

## Mapping Fusarium Head Blight Resistance in Durum Wheat and More

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Many previous studies have identified a number of quantitative trait loci (QTL) associated with resistance to fusarium head blight (FHB) in hexaploid wheat, mainly from the resistance source 'Sumai 3' or its derivatives. As very few sources of resistance are identified in durum wheat, attempts are made to transfer the resistance from various sources of hexaploid wheat to durum. In this study, location of resistance QTL from Chinese hexaploid resistance source, Wangshuibai in a durum background was done in a population consisting of 140 F<sub>2:5</sub> recombinant inbred lines (RILs). A total of 106 simple sequence repeats (SSR's) and eight sequence tagged sites (STS), many previously identified as linked to FHB QTL, covering a distance of 1007.7 cM (42-56% of the average durum map) of the genome were used to construct the linkage maps of all chromosomes. A QTL was identified at 14 and 21 d after inoculation between the loci *Xgwm533* and *Xsts138* on 3BS explaining 11 and 15% of the phenotypic variation respectively. Graphical genotyping on the top five resistant and susceptible lines showed the presence of QTL in the resistant lines and its absence in the susceptible lines. Further additional studies are needed to identify other QTL since a total of only 21% of the genotypic variation is explained by the QTL identified in this study.

Methods for physical mapping of chromosomes, which do not rely on meiotic recombination, are necessary for large genomes like wheat where uneven distribution of recombination and significant variation in genetic to physical distance ratios dramatically affect the capacity to order physical contigs in large portions of the chromosomes. In this context, physical mapping using a radiation hybrid (RH) mapping approach has proved valuable in a number of non-plant and plant systems. RH maps of chromosome 1D, utilizing 87 lines (irradiated with 35 Krad), and chromosome 3B, utilizing 187 lines (99 from 25 Krad and 88 lines from 35 Krad), were generated by mapping different marker classes without the need for polymorphism. Analysis of 1D RH panel with 378 marker loci identified a total of 2,312 obligate breaks for an average resolution of ~199 kb (size of chromosome/total breaks = 464 Mb/2,312 breaks). Remarkably, analysis of several large sequenced segments (3 Mb average size) of chromosome 3B with the 3B RH panels also indicated an average map resolution of ~200 Kb/break. Since this mapping resolution is within the range of BAC contig alignment, these panels have been used to align BAC contigs to regions of chromosomes 1D and 3B and to further refine the location of *species cytoplasm specific* (*scs<sup>ae</sup>*) locus on chromosome 1D. The *scs<sup>ae</sup>* locus could not be conventionally mapped in the durum alloplasmic background indicating an added benefit of RH panels.

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