

Genetic Mapping of Common Bunt Resistance Gene Bt6

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Abstract

A new factor for resistance to common bunt (*Tilletia caries*) called the Rio factor in the cultivar 'Rio' was reported by Stanford (1941) and later renamed to Bt6 by Metzger (1970).

Müllner *et al.* (2020) mapped a number of QTLs in mapping populations, where 'Blizzard' and 'Bonneville' were donors of resistance, including the QTL *Qbt.ifa-1B*. We fine-mapped the gene/loci using the same data set to the 11,637,599 bp interval 16,381,367 – 28,018,966 bp. The haplotype of 'Blizzard' and 'Bonneville' in this interval matched that of 'Rio' indicating that *Qbt.ifa-1B* could be Bt6. By phenotyping two RILs from the mapping populations with eight virulence races, it was found that their infection patterns matched that of 'Rio'.

Lunzer *et al.* (2023) mapped a QTL also named *Qbt.ifa-1B* at 1B in a 'Dimenit' (PI 166910) x 'Rainer' cross to the intervals 12.2–41.5 / 44.6–46.9 / 28.2–43.2 Mbp in different years. From a detailed analysis in the same dataset, it was found that the markers for Bt6 tracked the presence of *Qbt.ifa-1B*.

Validating the Bt6 markers in our own mapping panel, a perfect detection rate and a 5% false positive rate was found. Based on both marker position and phenotyping, we conclude that there is a high probability that Bt6 resistance gene is identical to the Bt4 resistance gene (Christensen and Borgen 2025).

References

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