

Genome wide association study of seedling leaf rust resistance in European winter wheat cultivars

Czembor P.C., Radecka-Janusik M., Mańkowski D.

Plant Breeding and Acclimatization Institute – National Research Institute

Radzików, 05-870 Błonie, Poland

Keywords

Brown rust, DArTseq markers, gene postulation, resistance, wheat cultivars

Abstract

Leaf rust caused by the biotrophic fungus *Puccinia triticina* Eriks. (*Pt*) is one of the most important fungal disease affecting wheat worldwide. Genetic resistance is the most economical, effective and ecologically sustainable method of controlling the disease. Almost 80 leaf rust resistance genes have been characterized. Efficient utilization of genetic resistance relies on an appropriate knowledge of the leaf rust resistance genes and their effectiveness in different environments. We applied a genome wide association study (GWAS) approach to identify resistance genes in 143 winter wheat cultivars recently registered in Poland, Germany, France, Switzerland, Denmark and United Kingdom. Identified significant marker-trait associations (MTAs) were verified on a panel of 36 Thatcher near-isogenic lines containing different *Lr* genes (Tc-LrNILs). Wheat cultivars and Tc-LrNILs were genotyped on DArTseq platform and phenotyped with 18 single *Pt* isolates at seedling stage. After filtering, out of 40 035 SNP only 2 983 were used in GWAS using restricted maximum likelihood (REML) approach and information on structure of the analyzed wheat set was included. We identified four resistance genes *Lr3bg* (6B), *Lr9* (6B), *Lr24* (3D) and *Lr26* (translocation T1BL.1RS) and several leaf rust resistance loci not present in Tc-LrNILs set on chromosomes 1B, 2A, 3B, 6B, 7A and 7D. Only one-third of the cultivars contained at least one of the identified resistance genes. For some resistant cultivars we were not able to identify *Lr* genes that might be attributed to the low resolution of *Pt* isolates used in the study.

Acknowledgments

This research was supported financially by the Polish Ministry of Agriculture and Rural Development, program Fundamental Research for Biological Progress in Crop Production (years 2014-2020).