



Mitotic and meiotic behavior of rye chromosomes in wheat - *Psathyrostachys huashanica* amphiploid x triticales progeny

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ABSTRACT. The dynamics of rye chromosomes during mitosis and meiosis was analyzed in a subset comprising 33 F_3 lines from the cross of wheat, *Psathyrostachys huashanica* amphiploid (AABBDDNsNs) and hexaploid triticales (AABBRR), as visualized by genomic *in situ* hybridization. The results indicated that 31 of the total lines contained 4-14 rye chromosomes. Twenty-eight combinations had more rye chromosomes than the F_1 hybrids, suggesting the occurrence of spontaneous quantitative increment. No *P. huashanica* chromosomes were detected in all of the combinations tested. Mitotic analysis showed that rye chromosomes progressed normally with the wheat counterparts without loss. However, abnormal meiosis was found in almost all lines.

Similar progression between wheat and rye genomes appeared from interphase to metaphase I. It was at anaphase I that many rye univalents lagged behind those of wheat, followed by equational division. This resulted in the formation of chromosomal segments and micronuclei at telophase I or II. Micronuclei could also be generated from the immobilized univalents in the periphery of cells. Synapsis and translocations between wheat and rye genomes, chromosome bridges, and unreduced gametes were detected. Therefore, it is proposed that rye chromosome elimination may involve chromatid lagging, fragmentation and micronucleation, or the immobilization of certain univalents during meiosis instead of mitosis in the relatively advanced generations. This mechanism, together with spontaneous incremental increase of rye chromosome number, permitted the generation of various germplasms for wheat improvement.

Key words: Wheat; Rye; Meiosis; Mitosis; Chromosome behavior; Genomic *in situ* hybridization