Supplementary Materials: Reaction-Diffusion Waves Coupled with Membrane Curvature

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SUPPLEMENTARY NOTES

Linear stability analysis

The fixed point (u_s, v_s) of reaction equations (2) and (3) is determined by solving $f(u,v)=0$ and $g(u,v)=0$:

$$u_s = \frac{2}{1+\sqrt{1+\frac{4}{A}}}, v_s = \frac{B}{u_s}.$$

Thus, $u_s \to 0$ at $A \to 0$ and $u_s \to 1$ at $A \to \infty$. It is the crossing point of the two nullclines in Fig. S1a. For a small perturbation $(\delta u, \delta v)$ around the fixed point, we determine the equations of the first order in δu and δv as follow:

$$\frac{\partial}{\partial t}\begin{pmatrix}\delta u\\ \delta v\end{pmatrix} = \mathbf{J}\begin{pmatrix}\delta u\\ \delta v\end{pmatrix},$$

$$\mathbf{J} = \begin{pmatrix} B - S_u + D_u\nabla^2 & {u_s}^2 \\ -B & -{u_s}^2 + D_v\nabla^2 \end{pmatrix},$$

$$S_u = \frac{u_s}{1-u_s}\left(\frac{1}{1-u_s}+1\right).$$

For a quasi-spherical vesicle, we obtain

$$\mathbf{J}_l = \begin{pmatrix} B - S_u - D_u\dfrac{l(l+1)}{r^2} & {u_s}^2 \\ -B & -{u_s}^2 - D_v\dfrac{l(l+1)}{r^2} \end{pmatrix},$$

based on the spherical harmonic expansion, where r is the radius of the sphere and $-l(l+1)$ is an eigenvalue of the Laplace–Beltrami operator ∇^2. In the present model, the conditions for the Hopf and Turing bifurcations are $B > S_u + {u_s}^2$ and $B >$

$\left(\sqrt{S_u} + u_s\eta\right)^2$, respectively, where $\eta = \sqrt{D_u/D_v}$. The phase diagram for $A = 1$ is presented in Fig. S1b.

Potentials for molecular dynamics simulation

For the molecular dynamics simulation in this study, we use the potential $U = U_S + U_V + U_\mathrm{b} + U_\mathrm{r} + U_\mathrm{cv}$, where U_S and U_V are surface area and volume constraint potentials, U_b and U_r are bond and repulsive potentials, and U_cv is a bending potential of membranes (F_cv is discretized using dual lattices). The constraint potentials are written as below:

$$U_S = \frac{1}{2}k_S(S - S_0)^2,$$

$$U_V = \frac{1}{2}k_V(V - V_0)^2,$$

where k_S and k_V are constraint coefficients, S_0 and V_0 are references of surface area and volume, respectively. We use the following parameter values:

$$k_S = \frac{4k_\mathrm{B}T}{a^2}, k_V = \frac{2k_\mathrm{B}T}{a^3}, S_0 = 0.41(2N - 4), V_0 = \frac{4\pi R^3}{3}V^*.$$

For the bond and repulsive potentials, we employ a well-like potential, which has broad and flat bottom and exhibits a rapid increase to ∞ at $l_{\mathrm{c}0} = 1.15a$ (bond) and at $l_{\mathrm{c}1} = 0.85a$ (repulsion). More details of the potential and method are described in Refs. 28 and 29.

Wave speed calculation method

The wave speed is calculated based on the distance traveled by the wave front per 0.1τ. We determined that spatial waves exist when $u_\mathrm{max} > 0.6$ and $u_\mathrm{max} - u_\mathrm{min} > 0.5$, where u_max and u_min are the maximum and minimum values of u on the vesicle, respectively. When waves exist, we identify the vertices for $u > 0.6$ as belonging to the wave region and the vertices adjacent to the nonwave regions as the wave edges (i.e., vertices on the inner boundaries between the wave regions and nonwave regions). The front edge is determined by the condition of v at the vertices, $v \geq v_\mathrm{min} + 0.4(v_\mathrm{max} - v_\mathrm{min})$, where v_max and v_min are the maximum and minimum values of v on the vesicle, respectively, because when the reaction-diffusion waves propagate, the

oscillation phase of v should shift from that of u toward the propagation direction (Fig. S2). If the wave topology does not change (i.e., when the waves do not merge or split) and the wave front has more than 10 vertices, we calculate the minimum displacement from each vertex to the vertices at the edge of the wave at the previous or next coordinates (vertex coordinates at time $\pm 0.1\tau$). If the standard deviation of the minimum displacement for each vertex is greater than $0.5a$, the calculation is rejected, if not, we calculate the average displacement as the distance traveled by the wave front.

SUPPLEMENTARY FIGURES

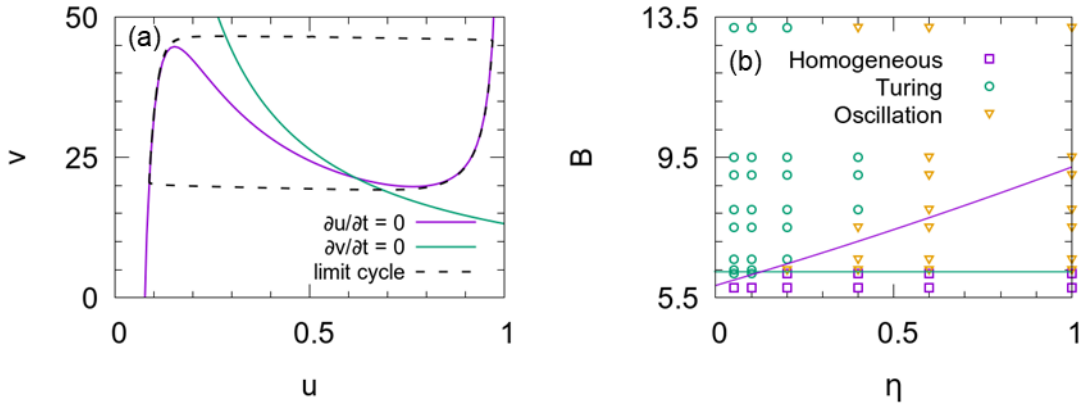

Fig. S1 (a) Phase plane of the Brusselator model with the modified protein unbinding process for $A = 1$ and $B = 13.2$. (b) Phase diagram for a spherical vesicle ($V^* = 1$) at $A = 1$ and $D_u = 4$ in the absence of membrane curvature feedback to the Brusselator. The purple and green lines on the phase diagram represent the Turing and Hopf bifurcation curves, respectively. The symbols represent the simulation results.

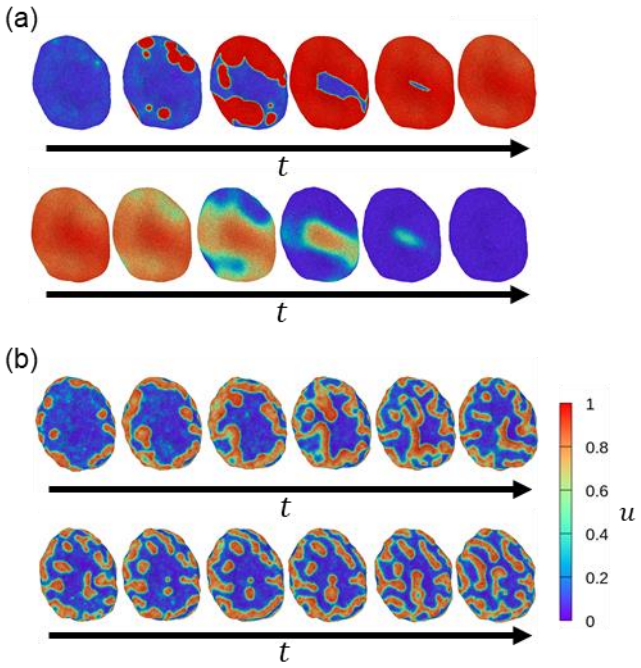

Fig. S2 Example snapshots of the pattern formation on discocyte-shaped vesicles ($V^* = 0.65$) for (a) $C_0R = 1, \kappa_1/\kappa_0 = 2$, and $D_u = 4$, and (b) $C_0R = 8, \kappa_1/\kappa_0 = 1$, and $D_u = 4$. The color indicates the concentration of the curvature-inducing protein u. Each frame step is 0.5τ for (a) and 2τ for (b).

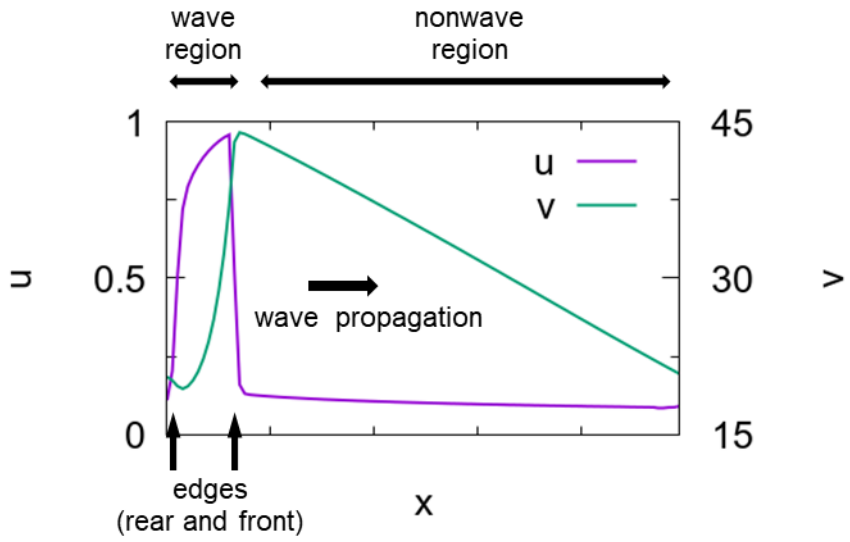

Fig. S3 Protein concentration profiles in a propagating wave in one-dimensional space. The front and rear wave edges have different concentrations of v because of the phase shift between u and v.

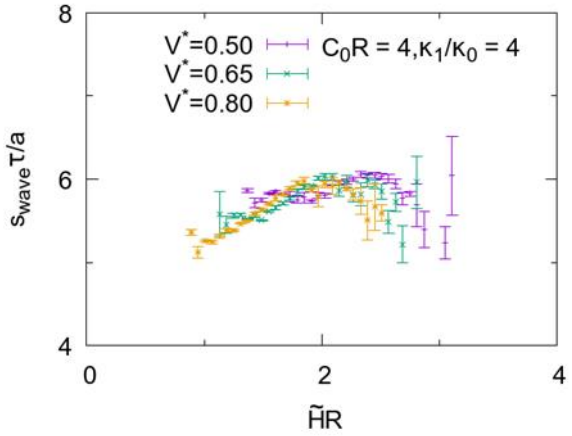

Fig. S4 Relationship between the membrane curvature and wave speed at $\kappa_1/\kappa_0 = 4, C_0R = 4, D_u = 1$, and $N = 15994$ for prolate shapes with $V^* = 0.5, 0.65,$ and 0.8.

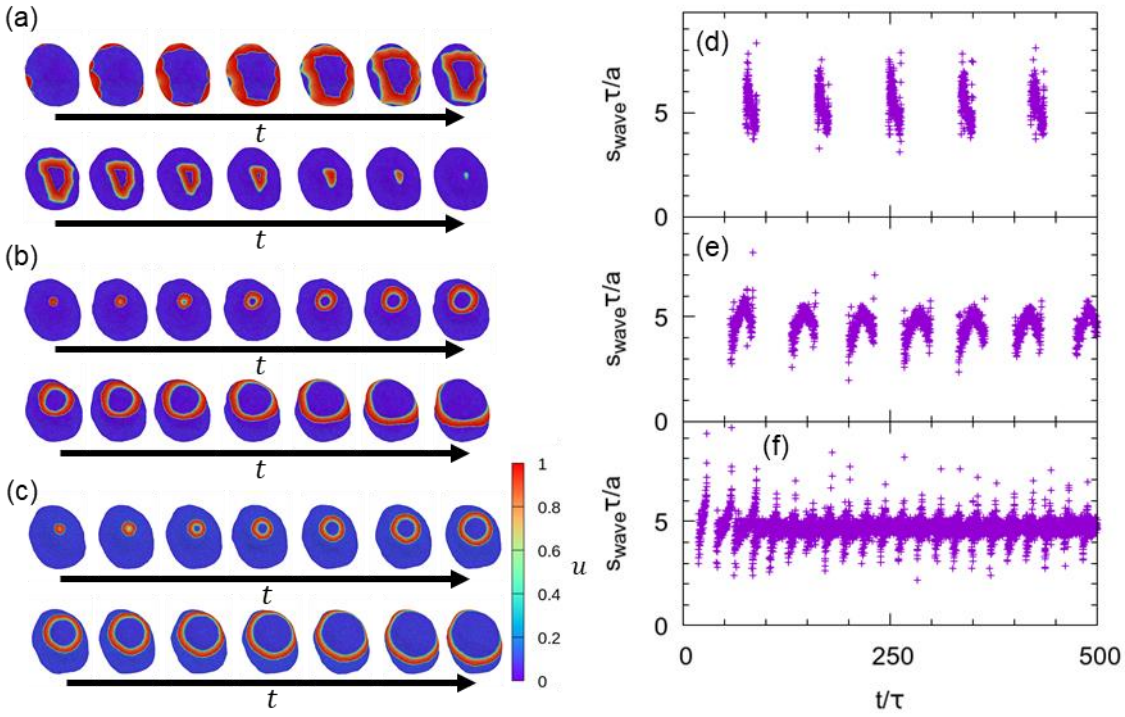

Fig. S5 (a–c) Typical sequential snapshots of the propagating reaction-diffusion waves for $N = 15994, V^* = 0.65, \kappa_1/\kappa_0 = 4, C_0R = 4,$ and $D_u = 1$ (a) with mechanochemical feedback and without a stimulated vertex, (b) with mechanochemical feedback and a stimulated vertex, and (c) without mechanochemical feedback and with a stimulated vertex. The color indicates the concentration of the curvature-inducing protein, u. Each frame step is τ. The corresponding movies are included in the ESI (Movie S4). (d–f) Time development of the wave speed under conditions corresponding to (a–c), respectively.

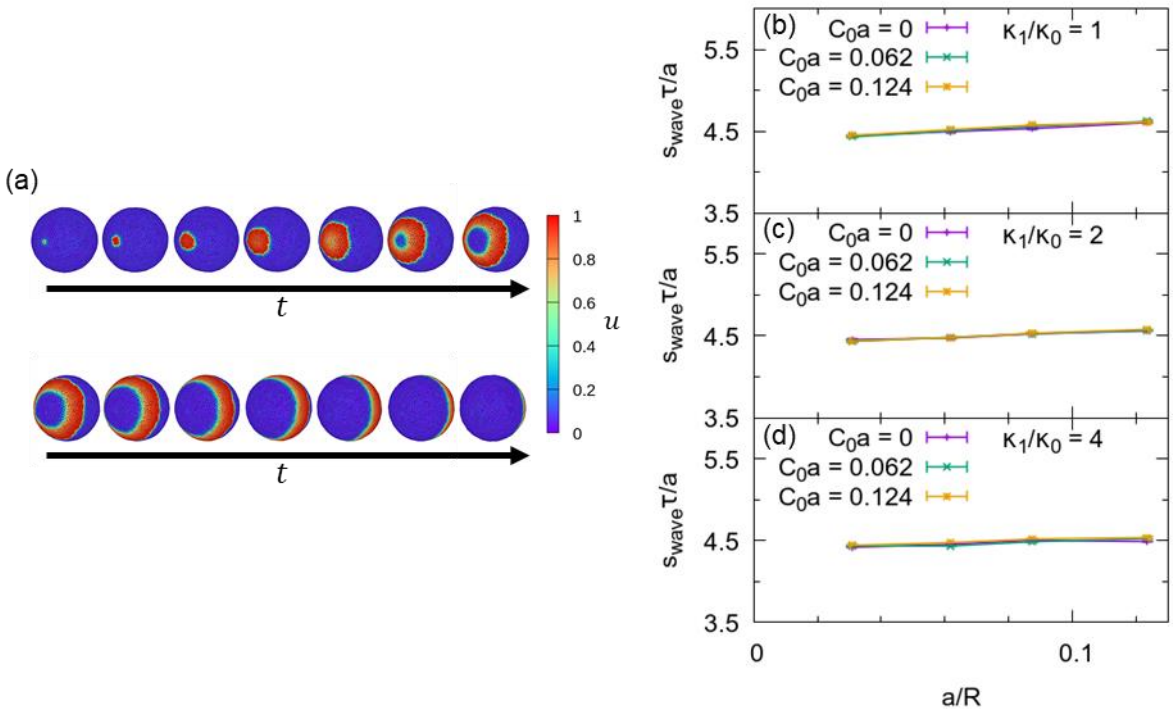

Fig. S6 (a) Example snapshots of the propagating waves on a spherical vesicle for $N = 4000, C_0a = 0.124$ $(C_0R = 2)$, and $\kappa_1/\kappa_0 = 4$. Each frame step is τ. (b–d) Wave speed for $N = 1006, 2004, 4000, 15994$ and $V^* = 1$ with a stimulated vertex and without mechanochemical feedback for $\kappa_1/\kappa_0 = 1, 2, 4,$ respectively.

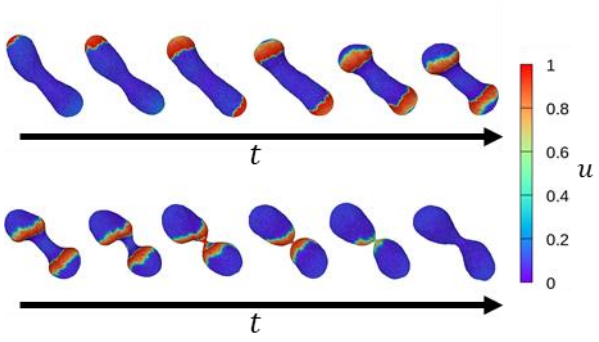

Fig. S7 Self-oscillation of a vesicle shape due to coupling between the membrane curvature and reaction-diffusion system for $N = 4000, \kappa_1/\kappa_0 = 4, C_0R = 4, D_u = 1, \tau = 400,$ and $V^* = 0.65$. Sequential snapshots of the shape oscillation. The color indicates the concentration of the curvature-inducing protein u. Each frame step is 1.25τ.

MOVIE CAPTIONS

Movies S1–S3. Propagating waves on deformable vesicles. Each frame step is 0.5τ. The data are the same as those depicted in Figs. 2b, e, and f, respectively. S1: $C_0R = 4, \kappa_1/\kappa_0 = 4,$ and $V^* = 0.8$. S2: $C_0R = 8, \kappa_1/\kappa_0 = 2,$ and $V^* = 0.65$. S3: $C_0R = 8, \kappa_1/\kappa_0 = 1, D_u = 16,$ and $V^* = 0.65$.

Movie S4. Propagating reaction-diffusion waves for $N = 15994, V^* = 0.65, \kappa_1/\kappa_0 = 4, C_0R = 4,$ and $D_u = 1$ with and without mechanochemical feedback (w/M and w/oM, respectively) and a stimulated vertex (w/S and w/oS, respectively). Each frame step is 0.5τ. The data are the same as those shown in Fig. S5a–c.

Movie S5. Self-oscillation of vesicle shapes for $N = 4000, V^* = 0.65, \kappa_1/\kappa_0 = 4, C_0R = 4, D_u = 4,$ and $\tau = 400$. Each frame step is 0.25τ. The data are the same as those shown in Fig. 6a.