

Transcriptional units form the elementary constraining building blocks of the bacterial chromosome

Amaury Bignaud^{1,5}, Charlotte Cockram^{1,2}, Justine Groseille^{1,2,5}, Céline Borde², Eric Allemand⁴, Agnès Thierry¹, Julien Mozziconacci³, Olivier Espeli², and Romain Koszul¹

¹ Institut Pasteur, CNRS UMR 3525, Université Paris Cité, Unité Régulation Spatiale des Génomes, F-75015 Paris, France

² Center for Interdisciplinary Research in Biology (CIRB), Collège de France, CNRS, INSERM, Université PSL, Paris, France

³ Muséum National d'Histoire Naturelle, Structure et Instabilité des Génomes, UMR 7196, Paris 75231, France

⁴ INSERM - U1163, Unité mécanismes cellulaires et moléculaires des désordres hématologiques et implications thérapeutiques, Institut Imagine, Paris, France.

⁵ Collège Doctoral, Sorbonne Université, F-75005 Paris, France

Transcription generates local topological and mechanical constraints along the DNA fiber, driving for instance the generation of supercoiled chromosomal domains in bacteria. However, the global impact of transcription-based regulation of chromosome organization remains elusive. Notably, the scale of genes and operons in bacteria remains well below the resolution of chromosomal contact maps generated using Hi-C (~ 5 - 10 kb), preventing to resolve the impact of transcription on genomic organization at the fine-scale. Here, we combined sub-kb Hi-C contact maps and chromosome engineering to visualize individual transcriptional units (TUs) while turning off transcription across the rest of the genome. We show that each TU forms a discrete, transcription-induced 3D domain (TIDs). These local structures impose mechanical and topological constraints on their neighboring sequences at larger scales, bringing them closer together and restricting their dynamics. These results show that the primary building blocks of bacteria chromosome folding consists of transcriptional domains that together shape the global genome structure.