

Common Bunt Resistance in Winter Wheat: A Cross-Chromosome Journey



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How to catch the big fish in the genetic ocean...

Common bunt is a **seed-borne fungal disease** caused by *Tilletia tritici* and *T. laevis*. **Organic farms** have a heavy cross to bear when their fields are infected, as common bunt **reduces grain yield and quality**, even at very low incidence. The **unpleasant fishy odour** of bunt balls can transform a wheat field swaying in the wind into a sea of rotten fish. Systemic fungicides are not allowed in organic systems, so **resistant cultivars** are considered the most effective management strategy.

Identifying and introgressing resistance to common bunt in winter wheat is **challenging and time-consuming**. We embarked on this journey of illuminating the effects of **QTL and resistance genes (*Bt*-genes)** on different wheat chromosomes as well as their interplay in crosses between **elite varieties and exotic resistance donors**.

Trade-offs between disease resistance from non-adapted sources and good agronomic performance are a common problem. This project **combines marker- and genomics-assisted selection** to lead breeding programs towards a successful selection strategy.



Figure 1: teliospore bunt balls are formed instead of kernels.

Mapping Project

403 RILs resulting from a cross between

PI166190 (*Bt9*, possibly *Bt11*) x Rainer

95 RILs resulting from a cross between

702-1102-C (putative *Bt8* or *Bt9*) x Rainer

with Rainer as the susceptible parent were subjected to artificial inoculation and planted in replicated field trials in 2019. All lines were selectively genotyped using KASP-markers putatively linked to *Bt9* on chromosome 6D.



Figure 2: common bunt teliospores in microscopic view.

Introgression Project

Back-cross-populations of crosses between elite cultivars and breeding lines with three different resistance donors were developed based on the work of Almuth Müllner (PhD-thesis in preparation) on mapping common and dwarf bunt resistance in:

1. Blizzard (resistance QTL on chromosomes 1A, 1B, 7A - [poster no.40](#))
2. Bonneville (1A, 1B, - [poster no.40](#))
3. PI119333 (turkish landrace, *Bt12* on 7D - [poster no.38](#))

From a BC₂F₁-population consisting of 609 lines, 108 heterozygous plants were selected and advanced to the BC₂F₂-generation or back-crossed again with elite cultivars to found a BC₃F₁-population.

Preliminary Results

1. PI166910

Incidence in the PI166910-RILs showed a clear 3:1 segregation pattern suggesting the presence of two resistance genes. All lines harboring the resistant allele for a nearly diagnostic *Bt9*-KASP-marker were resistant, but among those harboring the susceptible allele, a high percentage also showed resistance. Therefore we conclude that PI166910 possesses not only *Bt9* but also a second resistance gene, possibly *Bt11*.

2. 702-1102-C

RILs in the second population were segregating in a 1:1-manner, hinting at one resistance gene inherited from the resistant parent. Using KASP-markers located between 400 and 470 Mbp on chromosome 6D, this gene could be identified as *Bt9*.

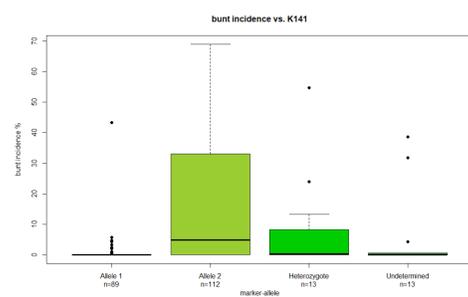


Figure 3: comparison of bunt incidence levels depending on the allele call for the nearly diagnostic *Bt9*-marker.

Preliminary Results

1. Marker-Assisted Foreground Selection

204 BC₃F₁ plants resulting from 30 crosses between BC₂F₁-lines and elite cultivars were genotyped with KASP-markers and 90 lines heterozygous at the introgressed resistance loci were selected. 2165 BC₂F₂-plants are currently being screened using KASP-markers to evaluate which ones possess the resistance QTL in a homozygous allelic state.

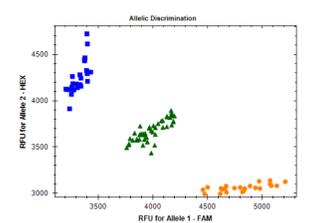


Figure 4: graphical result of KASP analysis. Blue: susceptible allele, green: heterozygotes, orange: resistant allele.

2. Genomics-Assisted Background Selection

SNP data were obtained by DArTcap-sequencing of 109 heterozygous BC₂F₁ lines. Based on these data, genomic estimated breeding values (GEBVs) were calculated using a GS model developed on data from SZD. 54 lines were selected based on their GEBVs as the BC₂F₂-generation.

Outlook

The presence of ***Bt9*** could be verified in both RIL-populations using a **nearly diagnostic KASP-marker**.

The second source of resistance in the PI166910-RILs (probably *Bt11*) will be evaluated by a **mapping approach**.

Outlook

Effectiveness of the introgressed QTL will be tested by **artificially inoculating** BC₂F₃- and BC₃F₂-lines and testing them in a field trial in 2021. Further cycles of marker-assisted and genomic selection will be carried out to develop **bunt resistant** lines with good **agronomic performance**.

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