

The mystery of chromosome structure

After more than a century of microscopic exploration, the intrinsic structure and chromatin organization of mitotic chromosome is still far from being solved. While we have an almost finished human genome map, from telomere to telomere (Nurk al. [Science 2022](#))¹, it is still difficult to figure out the exact folding pathway of chromatin during chromosome condensation despite the fact that numerous models with several different approaches have been suggested and tentatively demonstrated.

Two recent papers add new proposals to the field.

Sedat et al. (Sedat J, McDonald A, Kasler H et al. A proposed unified mitotic chromosome architecture. [PNAS 119 \(2022\)](#))² rely on the exact sequence and nucleosome number of chromosome 10, and on electron microscopy observation of interphase chromatin as a starting point. They present a revival of the super coiled organization suggested several years ago. Their computational model is worked out so that it fits perfectly with the observed and calculated length and width of the mitotic chromosome 10 and with the required compaction level. They use a single unified mechanism of compaction during the whole cell cycle. However, further observations are needed to validate the model.

For this, new methodologies that avoid alteration of chromatin structure are essential. This is, for example, the case of the new approach which allows the analysis of mechanical properties of chromosomes in their native state (Meijering AEC, Sarlós K, Nielsen CF et al. Nonlinear mechanics of human mitotic chromosomes. (Meijering al. [Nature. 2022](#))³ and which could be a way of testing the above mentioned model (and probably many others).

1. https://www.science.org/doi/10.1126/science.abj6987?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%20pubmed
2. <https://www.pnas.org/doi/full/10.1073/pnas.2119107119>
3. <https://www.nature.com/articles/s41586-022-04666-5>