

Centromeric DNA: the storage of genome “black matter” or determinant of centromere species identity?

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Centromeres are essential for chromosome segregation because they contain sites for landing kinetochores. Centromeres function to ensure proper distribution of genetic material to daughter cells during cell division, making them critical for genome stability, fertility, and healthy development, yet their DNA sequences evolve rapidly. In most organisms, the key determinant for the site of kinetochore assembly is epigenetic, requiring the deposition to nucleosomes a centromere-specific variant of histone H3 called CENH3 in plants, CENP-A in animals. Centromeres have remained largely underexplored being notoriously difficult to completely assemble due to the highly repetitive DNA sequences and complex structure, so the functional contribution of centromeric DNA to centromere identity remains elusive. Despite their importance, very little was known about the degree to which centromeric DNA share common properties between different species across different phyla. New approaches in genome sequencing and assembly methodology have enabled the gap-less reconstructing of entire eukaryotic chromosomes. Recent developments in long-read sequencing technology have allowed the assembly of centromeric DNA for the first time and have prompted a reassessment of fidelity of centromere function and the evolutionary dynamics of these regions. The mechanisms by which centromeric sequences and chromatin come together to functionally determine the relative fidelity of the centromere regions remains an open question. The report will present data on the molecular structure of centromeres of various eukaryotic species – human, primates, drosophila, cereals – discuss the evolutionary mechanisms of its formation and the possible role of DNA in these processes.

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