

## Tissue-dependent transcription of the rye centromeric histone CENH3 variants

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The assembly site for the kinetochore complex of active centromeres is defined by the chromosomal location of the centromeric modification of histone H3 (CENH3). The loss of CENH3 from centromeres leads to improper chromosomal segregation during cell division. In most diploid genomes, including cereals (maize and rice), in which the structure and copy number of *CENH3* have been determined, CENH3 is encoded by a single gene. However, some diploid species in the tribe Triticeae have two variants of *CENH3* gene. Previously we have shown the presence of two main forms of protein,  $\alpha$ CENH3 and  $\beta$ CENH3 in rye species (the genus *Secale*, belonging to the tribe Triticeae). In rye the average nucleotide identity between  $\alpha$ CENH3 and  $\beta$ CENH3 is 81–83 %, with main amino acid sequence difference in NTT domain and in  $\alpha$ 1-helix and loop 1 of HFD domain (CATD). Due to the presence of two main forms of the histone CENH3 instead of one, it is of great interest to study their functions. We suppose that the comparative study of the expression levels of  $\alpha$ CENH3 and  $\beta$ CENH3 in different tissues can shed light on this problem. Here we determine the expression levels of  $\alpha$ CENH3 and  $\beta$ CENH3 in various tissues of rye, *Secale cereale* var. ‘Imperial’. The highest level of expression of both *CENH3* forms was found in reproductive tissues (anther and carpel). The expression ratio of  $\alpha$ CENH3 and  $\beta$ CENH3 varies depending on the type of tissue, for example, the average expression level of  $\alpha$ CENH3 was higher than the average expression level of  $\beta$ CENH3 in leaves but they were comparable in carpels. Our results differ from the results obtained on barley, where expression level of  $\beta$ CENH3 significantly exceeded expression level of  $\alpha$ CENH3 in all studied tissues.

*Acknowledgements:* This research was financially supported by the Russian Fundamental Scientific Research Program (project 0310-2019-0003) and the Russian Foundation for Basic Research (grant 17-04-00748a).