

Genome wide association analysis for stripe rust resistance in barley seedlings and adult plant stage in India

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Barley stripe rust (*Puccinia striiformis* f. sp. *hordei*, PSH) occurs worldwide and is a major fungal disease in barley in Southern Asia. In order to identify and the estimate effects of loci underlying quantitative resistance to PSH, an association mapping panel of 261 barley genotypes consisting of released cultivars, advanced lines, differentials, and local landraces from the ICARDA barley breeding program and from North and South America, Europe, and Australia was screened for seedling and adult plant resistances to barley stripe rust. Seedling resistance evaluations were undertaken for 261 barley genotypes with the five prevalent PSH races, 0 (5S0), 24 (0S0-1), 57 (0S0), M (1S0), and G (4S0), individually at ICAR-IIWBR Shimla. The field screening was performed in two different locations, Durgapura (Rajasthan, India) in 2013 and 2014, and at Karnal (Haryana, India) in 2014 under artificial inoculation using a mixture of the five PSH races. The panel was genotyped with the DaRT-Seq high-throughput genotyping platform. The final markers sets used for this work comprises 13,182 PAV and 6,311 SNPs. Results of genome-wide association scans, using the PAV marker set, showed positive associations with resistance to PSH for both seedlings stage and adult plant stages. We identified 49 significant marker-trait associations corresponding to 32 QTL located across the seven barley chromosomes for stripe rust resistance at seedlings stage for the five races. A total of 21 significant marker trait associations resulting in 6 QTL were identified on all chromosomes except 7H for adult plant resistance. Common QTL for resistance to different races of PSH resistance at seedling stage were found on chromosomes 4H and 5H. For adult plant resistance we found a QTL on the long arm chromosome 5H stable across environments and years. Performing GWAS, using the SNP marker set we found 42 significant associations corresponding to 20 QTL, located on the seven barley chromosomes for seedling resistance for the five PSH races. For resistance at field screening, 17 positive associations corresponding to 10 QTL located on chromosomes 1H, 2H, 3H, 5H and 7H were found. The QTL detected in this study will be useful for future PSH resistance breeding efforts in the India and in other countries.