

Genome Wide Association Mapping of Net Form Net Blotch resistance in Barley reveals multiple disease resistance loci for resistance to biotrophic and necrotrophic pathogens

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The net form net blotch (NFNB) caused by *Pyrenophora teres f. teres* (*Ptt*) is an emerging barley disease in several countries. It causes severe yield and quality losses due to infection of leaves, kernels, and stems. Owing to inherent genetic diversity of *Ptt*, the incorporation of qualitative and quantitative resistance is important to obtain barley cultivars with durable resistance to NFNB. For this purpose, an association mapping panel named as HI-AM (High Input Association Mapping) was screened for resistance to NFNB at the seedling stage with two virulent Moroccan *Ptt* (*Ptt*40-3, *Ptt*45-3) under controlled conditions, and at the adult plant stage at four hot spot locations in Morocco during different cropping seasons (2016-17 and 2017-18). Genome wide association mapping (GWAM) was conducted using 13,182 PAV ((presence or absence variations) and 6,311 SNP markers (DaRTSeq) for mapping of seedling and adult plant resistance quantitative trait loci (QTL). GWAM analysis revealed 19 QTL for seedling stage and 35 QTL for adult plant stage resistance. Of the 54 QTL detected, our study validated 38 QTL already reported in literature while 16 QTL were novel. Seedling stage QTL explained together 40% of the genetic variance for seedling resistance to isolate *Ptt*40, and 69% for isolate *Ptt*45, whereas the genetic variance of QTL for adult plant stage resistance ranged from 35% to 85%. This panel was previously used for other GWAM studies including resistance to spot blotch and stripe rust of barley. By mapping of significant markers for three different diseases on the Morex genome version 3, we also identified 13 common QTL associated with resistance to net blotch and spot blotch and 3 QTL associated with resistance to all three disease. The identification and introgression of common QTL conditioning resistance to three diseases could help in attaining durable disease resistance to three major diseases of barley in North Africa.