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GENETIC AND CYTOGENETIC MAPS OF DURUM WHEAT-*THINOPYRUM PONTICUM* RECOMBINANT CHROMOSOMES: A TOOL TO FINELY DESCRIBE TRITICEAE 7L ARMS AND TO TARGET ALIEN TRAITS

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As one important result of wheat chromosome engineering, creation of arrays of wheat-alien recombinant chromosomes allows assignment of markers and genes to defined physical locations, hence improving knowledge of structural-functional organization of wheat and alien chromosomal regions. This, in turn, represents an important, prerequisite information for targeted alien gene transfers into wheat breeding lines.

With the initial purpose of introducing into durum wheat the *Lr19* (leaf-rust resistance) and *Yp* (yellow endosperm pigmentation) genes from the wild wheatgrass species *Thinopyrum ponticum*, several homoeologous recombinants were obtained involving the wheat 7AL and the alien 7AgL chromosome arms. Detailed genetic maps were developed and correlated to eight physical breakpoints concentrated in the distal half of the arm. Eighteen RFLP, 30 SSR, 4 STS and 16 EST markers were located to eight 7L syntenic subregions, to some of which candidate genes or phenotypes of interest were associated. Thus, *Lr19* location was restricted to a 1% 7AgL interval (FL = fractional length 0.77-0.78), while the *Yp* phenotype and a *Psy-1* phytoene-synthase candidate gene were assigned to a FL 0.78-0.90 segment. In the same 7AgL segment, in a region syntenic to a FL 0.86-1 interval of the 7AL arm, an effective QTL for Fusarium head blight (FHB) resistance is also present, which derives from a different *Th. ponticum* accession from the one containing the *Lr19+Yp* genes. New recombinant lines are currently being developed in which all the beneficial genes from both alien accessions are pyramided.

Comparative analyses of different recombinant lines indicate the presence of a segregation distortion factor in a FL 0.60-0.72 interval of the alien 7AgL arm, which could affect the potential exploitation of this specific 7AgL region.

A subset of the 7AL-7AgL durum wheat recombinant lines is being used in comparative trials aiming to identify location and possible mechanisms of genes/QTLs underlying the positive yield effects so far roughly associated with a sizable 7AgL translocation.