Materials Science

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Formation process of surfactant gel network structures

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Introduction

In a binary system consisting of surfactant and water, surfactant molecules self-assemble to form various kinds of structures such as lyotropic liquid crystals, spherical or cylindrical micelles and so on, by changing temperature, pressure and concentration. Below the Krafft temperature of nonionic surfactant aqueous solutions [$C_nH_{2n+1}(OC_2H_4)_mOH$], we have ever found that in $C_{16}E_7$ and water system, hollow vesicles are formed below the Krafft temperature. In the $C_{16}E_6$ system, on the other hand, lamellar domains randomly arrange as shown in Fig.1 [1,2]. In the mixed surfactant system, $C_{16}E_6$ and $C_{16}E_7$, intermediate structures between vesicles and network structures are formed.

In the present study, in order to investigate the effects of hydrophilic segments on the lamellar domain formation, we performed time resolved small and wide angle X-ray scattering (SAXS,WAXS) after the jump to the various quenched temperature in the mixed surfactant system.

Experimental

Measurements were performed on the beamlines 15A 4A and 9C. At 15A and 4A, the scattered beam was recorded using the CCD area detector covering the scattering vector q range from 0.03 to 0.3 Å^{-1}. At 9C, we used PSPC detectors for wide and small angle X-ray scattering, and the q range of the wider angle is 0.3 to 6.0 Å^{-1}. For the temperature jump, we used hot stage with kapton windows (TS62-mk1000). The temperature was changed from 16 to 14, 12, 10 ,8 and 6 °C, and scattered X-rays were detected after the temperature jump. The total concentration of surfactant is kept at 10 wt.%, and the mole ratio of $C_{16}E_7$ to $C_{16}E_6$ is varied from 0 to 1.

Results

Figures 2 is the time evolutions of the repeat distances d normalized by the initial repeat distance d_0 obtained from the Bragg peak in SAXS profiles, after the temperature jump. Each time evolution profile is obtained in the mixed surfactant system, with changing the mole fraction of $C_{16}E_7$. Up to the mole fraction 0.6, where the lamellar domains randomly arrange, the normalized d/d_0 increases within several minutes from the temperature quench, and reaches constant. On the other hand, beyond the mole ratio 0.6, d/d_0 increases continuously for about 10 minutes. In the case of the mole ratio 0.8 or the pure $C_{16}E_7$ systems, lamellar domains are shaped spherically, and we now consider that this swollen lamellar behavior is corresponding to the formation process of vesicles, and after vesicle formation completes, d/d_0 becomes constant.

In these results, we have concluded that in the region where the lamellar domains randomly arrange, the system goes to the equilibrium states, whereas in the case that the lamellar domains become vesicles, they are far from the equilibrium states and gradually are swollen with relaxing curvature energy of membranes.

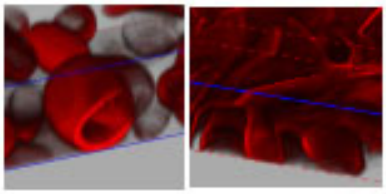

Fig.1 3D image of vesicles and network structures (randomly arranged lamellar domains), obtained from confocal microscope observation.

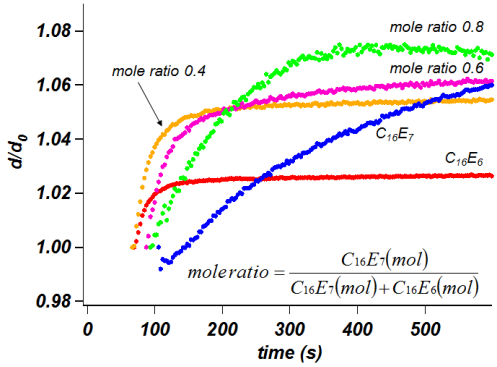

Fig.2 Time evolutions of the repeat distancies d normalized by the initial repeat distance d_0 obtained from the Bragg peak in SAXS profiles, after the temperature jump. Each time evolution profile is obtained in the mixed surfactant system, with changing the mole fraction of $C_{16}E_7$

References

[1] Y. Kawabata et al., J. Phys. Chem B, 113, 5686 (2009).
[2] Y. Kawabata et al., Phys. Chem. Chem. Phys., 13, 3484-3490 (2011).

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