

Selection of a diverse set of wheat genotypes for conducting genome wide association studies for nematode resistance

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Root lesion nematodes (RLN) of the genus *Pratylenchus* are known as pathogens on many crop species. The economic damage in crop production by RLN throughout the world is well documented. Two species of *Pratylenchus* (*P. neglectus* and *P. penetrans*) are also gaining importance on wheat in Germany causing high yield losses. The best way to avoid damage of RLN and reduce yield losses is the use of resistant or tolerant varieties. The goal of this study is to get information on the variability concerning the reaction of wheat to *P. neglectus* and *P. penetrans* infection and to identify QTL involved in resistance using a genome wide association genetics approach (GWAS). In this respect, the creation of a genetically diverse panel of wheat genotypes is a prerequisite. To achieve this, two different grouping approaches based on similarity and dissimilarity, i.e. K-medoids and Principal coordinate analyses (PCoA) were used for selecting 300 out of 890 genotypes.

Due to different platforms (15K and 90K) on which the 890 genotypes were analysed, 12,896 markers common in all sets were identified in a first step. Next, filtering was conducted for minor allele frequency (MAF) > 5%, maximum percentage of missing values <10%, and maximum percentage of heterozygous SNPs <12.5%. At the end, 10,979 markers were obtained, which were used for the analysis of genetic diversity, i.e. calculation of Rogers' distance (RD). Based on the RD result, the clustering of the 300 out of 890 genotypes was conducted using the K-medoids method. The result of the heatmap and PCoA confirmed that the 300 genotypes selected represent the maximum genetic diversity present in the 890 genotypes.

The set of 300 selected genotypes will be tested for nematode resistance and genome wide association studies will be conducted.