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Institute of
Biotechnology in
Plant Production

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IMPROVING CROPS

Detection of a major common bunt resistance QTL on wheat chromosome 6D present in the *Bt11* bunt differential line

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Common Bunt (CB)

Causal agents: *Tilletia caries* and *T. laevis*

Field Trials

1. winter wheat populations - sowing in **autumn**, first two weeks of November
2. **artificial inoculation** prior to sowing
3. **suspension** of CB teliospores in solution of 2 % **methylcellulose in water**
4. spores collected in previous years field trials on **wide range of genotypes**
5. collection in plots with **medium** (20 % - 50 %) infection levels
6. thorough **cleaning** from all plant residues
7. 0.3 mL of inoculum (= 0.09 g of spores) per 10 g of seeds

Artificial Inoculation

Inoculum Sources

IFA Housekeeping

- standard inoculum until 2020
- originally from **3 locations in AT**
- spore morphology: *T. caries*
- **high virulence**: *Bt2* and *Bt7*
- lower virulence: *Bt10*, *Bt13*, *BtP*

IFA Aggressive

- based on **infected 'Tilliko' heads** received in 2019
- collected at a farmers field in Austria
- morphologically same as Housekeeping
- standard inoculum from 2021 onwards
- **high virulence**: *Bt2*, *Bt7*, *Bt10*
- lower virulence: *Bt3* and *Bt13*

Phenotypic Scoring

common bunt incidence (CBI) in 100 randomly chosen spikes per plot

Project Overview

Aim

Genetic mapping of the resistance factor harboured by the differential line for *Bt11*, M822123 (PI 166910 × 'Elgin')

MP-PR1

- PI 166910 × 'Rainer'
- 120 recombinant inbred lines (RILs)
- 3 years

MP-PR2

- 'Rainer' × PI 166910
- 120 RILs
- 3 years

MP-PL:

- PI 166910 × 'Lukullus'
- 160 RILs
- 2 years

MP-MM:

- M822123 × 'Mulan'
- 105 RILs
- 4 years

Genotypic Data Analysis

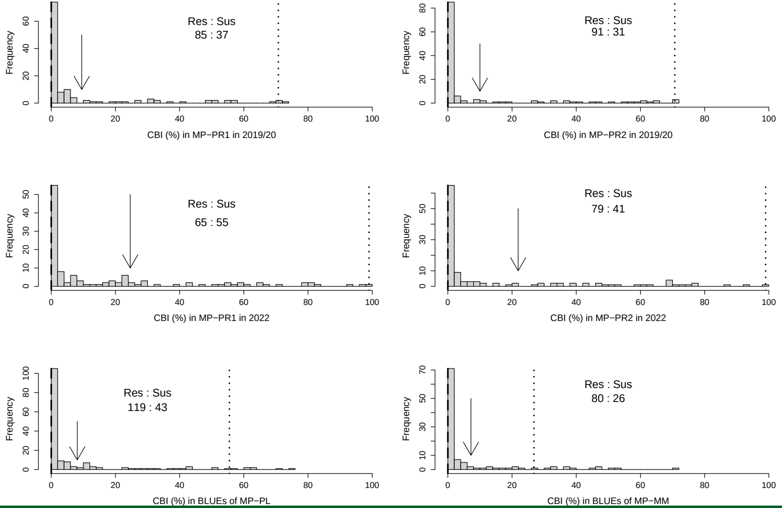
All RILs and parental lines genotyped with 25K wheat SNP array

- data filtered for
  1. marker call rate ($\geq 80\,\%$)
  2. marker segregation distortion ($p \leq 0.001$)
  3. genotype call rate ($\geq 80\,\%$)
- MP-PR1 and MP-PR2 no reciprocal crosses: different **sublines of PI 166910**
- analysis separately for individual MPs (between 1821 and 2795 SNPs)
- linkage groups (LGs) identified with R package *ASMap*
- LGs assigned to chromosomes based on marker positions in IWGSC RefSeq v2.1

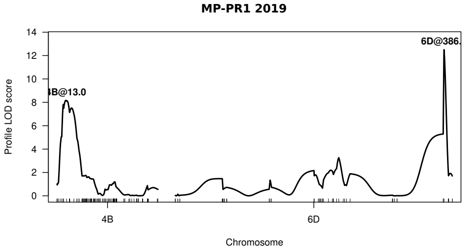
Results - General

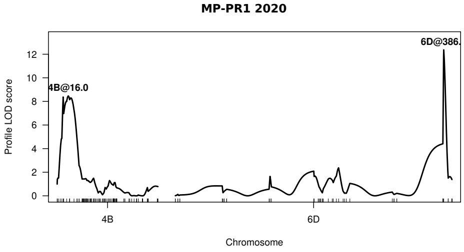
- 2022: **different bunt population** tested (only on MP-PR1 and MP-PR2)
- infection levels approx. 50 % **higher** in 2022
- PI 166910 and M822123: **completely resistant**
- susceptible parents **moderately** ('Mulan') to **highly** ('Rainer', 'Lukullus') infected
- high variation in CBI (0-99 %)
- high heritability estimates for CBI: 0.95 - 0.97
- negative correlations for plant height (PH) and CBI: $r = -0.13$ to $r = -0.25$

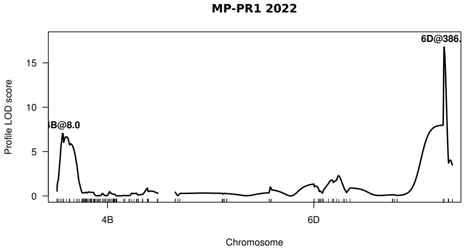
Results - Data Distribution

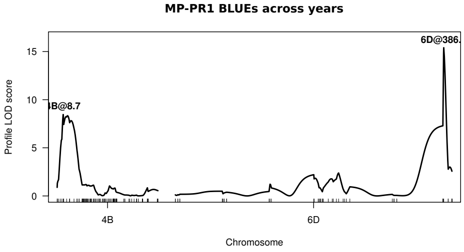


Results - MP-PR1 (PI 166910 × 'Rainer')


MP-PR1 2019

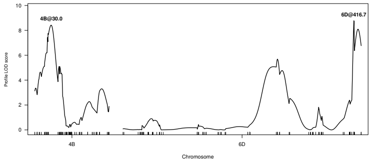

MP-PR1 2020


MP-PR1 2022

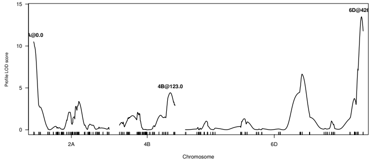

MP-PR1 BLUEs across years

Results - MP-MM (M822123 × 'Mulan')

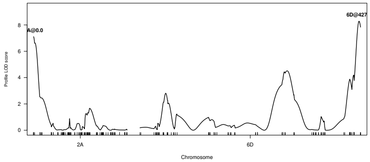
MP-MM 2015



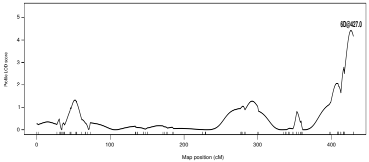
MP-MM 2016



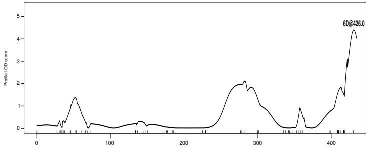
MP-MM 2020



MP-MM 2021



MP-MM BLUEs across years



Common Bunt Resistance QTL

Chrom	**cM**[a] (dist.)	**Mbp**[b] (pos.)	**PV %**[c]	**Experiment**
1B	5.4	12.2-46.9	34.8	MP-PR2: all experiments
2A	4.5	0.3-35.1	26.5	MP-MM: 2016, 2020
4B	38.0	11.5-28.6	22.0	MP-PR1: all experiments MP-PL: all experiments MP-MM: 2015, 2016
6D	13.2	482.8-495.2	33.9	all MPs, all experiments
7B	14.45	7.1-26.4	14.2	MP-PR2: 2019, 2020

[a] maximum distance spanned by the QTL in cM
[b] physical QTL position across experiments in Mbp
[c] average amount of phenotypic variation explained by the QTL across experiments

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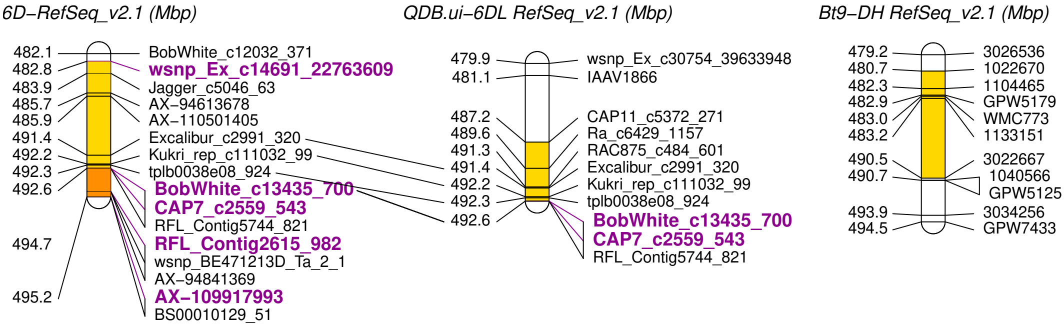
- overlapping with the *Bt9* locus: Steffan et al. (2017) and Wang et al. (2019)

Comparison Of Resistance Loci On Chromosome 6D



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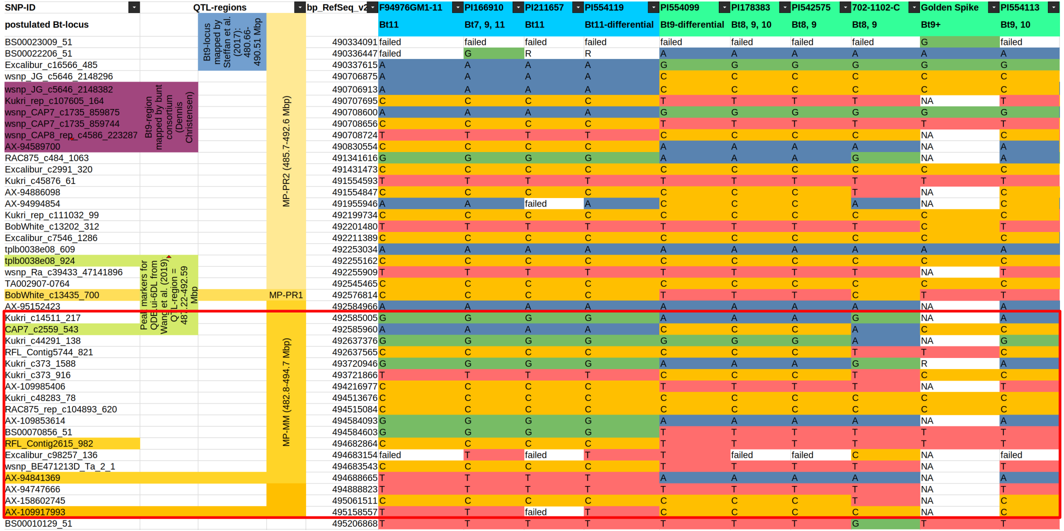
- overlapping with the *Bt9* locus: Steffan et al. (2017) and Wang et al. (2019)
- hard to fine-map because of **marker scarcity** in the region
- likely to be **different** from *Bt9* because:
    1. PI 166910 has the susceptible allele for *Bt9*-markers in Wang et al. (2019)
    2. *Bt9* does not provide full resistance against our bunt inoculum
    3. both resistance donors for our MPs are postulated to harbour *Bt11*
    4. *Bt11*-genotypes show a distinct haplotype in the QTL region, *Bt9*-genotypes do not
- with high probability corresponding to *Bt11*

Haplotype Comparison in the 6DL Region



SNP-ID	QTL-regions	bp_RefSeq_v2	F94976GM1-11	PI166910	PI211657	PI554119	PI554099	PI178383	PI542575	702-1102-C	Golden Spike	PI554113
postulated Bt-locus			**Bt11**	**Bt7, 9, 11**	**Bt11**	**Bt11-differential**	**Bt9-differential**	**Bt8, 9, 10**	**Bt8, 9**	**Bt8, 9**	**Bt9+**	**Bt9, 10**
BS00023009_51	Bt9-locus mapped by Steffan et al. (2017): 480.66-490.51 Mbp MP-PR2 (485.7-492.6 Mbp)	490334091	failed	failed	failed	failed	failed	failed	failed	failed	G	failed
BS00022206_51		490336447	failed	G	R	R	A	A	A	A	A	A
Excalibur_c16566_485		490337615	A	A	A	A	G	G	G	G	G	G
wsnp_JG_c5646_2148296		490706875	A	A	A	A	C	C	C	C	C	C
wsnp_JG_c5646_2148382	Bt9-region mapped by bunt consortium (Dennis Christensen)	490706913	A	A	A	A	C	C	C	C	C	C
Kukri_rep_c107605_164		490707695	C	C	C	C	T	T	T	T	NA	T
wsnp_CAP7_c1735_859875		490708600	A	A	A	A	G	G	G	G	G	G
wsnp_CAP7_c1735_859744		490708656	C	C	C	C	T	T	T	T	T	T
wsnp_CAP8_rep_c4586_223287		490708724	T	T	T	T	C	C	C	C	NA	C
AX-94589700		490830554	C	C	C	C	A	A	A	A	NA	A
RAC875_c484_1063		491341616	G	G	G	G	A	A	A	G	NA	A
Excalibur_c2991_320		491431473	C	C	C	C	C	C	C	C	C	C
Kukri_c45876_61		491554593	T	T	T	T	T	T	T	T	T	T
AX-94886098		491554847	C	C	C	C	C	C	C	T	NA	C
AX-94994854		491955946	A	A	failed	A	C	C	C	A	NA	C
Kukri_rep_c111032_99		492199734	C	C	C	C	C	C	C	C	C	C
BobWhite_c13202_312		492201480	T	T	T	T	T	T	T	T	C	T
Excalibur_c7546_1286		492211389	C	C	C	C	C	C	C	C	C	C
tplb0038e08_609		492253034	A	A	A	A	A	A	A	A	A	A
tplb0038e08_924	Peak markers for QDB.ui-6DL from Wang et al. (2019), QTL-region = 487.22-492.59 Mbp	492255162	C	C	C	C	C	C	C	C	C	C
wsnp_Ra_c39433_47141896		492255909	T	T	T	T	T	T	T	T	NA	T
TA002907-0764		492545465	C	C	C	C	C	C	C	C	C	C
BobWhite_c13435_700	MP-PR1	492576814	C	C	C	C	T	T	T	C	T	T
AX-95152423	MP-MM (482.8-494.7 Mbp)	492584966	A	A	A	A	A	A	A	A	NA	A
Kukri_c14511_217		492585005	G	G	G	G	A	A	A	G	NA	A
CAP7_c2559_543		492585960	A	A	A	A	C	C	C	A	C	C
Kukri_c44291_138		492637376	G	G	G	G	G	G	G	A	NA	G
RFL_Contig5744_821		492637565	C	C	C	C	C	C	C	T	T	C
Kukri_c373_1588		493720946	G	G	G	G	A	A	A	G	R	A
Kukri_c373_916		493721866	T	T	T	T	C	C	C	T	C	C
AX-109985406		494216977	C	C	C	C	T	T	T	T	NA	T
Kukri_c48283_78		494513676	C	C	C	C	C	C	C	C	C	C
RAC875_rep_c104893_620		494515084	C	C	C	C	C	C	C	C	C	C
AX-109853614		494584093	G	G	G	G	A	A	A	A	NA	A
BS00070856_51		494584603	G	G	G	G	T	T	T	T	T	T
RFL_Contig2615_982		494682864	C	C	C	C	T	T	T	T	T	T
Excalibur_c98257_136		494683154	failed	T	failed	T	T	failed	failed	C	NA	failed
wsnp_BE471213D_Ta_2_1		494683543	C	C	C	C	T	T	T	T	NA	T
AX-94841369		494688665	T	T	T	T	A	A	A	A	NA	A
AX-94747666		494888823	T	T	T	T	T	T	T	T	NA	T
AX-158602745		495061511	C	C	C	C	C	C	C	T	NA	C
AX-109917993		495158557	T	T	failed	T	C	C	C	C	NA	C
BS00010129_51		495206868	T	T	T	T	T	T	T	G	T	T

Conclusions

1. main resistance factor in our MPs: locus at **distal end of 6DL**
2. **unambigous distinction** of 6D locus from *Bt9* not possible in our data
3. strong arguments supporting mapping of *Bt11*
4. complete and **stable resistance**
5. valuable addition to known genetic resources for **resistance breeding**
6. **selection** with markers at 492.6 - 495.2 Mbp
7. attempts to **pyramid** 6DL locus with other major resistance factors in progress

Supervisors, Collaborators and Funding Agencies

- Hermann Bürstmayr and all colleagues at IFA-BP
- AgriGenomics DocSchool & Advisory Board:
    - Franziska Löschenberger (Saatzucht Donau GesmbH & Co KG)
    - Johann Sölkner (BOKU)
    - Jianli Chen (University of Idaho)
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- Heinrich Grausgruber and ECOBREED[1]

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Thank you for your attention!

No more slides