

Analysis of the spatial organization of the bacterial chromosome.

**Romain Mercier, Axel Thiel, Michele Valens, Frédéric Boccard and Olivier Espéli.
Centre de Génétique Moléculaire, CNRS, Gif sur Yvette , France**

The large size of bacterial genomes compared to cell dimensions imposes an extensive compaction of chromosomes compatible with the DNA transactions occurring during transcription, replication, recombination and segregation. Two different levels of chromosome organization have been identified. At a small scale, DNA supercoiling partitions the chromosome into topological microdomains averaging 10 kb. At a higher scale, in *E. coli*, cytological and genetic analyses based on long distance DNA interactions revealed a structuring process that spatially insulates four large regions of the chromosome called macrodomains (MD). Inside macrodomains, DNA interactions are readily detected, but collisions between DNA sites belonging to different macrodomains occur at low frequency. In addition to structured macrodomains, two particular regions called Non-Structured (NS) regions appeared to be more flexible. This macrodomain organization was directly visualized by analyzing the positioning and the segregation pattern of markers belonging to various macrodomains. The dynamic behavior of loci belonging to various macrodomains and less constrained regions is radically different. In macrodomains, constraints on mobility are apparent, whereas in Non-Structured regions, markers exhibit a greater mobility. We have recently identified a protein, MatP, and its binding sites that constrains the mobility of the DNA inside one of the macrodomain. The influence of long range chromosome organization on DNA constrains will be discussed.