Mapping Resistance to Spots and Blotches in Spring Barley

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Introduction

The development of spots after anthesis on the upper leaves of barley cultivars has become particularly pronounced in Scotland since 1995. The symptoms can be severe, resulting in premature loss of green leaf area with consequent losses in yield through reduced grain fill, which in turn can lead to a considerable increase in screenings, thus affecting malting premiums. There is debate as to whether the symptoms are due to a pathogen, potentially *Ramularia collo-cygni*, a physiologic reaction or an interaction between the two.

Physiologic Spots

Ramularia Like Spots

Previously, "target spot" was thought to be the result of a physiological reaction and the necrosis associated with the *mlo* powdery mildew resistance thought to be the cause of a yield decrease in cultivars carrying the gene. Target spot and similar leaf blotches generally appear between GS30 and GS50 but the *mlo* flecking can be more prevalent post anthesis. We have used two doubled haploid populations, one of which segregated for *mlo* to study leaf spots in spring barley. Those spots developing pre-anthesis were classified as physiologic spots (PS) and those post anthesis as Ramularia Like Spots (RLS).

Materials & Methods

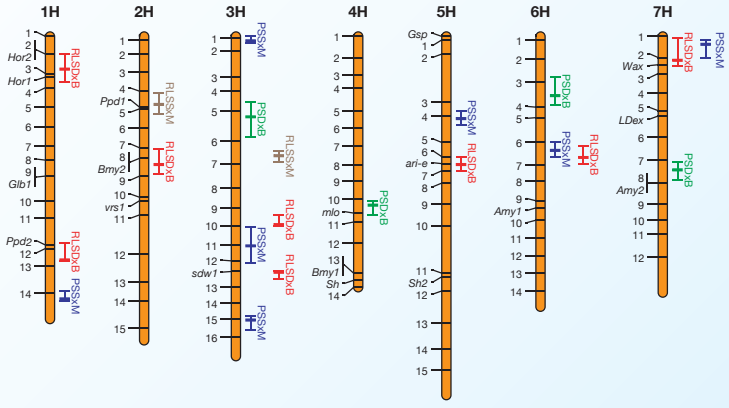
Two spring barley doubled haploid populations from the crosses Derkado x B83-12/21/5 and Steptoe x Morex were grown in field trials over several seasons and assessed for the development of PS and RLS, using a 1-9 scale with 1=resistant. ANOVA was used to estimate the amount of genetic variation for each trait and therefore its heritability. The overall means for each doubled haploid line from a cross were then combined with molecular marker and map data from the cross to identify Quantitative Triat Loci (QTL) affecting the two characters. The locations of these QTLs were compared by reference to the Barley Bin map.

Results

The parents of both mapping populations significantly differed in the amount of PS but such differences were not apparent for RLS. The doubled haploid mean was approximately equivalent to the mid-parent and the extreme DHs showed transgressive segregation, suggesting additive genetic control of the characters with dispersion of resistance genes between the parents. The heritability of PS was over 50% for both barley crosses but, where measurable, much less for RLS in Derkado x B83-12/21/5. There were significant but small correlations between the two characters (0.27 and 0.38 for Derkado x B83-12/21/5 and Steptoe x Morex respectively).

	Derkado x B83-12/21/5		Steptoe x Morex	
	PS	RLS	PS	RLS
Parent 1	4.0	3.6	5.0	5.0
Parent2	1.8	2.6	1.0	2.0
DH Min	1.4	2.2	1.0	2.0
DH Mean	3.1	3.6	2.8	4.0
DH Max	7.8	6.0	7.0	7.0
SED	0.6296	0.6761	0.8246	N/A
Heritability(%)	81.5	15.5	57.4	N/A

The largest QTL for PS was found in the region of *mlo* on 4H in DxB, consistent with the general association of *mlo* with leaf disorders. *mlo* was not associated with RLS, suggesting independence from *mlo.* The most significant QTL for RLS in DxB was located in the region of *sdw1* on 3H, with the dwarf allele from Derkado increasing susceptibility. QTLs for PS and RLS were co-located in just two instances but the PS QTL was detected in SxM and the RLS in DxB in both cases (6H and 7H), suggesting separate genetic control.



Conclusions

None of the QTLs identified for resistance to RLS in either cross would warrant deployment of Marker-Assisted Selection (MAS) in breeding for resistance to the disorder.

Considerable variation can be seen amongst elite breeding lines, however, and it is possible that there are some sufficiently strong genetic resistance effects that would be of value in MAS.

Whilst careful experimentation is needed to assess the phenotype, association with genotype may be possible through emergent High Throughput genotyping.