Surfing on protein waves: proteophoresis as a mechanism for bacterial genome partitioning

Jean-Charles Walter
Laboratoire Charles Coulomb, CNRS & Université de Montpellier, France

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1. Bacterial DNA segregation: the ParABS system
2. Dynamics: complexes surfing on protein waves
How is the bacterial genome segregated?

Repllication  Segregation  Division

Credit: J. Rech
Bacterial genome partitioning

Bacterial DNA segregation: the ParABS system

The ParABS operon

- ParA: “motor” protein (ATPase, Walker-type)
- ParB: binding protein (specific or non-specific binding)
- parS: centromere-like DNA sequence
The ParABS segregation system: molecular actors

Step 1. Formation of the partition complex

Step 2. Separation of the copies of DNA

Step 3. Positioning

3 components:
2 proteins (ParA & ParB)
specific binding sites (parS)

How to describe both segregation and positioning of macromolecular assembly in a fluid phase?
Molecular interactions and diffusion

ParA-slow (ATP) + ParA-fast (ADP) + nucleoid DNA

ParBS catalytic "cargo" scaffolding equipositioning

bound, slow unbound, fast

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Bacterial genome partitioning
Bacterial genome partitioning

Dynamics: complexes surfing on protein waves

Reaction-Diffusion equations (ParA) coupled to Brownian motion (ParBS)

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

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

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

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

Dynamics: complexes surfing on protein waves

Density profiles obtained with biological parameters

\[ \alpha < \alpha_c \]

\[ \alpha = \alpha_c \]

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

- Minimal reaction-diffusion system:
  → sufficient to explain segregation and positioning in ParABS

- Non-linear coupling between ParBS and ParA densities:
  → Self-consistent description of the 3 protein species

- Analytical analysis:
  → dynamical transition (stable/unstable regime)

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.

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Physical modeling
G. David
J. Dorignac
F. Geniet
V. Lorman
J. Palmeri
A. Parmeggiani

Molecular biology
R. Diaz
A. Sanchez
J. Rech
J-Y. Bouet

Super-resolution microscopy
D. Cattoni
A. Le Gall
M. Nollmann
Screening length

Bacterial genome partitioning
- Dynamics: complexes surfing on protein waves

Jean-Charles Walter
Supercritical pitchfork bifurcation

Infinite system (left) Supercritical pitchfork bifurcation diagram of reduced system in the $(K, \nu)$ space. (right) Dynamical phase diagram in the plane $(K, \sigma)$ where $K = \alpha m_0 / (4D\ell)$ and $\sigma$ is the dimensionless width of a gaussian source. The red curve represents the boundary (critical value $K_c$ vs. $\sigma$).
Periodic Boundary Conditions (left) Dynamical phase diagram in the plane $(K, \mu)$ where $K = \frac{\alpha m_0}{4D\ell}$ and $\mu = \frac{L}{\ell}$ is the dimensionless ratio between $L$ (size domain $2L$) and the screening length $\ell = \sqrt{D/k}$. (right) TW dimensionless velocity $v$ (positive) vs. parameter $K = \frac{\alpha m_0}{4D\ell}$ for different values of $\mu = L/\ell$ from 0.5 to 2 and for $\mu \to \infty$. The blue curve is the same as the upper part for infinite system, thus the right limit is recovered.
No-Flux Boundary Conditions (Log-log plot of the instability threshold $K_c(\mu)$ versus the system size to screening length ratio $\mu = L/\ell$ for a Dirac source.)