

Mapping QTL for resistance to net blotch (*Pyrenophora teres f. teres*) in a wild barley nested association mapping (NAM) population

Thomas Vatter¹, Doris Kopahnke¹, Klaus Pillen², Frank Ordon¹

¹ Julius Kühn-Institut, Institute for Resistance Research and Stress Tolerance, Quedlinburg

² Chair of Plant Breeding, Institute of Agricultural and Nutritional Sciences, Martin-Luther-University Halle-Wittenberg

Email of corresponding author: thomas.vatter@julius-kuehn.de

Net blotch, caused by the fungus *Pyrenophora teres f. teres*, is an important foliar disease of barley causing high yield losses. The identification of QTLs and underlying genes conferring resistance to this fungus is the basis for targeted and sustainable breeding approaches aiming to improve net blotch resistance in modern barley cultivars and to broaden the genetic base of resistance. Therefore, a SNP-based nested association mapping (NAM) approach was used to map QTL for resistance derived from *H. spontaneum* or *H. agriocrithon*. To achieve this, the barley nested association population (HEB-25) comprising 1420 BC₁S₃ lines in 25 families originating from a cross of 25 wild barley accessions (*H. spontaneum* and *H. agriocrithon*) with the cultivar Barke was screened for resistance in two-years

field trials using a summer-hill-design. Best linear unbiased estimates (BLUES) for average ordinate (AO) and reaction type (RT) were calculated. Using these and 5702 informative SNPs obtained from the 9k iSelect barley chip nested association mapping was conducted.

Results indicate a high variability in net blotch resistance between and within families of the NAM-population. A high correlation between AO and RT data was observed. In summary, SNPs highly associated to net blotch resistance were detected on all seven chromosomes of which some map to chromosome regions previously identified to be linked to net blotch resistance. In a next step, identified QTL will be analyzed in more detail to identify potential candidate genes.