Sym-1

Solution Conformation of an Antimicrobial Peptide Gaegurin 4

Jae-Eun Suk¹, Hwa-Jin Baek², Byeong-Jae Lee² and Kyou-Hoon Han¹
¹Biomol. Struct. Res. Unit, KRIBB, Yusong P. O. Box 115, Taejon, Korea
²Institute for Molecular Biology and Genetics, Seoul National University, Seoul, Korea

Gaegurin 4 is an antimicrobial peptide found in the skin of a Korean frog, Rana rugosa, known for its "wound-healing" effect for years. This 37-residue basic peptide binds to cell membranes and forms ion channels like other antimicrobial peptides but does not exhibit hemolytic activity. In order to understand detailed mode of action for gaegurin 4 we have been studying the structural transition of gaegurin 4 by determining their high-resolution conformations circular dichroism using and nuclear magnetic resonance spectroscopy in alcohol/water mixed solvents. NOE intensities and patterns, torsion angles, chemical shift indices and temperature coefficients are very sensitive to experimental conditions such as lipophilicity and temperature. In aqueous solution nascent turns and a short stretch of helix are present at room temperature. When lipophilicity of solution reaches a critical point gaegurin 4 becomes a fully extended amphipathic helix which continues into the "Rana box" disulfide loop. An intermediate helix is formed with flexible bends in the middle when (alcohol/water) ratio is close to 1. We speculate that such an intermediate helix represent the initial binding conformation at the early stage of peptide-lipid interations. As the peptide gets fully embedded in the hydrophobic stem of phospholipids a linear helix should be formed.