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Solution Structure of an Antimicrobial Peptide Gaegurin4

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The gaegurin 4 is an antimicrobial peptide from the skin of a Korean frog, *Rana rugosa*. They show a broad range of activity against prokaryotic cells but lyse eukaryotic cells poorly. Circular dichroism investigations revealed that the gaegurin 4 adopts mainly an α -helical conformation in both trifluoroethanol (TFE)/H₂O (1:1, v/v) mixture and in dodecylphosphocholine (DPC), sodiumdodecylsulfate (SDS) micelle environments, but flexible random structure in H₂O. Using ¹H-¹⁵N NMR spectroscopy, a complete ¹H and ¹⁵N resonance assignments have been obtained for the peptide gaegurin 4 in TFE/H₂O (1:1, v/v) mixture. The secondary structure, derived from the characteristic patterns of dipolar connectivities between backbone protons, chemical shifts, and three-bond J_{HNH α} coupling constants, consists of an α -helix with amphiphatic character and disulfide bridge between residues cys31 and cys37. The three-dimensional structure calculation of gaegurin 4 in TFE/H₂O mixture is in progress. In addition, we are planning to elucidate the structure in SDS micelles and in phospholipid bicelles, more membrane-mimetic environments.