Holocentric *Bombyx mori* chromosomes segregate into three genome-wide compartments

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The 3D genome contains a hierarchy of structures: chromosome territories, compartmentalization of active and inactive chromatin, and topologically associating domains (TADs). While the *B. mori's* genome architecture encompasses all three, it is distinct in its implementation of these classical features.

Most prominently, *B. mori* chromosomes segregate into three compartments. In addition to previously described active (A) and inactive (B) compartments, Hi-C maps reveal a third compartment that we term X. Unlike all previously documented compartments, X compartments do not prefer to interact with other X compartments. By modeling *B. mori* compartments as a block copolymer, we find compartment affinities alone cannot form X compartments.

Unlike most of the genome, X compartments also contain TADs. Loop extrusion, which forms TADs, weakens compartmentalization through active mixing of chromatin. Though loop extrusion is insufficient to form X compartments on its own, we find that adding extrusion to a three-compartment model successfully forms X compartments.

Finally, we find local compaction is associated with the histone mark H4K20me1. This mark has previously been linked to condensin activity in other organisms, hinting that *B. mori* TADs may be condensin, rather than cohesin-mediated.

Taken together, our modeling and analyses demonstrate how unique chromosome folding structures can arise through conserved biophysical mechanisms.