Bacterial DNA organization by ParB proteins

Miloš Tišma[1], Richard Janissen[1], Hammam Antar [2], Alejandro M. Gonzalez[1], Roman Barth[1] , Jaco van der Torre[1], Davide Michieletto[3], Stephan Gruber[2], Cees Dekker[1]

[1] *Department of Bionanoscience, Kavli Institute of Nanoscience Delft, Delft University of Technology, Delft, Netherlands*

[2] *Department of Fundamental Microbiology (DMF), Faculty of Biology and Medicine (FBM), University of Lausanne (UNIL),Lausanne, Switzerland*

[3] *MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine University of Edinburgh, Edinburgh, United Kingdom*

Bacterial chromosome segregation in the majority of species relies on ParABS system. ParB proteins can load on bacterial chromosomes using *parS* sequence and spread laterally, covering distances up to 10-15kb in vivo. Recent advances unveiled that ParB has a CTPase activity in multiple species, allowing for loading on parS site and lateral spreading in one dimension. While vital for chromosome segregation, it is unclear how ParB proteins maintain the dynamic partition complex following 1D spreading from the loading site. Here, we explore how ParB initiates the DNA condensation process and how this process is dynamically maintained. We use single-molecule visualization and AFM imaging to show that transient ParB-ParB bonds are essential for the DNA condensation, and we verify through Molecular Dynamics simulations that a transiency of these bonds is necessary. Furthermore, we use magnetic tweezer force spectroscopy to show that it is the N-terminal ParB-ParB interactions between different ParB dimers that is a prerequisite for DNA condensation, eliminating the need for a C-terminal opening in this process. The findings of our study explain how ParB can form a metastable partition complex during chromosome segregation.