

Identification and and location of genomic regions controlling adult plant resistance to barley leaf rust

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Barley leaf rust caused by *Puccinia hordei* is best controlled through genetic resistance. Among the available resistance classes, adult plant resistance (APR) is considered to be more durable because of its association with additive/and or epistatic effects of multiple genes. The diversity of APR is however narrow and to date only two sources (*Rph20* and *Rph23*) are known, and there is a need to identify and map new sources. To cater this need, we mapped a DH population, Baronesse/Stirling (B/S) using three-years of phenotypic data and more than 10K DArTseq molecular markers. QTL mapping indicated involvement of three consistent QTLs on chromosome 2H, 5H and 6H closely linked with *DArT_3985732*, *DArT_3986031* and *DArT_3264010* markers at a genetic distance 70.82, 15.56 and 61.69cM respectively. The QTL detected on chromosome 5H is in the same region where the APR gene *Rph20* is located in Flagship/ND24260 population. The parent Baronesse showed positive amplification when genotyped with marker *bPb-0837* (closely linked to *Rph20*) indicating that 5H QTL corresponds to *Rph20*. The other two QTL responsible for APR are potentially new and currently being fine mapped for developing closely linked markers for gene pyramiding and marker assisted selection.