Genetic Mapping of Common Bunt Resistance Gene BtZ

Dennis Kjær Christensen[1], Anders Borgen[2]

[1] Private, Gerding, DK-9520 Skørping

[2] Agrologica, Houvej 55, DK-9550 Mariager

Corresponding author: Dennis Kjær Christensen

E-mail: Dennis@fastcode.dk

Abstract

Once among the most devastating wheat diseases, common bunt caused by *Tilletia tritici* and *T. laevis* was successfully eliminated as a problem by the invention of seed dressings with hexachlorobenzenes (HCBs) in the 1950s. During the past decades, a continuously increasing area of agricultural land has been converted to organic management, refraining from the use of chemical pesticide applications, including seed treatments. Therefore, common bunt as a primarily seed-borne disease is experiencing a limited come-back since no alternative and equally effective treatments to seed dressings are available. The most sustainable and efficient way to avoid yield and quality losses due to bunt infections is the use of resistant cultivars. Seventeen different resistance genes have been characterized so far, and fifteen of them have been mapped and are available for applied breeding.

BtZ is introgressed into *Triticum aestivum* from *Thinopyrum intermedium* via the line Hybrid 599 / W0480. The cultivar Zarya has Hybrid 599 in its pedigree and is the main source of BtZ in European breeding material (Sandukhadze *et al* 2021).

No differential line has been agreed upon and BtZ is not part of the standard differential sortiment. Hybrid 599 and Zarya are obvious candidates.

Using 152 breeding lines, mainly from Cultivari, Germany, of which 103 where postulated to carry BtZ based on parental information and phenotyic results, for a GWAS gave a signal at 6D in the interval 3,118,642 – 4,572,453bp.

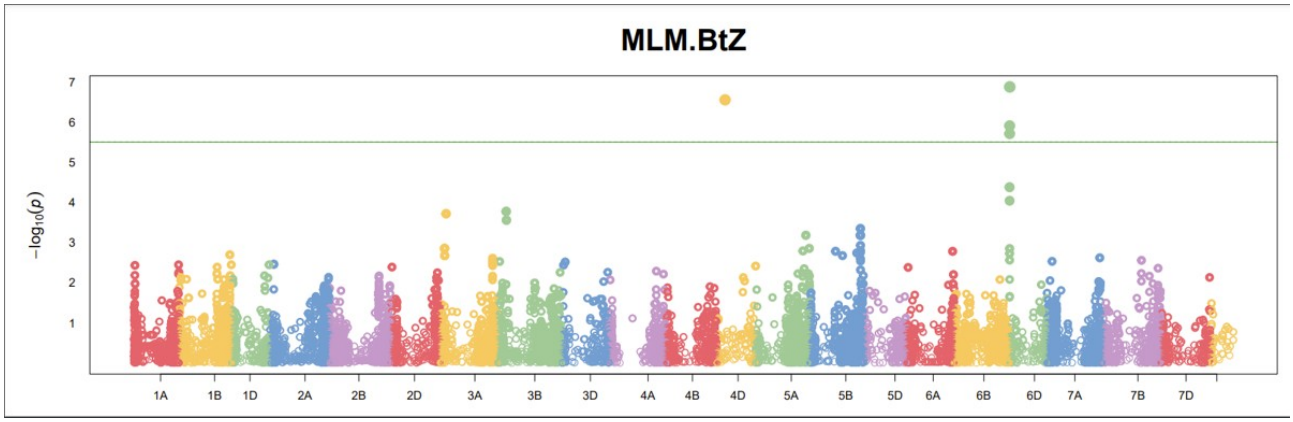

Figure 1: GWAS Manhattan plot made with the MLM method

The single marker at 4D was later found to be located at 6D and linked to the other markers.

Table 1: Significant markers from GWAS

RAC875_rep_c118305_446	C
Excalibur_c7731_2743	G
AX-158531240	T
Kukri_c73802_205	A

These four markers from the GWAS can be used to track the presence of BtZ in breeding material.

Our mapping population consists of 1192 lines and among them is a small RIL population with 14 lines from the cross of Inna (BtZ) and Starke II (Bt0). As the mapped interval is close to the telomere at 6DS, plenty recombination is happening and it was possible to narrow down the interval to 3,444,603 – 4,572,453 bp (wsnp_CAP12_c720_382116 - Kukri_c73802_205).

Table 2: Markers for MAS

wsnp_CAP12_c720_382116	G
BS00065960_51	C
Kukri_c73802_205	A

The two markers in brown define the interval and the one in green could be used for marker-assisted selection, but the markers from the GWAS are more effective.

Markers from the GWAS were a match in 70% of the 122 lines postulated to have BtZ alone or in combination with other genes. There are multiple possible reasons for this low match rate. Many lines have other resistance genes and phenotyping cannot clearly detect the presence of BtZ. It also appears that a lot of recombination is happening and this breaks linkage between the markers and the gene. For lines having BtZ alone, the marker match rate is 86% indicating that gene postulations errors in lines with multiple genes are the main source of error.

The false positive rate was 4%.

Bt10 has been mapped to an interval overlapping intervals for BtZ (Christensen and Borgen 2023). Alsp the phenotypic results are hard or even impossible to separate (Borgen et al 2023). Further investigation is needed to clarify this issue.

Acknowledgement

Phenotyping was done with support from the projects LIVESEED (H2020), BOOST (Organic RDD), DIVERSILIENCE (CoreOrganic Co-fund). Genotyping was supported by LIVESEED, Fonden for Økologisk Landbrug, Promilleafgiftfonden, and the European Consortium for Bunt Research.

Keywords

Wheat, gene mapping, common bunt, organic agriculture, resistance breeding, marker-assisted selection

References

Borgen, A., G. Backes, K-J Müller and H Spieβ 2018: Strategic use of virulence pattern to develop genetic markers for resistance to common bunt (*Tilletia caries*) in wheat. XX international Workshop on Smuts and bunts. pp. 24-25

Borgen, A., M. K. Forster, S. Sedaghatjoo, D. K. Christensenn and W.Maier 2023: Determination of virulence of European races of common bunt using a differential set of wheat cultivars. Proceedings of XXII International Workshop on Bunt and Smut Diseases.

Christensen, D and A. Borgen 2023: Genetic Mapping of Common Bunt Resistance Gene Bt10. Proceedings of XXII International Workshop on Bunt and Smut Diseases.

Sandukhadze BI, Mamedov RZ, Krakhmalyova MS, Bugrova VV. Scientific breeding of winter bread wheat in the Non-Chernozem zone of Russia: the history, methods and results. Vavilovskii Zhurnal Genet Selektsii. 2021 Jul;25(4):367-373. doi: 10.18699/VJ21.53-o. PMID: 35291231; PMCID: PMC8865402.