

Genome wide association studies for resistance of wheat to the root lesion nematode *Pratylenchus neglectus*

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The root lesion nematode (RLN), *Pratylenchus neglectus*, is a migrating endoparasite that is known as an economically damaging pathogen of wheat and many other crop species. Growing of resistant or tolerant cultivars is the most efficient, cost-effective and environmentally-friendly strategy to avoid yield losses caused by *P. neglectus*. The present study aims to identify resistant genotypes showing low infection to *P. neglectus* and to identify QTLs using genome wide association studies (GWAS).

A set of 149 diverse wheat genotypes was subjected for phenotyping by infection with 1000 nematodes at the University of Kiel. In parallel 9556 single nucleotide polymorphism (SNP) selected out of data present for these genotypes from the 15K and the 90K iSelect (SNP) chips turned out to be available for genome-wide association studies. In a first step

this marker set was mapped in the IWGSC RefSeq of wheat. After filtering for minor allele frequency (MAF) > 5%, maximum percentage of missing values <10%, heterozygosity (< 12.5%) and SNP imputation 8842, markers were selected for GWAS. The Mixed Linear Model (MLM) approach was applied to detect QTL for the number of nematodes in GWAS analysis employing kinship and population structure (Q matrix) estimated on 2050 informative markers selected on LD data.

First analysis identified five significant marker trait associations (LOD \geq 3) on chromosomes 1A, 2A, 4B, 6B and 6D of wheat genome.

Finally, GWAS will be performed in an extended set of 313 diverse wheat genotypes for which phenotyping is ongoing.