

Starke-II NIL based common bunt resistance gene mapping

Dennis Kjær Christensen | Anders Borgen

Agrologica, Houvej 55, DK-9550 Mariager, Denmark

dennis@fastcode.dk | borgen@agrologica.dk

Presented by: Anders Borgen

NordGen has a 6 genebank accessions developed by MacKay by crossing the variety Starke-II with bunt resistant lines, and backcrossed to Starke-II about 7-8 times while maintaining resistance. The precise protocol is unfortunately lost. The NILs possess Bt1(NGB-11503), Bt5(NGB-16106), Bt6 (NGB-11504), Bt9 (NGB-11505), Bt10 (NGB-11506) and an unknown gene (NGB-16160). The accessions have already been phenotyped, and resistant lines from each accession have been selected (Borgen et al. 2018A). In the LIVESEED project, all NILs and Starke II have been genotyped with the TG25K array (Bacanovic-Sisic et al 2021).

NILs and Starke II had all but 23-202 markers in 1-4 linkage groups in common. Linkage groups for each NIL was extracted and filtered against differential lines containing the Bt gene in question. Chromosomal locations of remaining markers were compared to suggested locations from the literature, enabling separating the major Bt gene from additional genes or QTLs.

- Bt1 was mapped to chromosome 2B in the interval 789,867,236-801,253,554 bp.
- Bt5 was mapped to chromosome 1B in the interval 285,345,287-285,608,205 bp. Corresponding markers in the bunt resistant varieties Globus and Tommi widely used in European bunt resistance breeding, confirms the phenotypic data indicating that these lines carry Bt5 resistance (Borgen et al. 2018B).
- Bt9 was remapped to chromosome 6D in the interval 469,248,476 bp – 469,919,743 bp. (Steffan et al. 2017; Wang et al. 2019)
- The Bt6 NIL (NGB-11504) seemed to be identical to the Bt9 NIL (NGB-11505) indicating missing information about this line, and no conclusion is therefore drawn for Bt6.
- Bt10 was remapped to chromosome 6D in the interval 1,773,421 bp – 11,407,937 bp. (Menzies et al. 2006)
- Unknown resistance in Starke NIL NGB-16160 is expected to be Bt12 and was remapped to chromosome 7D in the interval 7,073,045 bp – 10,835,093 bp. (Muellner et al., 2020)

All markers/intervals were analysed against the remaining 266 LIVESEED lines revealing that they were present in lines with and without the Bt gene. Whether the marker matches in other lines are linked to resistance or not is not known. An example is the presence of the Bt12 markers in Thule III having Bt13 (Goates 2012).

Aknowledgements

Thank you to NordGen for providing germplasm of the Starke-II NILs. Initial phenotyping of the NILs was supported by the COBRA-project (ERA-net CoreOrganic-II and Fonden for Økologisk Landbrug). LIVESEED projekt (H2020) supported phenotypic and genotypic data.

References

- Bacanovic-Sisic J, D Dennenmoser , A Borgen, C Vollenweider, K-J Müller, G.Backes2021: Network-based gwas revealed several candidates of genomic regions associated with rase-specific resistances to common bunt (*Tilletia caries*) in wheat. EUCARPIA conference: Breeding and seed sector innovations for organic food systems, March 8-10, 2021
- Borgen, A. J Svensson and L. Wiik 2018A: Evaluation of Nordic heritage varieties and NILs for resistance to common bunt (*Tilletia caries* syn. *T.tritici*). Abstract of the XX international Workshop on Smuts and bunts. Ed.: David Hole, Utah State University. P 19-23
- Borgen, A., G. Backes, K-J Müller, A. Gallehr, B. Scherrer and H Spieß 2018B: Identifying resistance genes in wheat against common bunt (*Tilletia caries*) by use of virulence pattern of the pathogen.. 69. Tagung der Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs, 19-21th November 2018, HBLFA Raumberg-Gumpenstein, Irdning, Österreich.
- Goates B.J 2012: Identification of New Pathogenic Races of Common Bunt and Dwarf Bunt Fungi, and Evaluation of Known Races Using an Expanded Set of Differential Wheat Lines. *Plant Disease* 96(3):361-369 DOI: 10.1094/PDIS-04-11-0339
- J. G. Menzies, R. E. Knox, Z. Popovic, and J. D. Procnier (2006). Common bunt resistance gene Bt10 located on wheat chromosome 6D. *Canadian Journal of Plant Science* • 1 December 2006 • <https://doi.org/10.4141/P06-106>
- Muellner, A. E., B. Eshonkulov, J. Hagenguth, B. Pachler, S. Michel, M. Buerstmayr, D. Hole and H. Buerstmayr (2020). Genetic mapping of the common and dwarf bunt resistance gene Bt12 descending from the wheat landrace PI119333. *Euphytica* volume 216, Article number: 83 (2020)
- Steffan, P.; A.M. Torp; A.Borgen; G.Backes; S.K. Rasmussen (2017): Mapping of common bunt resistance gene Bt9 in wheat. *Theoretical and Applied Genetics* DOI: 10.1007/s00122-017-2868-6
- Wang, R, T. Gordon, D. Hole, W. Zhao, K. Isham, J. M. Bonman, B. Goates, J. Chen (2019). Identification and assessment of two major QTLs for dwarf bunt resistance in winter wheat line 'IDO835'. *Theor Appl Genet.* 2019 Oct;132(10):2755-2766. doi: 10.1007/s00122-019-03385-2. Epub 2019 Jun 25.