Physical modeling of active bacterial DNA segregation

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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?

Replication → Segregation → Division

Credit: J. Rech

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Dynamics: partition complex surfing of protein waves

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

Oscillations of ParA

Le Gall et al, Nat. Comm. '16
Bouet's team, LMGM, unpublished

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How does ParAB work?

**Step 1.** Formation of the partition complex

**Step 2.** Separation of the copies of DNA

**Step 3.** Positioning

3 components:
- **a)** 2 proteins (ParA & ParB)
- **b)** specific binding sites (parS)

"Reaction-Diffusion" or "Filament pulling" mechanisms
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Bacterial DNA segregation: interactions of ParABS

\[ \text{ParA-ATP} \rightarrow \text{ParA-ADP} \rightarrow \text{DNA} \]

- ParBS
- DNA
- ParA-ATP
- ParA-ADP

- Catalytic "cargo"
- Scaffolding
- Unbound, fast
- Bound, slow

- \( k_1 \)
- \( k_2 \)
- \( D_1 \)
- \( D_2 \)

- Equipoisinging

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Dynamical steps: Reaction-Diffusion equations

ParA – ADP:

\[
\frac{\partial u}{\partial t} = D_1 \Delta u - k_1 u(r, t) + k_2 v(r, t) \sum_i S(r - r_i(t))
\]

ParA – ATP:

\[
\frac{\partial v}{\partial t} = D_2 \Delta v + k_1 u(r, t) - k_2 v(r, t) \sum_i S(r - r_i(t))
\]

\[
m_\gamma \frac{dr_i}{dt}(t) = \varepsilon \int_V \nabla v(r', t) S(r' - r_i(t)) \, d^3r'
\]

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

Threshold of dynamical stability obtained with Traveling Waves (TW) ansatz:
\[ u(x, t) = u(\xi); \quad v(x, t) = v(\xi), \text{ where } \xi = x - c_{\text{TW}} t \]

\[ |c_{\text{TW}}| = \frac{\alpha}{\epsilon / (m \gamma D^2)} \]

\[ \alpha_c = (\sigma C_0)^{-1} \]
Screening length

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Comparison with experiments

Model Experiments

Model Experiments

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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)


arXiv:1702.07372 [q-bio.SC]
Physical modeling
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Partition complexes: diameter $\sigma \approx 50 - 75\,nm$ containing $\approx 300$ proteins

→ porous particle with volumetric interactions
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Quasistatic hypothesis: calculation of the profiles

(a) static behaviour
\[ \alpha < \alpha_c \]

(b) slow displacement
\[ \alpha = \alpha_c \]

(c) fast displacement
\[ \alpha > \alpha_c \]