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SEGREGATION DISTORTION FOLLOWING INTROGRESSION OF *THINOPYRUM PONTICUM* DNA INTO DURUM WHEAT

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Segregation distortion (SD) is the deviation of observed genetic ratios from the expected Mendelian ratios of a given genotypic class within a segregating population. Genetic elements that cause SD may be potent evolutionary forces, particularly in terms of species differentiation and genome restructuring. Distorted segregation ratios may result from gametophytic competition, resulting in preferential fertilization or abortion of gametes or zygotes, with most systems affecting the male germline. Another generalization of SD studies is that the underlying mechanisms do not distort meiosis *per se* but rather alter the products of meiosis, often, but not exclusively, by rendering non-functional gametes that do not carry the driving allele(s). Segregation distortion (*Sd*) genes are therefore also referred to as gametocidal (*Gc*) genes.

SD has been observed in a wide variety of organisms, including fungi, plants, insects, and mammals. In plants, genomic regions harboring markers with abnormal segregation ratios have been reported in many crop species, including barley, pearl millet, tomato, rice, maize and wheat. Chromosomes carrying *Sd* genes have been also identified in several wild wheat relatives and their effect revealed upon hybridization with wheat. In most cases such alien chromosomes or chromosome segments are selectively or sometimes exclusively retained in the wheat background. This is the case for various *Aegilops* species and for species of the *Agropyron* and *Thinopyrum* genera. For at least some of these genes, direction and magnitude of the SD effect are determined by the genetic background of the recipient wheat. For instance, the *Sd1* gene, located on *Thinopyrum ponticum* 7AgL arm, proximal to the leaf-rust resistance *Lr19* gene, once incorporated into common wheat through 7DL-7AgL translocations, determined a wide range of effects, from preferential transmission to self-elimination, but also normal segregation of the carrier chromosome, depending on the allelic variation at several wheat "responder" loci. No knowledge is available on the mode of action of *Sd1*.

Among several *T. durum-Th. ponticum* recombinant lines we have previously produced and shown to carry different portions of 7AgL replacing wheat 7AL, normal segregation was observed for chromosomes with up to 28% of 7AgL, containing the alien *Lr19+Yp* genes. On the other hand, a line with 40% 7AgL (R23-1) exhibited reduced transmission of the recombinant chromosome through the male germline. Analysis of F2 and F3 progeny from the cross of R23-1 with different durum wheat varieties showed segregation ratios ranging from normal to highly distorted (always in the direction of self-elimination), due to effects ascribable to the varietal genotype, but with heterogeneity observed also among progeny of the same cross. Although previous mapping data suggested *Sd1* not to be included in the 7AgL segment of R23-1, this possibility cannot be completely ruled out. To investigate possible causes of the observed SD effect and define with more accuracy the location of its driving factor(s), meiotic and post meiotic stages of pollen development have been analyzed in R23-1 as compared to lines with 28% or 23% of 7AgL and their controls.

Preliminary results confirm R23-1 to be the only line presenting various irregularities, mostly affecting post-meiotic stages.