

Paralogous genes of centromeric histone CENH3 are actively expressed in the rye genome

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In most diploid plant species, centromeric histone H3 (CENH3) is encoded by a single copy of the gene. However, for rye species, as well as for other species of the tribe Triticeae, the presence of two genes, α CENH3 and β CENH3, was shown. The occurrence of CENH3 in chromatin is essential for kinetochore formation and proper centromere functioning. The presence of the CENH3 duplication raises the following questions: are both paralogs expressed during plant ontogenesis, is one of the paralogs a pseudogene, are both variants of the CENH3 protein involved in the formation of an active centromere, and is the centromere the only region of their localization? In this work, the transcription profiles of α CENH3 and β CENH3 were determined by the RT-qPCR method in two cultivars of rye *S. cereale*, 'Imperial' and 'Korotkostebel'naya 69'. It was found that both genes, α CENH3 and β CENH3, are expressed at all stages of individual development: in the tissues of seedling roots, coleoptiles, stems, anthers and carpels. The highest level of expression of both CENH3 variants was found in reproductive tissues (anthers and carpels); expression level of evolutionarily ancient α CENH3 exceeds that of the evolutionarily young β CENH3 in almost all tissues. The incorporation of two CENH3 variants into centromeres was investigated by immunostaining the chromosomes of Imperial with specific anti- α CENH3 and anti- β CENH3 antibodies. It was revealed that α CENH3 and β CENH3 are co-localized on centromeres in the interphase nucleus and in the metaphases of mitosis and the first division of meiosis. The presented data indicate the transcription of two CENH3 genes and the incorporation of functional CENH3 variants into centromeres differ in various tissues of rye during plant development.

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