

Is all centromeric DNA functionally competent for centromere identity?

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Centromeres are essential chromosomal regions that mediate the accurate inheritance of genetic information. Until now, centromeres have remained largely underexplored, especially in Triticeae genomes being 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. New approaches in genome sequencing have enabled the gap-less reconstructing of the sequences of entire eukaryotic chromosomes. However, the complete composition of centromeric DNA of such species as wheat, barley, rye remains unknown. Using a datasets of molecular markers, we conduct an in-depth analysis of gaps between contigs in individual chromosomes that were recently annotated as so-called pseudomolecules in genomic assemblies of rye, *S. cereale*. We estimated the centromere positions and determined the molecular nature of the DNA sequences in these loci. The report will present the composition and abundance of different DNA sequences in the centromeres of each rye chromosome and this comparison will be extended to other cereal species. This work is supported by RSF (No. 19-14-00051-P).

The main publications of authors on the subject of the abstract:

Elisafenko EA, Evtushenko EV, Vershinin AV. *The origin and evolution of a two-component system of paralogous genes encoding the centromeric histone CENH3 in cereals*//BMC Plant Biol (2021) 21: 541. doi: 10.1186/s12870-021-03264-3

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