Characterization of dosage compensation specific nuclear bodies

Eukaryotic genomes are compacted to fit inside nuclei while remaining accessible and functional, a process mediated by structural maintenance of chromosomes (SMC) complexes. In mammals, cohesin performs this role while in *C. elegans*, it is primarily condensin I. While many organisms form topologically associated domains (TADs) *via* chromatin loop extrusion limited by boundary elements, *C. elegans* autosomes lack TADs. In contrast, hermaphrodite X chromosomes form TADs through condensin I^{DC}, a specialized condensin I complex within the dosage compensation complex (DCC). Cleavage of condensin I/I^{DC} eliminates X-specific TADs and reveals nuclear speckles formed *via* phase separation of the Sex Determination and Dosage Compensation (SDC) proteins. In parallel, cleavage leads to widespread upregulation of X-linked genes, except within SDC bodies, suggesting that chromatin threads through these structures for gene regulation. The mechanisms by which SDC proteins recognize the X chromosome and mediate repression remain however unclear. To investigate SDC body composition, we tagged key DCC components SDC-1 and SDC-3 with the biotin ligase BASU for proximity labeling. SDC-1 labeling recovered known DCC components, validating our method. Notably, we also identified a previously uncharacterized protein. Fluorescent tagging showed that this protein aggregates in nuclear speckles. Ongoing work aims to define its role in dosage compensation, chromatin architecture, and gene regulation.