

Study of the leaf rust resistance gene *Lr52* by targeted sequencing

Bragina M.K.^{1*}, Afonnikov D.A.^{1,2}, Vasiliev G.V.¹, Salina E.A.¹

¹*Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

²*Novosibirsk State University, Novosibirsk, Russia*

* e-mail: koltunova@bionet.nsc.ru

At present, more than 30 genes that control a number of morphological and quantitative traits, resistance to abiotic and biotic factors, have been mapped on 5B wheat chromosome (5BL = 580 Mb and 5BS = 290 Mb), but research and chromosomal localization of loci with agronomic character remains relevant. In that work we identified and annotated 5BS wheat chromosome sequences for previously unstudied leaf rust resistance gene *Lr52*. *Lr52* localization in the position from 6654000 bp up to 6956436 bp on 5BS pseudomolecule (IWGSC RefSeq v1.0 genome) was determined by mapping of markers linked to the gene *Lr52*. We selected 5 plants with *Lr52* and 5 plants without *Lr52* from mapping population F4 (line *LrW* (52) × hybrid215) according to the data of KASP and SSR genotyping together with screening for resistance. These plants were sequenced using the SeqCap EZ Target Enrichment System (Roche). After quality control (FASTX-toolkit) the obtained sequences were assembled using the BWA-MEM mapping program and the SPAdes genomic assembler. As a result of assembled sequences analysis using blastn and blastx algorithms in GrainGene, Ensembl Plants and PRGdb databases, more than 500 sequences with homology with potential coding sequences were identified, of which more than 40 are putative resistance genes with the NBS, CC, LRR, Tm and kinase domains.

Acknowledgements: This work were supported by project No. 0324-2019-0039.