

Chromosome driven spatial patterning of proteins in bacteria

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Short Abstract — Asymmetric cell division in *Caulobacter crescentus* involves differentially positioning proteins between the mother and future daughter cell at the dividing cell's poles. It has been found that the polymerizing protein PopZ plays a major role in marking and capturing other proteins at the poles. But how PopZ itself achieves polar localization remains a mystery. We have developed a simple model for PopZ localization driven solely by attractive polymerizing interactions and self-avoidance with the bacterial chromosome. By changing either the volume fraction of PopZ or the chromosome we can reproduce the varied localization patterns that PopZ shows in experiment.

I. INTRODUCTION

THE organized spatial patterning of proteins in bacteria plays an important role in many cell biological processes from chemotaxis to cell division [1]. To what extent do these patterns emerge spontaneously or are they actively formed? The patterning of chemotaxis receptors (Che system) [2], the MinCDE system in *E. Coli* [3] and the polar localization of proteins in the asymmetrically dividing bacteria, *Caulobacter crescentus* [4] are examples where the patterns are thought to spontaneously form due to the specific molecular interactions in each system

In *C. crescentus*, different proteins localize at the two poles leading to the daughter cell adopting a different phenotype from the mother. Guiding this asymmetric localization is a scaffolding protein, PopZ that localizes to both poles [5, 6]. What mechanisms lead to the bipolar localization of PopZ? Experiments on PopZ localization have shown that it can go from diffuse to unipolar to bipolar patterns, even in *E. coli* in which no PopZ homolog exists [5, 6]. Further to these, experiments on filamentous cells showed that PopZ not only forms domains at the poles but also between the replicated chromosomes within the cells. This leads to the speculation that the polymerization of PopZ and DNA occlusion may be sufficient to drive PopZ's patterning [6], and that mechanisms such as membrane curvature may not be required to cause polar localization [7].

II. RESULTS

Here, we have conducted Monte Carlo simulations of a minimal physical model that produces all of the observed PopZ patterns. The bacterial chromosome is modeled as a self avoiding random walk. PopZ multimerization is modeled using particles with an attractive potential which allows PopZ domains to grow isotropically. There is no

interaction between the chromosome and PopZ other than self avoidance. The poles tend to be free of DNA providing an entropic force that drives PopZ domain formation there. PopZ domain formation depends on PopZ density and we predict that the various observed patterns can be explained due to either changes in the PopZ concentration or the volume fraction of the chromosome. We suggest new experimental tests that would further substantiate the model.

III. CONCLUSION

Using simulations, we have shown that protein multimerization along with DNA occlusion can be a sufficient mechanism to drive the spontaneous polar patterning of proteins in bacteria. The model shows that a transition from a unipolar to bipolar pattern can occur if the concentration of multimerizing protein increases, thereby breaking spatial symmetry, allowing for the possibility of differentiating the two poles. The patterning is driven in part from the entropy of the chromosome in addition to the energy gained from growing protein domains. This work extends prior theoretical [8, 9] and experimental work [7] that has focused on membrane curvature as the prime driving mechanism of polar protein localization.

REFERENCES

- [1] Shapiro L, McAdams HH, Losick R (2009) Why and How Bacteria localize proteins. *Science*. **326**, 1225.
- [2] Greenfield D et al., Self-Organization of the *Escherichia coli* Chemotaxis Network Imaged with Super-Resolution Light Microscopy. *PLoS Biol* 7(6): e1000137.
- [3] Raskin D, de Boer P (1999) Rapid pole-to-pole oscillation of a protein required for directing division to the middle of *Escherichia coli*. *PNAS*, 96: 4971-4976. And Hu Z, Lutkenhaus J (1999) Topological regulation of cell division in *Escherichia coli* involves rapid pole to pole oscillation of the division inhibitor Minc under the control of MinD and MinE. *Mol Microbiol* 34: 82-90.
- [4] Laub MT, Shapiro L, McAdams HH (2007) Systems Biology of *Caulobacter*, *annurev.genet.*41.110306.130346.
- [5] Bowman G. R. et al. (2008) A Polymeric Protein Anchors the Chromosomal Origin/ParB Complex at a Bacterial Cell Pole. *Cell*. Vol. **134**, 6, pp. 945-955.
- [6] Ebersbach G et al. (2008). A Self-Associating Protein Critical for Chromosome Attachment, Division, and Polar Organization in *Caulobacter*. *Cell*. Vol. **134**, Issue 6, pp. 956-968.
- [7] Lenarcic R. et al. (2009), Localization of DivIVA by targeting to negatively curved membranes. *EMBO J*. **28**, 2272.
- [8] Huang K.C., Mukhopadhyay R., Wingreen N. S., A Curvature-Mediated Mechanism for Localization of Lipids to Bacterial Poles. *PLoS Comput. Biol.* **2**, e151.
- [9] Howard M., (2004), A Mechanism for Polar Protein Localization in Bacteria, *J. of mol. Bio.* **335**, 2 P. 655-663.

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