INVITED SPEAKER

ARRAYS OF TRANSCRIPTIONAL UNITS REPRESENT THE STRUCTURAL FUNCTIONAL MATRIX OF THE BACTERIAL CHROMOSOME

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I will present how the multiscale functional organization (or "structure") of a bacterial chromosome can be addressed using genomics, genetics and imaging approaches. The folding of these gene-dense chromosomes consists of an assortment of intertwined structures, whose interaction with functional metabolic regulation remains sometimes unclear. In addition to small supercoiled plectonemic structures and large Mb-scale compartments, contact maps generated using chromosome conformation capture approach (Hi-C) have unveiled partitioning into medium-sized (~30 - 200 kb) chromosomal self-interacting domains or CIDs frequently (but not always) separated by long highly expressed genes (HEGs) at their boundaries. Because the gene and operon scale in bacteria remained close to the resolution limit of conventional Hi-C, the nature and functional relevance of CIDs remain elusive. Using a new sub-kb resolution Hi-C procedure, we observed that all transcribed genes, not just HEG, imprint Hi-C contact maps. To unravel the molecular mechanisms underlying this folding linked to transcription we engineered Escherichia coli strains carrying controlled expression systems that allow the observation of discrete transcription units while disabling whole-genome transcription. Using a combination of sub-Kb Hi-C and imaging approaches, we investigated the local and distal impact of a unit or pairs of transcription units. We show that transcription units form small compact domains that imprint a boundary in Hi-C contact maps and imposes two constraints on neighboring sequences, bringing them together while restricting their dynamics. Overall, our results suggest that the first stones of the multilayer bacterial chromosome folding correspond to small transcriptional domains.