

Supplementary Material for Charge Asymmetry Suppresses Coarsening Dynamics in Polyelectrolyte Complex Coacervation

Shensheng Chen and Zhen-Gang Wang*
Division of Chemistry and Chemical Engineering,
California Institute of Technology, Pasadena, CA 91125

A. Other simulation details

As per convention in DPD, the reduced number density is set to $\rho = 3.0$. The characteristic time scale is given by $\tau = \sqrt{mr_c^2/k_B T}$. The integration time step is set to $\delta t = 0.05\tau$. To prepare 125 pairs in large systems for studying coarsening dynamics, we first equilibrate one pair with a given λ in a $12r_c \times 12r_c \times 12r_c$ simulation box for $10^2\tau$, we then duplicate the small system 5 times in each direction to make the 125-pair systems in a $60r_c \times 60r_c \times 60r_c$ box. The positions and orientations of the polyion pairs become randomized on the order of $\sim 10\tau$, which is much shorter than the onset of coarsening ($> 100\tau$). The total simulation time is $5 \times 10^4\tau \sim 10^5\tau$. All the simulations are performed using the LAMMPS [1] platform.

B. PMF calculation between two polyion pairs

We use the adaptive bias force (ABF) algorithm [2, 3] implemented in LAMMPS [4] to calculate the PMF between two polyion pairs in a simulation box of $24r_c \times 12r_c \times 12r_c$. The center of mass distance r in the PMF calculation ranges from $0r_c$ to $15r_c$. The distance range is divided into consecutive windows of $0r_c \sim 1r_c$, $1r_c \sim 3r_c$, $3r_c \sim 6r_c$, $6r_c \sim 10r_c$ and $10r_c \sim 15r_c$ to improve the efficiency of the PMF calculations [3]. Each window is further divided into bins with equal width $0.1r_c$. The PMF in all windows reaches convergence before $5 \times 10^5\tau$.

C. Stability of a single droplet

To test the stability of a single droplet under charge asymmetry condition, we start our simulations with a single large, well-mixed droplet, and then turn on electrostatic interaction with a given charge asymmetry. Figure S1 shows that under good solvent condition ($\Delta a = 0$), droplets with $\lambda = 0.78, 0.82$ split into multiple clusters after we turn on electrostatics, indicating the equilibrium state at these asymmetry conditions should consist of multiple net-charged clusters. For $\lambda = 0.86$, the droplet stays stable during our simulation. However, this state

might still be a metastable state as the multi-cluster state

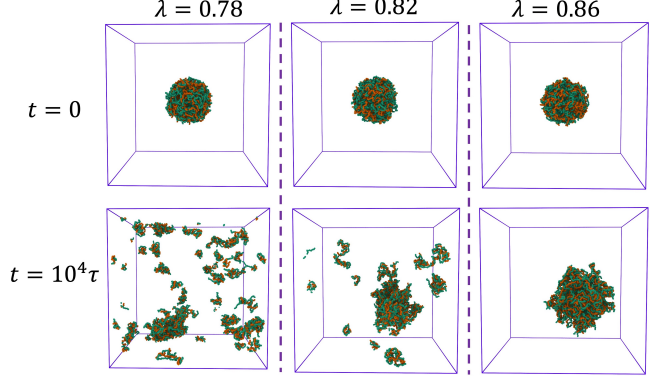


FIG. S1. Simulations starting a single well-mixed droplet at $\lambda = 0.78, 0.82, 0.86$, then turn on the electrostatics at good solvent condition.

could have lower free energy but might require high activation energy to split from a single droplet state.

D. Polarization between two charge-balanced droplets

To study the polarization as two charge-balanced pairs approach each other, we calculate the electric dipole moment of each pair given by $\vec{P}_\alpha = \sum_i q_{\alpha,i} \vec{r}_{\alpha,i}$, where $q_{\alpha,i}$ is the charge on monomer i and $\vec{r}_{\alpha,i}$ is its vector position, and the sum is over all monomers in pair α ($\alpha = 1, 2$). The total dipole of the system is then $\vec{P} = \vec{P}_1 + \vec{P}_2$. $P_{||}$ is the projection of the total dipole moment onto the center-of-mass vector between the two pairs. Since by symmetry, $\langle P_{||} \rangle = 0$, we characterize the polarization by the second moment, $\langle P_{||}^2 \rangle$.

In Fig. S1, we show $\langle P_{||}^2 \rangle$ for three values of $\Delta a = 0, 10$, and 25 . Polarization is stronger in systems with smaller Δa , with higher peak and wider range. Poorer solvent condition (larger Δa) results in weaker polarization, due to the compactness of the droplets.

* zgw@caltech.edu

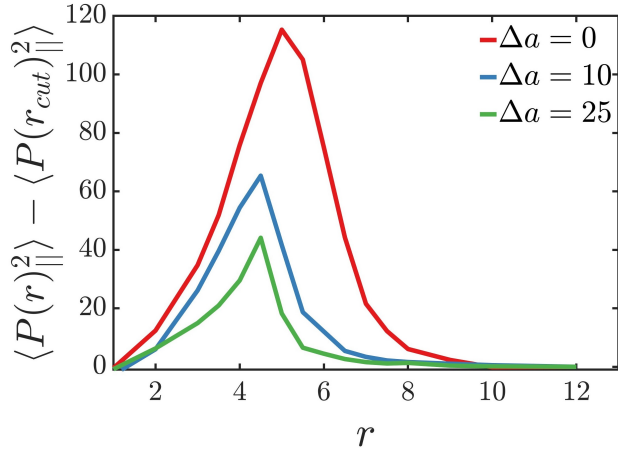


FIG. S2. Fluctuation of the longitudinal component of the polarization $\langle P_{||}^2 \rangle$ as a function of the center-of-mass distance between the two polyion pairs under different solvent conditions. $r_{cut} = 12r_c$.

- [1] S. Plimpton, Fast Parallel Algorithms for Short-Range Molecular Dynamics, *Journal of Computational Physics* **117**, 1 (1995).
- [2] E. Darve, D. Rodríguez-Gómez, and A. Pohorille, Adaptive biasing force method for scalar and vector free energy calculations, *The Journal of Chemical Physics* **128**, 144120 (2008).
- [3] J. Comer, J. C. Gumbart, J. Hénin, T. Lelièvre, A. Pohorille, and C. Chipot, The Adaptive Biasing Force Method: Everything You Always Wanted To Know but Were Afraid To Ask, *The Journal of Physical Chemistry B* **119**, 1129 (2015).
- [4] G. Fiorin, M. L. Klein, and J. Hénin, Using collective variables to drive molecular dynamics simulations, *Molecular Physics* **111**, 3345 (2013).