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Bacterial chromosome organization by condensins: functional analysis of MukBEF in E. coli

Abstract : Chromosome condensation and segregation are two essential processes for the transmission of genetic material in all living organisms. Indeed, chromosomes are composed of a DNA molecule and several families of proteins that perform various functions related to DNA. Ubiquitous SMC complexes in the living world are among these proteins that constitute the chromosome, and their study is of great importance in understanding the mechanisms of condensation, segregation, and their possible links.
The MukBEF SMC complex is the condensin of the bacterium *Escherichia coli.* Although MukBEF is essential under fast growth conditions, its deletion is tolerated under slow growth, and is characterized by the production of anucleate cells reflecting a defect in chromosome segregation. The chromosome conformation capture technique (3C-seq/HiC) has revealed that MukBEF promotes long-distance contacts throughout the chromosome, except in the Ter domain where it is inhibited by the MatP/*matS* system. During my thesis, I focused on characterizing the activity of MukBEF on the chromosome. I was able to demonstrate that the loading of MukBEF, unlike other bacterial condensins that have been studied, occurs without site specificity.Additionally, I identified that this loading is more efficient on newly replicated DNA. I also investigated the characterization of the inhibition mechanism of MukBEF by the MatP/*matS* system in the Ter domain. MatP is a protein that specifically binds to 28 *matS* sites distributed in the Ter domain. My results suggest a mechanism of inhibition that involves unloading MukBEF from the chromosome near the borders of the Ter domain. Furthermore, I demonstrated that 3 matS sites are sufficient to inhibit MukBEF, but the addition of additional sites strengthens the effectiveness of this inhibition. Moreover, the analysis of the distribution of *matS* sites in several bacteria suggests that increasing the number of *matS* sites and their density near the dif site aims to prevent MukBEF loading near the *dif* site.

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