3D Lampbrush Chromosomes Organization in Chicken Oocyte

Understanding how chromosomes fold in 3D space is one of the central questions in modern cell biology. Lampbrush chromosomes, with their spectacular chromomere–loop architecture, offer a uniquely accessible window into this problem.
A new study in Nucleic Acids Research by Lagunov et a. (1) presents the first genome-wide Hi-C (chromosome conformation capture) analysis of lampbrush chromosomes, integrating single-nucleus Hi-C, RNA-seq, NOMe-seq (Nucleosome Occupancy and Methylome sequencing), FISH mapping, and polymer simulations. The authors show that chromatin domains in lampbrush chromosomes are formed independently of CTCF (a key chromatin insulator protein that demarcates domain boundaries in somatic cells). Instead, their boundaries are defined by the orientation of transcription units, with convergently oriented gene pairs acting as insulating barriers. Active transcription repositions SMC (Structural Maintenance of Chromosomes) complexes and stiffens chromatin, driving the extrusion of lateral loops away from the chromosome axis. A biophysical model quantitatively reproduces these features, providing a unified mechanistic framework for lampbrush chromosome architecture.

1. https://academic.oup.com/nar/article/54/7/gkag316/8653609