Mapping the Membrane-Associated HIV Fusion Peptide Using Solid-State Nuclear Magnetic Resonance

The infection of human immunodeficiency virus (HIV) was initialized by the fusion process between the virus and host cell membranes. A ~20-residue hydrophobic fusion peptide was proposed to be crucial for understanding the mechanism of membrane fusion. Studies on the membrane-associated HIV fusion peptide oligomers using solid-state Nuclear Magnetic Resonance (NMR) are reported. Three aspects of the specific peptide-membrane system were investigated:

1. **Secondary structure of membrane-associated HIV fusion peptide oligomers.**

   The residue-specific conformation of HIV fusion peptide in a mimic phospholipids bilayer system was studied using NMR. A chemically synthesized fusion peptide oligomer was served as a model and it was observed that the secondary structure of HIV fusion peptide was affected by both the composition of membrane and the oligomerization of peptides.

2. **Tertiary structure of membrane-associated HIV fusion peptide.**

   The possible higher-order structure was detected using selectively $^{13}$C,$^{15}$N-labeled HIV fusion peptides. A Quantitative data analysis showed that ~50%-60% of the peptide could adopt anti-parallel $\beta$-sheet structure in the first 16 N-terminal residues. In addition, two registries were observed with approximately similar population.

3. **Membrane Insertion of HIV fusion peptide oligomers.**

   Interaction between peptide and membrane was probed by measuring the distance between a specific position on the peptide backbone and another specific position in the membrane bilayer. The up-to-date results revealed that different parts of the fusion peptide inserted into the membrane with different depth. Generally, the overall insertion could be modulated by the component of bilayer, and the insertion is related to the kinetics of the HIV fusion peptide induced lipid mixing.

**Reference:**

2. Qiang, W., Yang, J., and Weliky, D.P. *Biochemistry* 2007, **46**, 4997-5008