Genetic mapping of leaf rust (*Puccinia hordei* Otth) resistance in barley accession MBR1012

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Introduction

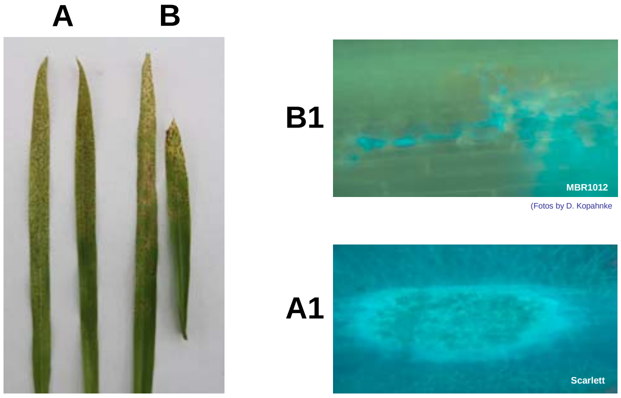
The fungal pathogen *Puccinia hordei* Otth is the causal agent of barley leaf rust, an economically important disease of barley in temperate regions, which can considerably reduce the yield of susceptible cultivars (Figure 1) up to about 60% (Cotterill et al 1992). Growing of resistant barley cultivars is an efficient way to control the disease, but the deployment of resistance genes is counteracted by the occurrence of new, virulent races of the pathogen. Therefore, there is a constant need for the identification of new sources of resistance. In order to explore the genetic variability in the barley gene pool of the Republic of Montenegro and the Republic of Serbia gene bank collections have been evaluated (Perovic et al 2003). Here we present results on the mapping of resistance to leaf rust isolates I-90 that is detected in the landrace MBR1012.

Fig. 1: Symptoms of *Puccinia hordei* Otth on leaves of the barley susceptible cultivar 'Scarlett'

Material and methods

In order to obtain information on the genetics of resistance to barley leaf rust isolate I-90 the resistant accession ´MBR1012´, was crossed with the susceptible cultivar ‚Scarlett' (Figure 2). A set of 65 DH lines was obtained and inoculated.

Five to ten grains per DH line were tested for resistance at the seedling stage. The seedling tests were performed according to Ivandic et al. (1998). The symptoms were rated according to the scale of Levine and Cherewick (1952) at 10–12 days after inoculation. For molecular work, bulked segregant analysis (BSA)-based genetic mapping using SSR markers was performed.

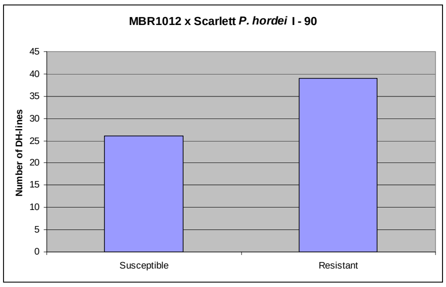


(Fotos by D. Kopahnke)

Fig. 2: Symptoms of *Puccinia hordei* Otth on leaves of the suscetible barley cultivar 'Scarlet' (A) and the resistant line 'MBR1012' (B). A1 a mature uredinium on the susceptible cultivar; B1 hypersensitive reaction on the resistant line

Disease scoring and bulked segregant analysis

The green house inoculation tests in Germany revealed that resistance is inherited in a monogenic manner (Fig 3). Based on phenotypic data bulked segregant analysis was carried out in order to map resistance and to detect closely linked molecular markers.



39r : 26s (Chi² 1r : 1s = 3.51); P= 0.061

Fig. 3: Results of segregation analysis for leaf rust isolate I-90. Results are obtained in green house trials on 65 DH-lines of MBR1012 (resistant) x Scarlett (susceptible)

Genetic mapping

A total of 140 genic and genomic SSR markers and 56 SNP-based markers were surveyed to identify polymorphisms between the resistant and the susceptible bulks and the two parental lines of the mapping population. Based on these results, the monogenically-inherited resistance to the isolate I-90 in barley line MBR1012 was genetically mapped on chromosome 1HS (Fig 4).

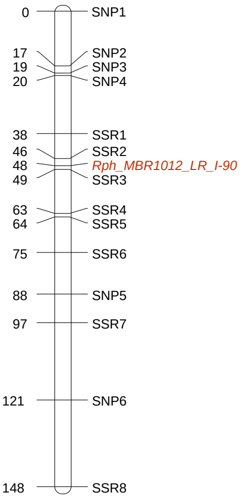


Fig. 4: Genetic map of new leaf rust resistance gene on chromosome 1HS derived from MBR1012

Discussion and conclusion

To promote the effective use of barley landraces in breeding programs, they need to be fully characterised and evaluated for agronomical traits as well as for disease resistance as the gene-pool of cultivated barley is largely depleted of major resistance genes for many plant pathogens. After detection of resistance to the available virulent isolates of pathogens, it is necessary to genetically map the corresponding genes in order to effectively incorporate them into adapted breeding lines. The results on the mapping of a new resistance gene to *Puccinia hordei* Otth isolate I-90 in the landrace MBR1012 opens the possibility to broaden the genetic base of resistance to *P. hordei*. However, the relation to *Rph4*, which is also located on chromosome 1H has to be analysed by tests for allelism.

References

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