

Screening of a wheat MAGIC population for resistance to stripe rust, leaf rust and Septoria leaf blotch

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Stripe rust (*Puccinia striiformis*), leaf rust (*Puccinia triticina*) and Septoria leaf blotch (*Zymoseptoria tritici*) are important fungal pathogens in wheat and cause yield and quality losses. In addition, the emergence of highly aggressive races with altered virulence patterns and the loss of effectiveness of fungicides increase the demand for wheat varieties with effective resistances. In this respect, the multi-parental Bavarian Magic Wheat (BMW-) population comprising 8 German elite wheat cultivars and being selfed six times was screened for resistance to these pathogens. In order to identify major resistance genes, a differential set of isolates consisting of different virulence/avirulence patterns for each of the three fungal pathogens has been used in detached leaf assays. Differences in the degree of resistance between the parental lines depending on the isolate used were observed.

To get additional information on quantitative resistances, field trials are performed at four different locations. At one of the locations genotypes are artificially inoculated with leaf rust, stripe rust and *Zymoseptoria tritici*. Respective genotypes were scored four times and the AUDPC, as well as the average ordinate (AO) were calculated. The 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 (0 % to 55 % in leaf rust trials). Based on phenotypic data and genotypic data available from the 20k iSelect chip, genome wide association studies (GWAS) will be conducted in order to identify major genes and quantitative trait loci (QTL).