Beukert et al.

Using a robotic high-troughput phenotyping method to detect leaf and stripe rust resistances in wheat genetic resources

Ulrike Beukert, Albrecht Serfling and Frank Ordon
Julius Kühn Institute, Institute for Resistance Research and Stress Tolerance, Quedlinburg
E-mail of corresponding author: ulrike.beukert@julius-kuehn.de

Bread wheat is one of the most important crops for human nutrition worldwide. To ensure food security, wheat production need to be increased by 60% till 2050. Yearly infections with leaf and stripe rust caused by *Puccinia triticina* and *Puccinia striiformis*, respectively, result in significant yield losses. Cultivation of resistant varieties carrying effective resistance genes is the most efficient and environmental friendly solution in order to avoid yield losses. Due to the emergence of virulent races the breakdown of existing resistances was observed in the past so that the identification of genotypes with up to now unknown resistances is an important task.

To achieve this, the wheat ex-situ collection of the IPK Gatersleben is analyzed for disease resistances, whereby precise phenotyping is a prerequisite for mapping of quantitative resistances. In order to characterize genetic resources of wheat, phenotyping of 9,700 winter wheat accessions in field trials and in greenhouse experiments was started. The detection and quantification of resistances is in addition achieved in detached leaf assays using high throughput technologies and digital imaging via the robotic platform Macrobot. Genotypes showing quantitative, race-nonspecific resistances are being detected and will be further characterized using microscopical and molecular techniques.

First results based on 5800 accessions revealed that 12.7% of the genotypes carry qualitative resistance against leaf rust, whereas 48.9% showed quantitative differences in resistance. 4.7% turned out to be resistant against both, *P. triticina* and *P. striiformis*.