Association mapping for resistance to Net Form of Net Blotch (*Pyrenophora teres* f. *teres*) and Spot Blotch (*Cochliobolus sativus*) in a diverse barley set

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Net Form of Net Blotch (NFNB) and Spot Blotch (SB) belong to the most important diseases of barley and are present in all barley-growing regions. Under optimal conditions both pathogens can cause high yield losses of 10% to 40% and also reduce grain quality. The most cost effective and environment-friendly way to prevent losses is growing resistant cultivars. In order to identify sources of resistance, more than 10,000 barley accessions were screened for resistance to NFNB and SB under greenhouse and field conditions. Out of these, 450 barley accessions expressing different levels of resistance were selected. The set comprises landraces and commercial cultivars from the centres of diversity.

Seedling resistance was assessed by conducting greenhouse experiments with two NFNB and SB isolates, respectively. For this, three week old plantlets were inoculated with a spore suspension of 5,000 spores/ mL and symptom assessment was carried out 14 dpi based on the rating scales by Tekauz (1985) and Fetch and Steffenson (1999). Additionally, field trials were conducted in Russia, Belarus and Germany. Disease severity was scored three times during the growing season to calculate the area under disease progress curve (AUDPC) and the average ordinate (AO). For both pathogens genotypic differences concerning resistance were observed.

Genotyping of the accessions was done with the Barley 9k iSelect chip. Marker data were filtered for a minor allele frequency (MAF) >5%, missing data <10% and heterozygosity <12.5% resulting in 5373 markers for conducting genome wide association studies (GWAS). On a reduced marker set of 508 markers kinship with a Modified Roger's Distance and population structure were calculated. The software STRUCTURE showed two sub-populations, i.e. two- and six-rowed genotypes. GWAS was carried out using the software GAPIT with a compressed mixed linear model (CMLM) including population structure and kinship. In order to get information on the reliability of the marker-trait associations, a cross validation with 1,000 runs was conducted. Detection rates of >20% were considered as reliable associations and detection rates of >50% were considered as particularly robust marker-trait associations. Regions associated with NFNB resistance were identified on all chromosomes. Regions associated with SB resistance were identified on chromosomes 1H, 2H, 3H, 4H, 5H, and 7H.

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