

Genetic Mapping of Resistance Genes to Common Bunt (*Tilletia caries*) in PI 119333

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Abstract

Goates (1996, 2012) added '1696' (PI 119333) as a differential line for the Bt12 gene. Müllner *et al* (2020) mapped a major resistance gene to the interval 6.5–10.8 Mbp at 7D proposing this to be the Bt12 gene. In the same mapping populations, an additional QTL was mapped to the 4B interval 20.6–706.5 Mbp.

Using the same dataset, we found, as the original authors did, that markers in the mapped 7D interval were not 100% linked to Bt12. All markers in large intervals around the 6.5–10.8 Mbp are monomorphic in the mapping populations and the candidate interval includes those and goes from 0 to 25 Mbp, excluding the 6.5–10.8 Mbp interval. Weak evidence also suggested the presence of two or more genes in the 7D candidate interval.

A subset of the RILs from the mapping populations were phenotyped with 8 different virulence races, and the infection patterns suggests two genes at 7D and two genes at 4B.

Detecting the locations of 18 recombination events across all RILs, the 4B chromosome could be divided into 19 intervals and comparing the donor parent in these intervals to the phenotyping results, a gene in each end of the chromosome was mapped.

- Bt_PI119333_4B_1: 1,306,080 – 15,855,852 bp
- Bt_PI119333_4B_2: 650,383,778 – 670,633,612 bp

Using additional data from the International Common Bunt Consortium Panel, both 7D genes were mapped to the 6,770,537 bp interval 14,162,621 - 20,933,158 bp. Hence, we conclude that Bt12 in line '1696' (PI 119333) is not a single gene, but a combination of at least 4 genes.

References

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