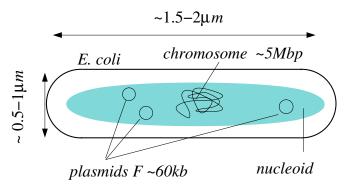
# Architecture of a bacterial DNA segregation apparatus: active caging of ParB by stochastic self-assembly nucleated from the centromere

#### Jean-Charles Walter

LMGM, CNRS & Université Paul Sabatier, Toulouse, France L2C, UMR5221 CNRS & Université Montpellier 2, France

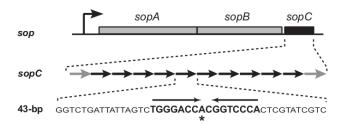
Interdisciplinary Views in Chromosome Structure & Function ICTP, Trieste, Italy
15-19 Septembre 2014

#### Intro: DNA segregation & Active partition system



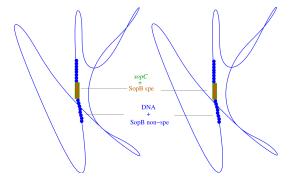
- Plasmid F: active partition system ParABS (=SopABC)
- Only type present on bacterial chromosome
- Most prevalent in low copy plasmids

#### The active partition system ParABS (SopABC)



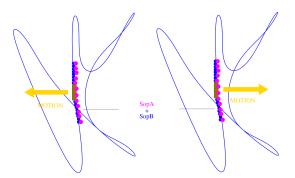
- SopA (ParA): motor protein
- SopB (ParB): binding protein
- sopC (parS): centromere-like DNA sequence

#### The partition system ParABS (SopABC)



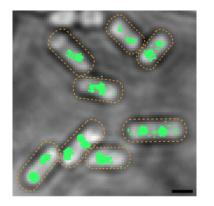
**Step 1**: formation of the partition complex on the two replicas (during/after replication)

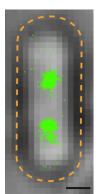
## The partition system ParABS (SopABC)



Step 2: Separation of the two replicas.

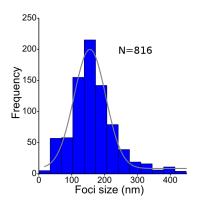
#### SopB is highly confined in foci

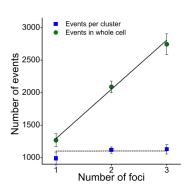




D. Cattoni & M. Nollmann, Single Molecule Localization Microscopy (PALM)

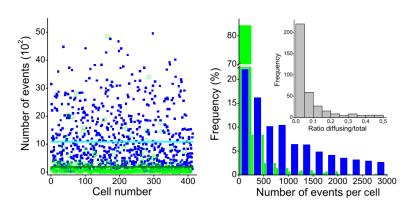
#### SopB is highly confined in foci



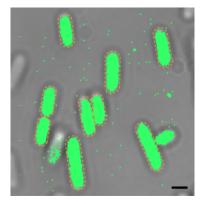


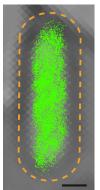
Foci diameter  $150 \pm 20$ nm

#### SopB is highly confined in foci

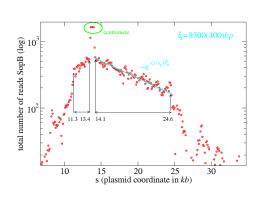


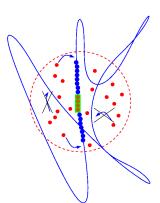
#### sopC is necessary to form foci





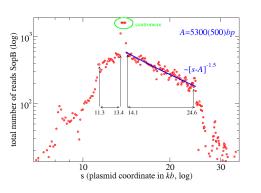
## Spreading of SopB along the plasmid: polymerization

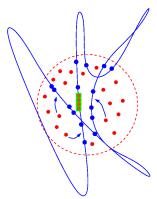




A. Sanchez, J. Rech, J-Y. Bouet, ChIP-sequencing

# Spreading of SopB along the plasmid: "stochastic binding"





# "stochastic binding": Preliminary quantitative calculation

Plasmid modeled by a Freely-jointed chain of Kuhn length a = 300bp

$$P_{binding}(s) = \int_0^\infty d^3 \vec{r} \; P(r,s) \, c_{SopB}(r) \propto rac{1}{[s-A]^{1.5}}$$

#### where

- $P(r,s) \propto s^{-1.5}e^{-3r^2/(2as)}$
- ullet  $c_{SopB}(r) \propto e^{-r^2/2\sigma^2}$
- $A = s_0 3\sigma^2/a^2$
- s<sub>0</sub> the position of the centromere

from the fitting of ChIP-sequencing data: foci of size 300nm



#### Conclusion

- ParB is highly confined in foci ( $\sim 10^3$  ParB per foci)
- Confinement requires spe and non-spe binding
- Propagation of ParB: cannot be explained by polymerization alone
- "Stochastic binding" scheme: conformation of the plasmid (further experiments, includes plectonemes in the model)
- Mechanism of caging of SopB?

Sanchez A, Cattoni D I, Walter J-C, Rech J, Parmeggiani A, Nollmann M & Bouet J-Y, submitted

LMGM, CNRS & Université Paul Sabatier, Toulouse, France Aurore Sanchez, Jérôme Rech, Jean-Yves Bouet

CBS, INSERM U554, UMR5048 CNRS & Université Montpellier 1&2 Diego Cattoni, Marcelo Nollmann

L2C, UMR5221 CNRS & Université Montpellier 2 A. Parmeggiani, J. Dorignac, F. Geniet, V. Lorman, J. Palmeri













### Titration of SopB

