Identification of genes for resistance against *Pyrenophora teres* f. *teres* and *Cochliobolus sativus* employing genome-wide association studies

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Pyrenophora teres f. *teres* (PTT) and *Cochliobolus sativus* (CS) are the causal agents of the net type of net blotch and spot blotch in barley, respectively. Both fungal pathogens are widely spread and cause high yield losses. The most cost effective and environment-friendly way to prevent and control these pathogens is growing resistant cultivars. In order to identify sources of resistance, in a first step more than 10,000 barley accessions including landraces and commercial cultivars were screened for resistance to PTT and CS under greenhouse and field conditions. Out of these, 450 barley accessions derived from the centres of barley diversity, and expressing different levels of resistance to respective pathogens were selected.

Next, greenhouse experiments were conducted with these 450 accessions with two PTT and CS isolates, respectively. Three week old plantlets were inoculated with a spore suspension of 5000 spores/mL and assessed for symptom expression 14 dpi. Additionally, field trials were conducted in Russia, Belarus and Germany. The disease severity was scored three times during the growing season to calculate the area under disease progress curve (AUDPC).In parallel respective genotypes were genotyped with the Barley 9k iSelect chip. Markers with a minor allele frequency (MAF) <5%, missing data >10% and heterozygosity >12.5% were removed prior to conducting genome-wide association studies (GWAS). The population structure was calculated based on 508 markers with high PIC (polymorphism information content) values covering the whole genome at an average distance of about 2 cM. GWAS was carried out using the software TASSEL 5 and a mixed linear model (MLM) including population structure and kinship and a false discovery rate of FDR=0.1.

In summary six regions associated with PTT resistance on chromosomes 1H, 2H, 3H, 5H, 6H and 7H and four regions associated with CS resistance on chromosomes 1H, 2H, 5H and 7H were detected. In the next step, additional field and greenhouse trials will be conducted to broaden the base of the phenotypic data and respective associations will be subsequently validated in different DH-populations.