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Molecular Self-Assembly Behavior in Simple Lipid as Membrane Model and its Stability using Molecular Dynamics Simulation

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【INTRODUCTION】

Self-assembly is a process that generates higher order complexes from simpler molecular building blocks. This mechanism plays a crucial role to form biological membrane due to the hydrophobic effect of lipid that consist of hydrophobic and hydrophilic features. Membranes were introduced as fluid mosaic model, but recently we know that membranes are more mosaic than fluid [1]. It implies that membrane structure is more complicated than thought before. Furthermore there are some limitations of experiment to describe the process of self-assembly. For this reason we investigate the properties of self-assembly using molecular dynamics simulation. Due to some interesting characteristics and availability of experiment data for comparison, we choose POPC (1-palmitoyl-2-oleoyl- phosphatidycholine) and POPE (1-palmitoyl-2-oleoyl- phosphatidylethanolamine) as lipid molecule shown in Fig. 1 and 2 [2,3].

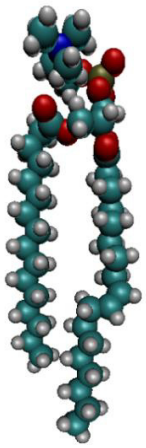

FIGURE 1. POPC lipid

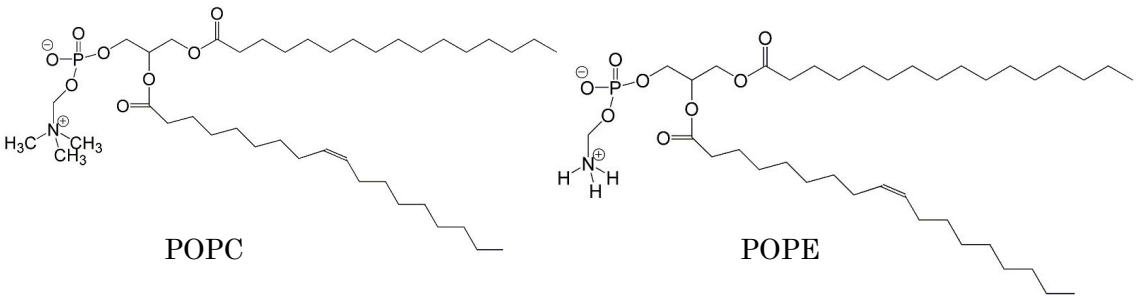

FIGURE 2. Molecular structure of POPC and POPE.

【METHOD】

In this simulation, lipid and water molecules are calculated in 3D and microcanonical ensemble NPT using AMBER program package [4] with force field 03 and TIP3P water. The initial structure of lipid model is generated by VMD software shown in Fig. 3. At first we determine the force field parameters and charge distributions by antechamber. In this study, we adopt the AM1-bcc charge for charge determine method. Lipid model are simulated in various condition. In this case, we simulate a) POPC in water b) POPC in salted water c) POPE in water, d) POPE in salted water. Each simulation is carried out in 300 K and 340 K under periodic boundary condition. Therefore we perform 8 simulations to investigate environment and temperature effects.

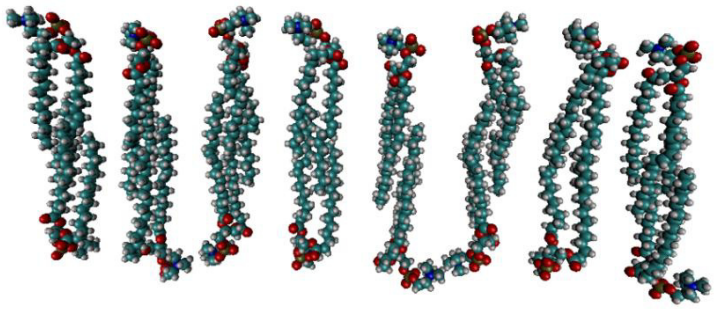

FIGURE 3. Initial coordinate of POPC lipid

【ANALYSIS】

We report the following issues: a) From the snapshot of MD simulation, we can classify the self-assembly structure into micelle, vesicle and membrane. We start with POPC lipid minimization in water environment and calculate RMSD as shown in Fig 4. b) We investigate the temperature effect in the formation of self-assembly c) We calculate: free energy, root mean square deviation (RMSD), radius of gyration (R_g), time relaxation, occurrence of cluster phase transition, lipid density and population lipid to distance. These parameters are calculated to obtain quantitatively the behavior of self-assembly. d) Finally we discuss the additional effect of salt environment on stability of structure [5,6]. This analysis is important to know what conditions make the lipid stable to form membrane. We focus on the explanation of self-assembly behavior, some properties related to this model and stability of structure formation.

This preliminary result can be used for our future work to simulate the stability of self-assembly in more complicated membrane structure as starting point in order to understand important problem in the relation between membrane structure and immune systems.

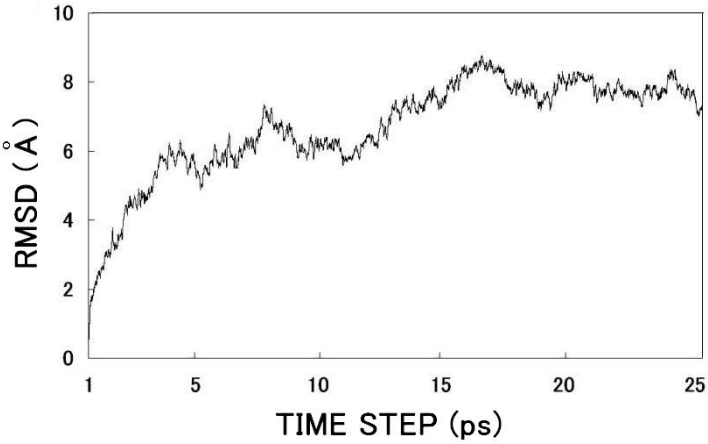

FIGURE 4. RMSD in POPC lipid

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