

POSITIVE EFFECTS ON YIELD-RELATED TRAITS OF DIFFERENT CHROMOSOMAL SEGMENTS OF THE WILD *THINOPYRUM PONTICUM* INTROGRESSED INTO DURUM WHEAT

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In order to maximize exploitation of useful genetic variability from the wild wheat relative *Thinopyrum ponticum*, previously developed durum wheat-*Th. ponticum* recombinant lines, carrying the *Lr19+Yp* genes, were subjected to field tests in central Italy (Viterbo) for two years (2009-10). Three recombinant lines, named R5-2-10, R112-4 and R23-1, possessing 23%, 28% and 40%, respectively, of their 7AL arms replaced by *Th. ponticum* homoeologous 7AgL distal segments, were used to assess the expression of several yield-contributing traits and eventually associate to defined 7AgL sub-regions putative yield QTL(s) previously ascribed to the presence of 70% of the alien arm. The recombinant lines used showed differential phenotypes for traits such as seed number/ear, tiller number/plant, above-ground biomass, flag leaf width, and grain yield. Line R112-4, in particular, resulted the most promising genotype in terms of overall yield potential, as its 28% 7AgL chromatin caused significantly increased values for tiller number at heading (+28%) and at harvest (+26%), as well as for biomass (+30%), altogether contributing to a significantly higher yield (+25%), at least in the more favourable conditions of 2010. On the other hand, line R23-1 produced the highest number of seeds/ear (+34% assessed on the first tiller), indicating that in the 7AgL segment present in this line and absent from the two others (28-40% distal 7AL arm) a putative QTL for seed number is located. However, as demonstrated by the remarkably lower yield shown by the same line R23-1, its 7AgL segment does not appear exploitable in durum wheat breeding, presumably due to a negative linkage drag determined by alien Segregation distortion genes. The information obtained represents an essential "first draft" of the identification of yield-related traits associated with 7AgL fragments already incorporated in various recombinant lines of durum and also bread wheat. Combined with the information coming from a dense 7AL/7AgL genetic map concomitantly developed, the possibility that specific markers for the different traits can be detected and hence used in MAS seems a feasible target.