

Physical modeling of active bacterial DNA segregation

Jean-Charles Walter

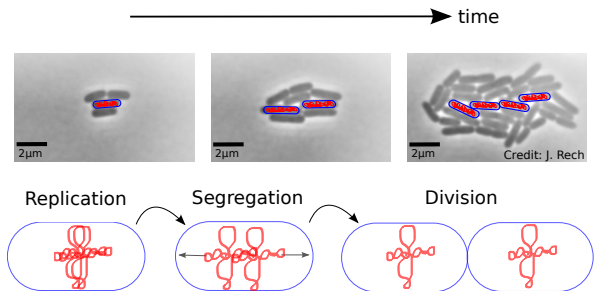
Laboratoire Charles Coulomb,
CNRS & Université de Montpellier, France

GDR Architecture et Dynamique Nucléaire
Paris Jussieu
March 30-31 2017

Outline

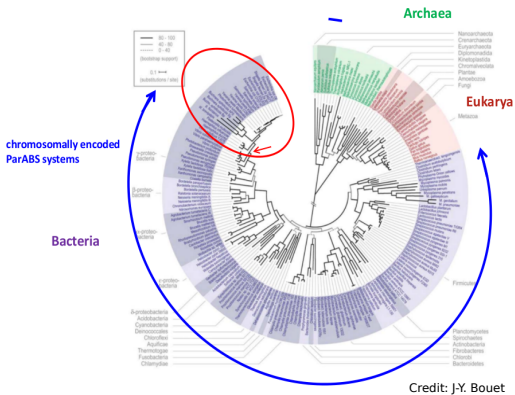
- 1 Bacterial DNA segregation: the system ParABS
- 2 Dynamics: complex surfing of protein waves

Segregation of bacterial DNA



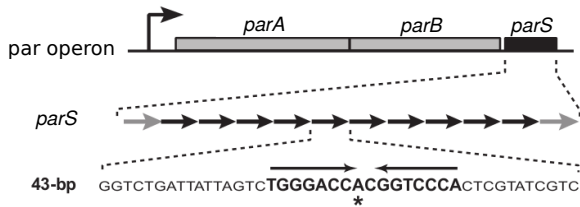
How is the bacterial genome segregated ?

Active segregation of bacterial DNA



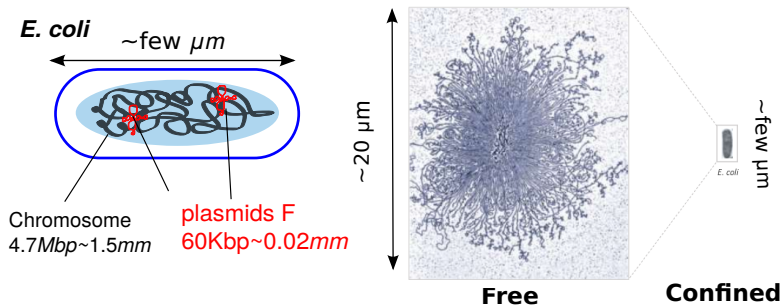
Partition system ParABS is strongly conserved

The ParABS operon

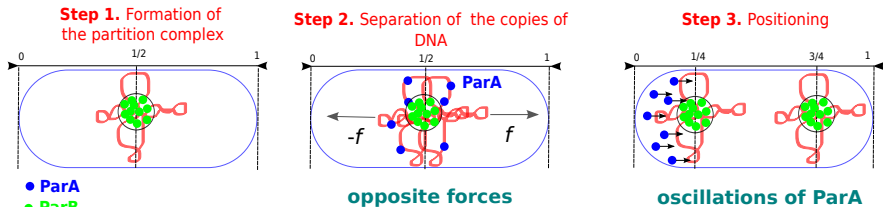


- ParA: “motor” protein (ATPase, Walker-type)
- ParB: binding protein (specific or non-specific binding)
- *parS*: centromere-like DNA sequence

Physical dimensions of bacteria



How does ParABS work ?



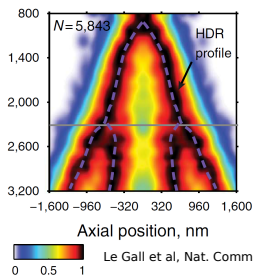
3 components:

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

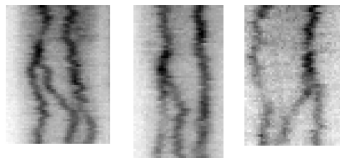
"Reaction-Diffusion"
or "Filament pulling"
mechanisms

Bacterial DNA segregation: experimental facts

Equipositioning of the complexes

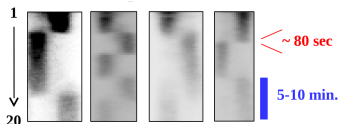


Le Gall et al, Nat. Comm. '16

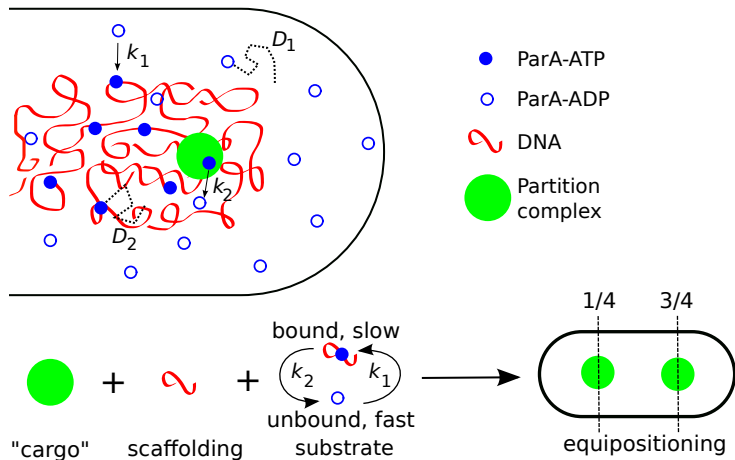


Bouet's team, LMGM, unpublished

Oscillations of ParA



Bacterial DNA segregation: interactions of ParABS



Dynamical steps: Reaction-Diffusion equations

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

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

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

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

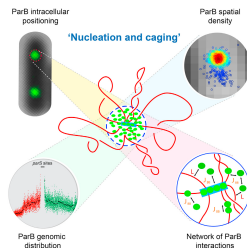
How does ParABS work ?

Cell Systems
Article



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

Aurore Sanchez,^{1,2} Diego I. Cattori,² Jean-Charles Walter,^{1,3,4} Jérôme Roch,^{1,2} Andrea Parmeggiani,^{4,5} Marcelo Nollmann,³ and Jean-Yves Boet^{2,3}

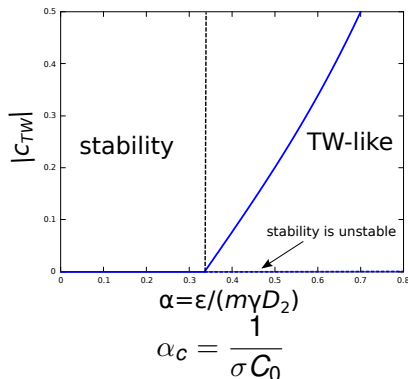


- Partition complexes: diameter $\sigma \approx 50 - 75\text{nm}$ containing ≈ 300 proteins
 → porous particle with **volumetric interactions**

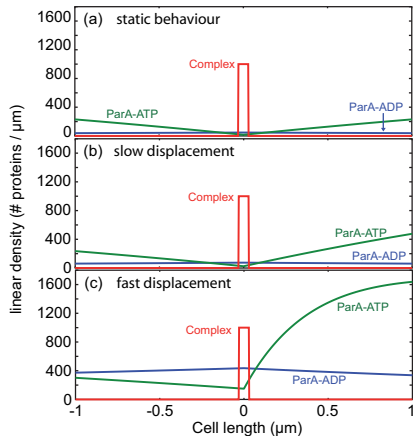
Dynamical instability

Threshold of dynamical stability obtained with TW *ansatz*:

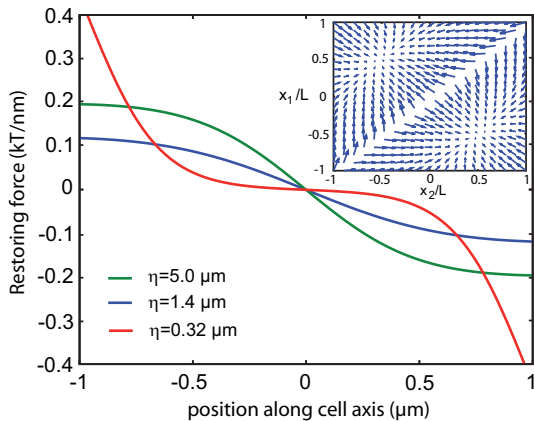
$u(x, t) = u(\xi)$; $v(x, t) = v(\xi)$, where $\xi = x - c_{TW} t$



Quasistatic hypothesis: calculation of the profiles

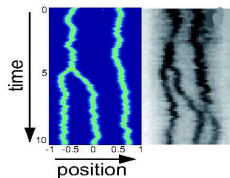


Screening length

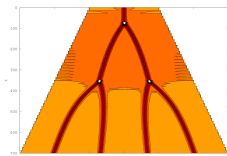


Comparison with experiments

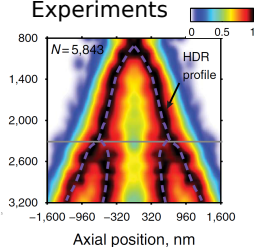
Model Experiments



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 particles”)

ChIP-sequencing

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



Super-resolution microscopy PALM

D. Cattoni
A. Le Gall
M. Nollmann



Physical modeling

G. David
J. Dornnac
F. Geniet
V. Lorman
J. Palmeri
A. Parmeggiani

