Conformational Comparison of μ-Selective Endomorphin-2 with Its C-Terminal Free Acid

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In order to make clear the structural function of C-terminal amide group of endomorphin-2(EM2:YPFF-NH_2) the conformations of EM2 and its C-terminal free acid (EM2OH:YPFF-OH) were analyzed by ^{1}H-NMR spectroscopy and X-ray crystal analysis.

The NMR spectra in trifluoroethanol(TFE) and water solvents indicated that both peptides were in equilibrium between the *cis*- and *trans*-rotamer around Tyr-Pro peptide bond, respectively. However they take almost trans rotmer in dodecylphosphocholine(DodPCho), micells, except for the EM2OH in water solvent at pH5.2. With the use of the proton-proton distance derived from ROESY cross peaks, possible fifty 3D structures are generated by dynamical simulated annealing method and were classified in four groups of two open and two fold conformers according to the folding of backbone structure.

On the other hand, two independent conformational isomers per asymmetric unit and seven water molecules were existed in the crystal structure of EM2OH. Both conformers were crystallized as neutral zwitterionic forms and took a folded-form with *cis*-configuration in around Tyr-Pro peptide bond.

Based on the conformational features of EM2 and EM2OH in solution and solid state, we would like to discuss the possible function of C-terminal amide group.

Keywords: NMR, x-ray conformation analysis, molecular conformation