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CHROMOSOME BIOLOGY

Different turfs for cohesin and condensin

The structural maintenance of chromosomes (SMC) complexes cohesin and condensin are ring-shaped protein machines that encircle the chromatin and control various aspects of chromosome function, including the formation of chromatin loops, sister chromatid cohesion and mitotic chromosome compaction. Schalbetter *et al.* now show that in the budding yeast *Saccharomyces cerevisiae*, mitotic chromosome compaction is achieved through *cis*-chromatin looping, and that cohesin and condensin have distinct roles in this process.

The authors employed Hi-C (genome-wide chromosome conformation capture) to study mitotic chromosome compaction. Hi-C contact maps produced from synchronized populations of yeast cells arrested in G1 or mitosis revealed that the frequency of contacts along chromosome arms between regions <100 kb apart was markedly increased during mitosis, whereas the frequency of longer-range intra-chromosomal contacts was reduced. This suggested that mitotic chromosome compaction results from the formation in *cis* of <100 kb chromatin loops. Chromatin compaction required only a third of the genome to be organized into loops, in contrast to metazoan chromosomes, in which the entire genome is organized into loops. This could explain the lower levels of mitotic chromosome compaction seen in budding yeast compared with metazoan chromosomes.

Next, the function of cohesin and condensin in forming *cis*-loops was examined by expressing inactive mutant complexes in mitotically arrested cells. Disruption of cohesin function prevented chromatin condensation and led to Hi-C maps that resembled those of cells arrested in G1. Thus, cohesin promotes the formation of chromatin loops along chromosome arms that are required for mitotic chromatin condensation. This function of cohesin is independent of its role in mediating sister chromatid cohesion, as chromatin compaction was still observed in mitotic cells in which DNA replication and the formation of sister chromatids were blocked.

Condensin deactivation did not cause genome-wide loss of mitotic compaction. Instead, condensin was necessary for higher-order chromatin compaction in specific genomic regions. Owing to the low level of chromosome compaction in budding yeast, the only region with readily visible compaction is the megabase array of ribosomal DNA (rDNA) repeats in chromosome XII, which is known to accumulate excessive levels of sister chromatid intertwines and thus requires additional compaction to facilitate its segregation. Mitotic compaction of the region between centromere XII and the rDNA repeats was dependent on condensin, but the mode of compaction was distinct from that mediated by cohesin: condensin enabled the formation of chromatin contacts >100 kb apart but had no role in the formation of contacts that are <100 kb apart. Centromeres also require condensin function, as its deactivation led to more contacts between centromeres of different chromosomes and decreased the resolution between centromeric regions of different chromosomes.

Together, the data indicate that in budding yeast mitotic chromosome compaction is achieved through *cis*-looping and that cohesin and condensin perform distinct roles in this process: cohesin is responsible for achieving relatively low levels of chromatin compaction genome-wide by forming small chromatin loops, whereas condensin supports higher chromatin compaction at specific loci by forming larger chromatin loops. Condensin function in yeast is similar to that of condensin in the longer and more repetitive metazoan chromosomes, which require higher levels of compaction.

In another study, Kakui *et al.* show that in the fission yeast *Schizosaccharomyces pombe*, condensin mediates mitotic chromosome condensation by forming long-range chromatin interactions. These long-range interactions replace the local chromatin contacts of interphase chromosomes, thereby leading to reduced chromatin motility during mitosis.

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> “mitotic chromosome compaction results from the formation in *cis* of < 100 kb chromatin loops”