

Durum wheat-*Thinopyrum ponticum* recombinant lines: a tool to finely describe homoeologous 7L arm regions

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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. To transfer into durum wheat the *Th. ponticum* *Lr19* (leaf-rust resistance) and *Yp* (yellow endosperm pigmentation) genes, several homoeologous recombinants were obtained involving the wheat 7AL and the alien 7AgL arms. Detailed genetic maps were developed and correlated to eight physical breakpoints concentrated in the distal half of the arm. Seventeen RFLP, 30 SSR, 4 STS and 17 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. Also, analyses of meiotic and post-meiotic pollen developmental stages in different recombinant lines suggested the presence of a segregation distortion factor, possibly *Sd1*, in a FL 0.60-0.72 interval. The same materials are 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.