Genetic Mapping of Common Bunt Resistance Gene Bt7

Dennis Kjær Christensen[1], Anders Borgen[2], Hermann Gregor Dallinger[3]

[1] Private, Gerding, 5020 Skørping

[2] Agrologica, Houvej 55, Mariager

[3]Institute of Biotechnology in Plant Production, University of Natural Resources and Life Sciences, Konrad-Lorenz-Strasse 20, 3430, Tulln

Corresponding author: Dennis Kjær Christensen

E-mail: Dennis@fastcode.dk

Abstract

The Bt7 gene was discovered by Briggs and Holton (1950) as one of two resistance factors, M1 and M2, in the variety Martin. M1 was later renamed to Bt1, and M2 to Bt7 (reference??). The two Martin factors were mapped using nullisomic and monosomic lines to chromosome 13 = 2B and chromosome 16 = 2D (reference??).

PI554100/ Selection 50077 is a selection from a cross of Martin with Elgin, and is now used worldwide as the common bunt differential lines for Bt7 (Goates 2012).

GWAS was conducted by using the MLM algorithm implemented in GAPIT R package (3.3), with kinship correction and population structure controlled by principal component analysis. The number of principal components was determined by the forward model selection implemented in GAPIT, using the Bayesian information criterion (BIC) to determine the optimal number of PCs to include.

We calculated linkage disequilibrium (r^2) in a region of x Mbp (according to the map provided by TG) around significant markers using the R package "gaston" (Gaston). To identify linkage groups within these markers, we clustered the resulting LD matrix hierarchically as implemented in R package stats (add citation) with treating the LD values as a distance matrix (dist = 1 - LD) and using method "ward.D2".

The mapping population consists of 1192 lines of which 301 was postulated to have Bt7, by pedigree analysis and multi race phenotyping (Borgen *et al* 2018), ~~to have Bt7~~, either alone or in combination with other genes. GWAS was run against these gene postulates.

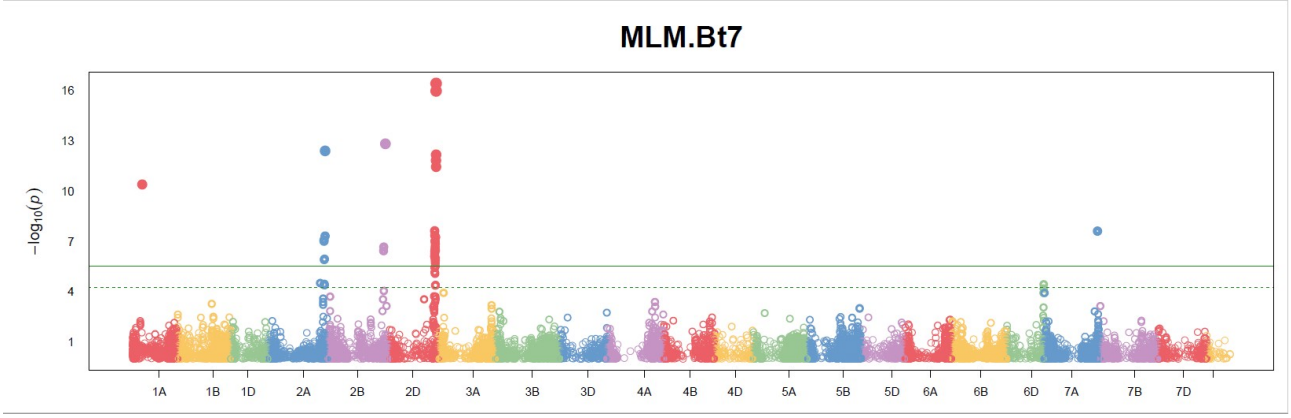

Figure 1: GWAS Manhattan plot made with the MLM method

The GWAS gave three distinct signals on the three homeologous chromosomes 2A/2B/2D. We investigated LD patterns in the regions around significant marker positions and aligned markers to the most recent IWGSC RefSeq v2.1 assembly. LD analysis showed that significant markers were in strong LD, indicating a single locus on one chromosome as the location of the resistance.

Three of the markers had unique alignments in the unfiltered physical map and all of them were at chromosome 2D on TG maps and BLAST results, suggesting that the signal is at chromosome 2D.

Using only markers from the 2D signal, the full genotype – phenotype relation was explained. In summary all analyses suggested that only one signal exists and it is located at chromosome 2D. This is in agreement with the result from the using nullisomic and monosomic analysis by Sears *et al* (1960).

GWAS resulted in a 7.33 Mbp bp interval 616,243,864 – 623,541,433 bp for the position of Bt7. Markers BS00110411_51 and wsnp_RFL_Contig4402_5154408 are flanking the interval and the three markers, RAC875_c30919_311, RAC875_rep_c114621_200 and wsnp_Ex_c42970_49408712 identify the Bt7 haploblock.

Table 1: Markers

BS00110411_51	C
RAC875_c30919_311	G
RAC875_rep_c114621_200	C
wsnp_Ex_c42970_49408712	A
wsnp_RFL_Contig4402_5154408	A

These three markers in brown can be used to track the presence of Bt7 and the two markers in green define the interval.

The markers matched in 87 % of lines postulated to have Bt7, but at the same time they matched in 28% of lines not postulated to have Bt7. In many cases it is not possible determine whether these lines represent false positives because the presence or not of Bt7 is masked by other genes, such as Bt9, Bt20 or BtZ.

Acknowledgement

Phenotyping was done with support from the projects LIVESEED (H2020), BOOST (Organic RDD), DIVERSILIENCE (CoreOrganic Co-fund). Genotyping was supported by LIVESEED, Fonden for Økologisk Landbrug, Promilleafgiftfonden, and the European Consortium for Bunt Research.

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Gaston **https://cran.r-project.org/web/packages/gaston/index.html**

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