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Active Thermodynamics of Cell Membranes

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Active thermodynamics of cell membranes

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 Introduction: Microvilli
 Microvilli height distribution
 Microvilli organization and morphology
 Conclusions and future directions: Neurons

Introduction: Microvilli





20.0 x 20.0 μ living epithelial cell (A6 cell line)

J. Gorelik et. al. ; PNAS 100, 5819-5822 (2003)



BLOOD (2004) <u>104</u>, 1396.

Mol. Cell. Endo. <u>217</u> (2004) 101

Introduction: Microvilli

Actin bundles:



Dynamic:

J. Gorelik et. al. ; PNAS 100, 5819-5822 (2003)

Microvilli

Schematic picture:



Actin polymerization driven motion



Our model: link actin polymerization with membrane curvature



Dynamics of Membranes Driven by Actin Polymerization

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Filopodia: Membrane proteins at the tip

Phospho-tyrosine -(PY), Cdc42, Src etc.

> Do these active proteins have a positive spontaneous curvature ?



Estuardo Robles, Stephanie Woo, and Timothy M. Gomez The Journal of Neuroscience, August 17, 2005 • 25(33):7669 –7681

Filopodial tip complex

 Also important are bundling proteins such as Fascin Tip contains formins, protecting actin from capping



Tatyana M. Svitkina,¹ Elena A. Bulanova,² Oleg Y. Chaga, Danijela M. Vignjevic,¹ Shin-ichiro Kojima, Jury M. Vasiliev,² and Gary G. Borisy The Journal of Cell Biology, Volume 160, Number 3, February 3, 2003 409–421



Equation of motion

$$\frac{\partial h}{\partial t} = -\omega h + An$$

Where:
$$\omega \propto F_0 / h_c$$
Restoring force $v_0 = A \langle n \rangle$ Growth velocity

And a noise term:

$$\left\langle \left(n - \left\langle n \right\rangle \right)^2 \right\rangle \neq 0$$

Microvilli: Height distribution

Observations:



J. Gorelik et. al. ; PNAS 100, 5819-5822 (2003)

Microvilli: Height probability distribution

From the equation of motion
→ Fokker-Planck equ.:

$$\frac{\partial P}{\partial t} = \frac{\partial}{\partial h} (\omega h P) + \frac{1}{2} \frac{\partial^2 P}{\partial h^2} \frac{A}{\omega} \langle n^2 \rangle - \frac{\partial P}{\partial h} A \langle n \rangle$$

At steady-state we get: $\partial P / \partial t = 0$

$$\Rightarrow P(h) = R_n e^{2hv_0/D_h} e^{-h^2\omega/D}$$

where:
$$D_h = A^2 \langle n^2 \rangle / \omega = (\Delta n / n_0)^2 v_0^2 / \omega$$

Describes the distribution of tip activity

Fluctuations in the size of the MV tip

Aggregation driven by spontaneous curvature:





Thermal

noise!

$$\left\langle n^2 \right\rangle = \frac{k_B T}{\partial^2 E_n / \partial n^2} \approx n_0^2 \frac{k_B T}{\kappa} \Longrightarrow \left(\frac{\Delta n}{n_0}\right)^2 \approx \frac{k_B T}{\kappa}$$

Typically $\kappa \sim 5-20 \text{ k}_{\text{B}}\text{T}$

Microvilli: Height probability distribution





MV-MV attractive interactions:

 $E_{curv} \geq E_{bend} \implies h_{ridge}$

Reduced membrane curvature energy between the MV:

 πK

 $\frac{\pi}{R}$

 $E_{bend} \approx$

Increased curvature energy of flattened tip:

Min. height for ridge:

Microvilli: ridges & height distribution

MV of unequal heights attract each other less then MV of equal heights

Additional restoring force:

$$-\omega(h-h_{nn})$$

MV in ridges: Height prob. distribution

Ridge height equation of motion:

$$\frac{\partial h}{\partial t} = -\omega h + A n_0 - \omega (h - h_{nn})$$

Exponential tails: due to force saturation

human blood lymphocyte

S. Majstoravich et. al. ; BLOOD (2004) 104, 1396.

Long Microvilli: Force saturation

Long MV: Height probability distribution

Dynamic → T_{eff}
 <u>"Thermodynamic</u>
 <u>"phase diagram</u>

 Linear aggregates due to positive spontaneous curvature of tip complex

T. Tlusty & S. Safran; Science <u>290</u> (2000) 1328

2D dipolar fluid, network of worm-like micelles etc.

- Assume single height of MV: <h>
- Excluded volume interactions
- Defects: free ends and 3-fold junctions

<u>Based on:</u> Zilman, A; Safran, S.A.; Sottmann, T.; Strey, R.; *Langmuir,* **20** 2199 (2004).

Microvilli: Energy of defects

Formation of networks

If the MV height increases, junctions multiply over ends:

Phase transition to a connected network:

 $\partial^2 F_{\prime}$ = 0

Spinodal

Free energy of gas of defects

$$F(\phi)/k_BT = (1-\phi)\ln(1-\phi) + \phi_e(\ln\phi_e - 1) + \phi_j(\ln\phi_j - 1)$$

+ $\phi_e\epsilon_e + \phi_j\epsilon_j - \frac{1}{2}\phi_e\ln\phi - \frac{3}{2}\phi_j\ln\phi$

 Φ is the area fraction of the MV $\Phi_e \& \Phi_j$ is the area fraction of the ends and 3-fold junctions respectively

Minimize with respect to independent defects' concentrations:

$$\phi_j = \phi^{3/2} e^{-\epsilon_j}$$
$$\phi_e = \phi^{1/2} e^{-\epsilon_e}$$

Using: *κ*=10 k_BT, *h*=400nm

Percolation line

Note: Large "effective" temperature

Using: κ =10 k_BT, ϕ =0.05

Percolation line

height-density phase diagram

Does it really behave as "active"thermodynamics ?

5.0 kV X1.50K 20.0.m

J. Gorelik et. al.

 Phase separation ? • What changes between cells ? • Equilibrium between systems in contact?

Conclusions

Spontaneous curvature of membrane proteins that activate actin polymerization drives Microvilli dynamics and morphology. Coupling of active and thermal fluctuations on different length and time scales: "Active-Thermodynamics"

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Theory

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Multi-scale Modeling

Thermal & actin-driven aggregation \rightarrow Tip formation

Thermal & actin-driven aggregation of $MV \rightarrow Network$ formation

Experimental challenge:

We need to characterize the physical parameters of the protein aggregates at the membrane:

What is the spontaneous curvature ?