Identification of resistance to stripe rust, leaf rust and Septoria tritici blotch in a multiparental wheat population

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The emergence of stripe rust (*Puccinia striiformis*) and leaf rust (*Puccinia triticina*) races containing virulence against common resistances genes and the loss of fungicide effectivity against Septoria leaf blotch (STB) increase the demand for wheat varieties with effective resistances to these pathogens. Therefore, 400 genotypes of the multi-parental Bavarian Magic Wheat (BMW-) population generated from eight German elite wheat cultivars were screened for resistance against these pathogens in order to conduct genome wide association studies (GWAS) and to develop closely linked molecular markers suitable for marker-assisted selection.

Phenotyping of the BMW-population was conducted in multi-years field trials at three locations. To ensure a reliable infestation, an inoculation was performed with leaf and stripe rust at one and with STB at all three locations using defined spore concentrations. Respective genotypes were scored two to four times and the area under the disease progress curve (AUDPC), as well as the average ordinate (AO) were calculated. In order to identify already known resistance genes, the parental lines were analysed with differential sets of isolates for all pathogens in detached leaf assays (STB) and whole plant tests (rust fungi).

Ratings of the field trials allowed the identification of quantitative differences and completely resistant genotypes with respect to leaf and stripe rust. Statistical analysis revealed significant differences ($p < 0.0001$) between the 400 lines of the BMW-population for all three diseases and showed a broad variability in the leaf rust (0 % to 64 %) and in the STB (0 % to 42 %) field trials, while most of the genotypes turned out to be resistant to stripe rust. The statistical evaluation of detached leaf assays showed significant impact on infestation for the genotype ($p < 0.0001$), isolate ($p < 0.0001$), and the respective interaction ($p = 0.0120$). Thus, it was possible to differentiate between highly aggressive and less aggressive isolates. In the whole plant test for leaf rust resistance, several effective resistances were detected, which are further characterized with molecular markers.

Based on the collected phenotypic data and the genotypic data available from the 20k iSelect chip, GWAS will be conducted in order to identify major genes and quantitative trait loci (QTL). The detected resistances that are present in the elite parent lines can be used quickly in new varieties to combine and improve resistances.