Genetic mapping of common bunt resistance gene *Bt1*

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Abstract

Common bunt is a soil and seed borne disease of wheat causing kernels to be replaced by sori balls of fungal spores. Common bunt is controlled in conventional agriculture by seed treatment but causes many problems in organic agriculture where seed cleaning, seed testing and plant resistance are the main tools available.

The *Bt1* gene was discovered by Fred N. Briggs in 1926 in the variety Martin (Briggs 1926). Briggs and Holton (1950) found that Martin has two resistance factors, M1 and M2. M1 was later renamed to *Bt1*, and M2 to *Bt7* (Metzger, 1970). The two Martin factors were located using nullisomic and monosomic lines to chromosome 13 = 2B (*Bt1*) and chromosome 16 = 2D (*Bt7*) (Sears, Schallearn, & Briggs, 1960). The Martin factor M1 was later found in Hussar, Odessa, White Odessa, Banner Berkeley, Regal, Sherman and Albit (Hybrid 128 x White Odessa) (E. N. Bressman 1932, Fred N. Briggs 1935, Fred N. Briggs 1929, E. N. Bressman 1931)

PI 554101/ Selection 2092 is used worldwide as the common bunt differential line for *Bt1* (Goates 2012).

NordGen has 6 genebank accessions developed by MacKay by crossing the variety Starke-II with bunt resistant lines and backcrossed to Starke-II about 7-8 times while maintaining resistance. The precise protocol is unfortunately lost. A NIL with *Bt1*, NGB-11503, exist. Albit is the *Bt1* donor.

The mapping population consist of 1192 wheat varieties and breeding lines that were phenotyped and genotyped in different trials in the LIVESEED, BOOST and DIVERSILIENCE projects. Each line was postulated to have or not have *Bt1* based on phenotype data and information about their pedigree. 62 lines were postulated to have *Bt1* alone or in combination with other genes.

A GWAS with gene postulates as input produced signals at 2B and 2D and the detailed analysis revealed that markers at 2D in reality are positioned at 2B and part of the same signal. The marker at 3A, Kukri_c18420_705, is known to be associated with spike fertility and is probably due to unaccounted for population structure.

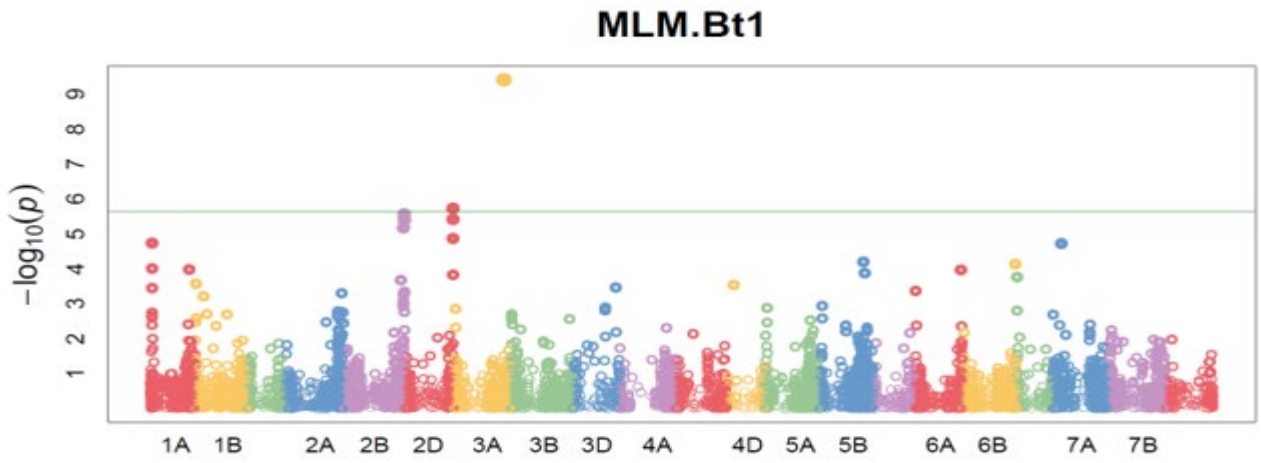

Figure 1: GWAS Manhattan plot made with the MLM method

Investigation of recombination events in the Starke II NIL / Starke II / Albit triplet together with a comparison of haplotypes for all *Bt1* postulated lines in our mapping population across an interval extending the GWAS interval at 2B allowed identification of the 11,043,031bp interval 799,983,180 – 811,026,211bp.

Markers were a match in 91% of lines postulated to have *Bt1*.

The false positive rate was 24%. For eight of these lines phenotyping cannot rule out that that they actually have *Bt1*, because resistance from other genes mask the effect of *Bt1*. Notable false positives was the *Bt2* differential line Selection 2075 / PI 554103 (Elgin x Selection 1403 / PI 554102). The *Bt11* differential line M82-2123 / PI 554119 also is a false positive as is the *Bt12* differential P78-24 / PI 554106 (1696 / PI 119333 x Elgin). Butaro is a parent of many lines in the population and is responsible for 26 false positives in them.

Table 1: Markers, Markers highlighted in brown define the interval. Markers highlighted in green can be used for MAS. Markers in orange are significant in the GWAS.

AX-158609666	A
Excalibur_c48404_59	C
wsnp_Ex_c15646_23969140	A
BS00065302_51	G
AX-94890379	G
BS00083998_51	G
Ra_c105904_187	C
Ra_c105904_1191	G
AX-158610188	A
AX-94808568	G
AX-158562114	C
Kukri_c49784_86	A
Excalibur_rep_c106698_235	A
BS00065264_51	G
Excalibur_c25043_357	A
Kukri_c900_1334	T
AX-95017900	G

Keywords

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

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