicated that there are two hypotheses, one is that all M2 peptides form the helical orientation with a single angle against the membrane surface and second is that M2 peptides form the mixtures of perpendicular (transmembrane) and parallel helical structures against the membrane surface. The results under the first assumption showed that the LD spectrum could be interpreted as the angle between the helix axis and the membrane normal would be 46°, while those under the second assumption showed that the ratio of M2 helix axes perpendicular and parallel to the membrane surface was 1: 1.1. We need further characterizations to understand the effect of the spontaneous curvature and fluidity on the membrane interaction, but the M2 conformation and orientation on the membrane obtained here would be helpful for disclosing the details of interaction mechanism between lipid membranes and M2.

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