

Phase Transition Behavior and Structural Analysis of Aggregates Formed by Multi-Branched Amino Acid–Sugar Hybrid Surfactant

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In recent years, there has been growing demand for the development of environmentally friendly surfactants. We have previously synthesized linear amino acid–sugar hybrid surfactants and investigated their aggregation behavior in aqueous solutions. However, the effect of hydrophobic chain architecture on aggregate structures has not yet been clarified. In this study, we synthesized a novel amino acid–sugar hybrid surfactant with a highly branched hydrophobic chain (*bC*₁₅GlyMal) and investigated the concentration-dependent phase behavior and aggregate structures in aqueous solutions by small-angle X-ray and neutron scattering (SAXS, SANS), dynamic light scattering, cryogenic transmission electron microscopy (cryo-TEM), polarized optical microscopy (POM), and rheology.

The concentration dependence of the SAXS profiles of *bC*₁₅GlyMal aqueous solutions is shown in Fig 1. The SAXS profiles at 1–10 mmol dm^{−3} and the SANS profile at 10 mmol dm^{−3} exhibited q^{-2} dependence in the low- q region, indicating the formation of vesicles. The vesicular bilayer structure was further confirmed by model fitting of the SAXS and SANS profiles using the Lamellar FF_HG model and the Kratky-Porod model, respectively, as well as by cryo-TEM observations at 5 mmol dm^{−3}. At 25–100 mmol dm^{−3}, the SAXS profiles retained the q^{-2} dependence in the low- q region, while diffraction peaks corresponding to lamellar interlayer spacings, along with bilayer form factor features, appeared, suggesting the coexistence of vesicles and lamellar domains. GIFT analysis further revealed an increase in the lamellar correlation length with increasing concentration, indicating enhanced lamellar ordering. At 250 and 500 mmol dm^{−3}, well-defined lamellar diffraction peaks indicated the formation of lamellar domains. Furthermore, at 750 and 1000 mmol dm^{−3}, POM revealed characteristic textures of a lamellar liquid crystalline phase. These results demonstrate that the multi-branched amino acid–sugar hybrid surfactant exhibits a unique concentration-dependent structural evolution from vesicles to lamellar domains and finally to lamellar liquid crystalline phase with increasing surfactant concentration. These findings suggest that the highly branched hydrophobic chains reduce the preferred spontaneous curvature, thereby promoting the formation of bilayer-based assemblies.

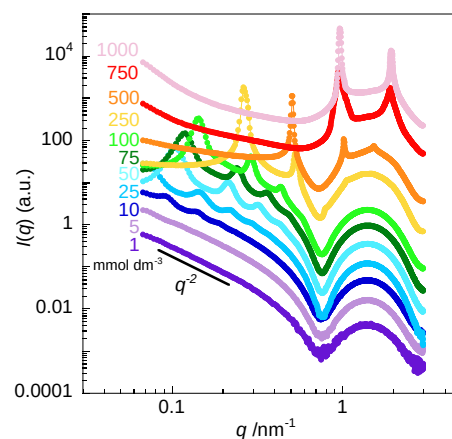


Figure 1. Concentration- dependent SAXS profiles of *bC*₁₅GlyMal solutions (1–1000 mmol dm^{−3}).