SECALOTRITICUM HYBRIDS AS A NEW MODEL FOR STUDYING THE ACTIVITY OF GENES ENCODING CENTROMERE-SPECIFIC PROTEIN CENH3

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The ultimate goal of remote hybridization is to make hybrids use as much of each of their parent's natural genetic potential or genetic diversity as they have. Of critical importance for increasing genetic diversity and developing hybrids with selective value could be the synthesis of rye-wheat amphiploids (×*Secalotricum*, ×*Secalotriticum* Rozenst = *Secale* L. × *Triticum* L.), with rye as the maternal form and wheat as the pollinator. Crosses like these are normally difficult to achieve due to incompatibility, and so rye-wheat amphiploids are not well studied. It was found by researchers of the Laboratory of Plant Cytogenomics of the Institute of Genetics and Cytology of the NAS of Belarus that the use of triticale as an intermediate agent donating wheat genomes in crosses with rye is efficient for overcoming progamic incompatibility of the original species. New hybrids, with rye as the maternal plant and triticale as the paternal source of the wheat genome, are collectively called secalotriticum. Secalotriticum represents better settings for enhancing the expression of the rye genetic systems and the manifestation of its valuable adaptive traits.

Differential staining of chromosomes revealed that the secalotriticum forms developed by crossing the parental tetraploid rye cv. Verasen' (RRRR, 2n=4x=28) to triticale cv. Mikhas' and Dubrava (AABBR'R', 2n=6x=42) followed by backcrossing are cytologically stable hexaploids (RRAABB, 2n=6x=42) without between-genome chromosome substitutions. We explored the expression of the main forms of centromere-specific histone *CENH3* in the hybrids. The coding sequences of the N-terminal tails (NTT) of the α forms of wheat and rye *CENH3* share a high percentage (99%) of nucleotide identity; however, a few positions display elevated levels of polymorphism. The NTT of αCENH3 in secalotriticum hybrids features a still higher percentage of nucleotide substitutions and, consequently, amino acid substitutions at such positions and the predominance of CENH3 forms typical of rye.

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