Digibreed
Optimizing Genomics Assisted Selection

PhD-candidate: Magdalena Ehn
Supervisor: Hermann Bürstmayr
Institute of Biotechnology in Plant Production, IFA Tulln
Contact: magdalena.ehn@boku.ac.at

University of Natural Resources and Life Sciences, Vienna

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

Common bunt (CB) 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.

Material and Methods

Plant Material

Three resistance donors conferring common bunt resistance via QTL located on **five different chromosomes** were crossed to **five elite winter wheat cultivars** in an initial step (see figure 2):

1. Blizzard (resistance QTL on chromosomes 1A, 1B, 7A, 7D)
2. Bonneville (QTL on 1A, 1B)
3. PI119333 (QTL on 4B, 7D (*Bt12*))

As shown in figure 2, a $\mathrm{BC_2F_2}$-population and a $\mathrm{BC_3F_2}$-population (both homozygous at CB resistance QTL through selfing) were developed based on these initial crosses. The introgressed exotic resistance loci are selected by marker-assisted selection (MAS) while selection for agronomic traits is done via genomics-assisted selection.

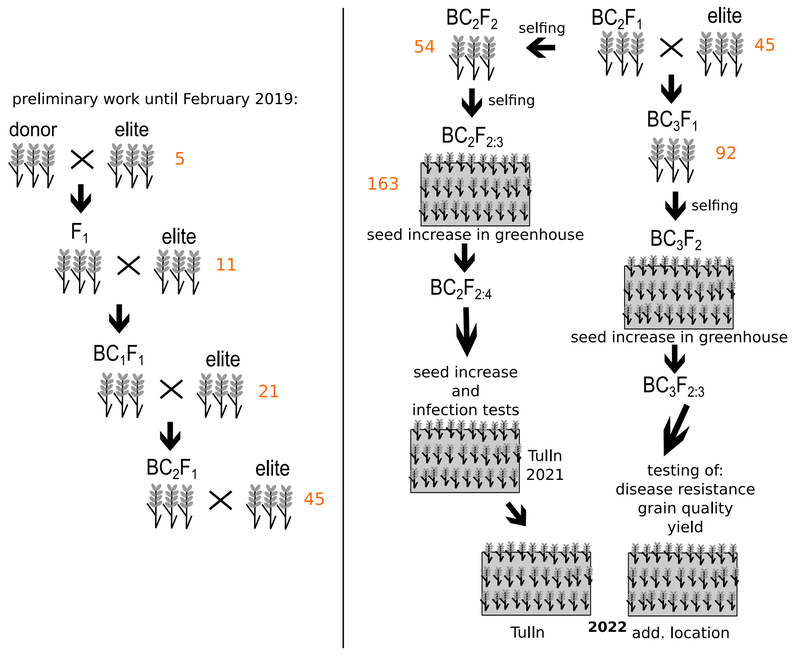

Figure 2: workflow-illustration. Left: preliminary crossing steps done by H. Bürstmayr before the start of the project. Right: steps to be carried out until the end of the project in 2022. Orange numbers indicate the number of (selected) lines in each generation.

Genotyping and Field Trials

Marker-assisted selection using the KASP-marker system: at least two polymorphic and flanking markers for each QTL.

Genome-wide marker data for genomic selection: DArTseq whole-genome sequencing and 10K SNP-chip array.

Field trials: artificial inoculation of seed samples with CB teliospore-suspension before sowing; incidence scoring in 150 spikes per $1.5\,\mathrm{m}$-double-row plot.

Preliminary Results

Foreground marker-assisted selection (MAS)

Screening with KASP-markers can be done during the vernalization phase of winter wheat, only selected plants are transferred into the greenhouse.

Advantage: fast and easy to use

Disadvantage: lack of suitable markers with increasing complexity of pedigrees

Background genomics-assisted selection (GAS)

Genomic estimated breeding values (GEBVs) were derived from a model trained on a huge winter wheat dataset from SZD. Lines with best predictions for important traits like yield and protein content were selected. A set of lines with average and worst GEBVs was included as controls.

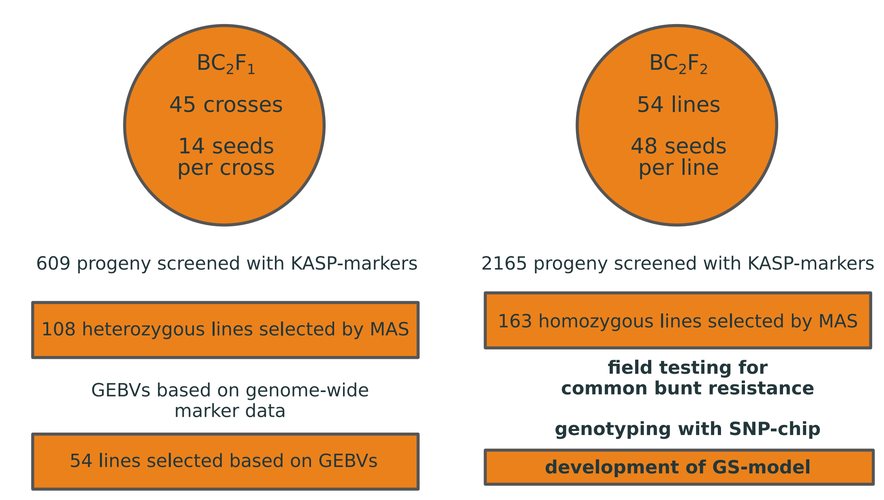

Figure 3: combined selection scheme with MAS and GS for the $\mathrm{BC_2}$-generation. Bold text marks selection steps which are still to be done.

Side-Projects

1. Simulation study: *in silico* testing of breeding scheme variations
2. QTL-mapping: of *Bt11* resistance gene from wheat line *M822123*

Outlook

- $\mathrm{BC_2F_{2:3}}$: sowing of field trials (inoculation, seed increase) for 2021
- $\mathrm{BC_3F_2}$: screening for CB resistance QTL; MAS for $\mathrm{F_{2:3}}$

Acknowledgements and References

Funding for this project is provided by the Austrian Academy of Sciences (OEAW) in the form of a DOC-Scholarship (grant 25453).
The research leading to these results has received funding from the European Union Horizon 2020 under the Grant Agreement number 771367, within the Research and Innovation Action (RIA).
Support by Saatzucht Donau (SZD) in the form of a databasis for GS and plant material is highly appreciated.

ecobreed
IMPROVING CROPS

[1] Cherewick, W. J. (1953). Smut diseases of cultivated plants in Canada. Can. Dep. of Agriculture, Ottawa.
[2] Matanguihan, J. B., Murphy, K. M., and Jones, S. S. (2010). Control of common bunt in organic wheat. Plant. Dis., 95, 92–103.
[3] Goates, B.J. and Bockelman, H.E. (2012). Identification of New Sources of High Levels of Resistance to Dwarf Bunt and Common Bunt among Winter Wheat Landraces in the USDA-ARS National Small Grains Collection. Crop Sci. 52:2595–2605.