

Multiscale Structuring of the E. coli Chromosome by Nucleoid-Associated and Condensin Proteins

As in Eukaryotes, bacterial genomes must be accurately folded to ensure their proper function. Bacterial genetic information is generally carried on a single circular chromosome with a unique origin of replication from which two replication forks proceed bidirectionally to the opposite terminus region. Here we investigated the higher-order genome architecture of the model bacteria *Escherichia coli*. We show that the chromosome is partitioned into two structurally distinct entities through a complex and intertwined network of contacts: the replication terminus (ter) region and the rest of the chromosome. Outside ter, the condensin MukBEF and the ubiquitous nucleoid-associated protein (NAP) HU promote DNA contacts in the megabase range. Within ter, the MatP protein prevents MukBEF activity and contacts are restricted to ~280 kb creating a domain with unique structural properties. We also show how other NAPs contribute to nucleoid organization, such as H-NS that constrains and insulates short-range interactions. Combined, these results reveal the contributions of major, evolutionary conserved proteins in a bacterial chromosome organization.

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