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Structural and Functional Study of Antimicrobial Peptide Using NMR Spectroscopy

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Structure of potent derivatives of gaegurin, an antimicrobial peptide from Korean frog, is studied by CD and NMR spectroscopy. Gaegurin did not show any secondary structure in aqueous environment, but adopted α -helix in aqueous TFE solution, SDS and liposome buffer. NMR study showed distinct difference in stability near proline residue in helix.

Tenecin 3, an antifungal protein isolated from hemolymph of meal worm, is purified and studied by CD and NMR spectroscopy. Tenecin 3 showed largely random structure in water and little change was observed by temperature and pH variation. Neither TFE nor SDS changed the conformation. Small dispersion of chemical shift and absence of characteristic NOE support that tenecin 3 has random propensity. The abnormal mobility in SDS-PAGE and gel filtration suggests that this protein exists as an extended chain in water.

Indolicidin is a potent cationic antimicrobial peptide isolated from cytoplasmic granule of bovine neutrophils. With high content of tryptophan and proline residues, it exhibited random structure in water or organic solution. SDS micelle, however, induced helix which is different from normal α -helix.