Genetic Mapping of Common Bunt Resistance Gene Bt9

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Abstract

R. J. Metzger found a resistance gene in the line C.I. 7090 / PI 57143 that was different from B1-Bt8 and hence named Bt9. C.I. 7090 / PI 57143 also contains Bt7. The Bt9 differential line is R63-6968 / PI 554099 which is a selection from the cross Elgin / PI 178383.

Bt9 was first mapped to the distal end of 6DL in a biparental population of 91 double haploid (DH) lines. The parents were PI 554099 (National Small Grains Collection, Aberdeen, Idaho, USA), carrying resistance gene Bt9, and common bunt susceptible-wheat cv. Cortez (Wiersum Plant Breeding, Winschoten, The Netherlands). (Steffan et al. 2017)

Bt9 was later mapped to the interval 469,830,275 – 471,017,889 bp (IWGSC RefSeq v1.0 positions) (491,342,078 – 492,585,860 in RefSeq 2.1 positions) in a biparental doubled haploid population with parents IDO835 (Bt9 donor) and Moreland by QTL mapping.

NordGen has a 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. One of the NILs possesses Bt9 (NGB-11505). The source of Bt9 in the Starke II Bt9 NIL is MK 2-6244 / NGB 21193. Comments in Nordgen state that it is Selection M73-2260 from PI 264255, but this is a Durum wheat named Akbasak.

Our mapping population have 1192 lines and 92 of them was postulated to have Bt9. Gene postulation was made difficult by the fact that many lines could have Bt8 + Bt9 or Bt9 +Bt11 and the presence of Bt8 or Bt11 will mask the presence of Bt9. A GWAS using the MLM method implemented in the R-package GAPIT was run with gene postulation as input.

The GWAS signal consists of four tightly linked markers in the interval 490,706,843 – 490,708,662 bp (RefSeq 2.1 positions).

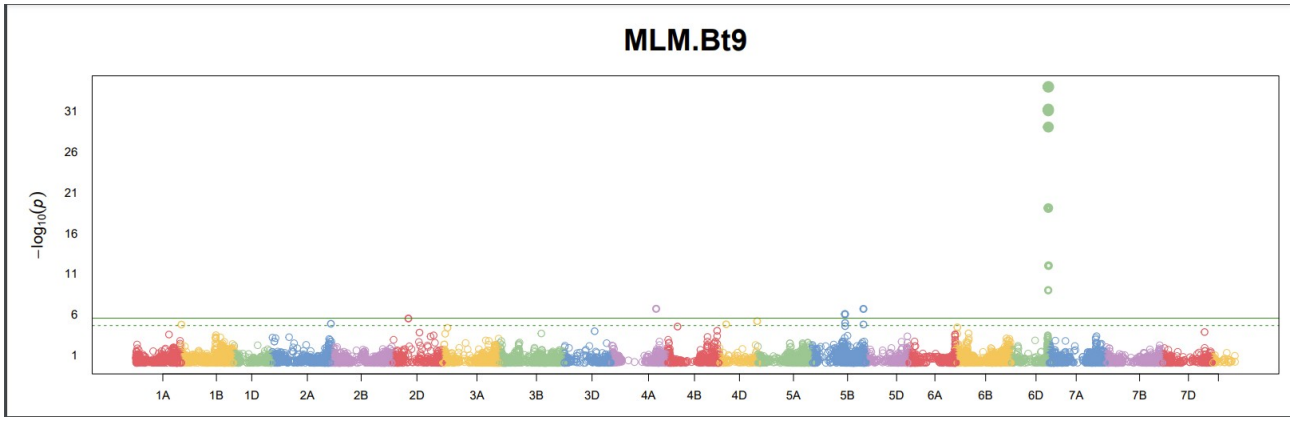

Figure 1: GWAS Manhattan plot made with the MLM method

Table 1: Significant markers in GWAS

wsnp_JG_c5646_2148296	C
Kukri_rep_c107605_164	T
wsnp_CAP8_rep_c4586_2232878	C
wsnp_CAP7_c1735_859875	G

An interval extending from approximately 10 Mbp below GWAS signal and to the end of the chromosome was used to search for recombination events in lines where one parent had Bt9, including the Starke II NIL. This lead to the discovery of the 1,005,254 bp Bt9 candidate interval 490,336,412 – 491,341,666 bp.

Table 2: Markers for MAS

BS00022206_51	A
wsnp_JG_c5646_2148382	C
wsnp_JG_c5646_2148296	C
Kukri_rep_c107605_164	T
wsnp_CAP8_rep_c4586_2232878	C
wsnp_CAP7_c1735_859875	G
AX-94589700	A
RAC875_c484_1063	A

The six markers in green/orange can be used to track the presence of Bt9.

Markers correctly identifies 84% of lines postulated to have Bt9 alone or in combination with other genes. For lines postulated to have Bt9 alone the hit rate is 98%. The false positive rate is 5%.

Some notable lines supposed to have Bt9 that does not match the markers are the Bt11 source Dimenit / PI166910, Malkesi / PI 178201 and Ark / CItr 15286.

Crosses for fine mapping should be designed to have maximum marker contrast inside the candidate interval, and multiple lines with 100% contrast are available, such as Ikarus (Bt5), Hypnos (Bt5) and T325-7717 (Bt0).

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Identification and assessment of two major QTLs for dwarf bunt resistance in winter wheat line 'IDO835'. Rui Wang, Tyler Gordon, David Hole, Weidong Zhao, Kyle Isham, J. Michael Bonman, Blair Goates, Jianli Chen. Received: 9 April 2019 / Accepted: 19 June 2019 / Published online: 25 June 2019© Springer-Verlag GmbH Germany, part of Springer Nature 2019