Genomics-based exploitation of wheat genetic resources for resistance to leaf rust and stripe rust

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To meet the raising wheat demand worldwide wheat production needs to increase by about 60% until 2050. Yearly infections of leaf and stripe rust caused by *Puccinia triticina* and *Puccinia striiformis* result in significant yield losses. The cultivation of resistant varieties carrying effective resistance genes is an efficient and resource-saving solution 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.

Therefore, the overall goal of Gene-Bank2.0 is to analyze the wheat ex-situ collection of the IPK Gatersleben by applying an integrated concept including cutting-edge genomics, phenomics, biodiversity informatics, and precision (pre)breeding.

Within this concept reliable phenotyping is a prerequisite for mapping of resistances against fungal diseases.

It is intended to characterize the entire wheat collection plus accessions from the secondary gene pool, i.e. in total around 22,000 genotypes, within a project time of 9 years with the aim to identify novel resistances which are not present in wheat elite cultivars.

In a first step 9,700 winter wheat accessions will be phenotyped in field trials and in greenhouse experiments with regard to leaf rust and stripe rust tolerance. (i) In order to detect and quantify resistances against rusts high throughput techniques (robotic platform Macrobot) will be used for the analysis of detached leaf assays. (ii) Genotypes showing quantitative resistances will be further characterized using microscopical and molecular techniques. (iii) Phenotypic data will be used for mapping the resistances and (iv) available markers will be used in order to detect resistances which are present already in cultivars.