flanking markers resulted in the identification of BAC supercontigs that cover 19.2 Mb of the *YrH52* gene region. Further work is underway to refine the physical map and identify candidate gene(s) for *YrH52*. A similar strategy is employed for positional cloning of *Yr15* and *YrG303*, also derived from *T. turgidum* subsp. *dicoccoides*. Collaboration with other groups was established to promote the positional cloning of other wheat genes that reside on 1BS. These results demonstrate the importance of the genomic resources developed by TriticeaeGenome consortium for accelerating positional cloning of target genes in the complex genome of wheat.

High-resolution mapping of areas of low recombination and polymorphism containing the hexaploid wheat loci Pis1 and C.

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Gene mapping and map-based cloning studies in wheat are often complicated by lack of marker polymorphism and/or recombination. Radiation hybrid mapping can address both problems as it relies on radiation-induced breaks to order markers. Due to the nature of RH panels markers are scored as presence/absence, eliminating the need for polymorphism. We utilized this approach to physically map genes based on multiple overlapping deletions induced by γ irradiation. *Pis1* is a wheat floral mutant producing three fully functional pistils per floret instead of the usual single pistil. Compactum (*C*) is responsible for club head phenotype and maps to the low-recombination, pericentromeric region of 2D. The location of *C* with respect to the centromere is not well established. *Pis1* has proven difficult to map in an F_2 population due to lack of marker polymorphism. In this study, independent RH mapping panels were assembled for both genes (282 RH lines for each of *Pist1* and *Compactum*). For each gene, a set of 94 lines were selected and characterized with ESTs and SSRs, specific to the targeted regions. We mapped *Pist1* gene on chromosome 2D (deletion bin 2DL-9) using 14 SSRs and 27 ESTs. Total map distance was 145.0 cR1500 covering ~98 Mb. Even in this region of a recombination hot spot, a cM/cR1500 ratio was found as 1:8; with a mapping resolution of ~750 kb. The closest ESTs flanking *Pist1* are co-segregating and spanned only six rice genes. *Pis1*-linked ESTs were then mapped on a genetic mapping F_2 (Multiovary/Winsome) population. For the *Compactum* locus, 25 ESTs and 16 SSRs were used in mapping. A total map length created was 158.8 cR1500 with average marker retention of 80% and map resolution of ~710 kb. The cM/cR1500 ratio in this region of chromosome was found to be 1:60. Two ESTs flanking *C* locus on this RH map span 15 rice genes. ESTs flanking the *C* locus were mapped on two different bi-parental genetic populations to confirm the outcomes of RH mapping. Putative candidates are being used for developing gene specific markers and work on fine mapping and their eventual cloning is underway.

The rye gene Pm8 conferring resistance to wheat powdery mildew is a homologue of the wheat powdery mildew resistance gene Pm3.

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During wheat breeding, chromosomes of the rye (*Secale cereale* L.) genome have been introgressed into the wheat genome to enhance tolerance to biotic and abiotic stresses. The most widely used wheat–rye translocation nowadays is the 1RS chromosome arm derived from the rye cultivar Petkus carrying three rust resistance genes and the powdery mildew resistance gene *Pm8*. In wheat, *Pm* genes mediate resistance against powdery mildew, a major fungal pathogen. *Pm8* was mapped at the same gene-rich region on the short arm of wheat homoeologous group-1 chromosome as the powdery mildew resistance gene *Pm3* of hexaploid wheat and was, therefore, proposed to be an ortholog of *Pm3*. Southern hybridization analysis showed that there is a sequence in rye and in *Pm8* wheat lines with homology to the *Pm3* promoter region. In a homology-based cloning approach based on primers derived from the cloned wheat powdery mildew resist-