Supporting Information for:

Co-assembly of amphiphilic triblock copolymers with DNA-polymer targeting ligands in solution

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I. SIMULATION METHOD AND MODEL INFORMATION

In the dissipative particle dynamics (DPD) method, the DPD particles represent the centroids of atomic cluster, which obey Newton's second law:

$$\frac{\mathrm{d}\vec{r}_i}{\mathrm{d}t} = \vec{v}_i, \ \frac{\mathrm{d}\vec{v}_i}{\mathrm{d}t} = \frac{\vec{f}_i}{m_i} \tag{1}$$

Where the $\vec{r}_i$, $\vec{v}_i$, $\vec{f}_i$ and $\vec{m}_i$ represent the position, velocity, force and mass of the *i*th DPD particles. The total force on each DPD particle is composed of three pair-wise additive forces:

$$\vec{f}_i = \sum_{j \neq i} (\vec{f}_{ij}^{\mathrm{C}} + \vec{f}_{ij}^{\mathrm{D}} + \vec{f}_{ij}^{\mathrm{R}}) \tag{2}$$

where the $\vec{f}_{ij}^{\mathrm{C}}$ stands for conservative force due to the excluded volume effect[1]. The remaining two forces are a dissipative force $\vec{f}_{ij}^{\mathrm{D}}$ and a random force $\vec{f}_{ij}^{\mathrm{R}}$. The dissipative force and the random force are coupled together to form a thermostat, which not only makes the temperature of the simulated system fluctuate within a certain range, but also keeps the total momentum of the system conserved. The aforementioned three types of forces along the center of DPD particle are given by

$$\vec{f}_{ij}^{\mathrm{C}} = a_{ij}\omega(r_{ij})\hat{r}_{ij} \tag{3}$$

$$\vec{f}_{ij}^{\mathrm{D}} = -\gamma\omega^2(r_{ij})(\hat{r}_{ij}\cdot\vec{v}_{ij})\hat{r}_{ij} \tag{4}$$

$$\vec{f}_{ij}^{\mathrm{R}} = \sigma\omega(r_{ij})\theta_{ij}\hat{r}_{ij} \tag{5}$$

where the $\vec{r}_{ij} = \vec{r}_i - \vec{r}_j$, $r_{ij} = |\vec{r}_{ij}|$, $\hat{r} = \vec{r}_{ij}/r_{ij}$ and $\vec{v}_{ij} = \vec{v}_i - \vec{v}_j$. The coefficient a_{ij} is a parameter representing the maximum repulsion strength between particles i and j. $\omega(r_{ij})$ is r_{ij} dependent weight function which provides the range of interactions between DPD particles, and the general form used in the simulation is

$$\omega(r_{ij}) = \begin{cases} 1 - r_{ij}/R_{\mathrm{c}ij} & r_{ij} \le R_{\mathrm{c}ij} \\ 0 & r_{ij} > R_{\mathrm{c}ij} \end{cases}, \tag{6}$$

where the $R_{\mathrm{c}ij}$ is the cutoff radius of all forces acting between DPD particles i and j in the system. Here we set $R_{\mathrm{c}ij} = (R_i + R_j)/2$, where R_i and R_j are the interaction radius of particle i and j. The constant γ is the friction factor, and the constant σ is the noise amplitude, corresponding to the maximum magnitude of the dissipative and random forces, respectively. According to the fluctuation-dissipation theorem, the simulated system can only conform to the statistical law of the canonical ensemble when $\sigma^2 = 2\gamma k_{\mathrm{B}}T$ is satisfied[2]. Here k_{B} is the Boltzmann constant and T is the system temperature. The θ_{ij} is a randomly fluctuating variable that satisfies the Gaussian statistics with zero mean and unit variance[3]. At the same time, θ_{ij} satisfies $\langle \theta_{ij}(t)\theta_{kl}(t')\rangle = (\delta_{ik}\delta_{jl} + \delta_{il}\delta_{jk})\delta(t-t')$. This relational expression not only guarantees that the random forces of different interacting particle pairs at different times are independent of each other, but also its symmetric relation $\theta_{ij} = \theta_{ji}$ guarantees the momentum conservation of the system.

In addition to this, the elastic force between the bonded DPD beads also need to be considered when describing the polymer system[4-6]. In our work the spring potential was employed to link the polymer beads in our study[7]. The spring potential is descripted as follows:

$$V_{\mathrm{bond}}(r_{ij}) = \frac{1}{2} k_{\mathrm{s}} (r_{ij} - r_0)^2, \tag{7}$$

Where k_s is the potential energy intensity constant, r_0 is the reference bond length. The angular potential is introduced to capture the rigidity of DNA strands. Similarly, the rigidity of three additional beads is enhanced by the angular potential:

$$V_{\mathrm{angle}}(\theta) = \frac{1}{2} k_{\theta} (\theta - \theta_0)^2, \tag{8}$$

Where k_θ represents the bending strength, and the larger the value, the stronger the rigidity of the DNA chain. θ_0 is the reference bond angle set in radians, and θ is the actual bond angle. The motion evolution of the DPD beads in the system is carried out at unit time t = 0.03 using the modified version of the velocity-Verlet algorithm proposed by Groot and Warren[8-11].

$$\begin{aligned}
&r_i(t+\vartriangle t) = r_i(t) + \vartriangle t v_i(t) + 0.5(\vartriangle t)^2 f_i(t), \\
&\tilde{v}(t+\vartriangle t) = v_i(t) + \lambda \vartriangle t f_i(t), \\
&f_i(t+\vartriangle t) = f_i(r(t+\vartriangle t), \tilde{v}(t+\vartriangle t)), \\
&v_i(t+\vartriangle t) = v_i(t) + 0.5 \vartriangle t (f_i(t) + f_i(t+\vartriangle t).
\end{aligned} \tag{9}$$

The $\tilde{v}$ is a prediction for the new velocity V, and the variable factor λ is set to 0.65. In our work, all the masses of DNA beads, polymer and solvent beads are normalized to 1. The interaction cutoff radius of polymer and solvent beads is set as R_c = 1 as unit length, and the energy scale is set to k_BT = 1. The value of the friction factor γ and the noise amplitude σ are set to 3 and 4.5, respectively.

II. ADDITIONAL FIGURES

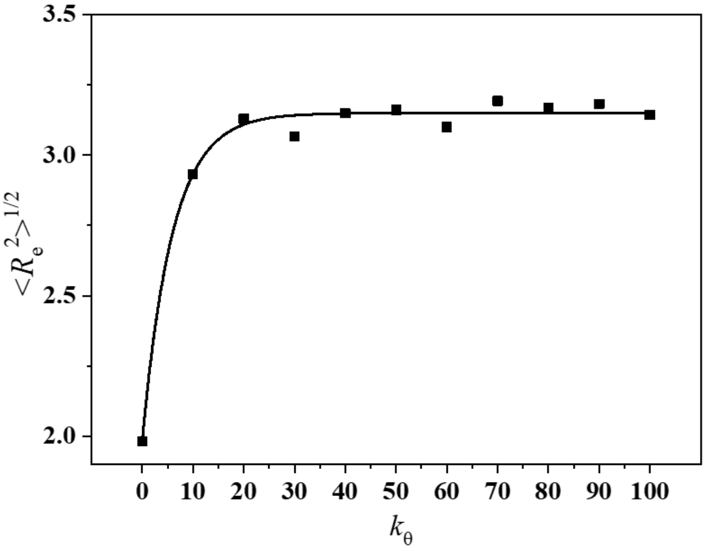


Figure S1. The root-mean-square end-to-end distance $< R_e^2 >^{1/2}$ of each DNA bead chain segment in the simulated system under different angle constants k_θ.

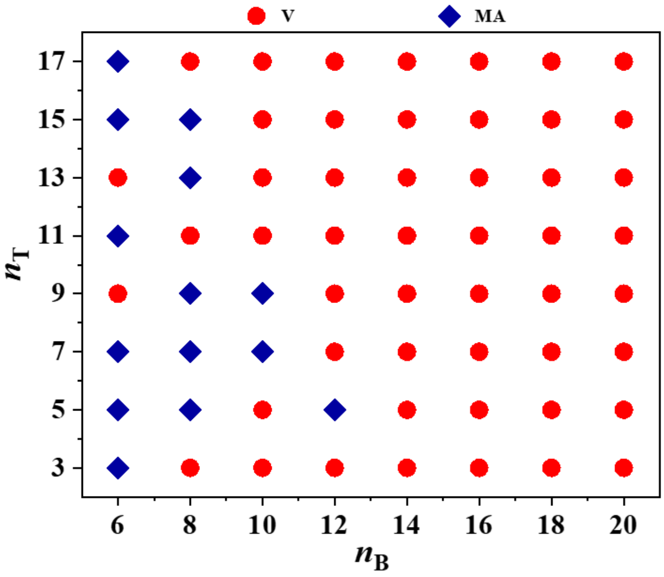
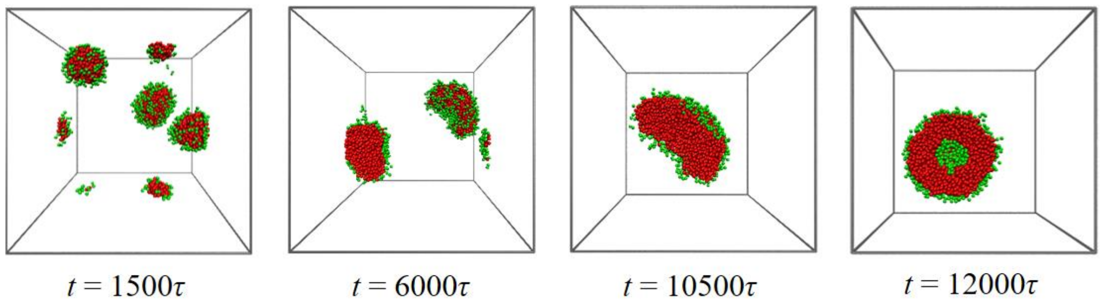
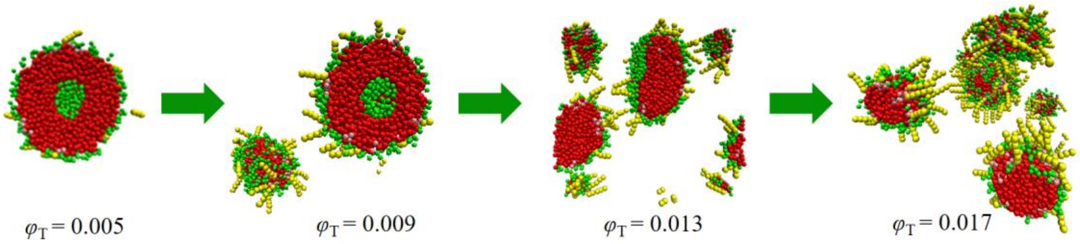


Figure S2. Phase diagram of the self-assembled aggregates formed by the co-assembly of amphiphilic triblock copolymers and targeting ligands at different values of n_B and n_T when φ_T = 0.005.



$t = 1500\tau$ $t = 6000\tau$ $t = 10500\tau$ $t = 12000\tau$

Figure S3. Dynamic process of self-assembly of amphiphilic triblock copolymers to form the polymeric vesicle ($\varphi_T = 0$, $\varphi_{AB} = 0.08$, $n_B = 16$).



$\varphi_T = 0.005$ $\varphi_T = 0.009$ $\varphi_T = 0.013$ $\varphi_T = 0.017$

Figure S4. Cross-sectional view of the aggregates in the system as φ_T changes when $\varphi_{AB} = 0.08$.

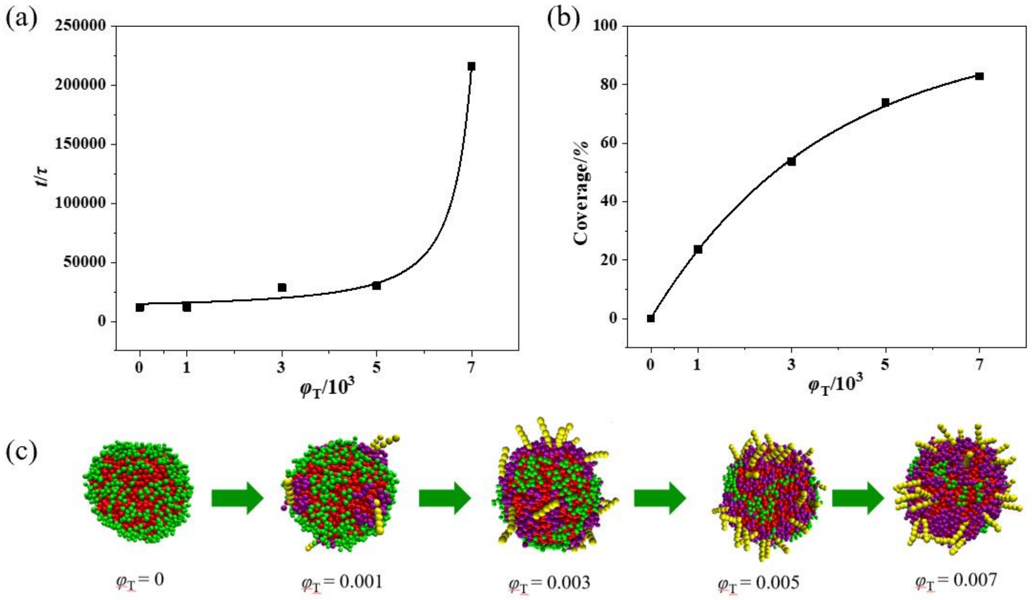


Figure S5. (a) The time required for the self-assembled targeting vesicles to form in the system, (b) the coverage of targeting vesicles as φ_T increases when $\varphi_{AB} = 0.08$ and (c) the morphology of the change in coverage of the targeting vesicles with the increase of φ_T (the purple part is the covered hydrophilic beads). Coverage is defined as the ratio of the number of covered hydrophilic beads (purple) to the total number of hydrophilic beads (green) on the outer surface. We name “covered” when the distance between the hydrophilic beads at the outer surface and the targeting ligand beads at the surface is less than or equal to 3.16, which is the root-mean-square end-to-end distance $< R_e^2 >^{1/2}$ of the targeting ligand.

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