

## Is Bt8 located at Chromosome 6D and closely linked to Bt10?

Dennis Kjær Christensen | Anders Borgen

Agrologica, Houvej 55, DK-9550 Mariager, Denmark

dennis@fastcode.dk | borgen@agrologica.dk

Presented by: Dennis Kjær Christensen

The biparental populations with the parents PI178383/Midas and PI178383/Rainer described in (Hagenguth, 2016) segregated, as there were two common bunt resistance genes in PI178383. As PI178383 is known to carry Bt8, Bt9, Bt10 and a minor factor, it is possible to speculate that two of the genes must be tightly linked. Bt9 and Bt10 are known to be located at chromosome 6D, but are not tightly linked. This leads to the hypothesis that Bt8 is closely linked to Bt10 or Bt9.

Comparing and filtering genotyping data for 6D from the TG15K array for PI178383, Hansel, Bt8 differential M82-2161, Bt9 differential M90-387, bt10 differential M82-2102, Stava, Starke II Bt9 NIL, Starke Bt10 NIL revealed that Bt8 and Bt10 may be located closely together at the short end of 6D in the interval 1,773,421 – 6,342,831 bp.

Crosses with PI178383 has led to several bunt resistant varieties, including the Swedish variety Stava. Stava miss the marker for Bt10 (J. G. Menzies, 2006) and Stava-crosses never gives lines that are infected with races virulent to Bt10. Stava has markers in the interval developed by Steffan et al 2017 indicating Bt9. Dwarf bunt at Gotland, Sweden, is virulent to Bt8 but not to Bt9 (Mascher et al 2016). Crosses with Stava is resistant to dwarf bunt at Gotland, and crossing with Stava does give bunt resistant lines of which some are resistant to dwarf bunt at Gotland (including Hellfrida), and some are not (including Magnifik). It is therefore most likely that Stava have both Bt8 and Bt9, whereas Magnifik has only Bt8.

A new race of *Tilletia laevis* has developed in Sweden virulent to Stava, and therefore must likely virulent to Bt8 and Bt9. This development jeopardize the strategy for Swedish bunt resistance breeding, but will in future make it easier to identify resistance genes by reactions to local virulent races.

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### References

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