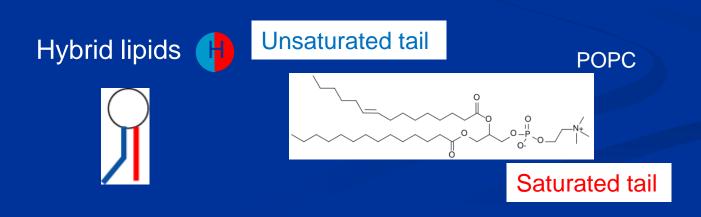
Line activity of hybrid lipids: stabilization of membrane rafts?

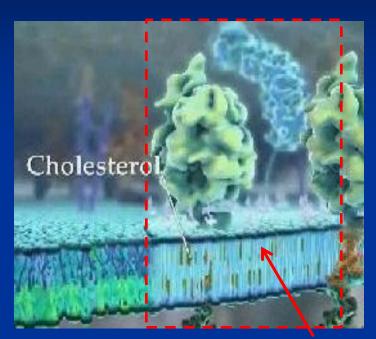
Tetsuya Yamamoto, Robert Brewster, Phil Pincus*, SAS

Department of Materials and Interfaces, Weizmann Institute of Science

*Materials Research Laboratory, University of California Santa Barbara



Lipid raft hypothesis – biological systems



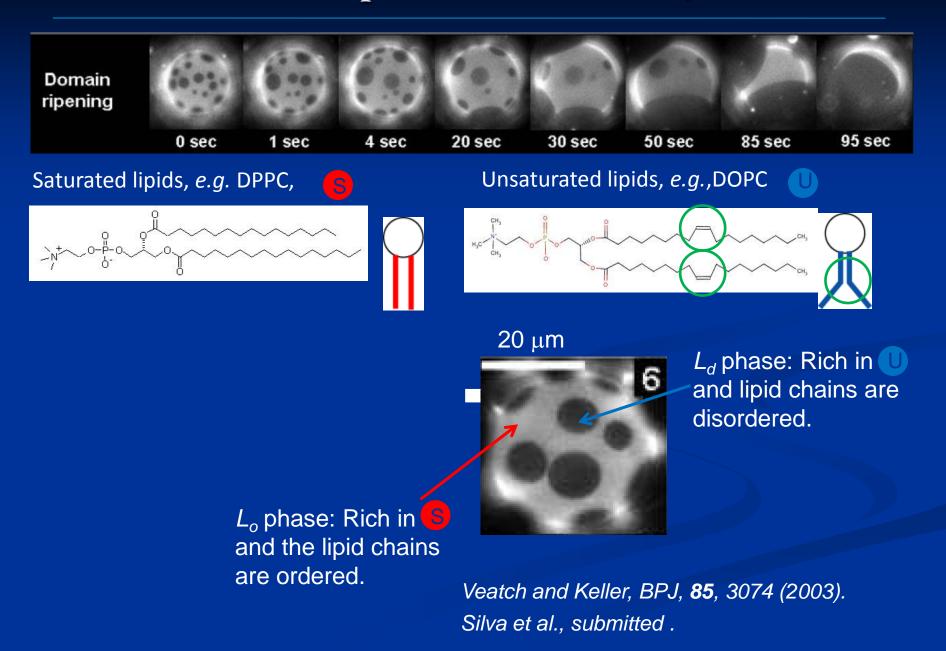
Lipid raft

(From: The Inner Life of the Cell http://multimedia.mcb.harvard.e du/anim_innerlife.html)

Lipid raft : small domains in biological membranes — controversial!

- Rich in saturated lipids
- Metastable or even stable
- The size of the domain is of the linear order of 10 − 100 nm.

Domains in lipid vesicles – DPCC, DOPC

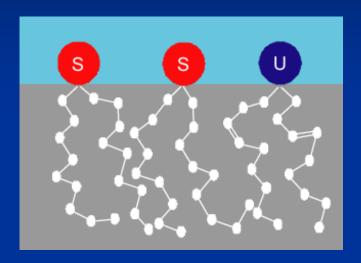


Phase separation: macroscopic or finite domains in lipid mixtures

- Phase separation implies positive line tension: separate into macroscopic domains
- How can finite domains be stable (in equilibrium)?
- Line active species reduces interfacial free energy: line analogy of surfactants
- Here, "lineactant*" chains match the two phases: only chain packing needed to explain effect

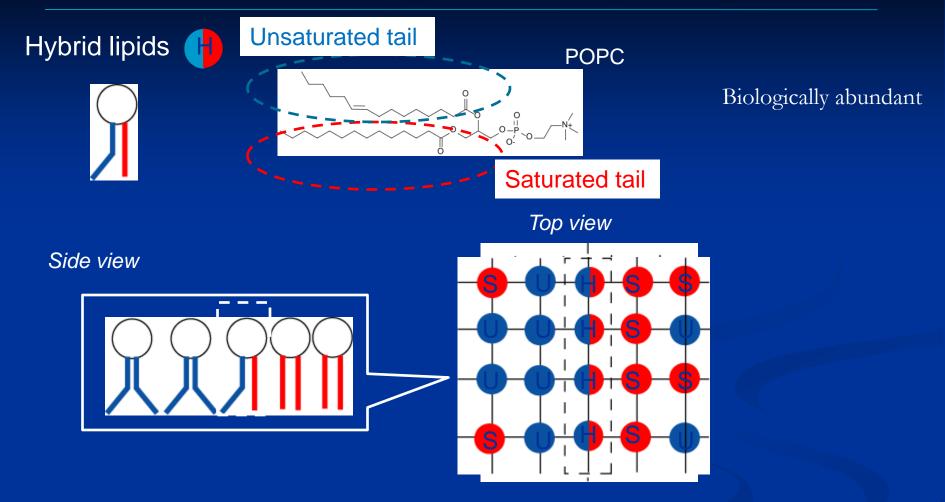
Chain packing theory of macroscopic phase separation

Chain packing "frustration" of saturated/unsaturated lipids is the driving force of phase separation of lipid membrane



- Phenomenological potential chain order
- Packing entropy
- Incompressibility of hydrophobic core

Line activity of hybrid lipid: reduces packing frustration



Line tension is reduced to zero for strong interaction (or low temperature).

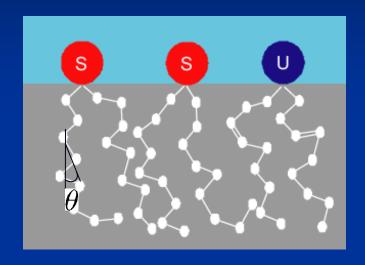
R. Brewster, P. A. Pincus, and S. A. Safran, Biophys. J., 97, 1087 (2009) and R. Brewster, S. A. Safran, Biophys. J. Lett., in press.

Objective

What is role of chain ordering in line activity of



?



Liquid crystal order parameter

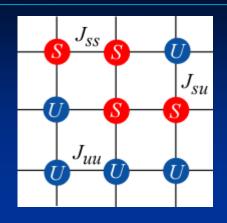
$$S = \langle \frac{3\cos^2\theta - 1}{2} \rangle \quad -0.5 \le S \le 1$$

θ: The angle between the bilayer normal and chain segment

Liquid crystal model to analyze how chain ordering drives phase separation and line activity of hybrid lipids

Lattice model for membrane without hybrid lipids

Lipids



Assumption:

The order parameter for U is ~ 0 , $(S_u \sim 0)$, because entropy >> interaction.

Mixing entropy

$$\psi(\mathbf{r})$$
: Local concentration of

$$G_{\mathsf{mix}} = k_B T[\psi(\mathbf{r}) \ln \psi(\mathbf{r}) + (1 - \psi(\mathbf{r})) \ln(1 - \psi(\mathbf{r}))]$$

Interaction energy

(favorable when neighboring chains are ordered - only interactions due to chain ordering)

$$G_{\text{int}} = -\frac{1}{2}J_{\text{SS}}\psi^2(\mathbf{r})S_s^2(\mathbf{r})$$

 $S_s({f r})$: Chain order parameter for

S

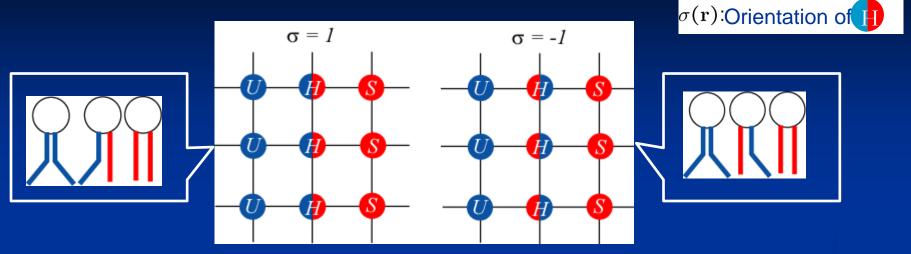
Entropy loss due to chain ordering

$$G_{\text{conf}} = 2k_B T[u_s S_s^4 - w_s S_s^3 + r_{0s} S_s^2] \psi(\mathbf{r})$$

P. G. de Gennes and J. Prost, The Physics of Liquid Crystals

Lattice model for membrane with





Orientation **dependent** part of the interaction energy

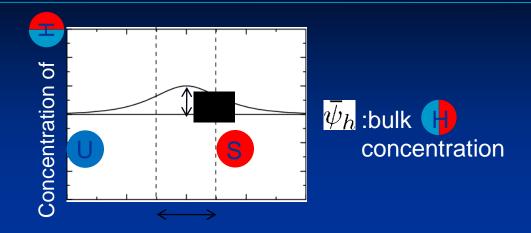
$$-\frac{1}{2}J_{SS}S_s(\mathbf{r})\psi_h(\mathbf{r})\sigma(\mathbf{r})\nabla(S_s(\mathbf{r})\psi(\mathbf{r}))$$

$$\psi_h({f r})$$
:
Local composition of

Orientational entropy

$$k_BT[rac{1+\sigma(\mathbf{r})}{2}\lnrac{1+\sigma(\mathbf{r})}{2}+rac{1-\sigma(\mathbf{r})}{2}\lnrac{1-\sigma(\mathbf{r})}{2}]\psi_h(\mathbf{r}).$$

Weak interaction (high temperature)



Line tension

$$\lambda = \lambda_0 \sqrt{1 - \alpha \psi_h^{\text{int}}} \quad \alpha > 0$$

 λ_0

:Line tension for S + U system with no hybrid

However, concentration of department adsorbed at interfaces is not enough to reduce the line tension to zero near critical point.

Strong interaction (low temperature)

Line tension

$$\psi_h^{\mathsf{int}} o \mathbf{1}$$

Width of interface ξ ~ Molecular size

Complete orientation

$$\lambda ~\sim~ -rac{1}{2}J_{
m SS}S_{
m int}-k_BT\lnar{\psi}_h$$



Average of **|** in the bulk.

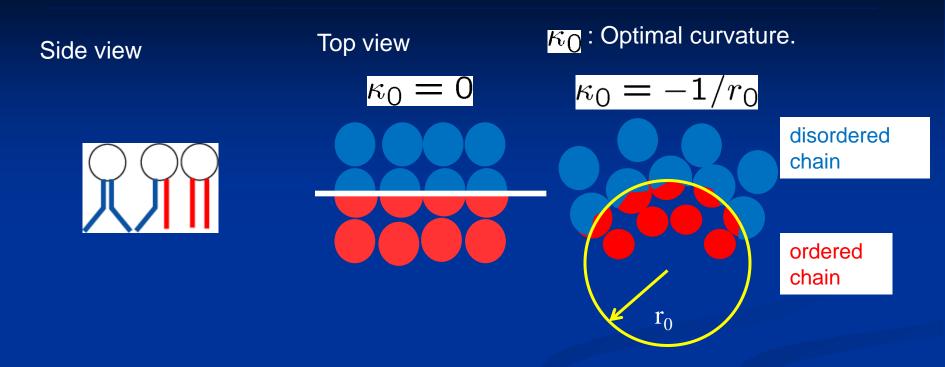




Chain order parameter of hybrid at the interface ~ 1

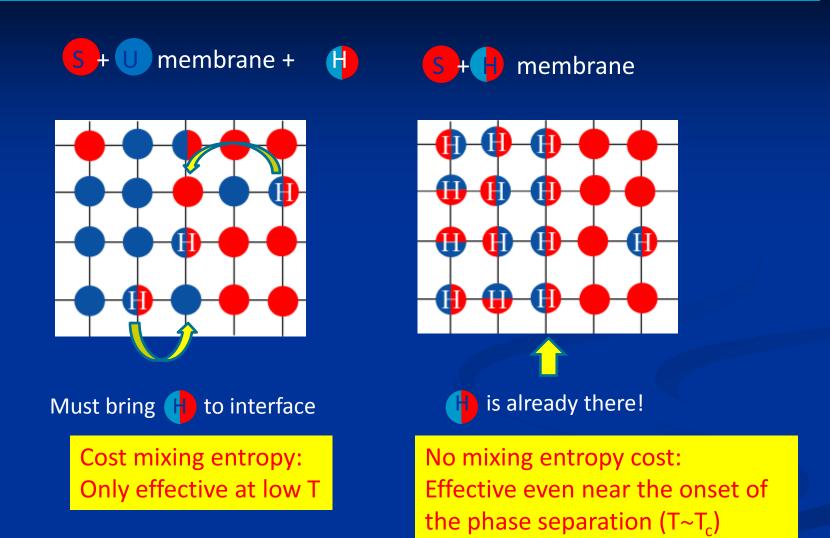
- Line tension is reduced to 0 with decreasing temperature
- Loss of mixing entropy limits this effect to low temperatures
 - Interfaces between domains stabilized by hybrid!
 - What is the stable size of the domains?

Domain size: 2D spontaneous curvature



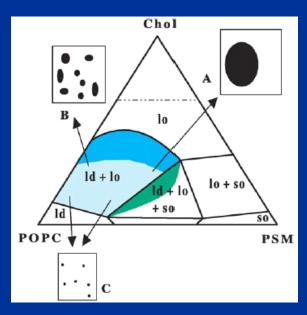
- Spontaneous curvature determines radius of domains stabilized by
- Subject to conservation constraints of S, U, and H (microemulsion)
- R. Brewster, SAS: Biophys. J. Lett., in press

Hybrid lipid more effective in line tension reduction in S+H

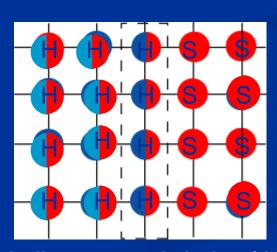


Hybrid + Saturated Lipids

- Hybrid saturated chain can have different order states
- In bulk (surrounded by other H) can be disordered
- Near interface with S phase will be more ordered
- Hybrid is line active in 2 component system due to the internal degree of freedom of chain order



(Almeida et al., JMB 2005)



Line active



Bulk



bulk: saturated chain of H disordered interface: saturated chain of H ordered H can be line active

Expts: Hybrid + Saturated

- Macroscopic or small domains
 - S+U+C clearly macroscopic
 - S+H+C ???
- Membranes of POPC, Palmitoyl SM, and cholesterol phase separate, in large domains (Veatch and Keller PRL 94, 148101 (2005)
- Type I (sat, unsat, chol) macroscopic phase separation
 Type II (sat, hybrid, chol) nanometric domains
 (Feigenson, Biochimia Biophys Acta, 2009)
- Ziblat et al. POPC needed to stabilize the membrane for experiments

Almeida et al., JMB 2005 Silva et al. – to be published

