

Physical modeling of active bacterial DNA segregation

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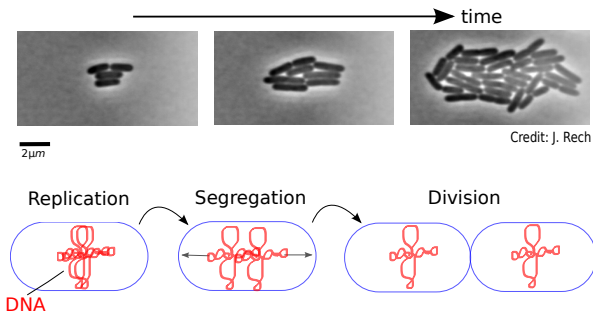
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Outline

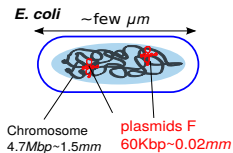
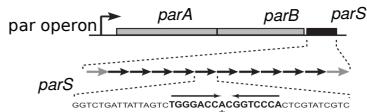
- 1 Bacterial DNA segregation: the system ParABS
- 2 Dynamics: partition complex surfing of protein waves

Segregation of bacterial DNA



How is the bacterial genome segregated ?

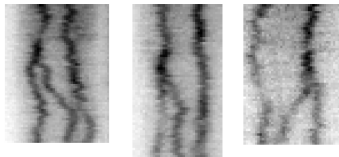
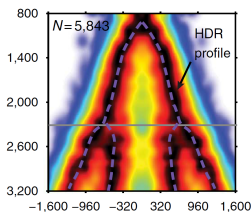
The ParABS operon



- ParA: “motor” protein (ATPase, Walker-type)
- ParB: binding protein (specific or non-specific binding)
- *parS*: centromere-like DNA sequence

Bacterial DNA segregation: experimental facts

Equipositioning of the complexes



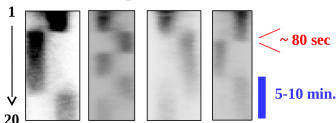
Bouet's team, LMGM, unpublished

Axial position, nm

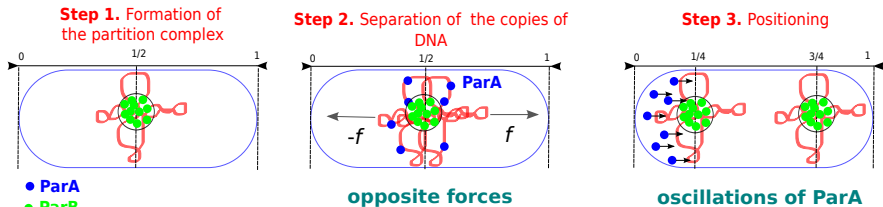


Le Gall et al, Nat. Comm. '16

Oscillations of ParA



How does ParABS work ?

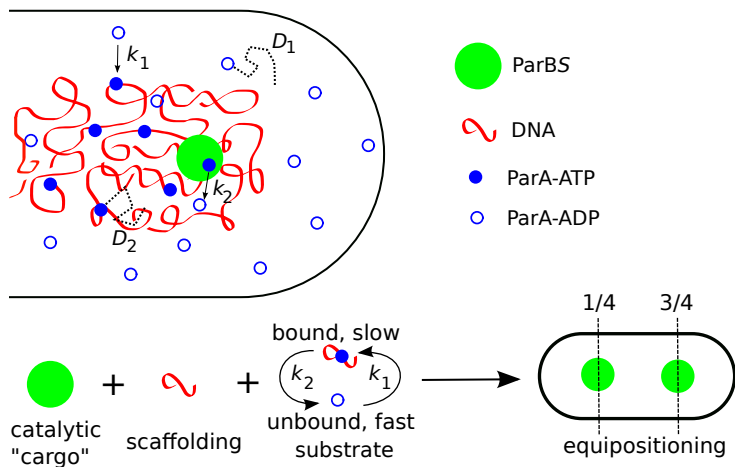


3 components:

- 2 proteins (ParA & ParB)
- specific binding sites (*parS*)

"Reaction-Diffusion"
or "Filament pulling"
mechanisms

Bacterial DNA segregation: interactions of ParABS



Dynamical steps: Reaction-Diffusion equations

$$\text{ParA} - \text{ADP} : \quad \frac{\partial u}{\partial t} = D_1 \Delta u - k_1 u(\mathbf{r}, t) + k_2 v(\mathbf{r}, t) \sum_i S(\mathbf{r} - \mathbf{r}_i(t))$$

$$\text{ParA} - \text{ATP} : \quad \frac{\partial v}{\partial t} = D_2 \Delta v + k_1 u(\mathbf{r}, t) - k_2 v(\mathbf{r}, t) \sum_i S(\mathbf{r} - \mathbf{r}_i(t))$$

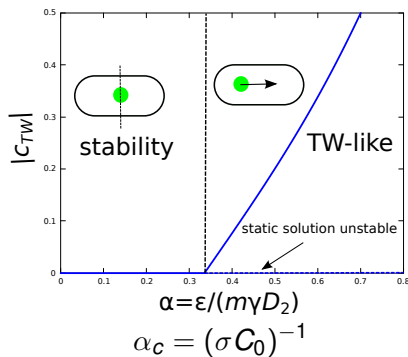
$$m\gamma \frac{d\mathbf{r}_i}{dt}(t) = \varepsilon \int_V \nabla v(\mathbf{r}', t) S(\mathbf{r}' - \mathbf{r}_i(t)) d^3\mathbf{r}'$$

- **Feedback** between the partition complexes and ParA densities
 → Non-linear system with **dynamical instability**

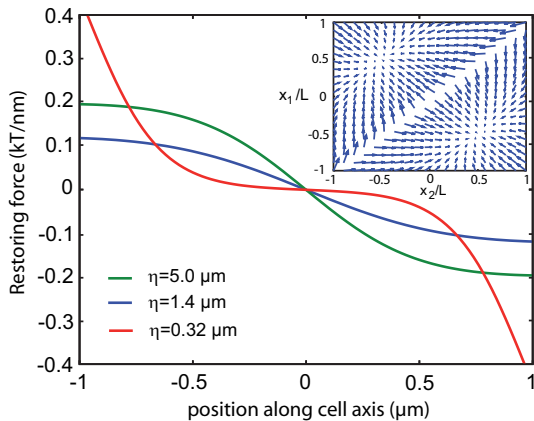
Dynamical instability

Threshold of dynamical stability obtained with Traveling Waves (TW) *ansatz*:

$$u(x, t) = u(\xi); \quad v(x, t) = v(\xi), \quad \text{where } \xi = x - c_{TW} t$$

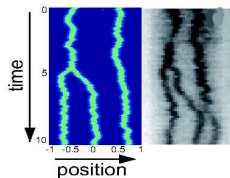


Screening length

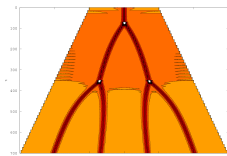


Comparison with experiments

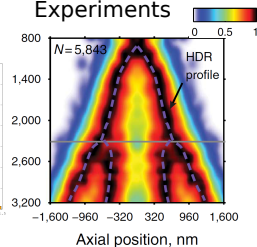
Model Experiments



Model



Experiments



Summary

- **Minimal reaction-diffusion** system without extra mechanism:
→ sufficient to explain segregation and positioning in ParABS
- Equation of motion of the complex
→ **coupling with the density of ParA** allowing a transient regime
- **Volumetric interaction** within the complex with ParA (porous catalytic particles)

JCW, Dorignac J., Lorman V., Rech J., Bouet J.-Y., Nollmann M., Palmeri J., Parmeggiani A. & Geniet F., *Surfing on protein waves: proteophoresis as a mechanism for bacterial genome partitioning*, *Phys. Rev. Lett.* **119**, 028101.

arXiv:1702.07372 [q-bio.SC]

Physical modeling

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Super-resolution microscopy

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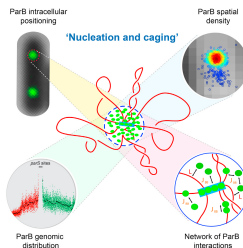
How does ParABS work ?

Cell Systems
Article



Stochastic Self-Assembly of ParB Proteins Builds the Bacterial DNA Segregation Apparatus

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- Partition complexes: diameter $\sigma \approx 50 - 75\text{nm}$ containing ≈ 300 proteins
 → porous particle with **volumetric interactions**

Quasistatic hypothesis: calculation of the profiles

