

Genome wide association studies of barley net blotch resistance in Morocco

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ABSTRACT

Net blotch of barley caused by *Pyrenophora teres f. teres* (net form) and *Pyrenophora teres f. maculata* (spot form) are important foliar diseases of barley crop worldwide. In Morocco, the yield losses can reach up to 35% on susceptible cultivars under severe disease incidence. The resistance to Moroccan isolates is poorly understood and very few sources of resistance are available. The objectives of this study are to identify the genomic regions conditioning resistance to net form of net blotch (NFNB) and spot form of net blotch (SFNB), in 336 barley genotypes originating from ICARDA germplasm, as well as to identify markers tightly linked with these loci, to help in better integration of resistance in improved germplasm. An Association Mapping panel (AM-15) was genotyped using 9K iSELECT SNP markers. The panel was phenotyped in three hotspot locations in Morocco (Marchouch, Jemma Shaim, and Sidi El-Aidi research stations) for seedling and adult stage resistance in α -lattice design experiment. Association analysis using mixed linear model (structure and kinship as covariate) were employed to identify SNP markers associated with net blotch resistance. A total of 92 marker-trait associations were detected. Seven and six QTLs associated with resistance to NFNB resistance at seedling and adult stage respectively were identified on all seven barley chromosomes. A total of seven QTLs associated with seedling resistance to SFNB were identified on chromosomes 3H, 5H and 7H while four QTLs located on 3H and 7H were associated with adult stage resistance. Out of the 24 identified QTLs, five correspond to previously mapped net blotch resistance QTLs, QRpt6, QRpts4 and Rpt7. The 19 novel loci identified in the current study may represent a broad spectrum of net blotch resistance and will be useful in marker-assisted barley improvement.

SECTION:

Biotic stresses

Plant Breeding and Genetics Education