Preliminary Genetic Mapping of Common Bunt Resistance Gene Bt13

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Abstract

Two kinds of plant resistance against common bunt exists. Race specific qualitative resistance following the gene for gene principle by Floor and non-race specific quantitative resistance. Until now seventeen genes named Bt1-Bt15, Btp and BtZ are known to confer race specific resistance and they make up the set of differential lines used to differentiate virulence races. The differential lines carrying Bt14 and Bt15 are the Durum varieties Doubbi and Carleton, while the remaining lines are *Triticum aestivum*.

The Bt13 gene was identified and added to the differential line reference set by Blair Goates (Goates 2012). Thule III (PI 181463), not to be confused with the Swedish cultivar Thule III (NGB 6714) (Borgen 2014), is used as the differential line for identifying the Bt13 resistance gene (Goates, 2012).

1192 wheat lines were phenotyped using a design described in Borgen *et al* (2018) and genotyped using TG25k SNP markers in different trials in the LIVESEED, BOOST and DIVERSILIENCE projects. Each line was postulated to have or not have Bt13 based on phenotypic data and information about the pedigree. Our mapping population has strong population structure regarding Bt13 because Thule III is a direct parent of most of the 64 lines postulated to have Bt13. For this reason there are a many sporadic significant markers scattered across chromosomes.

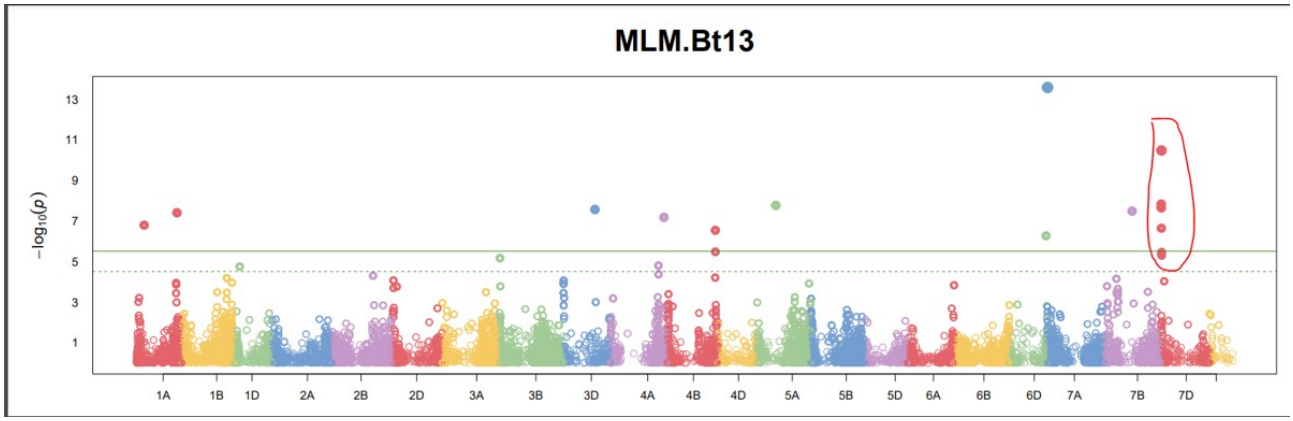

Figure 1: GWAS Manhattan plot made with the MLM method

At chromosome 7D in the interval 6,820,874 – 11,141,495 bp we have what appears to be the correct signal. The marker at 7A, which is the most significant of all, was investigated further and was found to

placed at 7D by linkage analysis in the BOKU Bt12 mapping population. Furthermore, a BLAST against RefSeq 2.1 had 7D 8,602,319 bp as a possible (and very likely) location. The likelihood that the 7D signal is the correct one is strengthened by this placement of the most significant marker in the middle of it.

Table 1: Significant markers at 7D

TA001746-1415	G
AX-158595238	T
Kukri_c80931_147	A
IAAV9104	C
AX-111707392	T
RFL_Contig1323_544	G

The Bt13 signal is identical to the Bt12 interval mapped by Muellner *et al.* (2020). For this reason, the Bt13 GWAS markers also matches in most lines containing Bt12. This 7D haploblock can be considered a signature shared between Bt12 (including Snow Mold Tolerant Selection 1 / CItr 14106 and Snow Mold Tolerant Selection 2 / CItr 14107) and Bt13 containing lines and also with Erythrospermum 5221 / PI 572845, TU86-42-01-6 / PI 560848 and PI560603-sel-wclrs / PI 636148 having unknown resistance.

A detailed analysis of cross-over events in lines having Thule III in the pedigree in an extended interval around the GWAS signal was done to get a candidate interval. The two Bt13 postulated lines SegThul LS180 and SegThul LS169 had recombination in the GWAS interval, between markers at 9,201,720 and 9,642,370 bp. The three lines SegThul-veksel LS158 (No Bt13), SegThul LS168 (Bt13) and SegThul LS173 (Bt13) had recombination in the GWAS interval, between markers at 9,201,720 and 9,642,370 bp and also between 5,005,433 and 5,357,634 bp. From these five lines we get the final candidate interval 5,005,433 - 9,642,370 bp.

Table 2: Markers

AX-158555104	C
AX-94804328	C
Kukri_c37227_579	A
AX-95237430	G
Ra_c30952_531	T
AX-158544378	T
AX-94708419	G
TA001746-1415	G
AX-158595238	T
Kukri_c80931_147	A
IAAV9104	C

Markers in blue define the interval. Markers in green can be used for MAS. Markers in red letters are significant in the GWAS.

The MAS markers match in 95% of Bt13 postulated lines and the false positive rate is 7%. The low false positive rate is partly explained by the presence of very few Bt12 containing lines in the mapping population.

Acknowledgement

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Keywords

Wheat, gene mapping, common bunt, organic agriculture, resistance breeding, marker-assisted selection

References

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