

Association mapping for common bunt resistance in wheat

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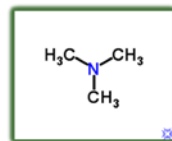
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Wheat screened for their resistance reaction towards common bunt in the field

- 248 wheat accessions
 - Most were susceptible to common bunt; 25 lines showed less than 10% infection
 - 32 spring type, 191 winter type and 25 with unknown vernalization requirements
 - Central 191, Northern 62, Western 31, Europe; 35 NSGG (Idaho) Bt1-Bt13 (Goates, 1996); 19 unknown origin, 41 landraces
 - 189 varieties released from 1886 to 2010!
- Genotyping
 - DArT markers (Triticarte 2012) approx. 7000 markers
- Field: Mariager (56°39 N 10°01 E), Denmark; year 2011, 2012

- Trouble maker:



Inoculations, fields and evaluation 2011 and 2012

- Common bunt teliospores bulk collection
 - Spores from different sites in Denmark representing a virulence spectrum (obtained from Bent J. Nielsen)



- Seeds inoculated by dusting,
 - 50-80 seeds per accession per 1 meter row
 - Winter sown (October), Spring sown (April)



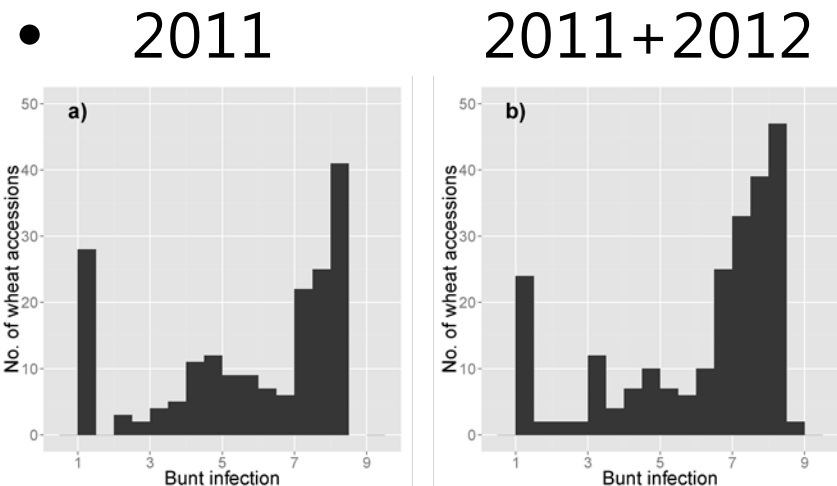
- Resistance scoring
 - After heading, early summer
 - % of spikes with a least 1 bunt sorus
 - Log-transformation of scale

| Percent infection | Log1-9 scale | Log1-2 scale |
|-------------------|--------------|--------------|
| 0 | 1.0 | 1 |
| 1 | 1.9 | 1 |
| 2 | 2.5 | 2 |
| 3 | 3.0 | 2 |
| 4 | 3.4 | 2 |
| 5 | 3.7 | 2 |
| 10 | 4.8 | 2 |
| 15 | 5.5 | 2 |
| 20 | 6.0 | 2 |
| 30 | 6.7 | 2 |
| 50 | 7.7 | 2 |
| 100 | 9.0 | 2 |

Infection data for 2011 and 2012

- Out of 248 wheat, 239 accession were scored both years, 234 in 2011 and 243 in 2012
- %-infection by winter- and spring-type
- 25 accessions less than 10% infection
- Correlation for bunt scores between years were high: $r^2 = 0.64, p < 0.001$
- Phenotypic variation
 - 79% were genetic effects
 - 11% were G x Year effects
 - 4% Year effect

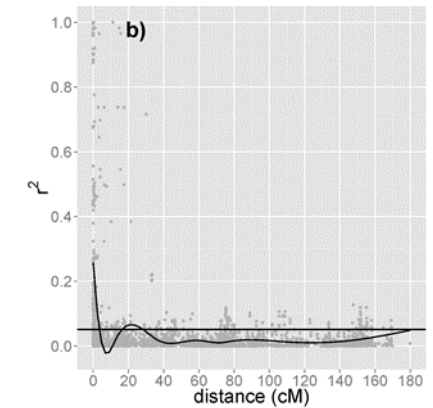
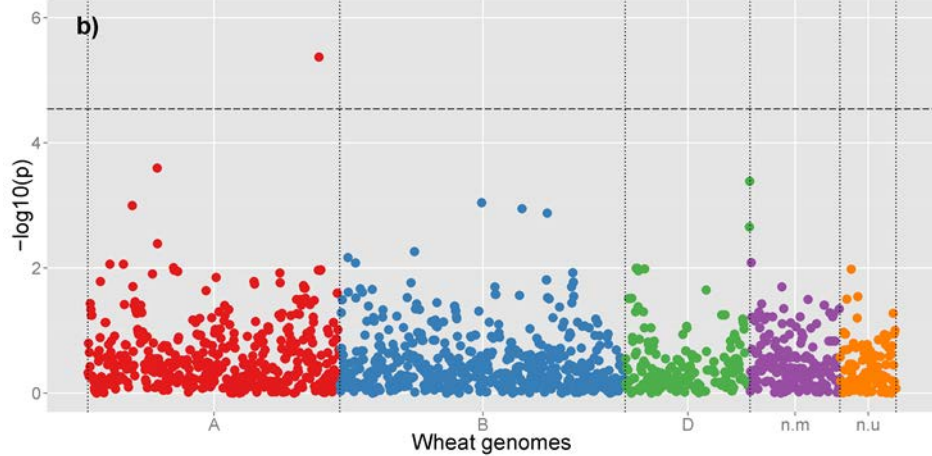
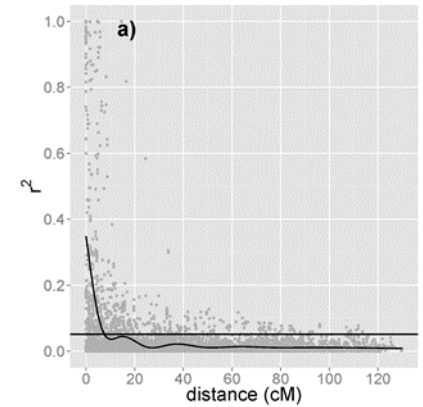
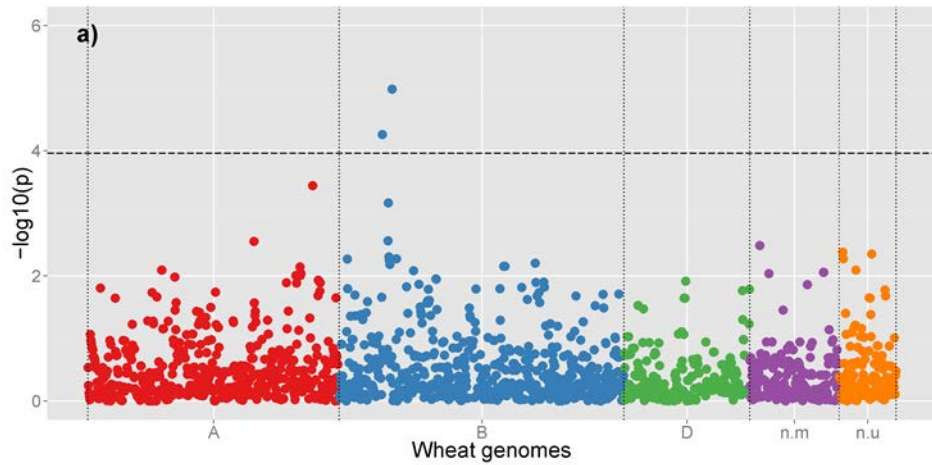
| Infection | Type | 2011 (%) | 2012 (%) | Average (%) |
|-----------|--------|----------|----------|-------------|
| Minimum | spring | 12 | 4 | 19 |
| | winter | 0 | 0 | 0 |
| Maximum | spring | 92 | 54 | 60 |
| | winter | 100 | 73 | 82 |
| Mean | spring | 49 | 25 | 36 |
| | winter | 43 | 27 | 35 |
| | all | 44 | 27 | 35 |



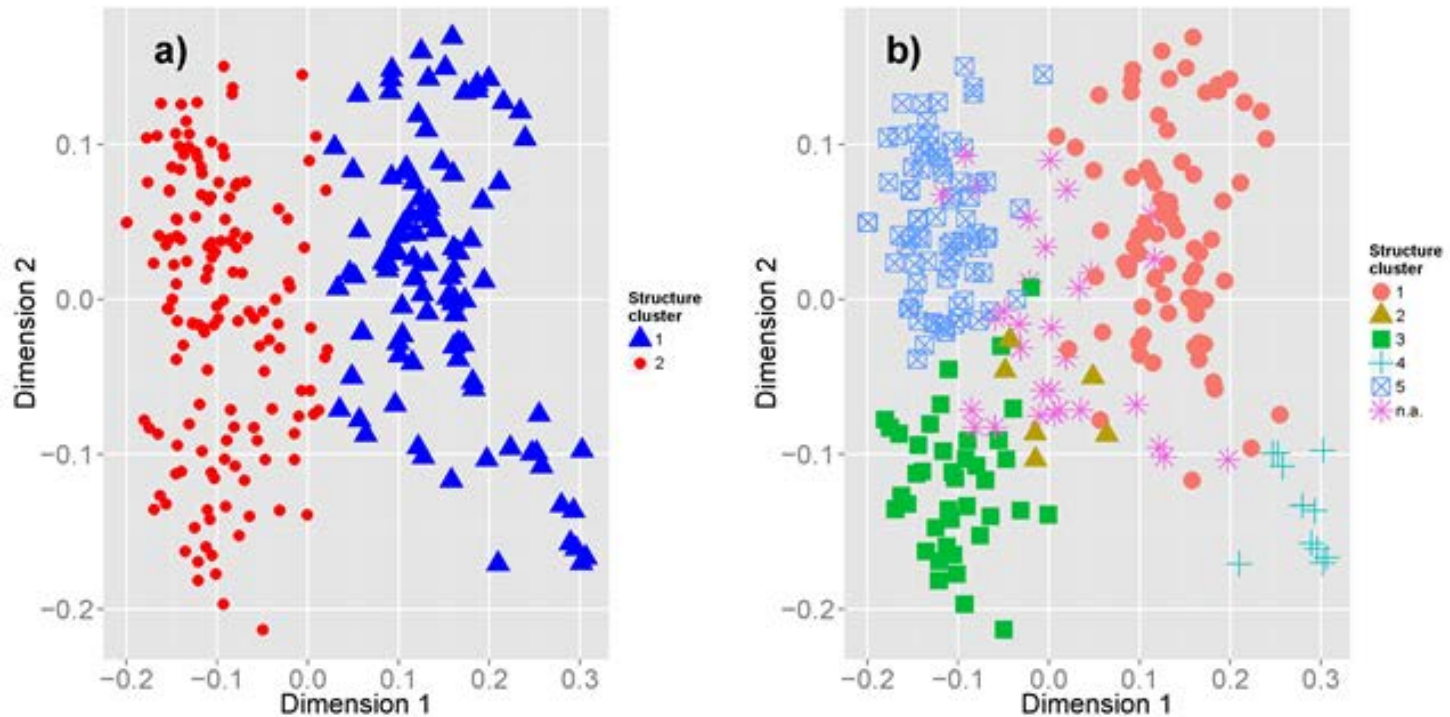
Distribution of 1452 polymorphic DArT markers

| Chromosome | <i>n</i> | average distance (cM) | maximum distance (cM) |
|------------|----------|--------------------------|--------------------------|
| 1 A | 130 | 1.2 | 19.6 |
| 2 A | 63 | 1.9 | 15.1 |
| 3 A | 61 | 3.5 | 29.5 |
| 4 A | 60 | 1.8 | 54.5 |
| 5 A | 25 | 5.0 | 60.9 |
| 6 A | 125 | 0.9 | 34.5 |
| 7 A | 85 | 2.1 | 28.9 |
| 1 B | 93 | 1.2 | 15.1 |
| 2 B | 124 | 1.1 | 9.2 |
| 3 B | 132 | 1.0 | 12.9 |
| 4 B | 33 | 3.5 | 27.1 |
| 5 B | 76 | 2.1 | 20.7 |
| 6 B | 104 | 1.3 | 20.0 |
| 7 B | 66 | 3.5 | 69.6 |
| 1 D | 36 | 2.6 | 14.6 |
| 2 D | 41 | 2.8 | 27.8 |
| 3 D | 46 | 3.5 | 95.4 |
| 4 D | 3 | 24.3 | 0 |
| 5 D | 2 | 80.9 | 76.4 |
| 6 D | 20 | 6.7 | 94.1 |
| 7 D | 127 | 1.4 | 56.3 |
| A genome | 549 | 2.3 | 60.9 |
| B genome | 628 | 2.0 | 69.6 |
| D genome | 275 | 17.5 | 95.4 |

Manhattan plots 2011 and 2011+2012



Structure in the population of 248 wheat



QTL identified on 2B and 7A in this population of 248 wheat accessions

- Based on 2 year field

| QTL | Marker | Chr. | Pos. | MAF | Year | Scale | p | q | p perm. | R ² | Effect |
|--------------|------------|------|-------|------|------|---------|----------|-------|---------|----------------|--------|
| Q Cbt.cph-2B | wPt.744022 | 2 B | 10.88 | 0.41 | 2011 | log-1-9 | 0.00001 | 0.016 | 0.00011 | 0.07 | 0.76 |
| Q Cbt.cph-2B | wPt.0100 | 2 B | 4.21 | 0.49 | 2011 | log-1-9 | 0.00006 | 0.042 | 0.00011 | 0.06 | 0.68 |
| Q Cbt.cph-7A | tPt.6221 | 7 A | 55.13 | 0.05 | mean | log-1-2 | 0.000004 | 0.005 | 0.00003 | 0.08 | 0.23 |

- From 2014 Thesis

Table 1 Bt genes and QTL for common bunt resistance in wheat for which chromosomal locations are known.

| Gene | Chromosome | Reference |
|------------------------|------------|----------------------------------|
| Bt 1 | 2 B | Sears et al (1960); Gupta (2007) |
| Bt 4 | 1 B | Schmidt et al (1969) |
| Bt 9 | 6DL | Steffan et al (2014) |
| Bt 10 | 6 DS | Menzies et al (2006) |
| Q Cbt.crc-1B.1 | 1 BS | Fofana et al (2008) |
| Q Cbt.crc-1B.2 | 1 BL | Fofana et al (2008) |
| Xgwm 374 ^a | 1 BS | Wang et al (2009) |
| Xgwm 273 ^a | 1 B | Dumalasová et al (2012) |
| Xgwm 408 ^a | 5 B | Dumalasová et al (2012) |
| Q Cbt.crc-7A | 7 AL | Fofana et al (2008) |
| Xpsp 3050 ^a | 7 A | Dumalasová et al (2012) |
| Xgwm 43 ^a | 7 B | Dumalasová et al (2012) |
| Q Cbt.spa-7B.1 | 7 B | Knox et al (2013) |

^a For QTL which were not designated following McIntosh et al (1998) the name of the nearest flanking marker is given.

- According to Muellner et al. 2021 a total of 24 QTL for common bunt has been identified by adding 1AL, 7AL
- Gordon et al. 2020 QTL 6DS
- Wang et al. 2019 QTL 7AL
- Bokore et al. 2019 5A, 7A
- Singh et al. 2016 1B, 4B, 5B, 6D, 7D

Thanks to

- P.M. Steffan: Biotechnology Assisted Wheat Breeding for Organic Agriculture (Ph.D. thesis 2014, University of Copenhagen)
- Steffan, Borgen, Torp, Rasmussen, Backes: Association mapping for common bunt resistance in wheat. (in preparation)
- P. M. Steffan, A. M. Torp, A. Borgen, G. Backes, S. K. Rasmussen: Mapping of Common Bunt Resistance Gene Bt9 in Wheat. *Theor Appl Genet* (2017) 130: 1031–1040 DOI: 10.1007/s00122-017-2868-6

