

The association mapping of quantitative resistance loci to net blotch and spot blotch in barley

Rožanova I.V.^{1,2*}, Lashina N.M.³, Efimov V.M.², Afanasenko O.S.³, Khlestkina E.K.^{1,2}

¹*N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR), St. Petersburg, Russia*

²*Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

³*All-Russian Institute of Plant Protection, St. Petersburg, Russia*

* e-mail: i.rožanova@vir.nw.ru

Spot blotch, caused by *Cochliobolus sativus*, and net blotch, caused by *Pyrenophora teres* f. *teres* are two of the most widespread and harmful diseases in barley. The identification of genetic loci associated with resistance to both *C. sativus* and *P. teres* is the important task for future marker-assisted selection. The goal of the current study was to identify loci conferring seedling resistance to different pathotypes of *C. sativus* and *P. teres* in the Siberian spring barley core collection. The collection included 96 spring barley cultivars and lines was created. All of them were phenotyped at the seedling stage with two *C. sativus* isolates (Kr2 and Ch3) and four *P. teres* isolates (S10.2, K5.1, P3.4.0, A2.6.0). About 42–47 % and 15–40 % genotypes were resistant to spot blotch and net blotch, respectively. A total of 94 genotypes were analyzed with the barley 50K Illumina Infinium iSELECT assay. 27,319 SNPs from total 44,040 SNPs passed filtering threshold and were used for association mapping. The GLM analysis revealed 3 and 27 SNPs for spot blotch isolates (Kr2 and Ch3) and 6, 3, 29 and 3 SNPs for net blotch isolates (S10.2, K5.1, P3.4.0, A2.6.0), respectively. In total three genomic regions on chromosomes 1H, 2H and 3H were assisted with resistance to spot blotch and seven genomic regions on chromosomes 1H, 2H, 3H and 6H were assisted with resistance to net blotch. The data were assessed using PASS, Tassel 5 and R. Information of SNPs related can be used further for development of DNA-markers convenient for diagnostics of resistance-associated alleles in barley breeding programs.

Acknowledgements: This study was supported by RSF No. 16-14-00086.