Identification and mapping of QTL for *Zymoseptoria tritici* resistance in the winter wheat accession HTRI 1410

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Zymoseptoria tritici, the causal agent of Septoria tritici blotch (STB) causes yield losses up to 30 – 50% in wheat, globally. Growing of resistant cultivars is the most cost effective and environmentally friendly way to avoid these losses. *Zymoseptoria tritici* causing leaf spot can be found worldwide and has gained importance due to changes in wheat cultivation.

Aims of the proposed project are the exploitation of the Zymoseptoria resistance of gene bank accession HTRI 1410 via genetic analyses and development of molecular markers and its utilization in wheat breeding, in order to broaden the genetic basis of *Z. tritici* resistance in wheat.

In extensive screening programmes for resistance, the gene bank accession HTRI 1410 turned out to be resistant in field tests and will be tested in greenhouse tests against 22 STB isolates carrying virulences against the 18 STB genes described up to now. In order to get information on the genetic background of the STB resistance in HTRI 1410, a DH-population consisting of 135 lines derived from crosses of HTRI 1410 to three susceptible cultivars was generated.

The leaf infestation after artificial infection of the DH population was repeatedly estimated the last two years at three different locations in Germany and the area under the disease progress curve determined. Statistically significant phenotypic differences between the DH lines as well as between locations were detected. In addition climate chamber and greenhouse experiments with STB-isolates being avirulent on HTRI 1410 but virulent on the other parental lines will be conducted.

In parallel, this population has already been genotyped by the 90 k iSelect chip. The genotypic data were used for map construction. About 6.100 SNPs turned out to be polymorphic between the resistant cultivar and the susceptible lines. In total 1.118 marker has been mapped on the A genome with an average distance of 3.46 cM, 1.326 marker were mapped on the B genome with an average distance of 2.76 cM and on the D genome 267 markers were mapped with an average distance of 5.69 cM. QTL analyses based on two years phenotypic data is in progress and first results of these studies will be presented.