Occurrence and variability of polyembryonic seedlings in triticale-wheat hybrid line

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Polyembryony is suggested as an important feature due to producing more plants per unit area by using the same number of seeds. However, yet little is known about this reproductive phenomenon to increase its frequency up to 100 percent for involving in the breeding process. In our work the constant polyembryonic line #908 (2n = 42) was spontaneously derived from the crosses of triticale (genome AABBRR (T. durum/ Ae. squarrosa//Secale cereale ssp. segetale), 2n = 42)) with common wheat T. aestivum var. velutinum (genome AABBDD, 2n = 42). Correlated positively with the spike fertility the polyembryonic seed frequency of this line is varying from 0.26 % to 11.98 % per plant. The highest frequency distribution of polyembryonic seeds was observed in central spikelets and basal (closest to the rachis) florets of spike, i.e. in the positions favoring seed formation. Polyembryonic seedlings morphologically can be divided into following types: i) with common coleoptile; ii) with half or completely conjoined coleoptiles, and iii) with splitted coleoptiles. With low frequency the conjoining was observed also for leaves and roots either in mono- and polyembryonic seedlings of this line. The highest frequency of appearance is for twin plants with splitted coleoptiles, followed by triple, quadruple, quintuple and sextuple. Seeds with more than double seedlings can combine its splitted with common or conjoined coleoptile(s). Seedlings from the same polyembryonic seed can develop either equally or unequally determining a wide variation of plant height and spike fertility traits. The trait exhibits a recessive mode of inheritance in the crosses with other poly- and non-polyembryonic lines. Compared with the monoembryoid the polyembryoid seeds were more sensitive to high doses of gamma radiation. GISH analysis showed that line #908 has 14 rye chromosomes, i.e. it is hexaploid triticale. It can be assumed that the increased polyembryony frequency is associated with a specific combination of the genes of the A- and B-genomes of T. durum and T. aestivum resulting from crosses.