

Abstract: Centromeres can be classified into two different types, each with unique structural characteristics: monocentromeres, where one specific domain in each chromosome is designated for centromere function, and holocentromeres, where the domains are distributed along the length of the chromosomes.

Holocentromeres have evolved multiple times independently in eukaryotes including in the Lepidoptera and Nematodes. The first holocentric architecture that has been determined is the one from the nematode *C. elegans*. It was found that centromeres formation occurs in larger chromosomal domains anticorrelated with RNA polymerase II occupancy and high nucleosome turnover. In addition, more recent studies from our lab characterized the molecular organization of the *B. mori* (silk moth) holocentromere. It was found that, similar to *C. elegans*, centromere formation appeared to be shaped by the chromatin landscape in that centromeres are excluded from regions with high nucleosome turnover. The similarity between the two holocentromere organizations is interesting given the fact that both species build their centromeres on opposite sets of inner kinetochore components. In *C. elegans*, centromeres are built on CENP-A and its direct DNA binding partner CENP-C. *B. mori*, in contrast, has lost both of these components but assembles its inner kinetochore on a homologous set of constitutive centromeres associated network (CCAN) components. For my project I systematically compared centromere organization between the two species to relate those to the linear organization of the *C. elegans* and *B. mori* genomes. In addition, I also aim to reconstitute CENP-A, obtained from *C. elegans*, into the kinetochore and centromere of *B. mori* to determine additional factors that contribute to the centromere profiles in this organism.