

Is Bt8 at Chromosome 6D?

And Closely Linked to Bt10?

Me

- Dennis Kjær Christensen
- Denmark
- Engineer in electronics
- Programmer
- Automated SW test
- Hobby wheat nerd

Inspiration

MASTER THESIS

**Breeding for organic agriculture:
Evaluation of common bunt resistance
in three winter wheat populations
derived from M822123, PI178383 and
PI560841-bcl**

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Population(s)

- PI178383, a Turkish landrace containing the resistance genes *Bt8*, *Bt9* and *Bt10* and a minor resistance factor.
- Crossed to Midas/Rainer
- Two populations treated as one

Segregation Ratio 3:1 -> Two genes

PI178383/PS (n=129)	1:1	97 (88)	32 (41)	64.50	64.50	32.752 (17.124)	1.047e-08 (3.502e-05)
	3:1	97 (88)	32 (41)	96.750	32.25	0.003 (3.165)	0.960 (0.075)
	7:1	97 (88)	32 (41)	112.88	16.13	17.862 (43.855)	2.376e-05 (3.536e-11)

Hypotesis

- Three genes present in PI178383 – Bt8, Bt9, Bt10
- Segregating as two
- Two must be linked
- B9 and Bt10 on 6D in opposite ends -> loose linkage
- Bt8 close to Bt9 or Bt10 -> tight linkage
- Is Bt8 close to Bt9 or Bt10?

Additional Material

- Genotyping data for 6D from the TG15K array for PI178383, Hansel, M82-2161 (Bt8 differential), M90-387 (Bt9 differential), M82-2102 (Bt10 differential), Stava, Starke II Bt9 NIL, Starke Bt10 NIL.

Marker Analysis

- Simple compare for all 6D markers
- Marker matches for Bt8 lines in the interval 1,773,421bp – 6,342,831bp
- Marker matches for Bt10 lines in the interval 1,773,421bp – 9,973,090bp
- Marker matches for Bt9 lines in the interval 460,469,869bp – 472,890,118bp
- Ignoring a few markers looking out of place or as false positives

The Future

- Test markers in many lines known to have Bt8
- Prefer testing in a biparental mapping population
- Or even do a proper GWAS!

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