1. Introduction

Blood is composed primarily of red blood cells (RBCs) suspended in plasma with volume fraction about 40–50%. A human RBC is a nucleus-free cell; it is essentially a membrane encapsulating hemoglobin solution. The membrane consists of a lipid bilayer supported by an attached spectrin-based cytoskeleton. Under physiological conditions, the RBC has a biconcave shape when not subject to any external stress and is approximately 8.0 μm in diameter and 2.0 μm in thickness. A giant vesicle, which is a cell-size membrane envelope, mimics essential characteristics of the RBC such as its equilibrium biconcave shape, tank treading and tumbling motions under shear flow. Thus, membrane vesicles have gained popularity as a model system to study the RBC dynamics and membrane biophysics in general.

It is well known that membrane vesicles are highly adaptive structures having a rich variety of shapes. The study of shape and topological changes of membrane vesicles can be helpful to understand the features of cell shape arising from the properties of the membrane itself, without the presence of a cytoskeleton. In past decades, membrane vesicles attracted considerable attention in both experimental and theoretical studies. \(^\text{5–12}\) The experimental results confirm the hypothesis that the shape of a vesicle is mainly determined by bending elasticity and thus by curvature. A number of computational models have been employed to explain the variety of shapes exists. For instance, the cost for bending is described by several continuum models based on the Helfrich energy: the spontaneous curvature (SC) model, the bilayer couple (BC) model, and the area-difference elasticity (ADE) model. \(^\text{13–14}\) These models and their variants allow the prediction of energy-minimizing shapes for a given parameter set. For example, Yuan et al. simulated the shape transformations of membrane vesicles by incorporating a volume-control algorithm into mesoscopic fluid membrane model. \(^\text{15,16}\) Through coarse-grained molecular dynamics (CGMD) simulations, they found that the shape deformations of membrane vesicles depend on the volume change rate: a slow volume change rate promotes dumbbell to tube shape transformation, while for fast volume change rate the membrane vesicles follow a biconcave-stomatocyte-inward budding transformation pathway. Markvoort et al. studied the effect of small changes in the lipid heads on the membrane vesicle shapes from CGMD simulations. \(^\text{17,18}\) They found that small asymmetries in the lipid bilayers can result in high spontaneous curvature and large vesicle deformations. The shape deformation of membrane vesicles can also be caused by temperature changes. For example, Liu et al. obtained the phase diagram for shapes of membrane vesicles with a variation in temperature difference. \(^\text{19,20}\) Several interesting vesicle shapes, including stomatocyte, multiridge, double-layer, and compact solid-like shapes, were found in their CGMD simulations. Besides, the shape deformations of membrane vesicles are related to the internal circumstances. Using a field-theoretic approach, Oya et al. studied the equilibrium shape deformations of membrane vesicles by combining the phase field theory for membrane and self-consistent field theory (SCFT) for polymers. \(^\text{21}\) Simulations on the coupled model system show the shape deformations of the membrane vesicles can be induced by the presence of enclosed flexible polymers.
Presently, membrane vesicles can be prepared from compounds such as surfactants, phospholipids and block copolymers. Their common feature is the presence of hydrophilic heads and hydrophobic tails in the molecules. When they are exposed to water, they organize themselves into a bilayer membrane with all of their tails pointing toward the center of the bilayer. The bilayer membrane can also spontaneously close and form a bilayer vesicle to avoid exposure of their hydrophobic core to water. Regarding the membrane architecture of the bilayer vesicle, the similarity between polymer vesicles and lipid vesicles is in the sense that both species are composed of a bilayer of amphiphiles enclosing an aqueous compartment; however, there are also some big differences. The building blocks of lipid vesicles, i.e., phospholipids, are in most cases with a molecular weight well below 1 kDa, whereas a polymer vesicle is formed from amphiphilic block copolymers with a molecular weight up to 100 kDa. This higher molecular weight of the building blocks establishes itself in a lower critical micelle concentration, resulting in a tougher, less permeable and more robust membrane. Furthermore, by contrast to lipid vesicles the chemical composition and thickness of polymer vesicle membranes can be adjusted by tuning the length and composition of the building blocks. These features render polymer vesicles attractive alternatives to lipid vesicles as an interesting candidate for in vivo imaging and cellular delivery.

Polymer vesicles have attracted considerable attention in recent years for both theoretical and experimental studies. In a previous study, we simulated the shape transformations of single-component membrane vesicles by introducing an asymmetry in the membrane. A plethora of complex vesicle shapes is revealed by the simulations, including some novel ones such as toroidal, long rod-like, and inverted vesicles.

It is generally believed that the phase separated polymers act as building blocks to construct the membrane vesicles. For example, as shown in Fig. 1(a), the ABA-typed units will laterally join together to form the monolayer of the vesicle wall, while the AB-typed units will pack into the bilayer structure. For monolayer vesicles, their shape deformations can be induced by the spontaneous curvature of the membrane; for bilayer vesicles, the shape deformation can also be induced by the area difference between the exterior and interior layers of the membrane. Considering the special bilayer structure, the asymmetry between the two layers is an efficient way to deform the shapes of bilayer vesicles; however, to the best of our knowledge, no studies of shape transformations of polymeric bilayer vesicles using particle-based method have been reported.

In this paper, we study the shape transformations of bilayer vesicles composed of two-component amphiphilic diblock copolymers and compare with the BC model. We employ the dissipative particle dynamics (DPD) method, which is a mesoscopic CG simulation method for soft matter and polymeric systems. The DPD model used here is coarser than that used in previous studies, which conducts efficient simulations of membrane vesicles and gives access to longer time and length scales than those achievable with conventional MD simulations. A plethora of complex vesicle shapes, including some axisymmetric ones such as cigar shape, pear shape, dumbbell shape and discocyte shape, and several non-axisymmetric ones such as boomerang shape, starfish shape, and racket-like shaped vesicles, is observed from the DPD simulations. Now we can believe that polymer vesicles undergo shape transformations and show morphological diversity comparable to that of lipid vesicles according to external/internal circumstances.

The rest of this paper is organized as follows: In Section 2 we describe the simulation method and employed DPD model. We present and discuss the simulation results in Section 3. Finally, in Section 4, we summarize the findings and present the conclusions.

2. Simulation model and method

The simulations presented here are based on the DPD method, for completeness, the method and the model are briefly reviewed below, whereas details on the DPD method and model are available elsewhere.

In a DPD simulation, a particle represents the center of mass in a cluster of atoms, and the position and momentum of the particle is updated in a continuous phase but spaced at discrete time steps. Particles $i$ and $j$ interact with each other via pairwise conservative, dissipative, and random forces, which are given by

$$F_i = \sum_{j \neq i} b_{ij} \omega(r_{ij}) \hat{r}_{ij} - \gamma v_i \hat{v}_i (r_{ij} v_i) \hat{v}_j + \sigma v_i (v_i^2 - \langle v_i^2 \rangle) \Delta t^{-1/2} \hat{r}_i,$$

where $b_{ij}$ is a maximum repulsion between particles $i$ and $j$; $r_{ij}$ is the distance between them, with the corresponding unit vector $\hat{r}_{ij}$. Also, $v_i$ is the difference between the two velocities; $\zeta_i$ is a random number with zero mean and unit variance, and $\gamma$ and $\sigma$ are parameters coupled by $\sigma^2 = 2\gamma k_B T$, where $k_B$ is the Boltzmann constant and $T$ is the temperature.

The total force can also have an elastic contribution, which is derived from the harmonic force used to connect two
consecutive particles in the amphiphilic molecules. The harmonic spring force with a spring constant of $k_s$ and an equilibrium bond length of $r_s$ in our simulations has the form

$$F_i^S = k_s(1 - r_s/r_i)\vec{r}_{ij}.$$  

(2)

In the DPD method, the dissipative force and the random force act as heat sink and source, respectively, and the combined effect of the two forces acts as a thermostat, which conserves momentum and thus provides the correct description of hydrodynamics for the system. Also, a common choice of the soft repulsion for the conservative force permits us to use larger integration time steps than are usually allowed in MD. Thus, DPD is a simple but very effective simulation method that represents hydrodynamic interactions correctly.

Within the mesoscopic approach, an amphiphilic molecule is represented by a CG model. In order to simulate polymer-based asymmetric membranes as well as vesicles in solvent, we consider the amphiphilic linear diblock copolymers. For the sake of simplicity, we focus on the simple models of amphiphilic molecules as shown in Fig. 1(b). They are built by one hydrophilic head particle (denoted by A or C) and four hydrophobic tail particles (denoted by B). Two types of amphiphiles, which are denoted by $A_iB_n$ and $C_iB_n$, have the same architecture but segregate from each other. The main features of these models are the preferred interaction between hydrophilic particles and solvent, and the preferred interaction of the hydrophobic particles with each other. For a comparison study, in Section 3.2 we also simulate the shape deformation of bilayer vesicles formed from $A_iB_n/C_iB_n$ and $A_iB_n/C_iB_n$ amphiphilic diblock copolymers. Solvent particles (denoted by S) are included explicitly in the simulation; however, for clarity, only the hydrophobic particles are shown in the following figures.

We use 9600 constituent particles of the amphiphilic molecules (1080 repeat units of $A_iB_n$ and 840 repeat units of $C_iB_n$) in a simulation box of $40r_c \times 40r_c \times 40r_c$, with a particle number density of 3. Therefore, the total number of DPD particles in the system is 192 000, and the concentration of the amphiphilic molecules is 5.0 vol%. The simulations are performed using a modified version of the DPD code named *MyDPD*. The time integration of the motion equations is computed through a modified velocity-Verlet algorithm with $\lambda = 0.65$ and time step $\Delta t = 0.01r_c$, where $r_c$ is a characteristic time in DPD units.

Based on previous computational studies, the repulsive parameter related to the interaction between two alike particles is set at $b_{ii} = 25.0$ ($i = A, B, C, S$), causing the simulated compressibility of these DPD particles at room temperature to correspond to the experimental value. As suggested by Laradji and Sunil Kumar, the hydrophobic and hydrophilic interactions emerge from the relative interaction strengths $b_{ij}$. With this, the value of the parameter between two particles, one of which is hydrophilic and the other hydrophobic, is $b_{AB} = b_{BC} = 80.0$, which is considered to be a sufficiently large value for the strong segregation. Additionally, in order to consider the segregation between the two different types of amphiphiles, the parameter between hydrophilic particles A and C is set at $b_{AC} = 50.0$.

To model the amphiphilic nature of block copolymer, the repulsion parameter between the hydrophilic and solvent particles is made smaller than the repulsion parameter between two alike particles, i.e., $b_{AS} = b_{CS} = 20.0$. Likewise, the parameter related to the interaction between the hydrophobic and solvent particles is made larger than the repulsion parameter between two similar particles, which ensures that the hydrophobic segment of amphiphilic molecule is sufficiently shielded from the solvent. In this study, we choose $b_{BS} = 100.0$. In addition, regarding the elastic contribution to the interaction energy, the spring constant is given by $k_s = 10.0$, and the equilibrium bond length $r_s = 0.86$. With these parameters, a bilayer vesicle with the exterior layer consisting of hydrophilic particles A and interior layer consisting of hydrophilic particles C can be formed, as seen in Fig. 1(b).

3. Results and discussion

3.1. Shape transformations of bilayer vesicles

In this section, we present the shape transformations of the bilayer vesicles formed from the $A_iB_n/C_iB_n$ amphiphilic diblock copolymer systems. As described in previous simulations based on DPD model, the large repulsive interaction parameters in DPD simulations are chosen so that the bilayer vesicle is impermeable to solvent particles, which implies that the number of solvent particles inside the closed vesicle is almost constant. It is hard to change the shape for a spherical vesicle without changing its interior volume; therefore, the initial configurations for the following simulations are all derived from a vesicle for which a certain number of solvent particles are removed from its interior and placed into the outer region.

In order to provide a quantitative insight into the characteristics of the shape transformation behaviors of the bilayer vesicles, we employ theoretical models for comparison. In simulations, the vesicle membrane formed from amphiphilic block copolymers has a finite thickness, therefore, it is interesting to compare the simulation results to a theoretical model involving a finite-thickness membrane; however, to the best of our knowledge, such a model does not exist at present. In the DPD model, the large repulsive interaction parameters are selected so that the two layers of membrane vesicle cannot easily exchange amphiphilic molecules, thus, the number of amphiphilic molecules in each monolayer is fixed and kept at an approximately constant value during the simulations, which is in accordance with the assumption of the existing BC model. Hence, the BC model is used for comparison in this study.

For the BC model, the phase diagram depends only on two dimensionless variables, the reduced volume, $v$, and the reduced area difference between the exterior and interior layers, $\Delta a$, defined by

$$v = \frac{V}{V_0} = \frac{V}{4\pi/3R_0^3}, \quad \Delta a = \frac{\Delta A}{A_0} = \frac{A_{ex} - A_{in}}{4\pi R_0^2},$$  

(3)

where $R_0$ is the radius of a sphere with the same area. In DPD simulations, $\Delta a$ is determined by the DPD repulsive interaction parameters of amphiphilic block copolymers. A difference in repulsive interactions between the two different hydrophilic...
blocks in amphiphilic molecules introduces a difference in area occupied per amphiphilic molecule, resulting in an asymmetry in the membrane. Specifically, the shape transformations of membrane vesicles are observed by varying the difference of repulsive interactions, \( \Delta b = b_{AA} - b_{CC} \), in the range from 0.0 to 25.0 by changing the repulsive parameters of \( b_{AA} \) in the range from 25.0 to 50.0; \( b_{CC} \) is obtained through the relation \( b_{CC} = 50.0 - b_{AA} \).

To describe the shape transformations of simulated vesicles in terms of the BC model, the triangulated surface model is used to estimate these two dimensionless variables. The density of particles forming the membrane vesicle is computed on a three-dimensional (3D) grid with a series of nodes, and the density isosurfaces can be represented using the triangular surface meshes connecting the corresponding nodes. The membrane of the bilayer vesicle has two layers and two different isosurfaces (where the density is midway between the hydrophilic and hydrophobic domains), i.e., the outer isosurface between hydrophilic A and hydrophobic B domains and the inner one between hydrophilic C and hydrophobic B domains. In this study, we use the outer isosurface to estimate the area of the exterior layer, \( A_{\text{ex}} \), while using the inner one to estimate the area of the interior layer, \( A_{\text{in}} \). The membrane area difference, \( \Delta a \), is then estimated according to the eqn (3).

The volume of the bilayer vesicle is calculated by measuring how many vertices of a dense regular grid happen to be within the middle surface of the bilayer membrane, which is located in the middle between the inner and outer isosurfaces. The values of reduced volumes are listed in Table 1. For a spherical vesicle, we obtain a reduced volume of \( \nu \approx 1.0 \). A reduced volume of \( \nu \approx 0.80 \) can be obtained after 21% of the interior solvent particles are removed from the interior of the bilayer vesicle. Similarly, if 70% of the interior solvent particles are removed, we obtain a vesicle with a reduced volume of \( \nu \approx 0.55 \).

A simple estimation can be given here. The original vesicle has a radius \( (R_0) \) of 7.8\( r_c \) and thus a volume \( V_0 = (4/3)\pi R_0^3 \approx 1988r_c^3 \). The membrane thickness \( l_{\text{inc}} \) is estimated to be 3.3\( r_c \), and the inner radius of the vesicle is 6.2\( r_c \) with a volume \( V_{\text{in}} \approx 998r_c^3 \). If we assume that the membrane does not change in volume, then a reduced volume \( \nu \approx (V_0 - V_{\text{in}} \times 0.21)/V_0 = 0.89 \) is achieved by removing 21% of the interior solvent, and by removing 70% of interior solvent, the reduced volume drops to \( \nu \approx (V_0 - V_{\text{in}} \times 0.70)/V_0 = 0.65 \). Actually, the removal of a certain number of solvent particles from the interior of the vesicle into its outer region leads to a tiny increase in the membrane thickness, which can influence the volume of the bilayer vesicle. Thus, the calculated reduced volumes decrease faster than these estimated numerical values. Moreover, the strong repulsions are chosen in the DPD model so that the two layers of membrane vesicle cannot easily exchange amphiphilic molecules, which prevents the penetration of the amphiphilic molecules in inner layers through the membrane, resulting in a possible excess membrane area in the inner layer of the vesicle, and the volume of the bilayer vesicle is calculated at the middle surface rather than the inner surface of the bilayer membrane, so, the dependence of the reduced volume, \( \nu \), on the fraction of the solvent removed from the spherical vesicle is not linear.

For a spherical vesicle, we obtain both the reduced volume \( \nu \) and the reduced area difference \( \Delta a \) of approximately 1.0. The spherical vesicle deforms to different shapes depending on the values of \( \nu \) and \( \Delta a \). A selection of vesicle shapes along with the corresponding experimental observations and theoretical calculation based on the BC model is displayed in Fig. 2. In the order from low to high values of reduced volume \( \nu \), discocyte shape (Fig. 2a), triangular oblate shape (Fig. 2b), cigar shape (Fig. 2c), stomatocyte shape (Fig. 2d), elliptoocyte shape (Fig. 2e), and pear-shaped (Fig. 2f) vesicles are observed. The shapes appear in the same order as predicted in theory⁴⁰ and observed

Table 1 Obtained reduced volume values of bilayer vesicles by removing percent of solvent from the interior of the vesicle to the outer region. The symbols in the Table denote: \( p \) represents the fraction of solvent removed from the interior of the bilayer vesicle; \( V \) represents the volume of the bilayer vesicle; \( \nu \) represents the reduced volume of the bilayer vesicle, which is calculated using eqn (3). We find that the original spherical vesicle has a volume \( V_0 = 1988r_c^3 \) if there is no solvent particles are removed from the interior of the vesicle.

<table>
<thead>
<tr>
<th>( p ) (%)</th>
<th>0</th>
<th>10</th>
<th>20</th>
<th>30</th>
<th>40</th>
<th>50</th>
<th>60</th>
<th>70</th>
<th>80</th>
</tr>
</thead>
<tbody>
<tr>
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<td>1988</td>
<td>1814</td>
<td>1635</td>
<td>1519</td>
<td>1415</td>
<td>1314</td>
<td>1172</td>
<td>1093</td>
<td>1014</td>
</tr>
<tr>
<td>( \nu )</td>
<td>1.00</td>
<td>0.91</td>
<td>0.82</td>
<td>0.76</td>
<td>0.71</td>
<td>0.66</td>
<td>0.59</td>
<td>0.55</td>
<td>0.51</td>
</tr>
</tbody>
</table>

Fig. 2 Selected vesicle shapes compared to experimental observations⁴⁰ and theoretical stationary shapes computed within the BC model.⁴ⁱ Experimental data are obtained at: discocyte \( (\nu; p = 0.51, \Delta a = 1.05) \), triangular oblate shape \( (\nu; p = 0.53, \Delta a = 1.24) \), cigar shape \( (\nu; p = 0.54, \Delta a = 1.52) \), stomatocyte shape \( (\nu; p = 0.58, \Delta a = 0.77) \), elliptoocyte shape \( (\nu; p = 0.68, \Delta a = 1.22) \), and pear shape \( (\nu; p = 0.91, \Delta a = 1.07) \). Simulation data are obtained at: Discocyte shape \( (\nu; p = 0.51, \Delta a = 1.09) \), triangular oblate shape \( (\nu; p = 0.55, \Delta a = 1.59) \), cigar shape \( (\nu; p = 0.60, \Delta a = 1.44) \), stomatocyte shape \( (\nu; p = 0.65, \Delta a = 0.99) \), elliptoocyte shape \( (\nu; p = 0.71, \Delta a = 1.17) \), and pear shape \( (\nu; p = 0.86, \Delta a = 1.19) \).
in experiment,\textsuperscript{40} even though the values of \( r \) and \( \Delta a \) have some difference between the simulation results and the experimental data. Also, the shape transformations observed here include shapes that persist for several hundred thousand time steps or longer (Fig. 2a, c, d and f) and transient shapes which evolve at a much shorter time scale (Fig. 2b and e). However, both the persistent and the transient shapes are in agreement with the experimental observation\textsuperscript{40} and are consistent with the theoretical prediction by the BC model.\textsuperscript{41}

To illustrate the effect of the reduced volume \( r \) and reduced area difference \( \Delta a \) on shape deformations of the bilayer vesicles and to compare with the BC model, we systematically vary these two parameters and examine the modulated shapes for a series of DPD simulations. Fig. 3 presents the corresponding diagram of morphologies as a function of \( r \) and \( \Delta a \). Overall, the trend of the simulation diagram agrees with the theoretically predicted boundaries except for a slight shift of the left boundary of the appearance of the cigar/dumbbell shapes. The spherical vesicle deforms to achieve stomatocyte at small boundary of the appearance of the cigar/dumbbell shapes. The predicted boundaries except for a slight shift of the simulation diagram agrees with the theoretically predicted boundaries except for a slight shift of the left boundary of the appearance of the cigar/dumbbell shapes. The spherical vesicle deforms to achieve stomatocyte at small boundary of the appearance of the cigar/dumbbell shapes. The predicted boundaries except for a slight shift of the left boundary of the appearance of the cigar/dumbbell shapes.

Most studies on vesicle shapes have a reduced volume between 0.5 and 0.7. In this regime the spectrum of shapes is diverse, and some more complex vesicle shapes such as boomerang and starfish can be obtained.\textsuperscript{41,42} Next, we extend the range of reduced volume down to 0.5. From Fig. 3, we find that the axisymmetric shapes, such as dumbbells, cigars, and necklaces, appear at large enough \( \Delta a \), and the discocytes at low \( \Delta a \) near 1.03 which is almost independent of \( r \). Moreover, the non-axisymmetric shapes involved in the transition between the discocytes and the dumbbell/cigar shapes is found to be dominated in the central part of the diagram, and the location of the dumbbell/cigar shifts to larger \( \Delta a \) as \( r \) is decreased. This is consistent with the predictions.\textsuperscript{41}

Fig. 4 shows the shapes of bilayer vesicles for reduced volume ranging from 0.50 to 0.70. One important feature revealed in the DPD simulations is the existence of multi-armed vesicle shapes. At \( r = 0.70 \), the axisymmetric dumbbell shape is obtained from the spherical vesicle. When the reduced volume \( r \) is decreased to 0.62, the racket-shaped vesicle is obtained with a flattened body and an elongated arm. As \( r \) is decreased further, the vesicle shapes with multi-arms become more prominent. At \( r = 0.56 \), the vesicle shape develops two arms, and a boomerang-shaped vesicle is obtained. Three-armed starfish shape appears as \( r \) is decreased to 0.53. At \( r = 0.50 \), the four-armed starfish shape appears; however, it gradually transforms into a three-armed starfish. These results agree with the previously reported result that the three-armed starfish-vesicles are the most stable equilibrium shapes in a region of the phase diagram with the reduced volume 0.50 \( \leq r \leq 0.60 \).\textsuperscript{41} This is even more explicitly demonstrated by the shape transformation of the bilayer vesicle at \( r = 0.50 \) during the time evolution, as shown in Fig. 6. During this transformation where a series of estimated \( \Delta a \) are combined with their corresponding vesicle shapes, we find that \( \Delta a \) first rapidly increases, and the spherical vesicle is transformed continuously into a four-armed starfish shape. Then \( \Delta a \) decreases and smoothly approaches saturation with time, the vesicle gradually buries an arm of its own. The four-armed starfish is transformed continuously into a three-armed starfish.

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**Fig. 3** \( r-\Delta a \) phase diagram of two-component bilayer vesicle. The different classes of vesicle shapes are color-coded. The solid line in the left represents the boundary in the stomatocyte–discocyte transition, while the solid line in the right and the dashed line describe the boundary location of the cigar/dumbbell shapes predicted by the BC model\textsuperscript{41} and observed in DPD simulations, respectively. Overall, the trend of the simulation diagram agrees with the theoretically predicted boundaries except for a slight shift of the left boundary of the appearance of the cigar/dumbbell shapes.

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**Fig. 4** Shape transformations of bilayer vesicles as a function of the reduced area difference \( \Delta a \) at the reduced volume \( r = 0.80 \).
vesicle shape. Over time, the arms appear to grow or shrink randomly while preserving the initial volume of the vesicle and as well as the arm diameters.

3.2. Dependence of the building blocks on the shapes of bilayer vesicles

In this study, the block length is comparable to the thickness of bilayer membrane; thus, the vesicle shapes may depend on the actual discretization of the building blocks. We then examine the dependence of the shape deformation and stability of the bilayer vesicles on the chain length of the block copolymers by changing the hydrophobic block length ranged from \( n = 3 \) to 5. Fig. 7 shows the effect of the hydrophobic block lengths on the shapes of bilayer vesicles. Fig. 7(a)–(c) show some stationary shapes of bilayer vesicles for several values of \( n \) and \( \Delta a \) with different building blocks in amphiphilic block copolymers: (a) \( A_1B_5/C_1B_5 \), (b) \( A_1B_4/C_1B_4 \), and (c) \( A_1B_3/C_1B_3 \).

we find that the vesicle shapes are dominated by flattened oblate shapes for the \( A_1B_3/C_1B_5 \) amphiphilic diblock copolymers. For example, a flattened ellipsoidal shape can be observed at \( \nu = 0.81 \). As \( \nu \) is reduced to 0.73, we find a racket-like vesicle shape. A further decrease in \( \nu \) leads to the formation of flattened boomerang. At still smaller volume, the flattened boomerang is transformed to a normal one by reducing its flattened body and elongating its arms. Further decrease in \( \nu \) to even smaller value causes the formation of triangular and asymmetric oblate shapes, in which the characteristic cross-section is an asymmetric oblate shape with several end-caps. Compared to the vesicle shapes formed from \( A_1B_5/C_1B_5 \) amphiphilic diblock copolymers, more prolate/pear shapes, including the elongated three-armed vesicle shape, appear for the \( A_1B_3/C_1B_3 \) and \( A_1B_4/C_1B_4 \) amphiphilic diblock copolymers, which indicates that the bilayer vesicle tends to prefer prolate/pear shapes when the hydrophobic block length is decreased. In particular, for the vesicle shapes formed from the \( A_1B_3/C_1B_3 \) diblock copolymers, the prolate/pear shapes extend more along the axial direction and become elongated prolate/pear shapes.

A vesicle may change its shape, volume, or surface area, due to the change in properties of its membrane and/or the presence of external/internal circumstances. To understand why the bilayer vesicle formed from the amphiphilic molecules with shorter hydrophobic block lengths favors prolate/pear shapes over oblate shapes, we estimate the bending modulus of the bilayer membrane. The bending modulus, which is one of the basic parameters of bilayer membrane, describes a kind of capability for a vesicle that can resist perturbation and deformation. Microscopic models\(^{43}\) show the bending modulus, \( \kappa \), should scale as the area expansion modulus, \( K_A \), multiplied by the square of the membrane thickness, \( l \), given by

\[
\kappa = K_A \frac{\Delta \alpha}{C},
\]

where \( C \) is a normalization constant. Therefore, the bending modulus is increased progressively with the increase of the
chain length, which implies that vesicles with less bending rigidity behave more like fluids, susceptible to extra-pressure and tensile stress as well as external/internal circumstances, and will be seriously deformed; thus, the multi-armed vesicle shapes appear. One more interesting result from the DPD simulations is the appearance of the toroidal vesicle shape at smaller \( \nu \). One possible reason for this shape is the thin membrane. In this case, the triangular oblate shape becomes unstable, and it pinches off at the center and transforms into a toroidal structure with a torus.

As we know, when amphiphilic molecules are exposed to water, they organize themselves into a bilayer membrane with all of their hydrophobic tails pointing toward the center of the bilayer. A difference in repulsive interactions between the two different hydrophilic blocks in amphiphilic diblock copolymers introduces an asymmetry in the bilayer, resulting in a spontaneous curvature. Following Markvoort et al.,\(^7\) a bilayer with two large domains consisting of amphiphilic diblock copolymers is simulated in a periodic box to obtain the spontaneous curvature. Specifically, in the left half of the bilayer, the lower layer consists of hydrophilic particle C while the upper layer of hydrophilic particle A. In the right half of the bilayer this is exactly the other way around, such that two domains with opposite curvature are formed. In the DPD simulations, the bilayer membrane is oriented perpendicular to the \( x \)-axis, and the area of the \( yz \)-plane is changed in order to control the bilayer tension to be constant with the given value.

A resulting highly curved bilayer membrane in the case of amphiphilic diblock copolymers \( A_1B_4/C_1B_4 \) is shown in Fig. 8(a). When we decrease the length of hydrophobic block from \( n = 4 \) to 3, a bilayer membrane with a higher curvature is obtained; see Fig. 8(b). Here again, the domains in the upper and lower layers of opposite type remain coinciding for the curved bilayer. The spontaneous curvature of the bilayer membrane can be estimated by comparing the curves obtained from the DPD simulations with predictions for membrane shapes from a spontaneous curvature model.\(^23\) From comparison of the curves with the bilayer membranes, an approximate spontaneous curvature of \( \kappa = 0.045 \) is obtained for \( A_1B_3/C_1B_3 \) amphiphilic diblock copolymers, \( c = 0.09 \) for \( A_1B_4/C_1B_4 \) amphiphilic diblock copolymers, and 0.012 for \( A_1B_3/C_1B_3 \) amphiphilic diblock copolymers, which indicates that the spontaneous curvature value is increased with the decrease of the hydrophobic block length.

Thus, the vesicle will respond differently to the increase of the spontaneous curvature and adjust its shape according to its globe factors, including interactions between different types of hydrophobic particles, the reduced volume and the bending elastic energy for the closed and finite-sized bilayer vesicles.

4. Conclusion

In this paper, we studied shape transformations of bilayer vesicles by particle-based models of two-component amphiphilic diblock copolymers using the dissipative particle dynamics (DPD) approach. A plethora of complex vesicle shapes, including axisymmetric ones like sphere shapes, oblate shapes, pear shapes and dumbbell shapes, as well as non-axisymmetric ones like boomerang shapes, three- and four-armed starfish shapes, are obtained in the DPD simulations. The results are in agreement with previous experimental as well as theoretically predicted shapes, but our simulations also show some differences and moreover allow the study at a molecular level; thus, to be able to fully predict the shapes of our relatively small vesicles, the theoretical models should be extended to include explicitly the bilayer thickness. The simulations also show that the actual discretization of the building blocks of amphiphilic molecules exerts a considerable influence on the shape transformations of polymer vesicles, and the appearance of more pronounced multi-armed vesicle shapes is a consequence of finite thickness of polymer bilayer membrane. These findings demonstrate that the shape transformations for lipid vesicles is also possible for polymer vesicles and confirm that the DPD method is an effective but simple simulation technique for understanding the behavior of polymer vesicles.

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