

Fine mapping and validation of highly effective, previously unexploited leaf and yellow rust resistances from wheat genetic resources

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Several rust-resistance genes for wheat have been identified and cloned in recent decades. Annual infections with leaf rust and yellow rust caused by *Puccinia triticina* and *Puccinia striiformis*, respectively, result in significant yield losses of up to 50% and quality losses. The integration of unused germplasm shows potential for breeding new cultivars with improved resistance genes. Therefore, identifying genotypes with new, previously unknown resistances is an important task to avoid epidemics caused by cereal rust and minimize yield losses in an environmentally friendly way. To achieve this, the main goal of the project Genebank is to transform the *ex-situ* wheat collection of the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben into a collection actively used in breeding. In the first two phases of the project, the Julius Kühn Institute (JKI) Quedlinburg has already tested about 9600 winter wheat and 2700 spring wheat accessions of the IPK Gatersleben *ex-situ* genebank in field and greenhouse tests for their resistance to defined highly aggressive races of yellow and leaf rust. Based on the phenotypic data obtained in combination with sequencing data, a GWAS identified yellow rust resistance QTL on nearly all wheat chromosomes as well as 194 leaf rust resistance-associated loci on chromosomes 1B, 4A, 4B, 6B and 6D, including resistance sources already used in elite material. Most of these resistances are active at the seedling stage. Moreover, some unknown resistances could be identified in adult plants in different field trials.

The third phase of the project aims to exploit resistances that have not yet been used in breeding. Using the Macrobot platform as a high-throughput phenotyping method, new resistance loci to yellow and leaf rust will be fine-mapped and validated using several races with different virulence patterns. Strategies for validating the resistance associations will be pursued, considering the size of the resistance-associated regions. The goal is to build a publicly accessible library of donors that are carriers of rare resistance loci to different races of powdery mildew, yellow rust and leaf rust. Furthermore, the genetic background will be analyzed, so that potential candidate genes will be detected.