

THE CENH3 GENE ENCODING CENTROMERE-SPECIFIC HISTONE H3: ACTIVITY IN TRITICALE

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Remote hybridization often causes genome rearrangements, which may lead to elimination of one of the parents' chromosomes even after successful fertilization and combining two genomes in the hybrid cell. Crosses between wheat and rye species proved to be by far the most successful remote hybridization events in that the progeny is reproducible and the allopolyploid hybrids – triticales (*Triticum x Secale*, (\times *Triticosecale* Wittmack)) – can be introduced in breeding practice.

Centromeres regulate faithful chromosome segregation during cell division. CENH3, a specialized modification of histone H3, is a permanent component of centromeric chromatin. CENH3 consists of a conserved C-terminal domain (HFD) and a more variable N-terminal tail (NTT), which plays an important role as CENH3 is incorporated to centromeric chromatin during cell division. This work provides the results of a cytogenetic analysis of triticales (AABBDDRR, $2n=8x=56$), developed by crossing the isogenic line of hexaploid wheat *T. aestivum* cv. Triple Dirk D (AABBDD, $2n=6x=42$) and the rye *S. cereale* cv. Korotkostebel'naya 69 (RR, $2n=2x=14$) and a comparative analysis of the expression of the main forms of *CENH3* in the parental species and hybrids. The coding sequences of the NTT of the α forms of wheat and rye *CENH3* are 213 bp in length each and have 99% nucleotide identity. The amino acid sequences of CENH3 from the parental rye cultivar possess specific positions with nonsynonymous amino acid substitutions that make them differ from those in wheat. All rye-specific amino acids are also present in the α CENH3 forms observed in the hybrid cells and the presence of these amino acids in the hybrids serves as a measure of expression of the parental *CENH3* in the hybrids. This suggests that triticales, with their hybrid genomes, express *CENH3* copies that are typical of each of the parents.

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