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## Alternations of chromosome number or structural changes of chromosomes

Alternations of chromosome number or structural changes of chromosomes appear quite often in hybrids. Those changes can result in genetic diversity or can even drive to new species formation. Chromosome aberrations can be triggered as a result of physical factors (such as: radiation, temperature), chemical factors (colchicine) or genetic factors (abnormal expression of genes, responsible for pairing of homologs; gametocidal genes).

Such chromosome deviations are widely used for the transfer of alien germplasm into cultivated species. Hybridization is a starting point, which leads to the introgression of desirable loci. Polyploidization is a specific kind of hybridization, which results in the inheritance of an additional, complete set (or sets) of chromosomes. This phenomena can appear naturally in the wake of abnormal cell division (failures during meiotic or mitotic cell division) or by fusion of unreduced gametes. Both mechanisms lead to multiplication of chromosome set. There are two kinds of polyploidy organisms. Those with multiplied own sets of chromosomes are called autopolyploids (e.g. potato). By contrast polyploids originated from the cross-hybridization of two different species are known as allopolyploids (e.g. canola, wheat, triticale).

Both autopolyploids and allopolyploids are common among domesticated plant species. Generating synthetic amphidiploids containing the genomes of different cereal species provides new insights into polyploid evolution, which can help to understand the mechanism and evolutionary aspects of polyploidy. It can also facilitate the transmission of valuable genetic properties from wild species to cultivated plants (Apolinarska et al. 2010; Kwiatek et al. 2012; Kwiatek et al. 2013).

In general, F1 hybrids obtained by the intergeneric cross-hybridization are sterile, mostly because of the lack of functional gametes. This is connected with different ploidy level of the parental components and the expression of Ph1 gene located on chromosome 5B in triticale, responsible for homologous chromosome pairing during meiosis (Riley and Chapman 1958; Lukaszewski and Kopecký 2010).

If parents are of distant genome affinity and differing chromosome pair number, the F1 offspring will be unable to produce chromosomally identical and balanced gametes. However, especially in the evolution of the majority of polyploid plants, those obstacles were overcome with the pivotal-differential origin pattern. Evolution of wheat (*Triticum aestivum* L.;  $2n=6x=42$  chromosomes) is an excellent example of such pattern of allopolyploidization, through

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hybridization among species from the plant genera *Aegilops* and *Triticum*. There are two explanations of speciation in this group. First, monophyletic evolution hypothesis is that a single wild progenitor was an ancestor of particular species or genomes. Second theory, called polyphyletic evolution, says that the wild progenitor could have been introduced into several spontaneous crosses with other species and faced with multiple events of recombination (Zohary 1999). According to the polyphyletic hypothesis, the rate of parental genome modification in the case of evolution of polyploid species is different. In this instance, one genome is closely related or even identical to the parental one (pivotal genome), while the second - differential genome (or genomes) is much more genetically diversified (Feldman and Levy 2012).

Polyploid wheats include two evolutionary lineages: Emmer wheats (AuAuBB) and Timopheevi wheats (AuAuGG) (Spoor 2001) where Au-genome is the pivotal one. Both of them are supposed to have originated from two independent crosses involving progenitors of *Triticum urartu* Thum. ex Gandil (Au-genome, paternal component) and *Aegilops speltoides* Tausch (S-genome, maternal component).

On the one side, it is hypothesized that B-genome is monophyletic in origin and was derived directly from *Ae. speltoides*. On the other side, B-genome is of polyphyletic origin, and it is assumed that it has derived from more than one diploid species. Moreover, two pivotal genomes, D and U, were identified in *Aegilops* genus, where all polyploid species were subdivided into two clusters. The D-genome cluster includes a diploid *Ae. tauschii* and six polyploid species of *Vertebrata* and *Cylindropyron* sections, while the U-genome cluster included a diploid *Ae. umbellulata* and eight polyploid species of *Pleionathera* section (Kihara 1954; Feldman 1965; Kilian et al. 2011).

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