Preliminary Genetic Mapping of Common Bunt Resistance Gene Bt2

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Abstract

The resistance gene Bt2 to common bunt (*Tilletia caries*) was discovered by (Briggs, F. N. 1926/1929/1930) in the variety 'Hussar' (along with Bt1) and therefore originally called the Hussar factor. Metzger (1970) renamed the resistance Bt2 and proposed 'Selection 1403' (PI 554102), '1075' and '1102' (PI 554097) as differential lines for this gene.

1561 varieties and breeding lines being part of the International Common Bunt Consortium mapping panel were phenotyped with multiple virulence races and resistance genes were postulated based on this and the pedigrees (Borgen and Christensen 2023).

A GWAS using the MLM method (GAPIT 3.1) was performed against the gene postulates using 24145 markers from the TG25K/TG26K SNP array, giving significant signals at chromosome 1D, 2B, 5B, 5D and 6D.

A detailed investigation revealed that the three loci at 1D, 2B and 5D contained resistance genes from different donors all giving the same phenotyping pattern with respect to the 10 virulence races used.

Candidate intervals for all loci were determined by locating cross-overs in parent1/parent2/offspring triplets. Refinement of the Bt2 interval was done by haplotype comparison using 'Hussar' (CItr 4843).

The Bt2 gene in 'Hussar' and differential lines 'Selection 1403' (PI 554102), and 'Selection 1102' (PI 554097) was found to be at 1D in the 2,976,429 bp interval 41,696,687 – 44,673,116 bp, containing 12 High Confidence RefSeq 2.1 (HC) genes.

The additional gene at 2B, resulting in the same phenotypic reaction as Bt2 preliminarily named Bt_Bussard_2B, was mapped to the 4,427,263 bp interval 8,697,088 – 13,124,351 bp, containing 61 HC genes.

The additional gene at 5D, resulting in the same phenotypic reaction as Bt2, preliminarily named Bt_Magnifik_5D, was mapped to the 2,539,663 bp interval 44,030,824 – 46,570,487 bp, containing 26 HC genes.

References

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