Identification 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 61.69 cM 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.