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Abstracts

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CHARACTERIZATION OF THE CENTROMERIC HISTONE H3 (CENH3) IN GENUS *SECALE* AND ITS PHYLOGENETIC RELATIONSHIPS

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Motivation and Aim: Rye (*Secale*) is a small genus that includes the species adapted to a wide range of abiotic and biotic stresses and possessing two types of pollination system. Traditional rye varieties are panmictic populations displaying high levels of heterozygosity and heterogeneity, which might have resulted from outcrossing pollination and facilitated interspecies hybridization. We aimed to study the molecular structure of genes encoding centromere-specific histone H3 (*CENH3*), a key component of centromere specification and function, in 14 *Secale* species and subspecies and their phylogenetic relationships with species in their most closely related genera, *Triticum* and *Hordeum*. **Methods and Algorithms:** We cloned and sequenced the *CENH3* genes from 14 species and subspecies across *Secale*. To determine the extent of *CENH3* evolution, we compared Ka/Ks (nonsynonymous/synonymous substitutions) ratios for all coding sequences of a species within genus *Secale* and between other genera using DNAsp. We used the mixed effects model model of evolution (MEME) to evaluate selection at the codon level in genus *Secale*.

Results: Diploid rye encodes two paralogous *CENH3* genes, which are transcribed into two main forms α *CENH3* and β *CENH3*. They differ in size, intron-exon structure and amino acid substitutions and originated from a duplication event in the common ancestor before the barley and wheat-rye lineages split. A sequence alignment of *CENH3* from *Secale* species and subspecies display a surprisingly high level of similarity, despite the differences that they have in morphology, life-cycle duration and pollination systems as well as environmental and growing conditions. The *CENH3* proteins are strictly controlled by genetic factors responsible for purifying selection. Diversifying selection operates at a very few sites in cross-pollinating rye species. In contrast, considerable differences between *Hordeum* species suggest that the *CENH3* are rapidly evolving in this genus. A comparison between *Hordeum*, *Secale* and *Triticum* species demonstrates that the structure of *CENH3* in the subtribes Hordeinae and Triticinae evolved at different rates. The high similarity between rye and wheat *CENH3*s is indicative of an evolutionary stability and conservation of the genetic factors that control the *CENH3* structure in the subtribe Triticinae. The assumption that multiple cycles of remote hybridization and attendant domestication served as a factors stabilizing the *CENH3* structure and that these factors were more powerful within *Secale* and *Triticum* than in *Hordeum*, will be discussed.

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