Can susceptibility to net blotch in barley be explained by sensitivity to necrotrophic effectors?

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Net blotch is a major barley disease in Norway caused by the necrotrophic fungus *Pyrenophora teres* leading to yield losses of up to 40%. At present, resistance of Norwegian cultivars is insufficient. The closely related wheat pathogens *Parastagonospora nodorum* and *Pyrenophora tritici-repentis* secrete necrotrophic effectors (NEs) which act as virulence factors in order to gain entry into and nutrients from the host. NEs cause a hypersensitive response (cell death) in the presence of corresponding dominant host susceptibility factors. The first *P. teres* NE was recently identified in a Canadian isolate (Liu et al. 2014).

The main objective of this study is to examine the potential role of NEs and corresponding host receptors in explaining susceptibility to net blotch in Norwegian barley. This knowledge together with an understanding of the genetic background of the Norwegian net blotch population will be utilized to speed up resistance breeding.

By collecting ca. 350 naturally infected barley samples from different regions, a representative isolate collection has been established which will be genotyped in order to assess genetic diversity and population structure of the Norwegian net blotch population. Selected isolates and their culture filtrates will be screened for specific reactions against a) differential barley lines to investigate the role of NEs, b) a collection of ca. 200 barley lines for association mapping and c) segregating mapping populations to characterize novel NE-host susceptibility interactions and to map the corresponding sensitivity loci. Effector protein candidates will be purified and further analysed to verify their effect on disease development.

In the 2014 field testing, net blotch susceptibility ranged from 14% to 69% diseased leaf area with a population average of 32%. The most resistant current variety was Fairytale with 28% susceptibility while all other current variety were above average susceptible with ‘Helium’ and ‘Tiril’ being among the four most susceptible lines. The field data also indicated recent changes in the pathogen population. For instance ‘Heder’ was the most susceptible of all entries 2013 and averagely susceptible in 2014, while it previously had been considered to have good resistance. ‘Arve’ was widely grown in the 1990s and considered highly susceptible, but was rated moderately resistant during the field testing in 2013 and 2014. Preliminary screening with a small number of isolates revealed a resistance/susceptibility QTL on barley chromosome 3H in the ‘Hector’ x NBD112 mapping population and two resistance QTL on 3H and 6H in the CI5791 x ‘Tifang’ mapping population under greenhouse conditions.

Reference