Electronic Supplementary Material (ESI) for Soft Matter.

Enhanced stability of cross-linked and charged unimolecular micelles from multigeometry triblock copolymers with short hydrophilic segments: Dissipative Particle Dynamics Simulation

Jianchang Xu,[a] Jing Zhang,[a] Di Xiong,[b] Wenjing Lin,[c] Liyang Wen,[a] and Lijuan Zhang*[a]

[a] Guangdong Provincial Key Lab of Green Chemical Product Technology, School of Chemistry and Chemical Engineering, South China University of Technology, Guangzhou 510640, China.

[b] School of Chemical Engineering, Xiangtan University, Xiangtan 411105, China.

[c] School of Chemical Engineering and Light Industry, Guangdong University of Technology, Guangzhou 510006, China.

Supporting Information

1. DPD Methods

DPD simulation adopts a soft repulsive potential and a momentum-conserving thermostat together to control the interactions between beads representing a group of atoms. The force $\mathbf{f}_i$ acting on bead i can be described as the equation (1).[1]

$$\mathbf{f}_i = \sum_{i \neq j} \left(\mathbf{F}_{ij}^{C} + \mathbf{F}_{ij}^{D} + \mathbf{F}_{ij}^{R} \right) + \mathbf{f}_i^{S} + \mathbf{f}_i^{A} \qquad (1)$$

The conservation force ($\mathbf{F}_{ij}^{C}$) is defined by soft repulsive force to ensure excluded volume. The dissipative force ($\mathbf{F}_{ij}^{D}$) corresponds to the viscous drag that depends both on the position and relative velocities. The random force ($\mathbf{F}_{ij}^{R}$) maintains energy input into the system to eliminate the dissipation. $\mathbf{F}_{ij}^{D}$ and $\mathbf{F}_{ij}^{R}$ serve jointly as a momentum-conserving thermostat. The spring forces $\mathbf{f}_i^{S}$ and $\mathbf{f}_i^{A}$ describe the bond-stretching and bond-bending interactions respectively. Excluded volume $\mathbf{F}_{ij}^{C}$ is given as the equation (2).

$$\mathbf{F}_{\mathrm{ij}}^{\mathrm{C}} = \begin{cases} a_{\mathrm{ij}}(1 - r_{\mathrm{ij}})\hat{\mathbf{r}}_{\mathrm{ij}} & \mathrm{r}_{\mathrm{ij}} < 1 \\ 0 & \mathrm{r}_{\mathrm{ij}} \geq 1 \end{cases} \qquad (2)$$

Where a_{ij} describes the strength of repulsive interaction between particle i and j. $\mathbf{r}_{\mathrm{ij}} = \mathbf{r}_{\mathrm{i}} - \mathbf{r}_{\mathrm{j}}$, $r_{\mathrm{ij}} = |\mathbf{r}_{\mathrm{ij}}|$, $\hat{\mathbf{r}}_{\mathrm{ij}} = \mathbf{r}_{\mathrm{ij}}/|\mathbf{r}_{\mathrm{ij}}|$.

The repulsive parameters a_{ij} between beads i and j can be obtained from the underlying atomistic interaction that is linearly related to the Flory-Huggins parameters (χ_{ij}).[2]

$$a_{\mathrm{ij}} = a_{\mathrm{ii}} + 3.50\chi_{\mathrm{ij}} \qquad (3)$$

Herein, $a_{\mathrm{ii}} = 25k_{\mathrm{B}}T$ at a density $\rho = 3$, and the value of $k_{\mathrm{B}}T$ is defined as 1 (Groot and Warren suggested that $\rho = 3$ and $a_{\mathrm{ii}} = 25\mathrm{k_B T}$ are reasonable parameters for liquids). k_{B} is the boltzmann constant and T is temperature. The χ_{ij} values can be calculated from the solubility parameters using the equation (4), which establishes a connection between atomistic molecular dynamics (MD) and mesoscale DPD methods.

$$\chi_{\mathrm{ij}} = \frac{\Delta E^{\mathrm{mix}} V_{\mathrm{r}}}{RT\Phi_{\mathrm{i}}\Phi_{\mathrm{j}}V} \qquad (4)$$

Here, R is the gas constant. Φ_{i} and Φ_{j} are the volume fractions of bead i and j, respectively. V is the total volume, and V_{r} is a reference volume. ΔE^{mix} is the mixing energy of two different types of beads, which can be calculated by the equation (5).

$$\Delta E^{\mathrm{mix}} = E_{\mathrm{ij}} - (E_{\mathrm{i}} + E_{\mathrm{j}}) \qquad (5)$$

where E_{ij} is the potential energy of binary mixture, E_{i} and E_{j} are the potential energies of pure components i and j, respectively.

2. Repulsion Parameter

In acidic solution, DEAEMA is protonated at its tertiary amine groups to obtain DEAHEMA, and Cl^- ions were added for electrical neutrality. Pure and binary systems were built by the amorphous cell algorithm in Materials Studio (Accelrys Inc.) and subsequently subjected to up to 10 000 steps of energy minimization until an energy convergence of 0.0001 kcal/mol and a force convergence of 0.005 kcal/mol/Å were reached. The cutoff distance for van der Waals interactions was 12.5 Å, with a spline width of 1 Å and a buffer width of 0.5 Å. Ewald summation was used with an accuracy of 0.001 kcal/mol. Both pure and binary systems were simulated for 2 ns under the NPT condition, at 298 K and 1 atm controlled by the Nose- Hoover (*Q* ratio is 0.01, decay constant is 0.1 ps) and Berendsen (decay constant is 0.1 ps) methods, respectively, and the final 1 ns was used to calculate the potential energy.

3. Mixing Energy and Interaction Parameter

The mixing energy (E_{mix}) and interaction parameter (χ) were used as the criterions for the evaluation of the miscibility of blends, which reflects the strength of intermolecular interactions between different components. E_{mix} and χ were conducted in Blends module using Materials Studio (Accelrys Inc.). Geometry optimization was performed firstly using smart algorithm (cascade of steepest descent, conjugate gradient, and quasi-Newton methods). After that, molecular docking is conducted based on the modified Flory−Huggins theory. The mutual interactions between different components (DEAEMA and MMA (or EO or H_2O), DEAHEMA and MMA (or EO or H_2O), DEAEMA and DEAHEMA) were investigated separately. The mixing energy (E_{mix}) and the interaction parameter (χ) were calculated. The energy samples, energy bin width, cluster samples and iterations per cluster were set to 1000000, 0.02 kcal/mol, 10000 and 200 respectively. The forcefield was switched to COMPASS. The cutoff distance for van der Waals and Electrostatic interactions were 15.5 Å, with a spline width of 1 Å and a buffer width of 0.5 Å.

4. Solvent Accessible Surface Area

Figure S1 shows a volume field for a simple diatomic molecule created using the Solvent task. A slice has been added, showing the location of a van der Waals (vdW) surface and two solvent accessible surfaces. The blue and red circles illustrate solvent probe position and radius. As shown in the figure, the surface that intersects with the vdW radii of the atoms in the structure is known as vdW surface. The solvent accessible surface is the locus of the probe center as the probe rolls over the scaled vdW surface, in accessible regions only. Hence, the solvent accessible surface area (*SASA*) is related to the probe radius.

The solvent accessible surface area is analyzed through the Solvent task of the “Atom

Volumes & Surfaces" module. Firstly, the measured radius of *SASA* (the sum of the scaled vdW and probe radii) needs to be determined. The radial distribution functions of water molecules as a function of distance from O atoms of different components (EO, MMA, DEAEMA and DEAHEMA) was analyzed with all atom model by molecular dynamics method. It is found that the *RDF*s of water molecules all begin to appear at 2.5 Å, indicating that solvent accessible region of water molecules is 2.5 Å around the blocks. Because the radii of different beads are 3.83 Å in DPD simulations, the measured radius of *SASA* is fixed to be 6.33 Å. Secondly, the coarse-grained beads of micelles are converted into O atoms at the corresponding positions using the script because the solvent accessible surface cannot be analyzed in DPD simulations. Finally, the probe radius needs to be determined. Because the measured radius of SASA and the vdW radius of O atom are 6.33 and 1.32 Å respectively, the probe radius is fixed to be 5.01 Å, which can ensure that the results of SASA are not affected by the model transformation (Second step). Thus, the initial solvent radii in the "Atom Volumes & Surfaces" module is set to 5.01 Å.

5. Judgement of Equilibrium State

To check whether the self-assembled structures reach equilibrium, the time dependency for the properties including probability of unimolecular micelles (*P*), radial number density (*RND*) and radii of gyration (R_g) was studied. As shown in Figure S2 and Table S1, the *P* values remain unchanged at 100, 150 and 200 ns. The peak positions and values of *RND* curves for MMA, DEAHEMA and EO blocks are about the same with the increasing simulation time. The R_g values of MMA, DEAHEMA and EO blocks have a negligible change with the increase of simulation time. Results of *P*, *RND* and R_g values demonstrate jointly that the timesteps of 4.33×10^5 used in the study are sufficient to reach equilibrium.

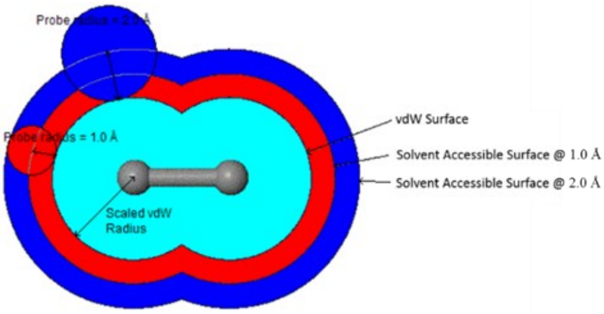

Fig. S1 The van der Waals and solvent accessible surfaces

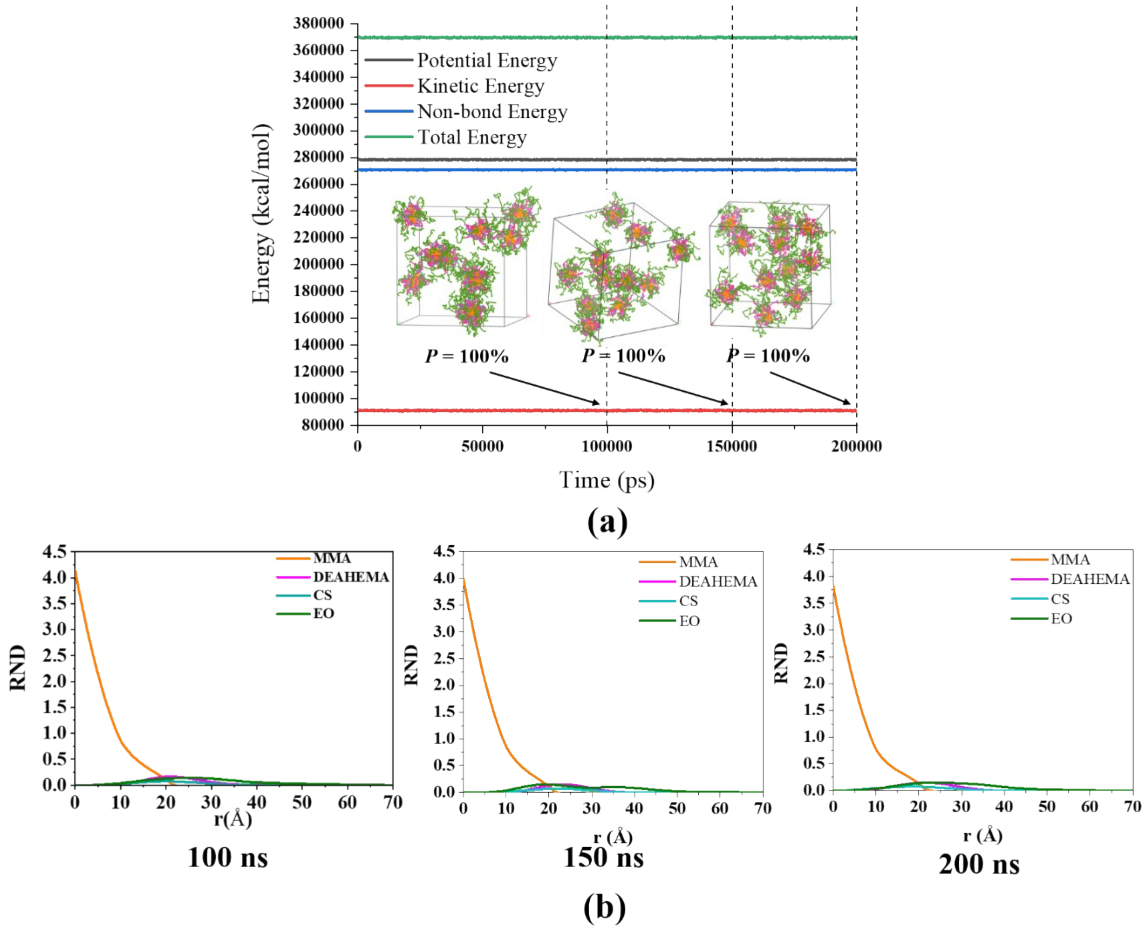

Fig. S2 (a) The unimolecular micelles (*P*), (b) radial number density (*RND*) with the increase of simulation time.

Table S1. The radii of gyration (R_g) of MMA, DEAHEMA and EO blocks with the increase of simulation time.

Time (ns)		**100**	**150**	**200**
R_g **(Å)**	**MMA**	11.86	11.85	11.86
	DEAHEMA	26.10	26.10	26.17
	EO	41.2	40.02	40.05

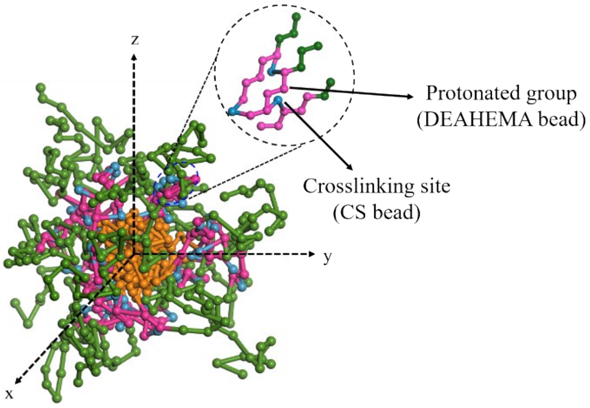

Fig. S3 Schematic illustration of a crosslinked and charged unimolecular micelle. Color scheme: EO, green, MMA, orange, DEAHEMA, pink and crosslinking site, light blue.

Table S2. The crosslinking degrees of multiheometry triblock copolymers with different hydrophilic/hydrophobic segment ratios.

Hydrophilic/ hydrophobic segment ratio	**Crosslinking degree (%)**			
	Brush-like graft copolymer	**Cyclic graft copolymer**	**Hyperbranched block copolymer**	**Star-like block copolymer**
3:1	**49.52**	**49.52**	**40.95**	**49.52**
4:1	**48.57**	**49.52**	**41.90**	**48.87**
5:1	**48.57**	**49.52**	**41.90**	**48.57**
6:1	**49.52**	**49.52**	**41.90**	**48.57**
7:1	**49.52**	**49.52**	**41.90**	**48.57**
8:1	**48.57**	**49.52**	**41.90**	**49.52**

References

1. S. Ma, Y. Hu and R. Wang, *Macromolecules*, 2015, **48**, 3112-3120.
2. R. D. Groot and P. B. Warren, *The Journal of Chemical Physics*, 1997, **107**, 4423-4435.