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Genetic and epigenetic reprogramming of the wheat genome upon allopolyploidization 🕮

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Abstract

In the past few years we have analysed alterations in genome structure and expression that occur in wheat upon allopolyploidization. Our major findings in natural and synthetic allopolyploid wheat are reviewed here. It was found that allopolyploidization brings about rapid genome evolution through the instantaneous generation of a variety of cardinal genetic and epigenetic alterations comprising: (1) non-random elimination of coding and non-coding DNA sequences, (2) epigenetic changes such as DNA methylation of coding and non-coding DNA leading, among others, to gene silencing, and (3) activation of retroelements, which in turn alters the expression of adjacent genes. These changes were reproducible, occurring in the F1 hybrids or in the first generation(s) of a series of nascent allopolyploids corresponding to various interspecific and intergeneric combinations. Moreover, these changes were similar to those that occurred twice in nature: first, at the transition from diploid to tetraploid wheat (IN 0.5 Mya) and, second, at the transition from tetraploid to hexaploid wheat (**1**9500 years ago). Elimination of non-coding sequences augments the differentiation of homoeologous chromosomes at the polyploid level, thus increasing the physical divergence between homoeologues and contributing to the diploid-like meiotic behaviour of polyploid wheat. Transcriptional and post-transcriptional alterations of gene activity, including transcriptional activation of retroelements, led to novel expression patterns. These phenomena emphasize the plasticity of the genome with regard to both structure and gene expression. This plasticity in turn might improve the adaptability of the newly formed allopolyploids and facilitate their rapid and successful establishment in nature.

Keywords: *Aegilops*, allopolyploidy, DNA rearrangements, gene silencing, genome evolution, polyploidy, retrotransposons, *Triticum*

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