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PLANT SCIENCES

Peroxidase gene profiling indicates a role of peroxidase genes of barley in determining level of basal resistance to rust and powdery mildew

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Introduction

Previous studies have indicated that Peroxidases (PRX) may promote susceptibility [1] or defense [2] against pathogen infection in various plant species. We applied a motif-directed profiling strategy [3] to determine the association of PRX genes with QTLs for resistance of barley to rust and powdery mildew fungi.

Barley populations

We used two mapping populations, L94 x Vada (L xV) and Vada x SusPtrit (VxS). Marker linkage maps and rust and mildew disease data were available [4, 5].

Motif-directed profiling

Primers targeted the conserved motives FHDCV or VSCADI. Twelve degenerate primer-enzyme combinations resulted in 1292 amplification products, 185 of which were polymorphic and mapped.

Mapping of the prx-markers

Prx profiling markers tended to map in clusters (Figure 1).

Estimated number of prx-clusters

The total number of PRX clusters was estimated by a re-sampling procedure. The relation between sample size and average number of realized clusters in the sample suggested about 40 of such clusters in barley (Figure 2). This is similar to what has been reported for rice and Arabidopsis.

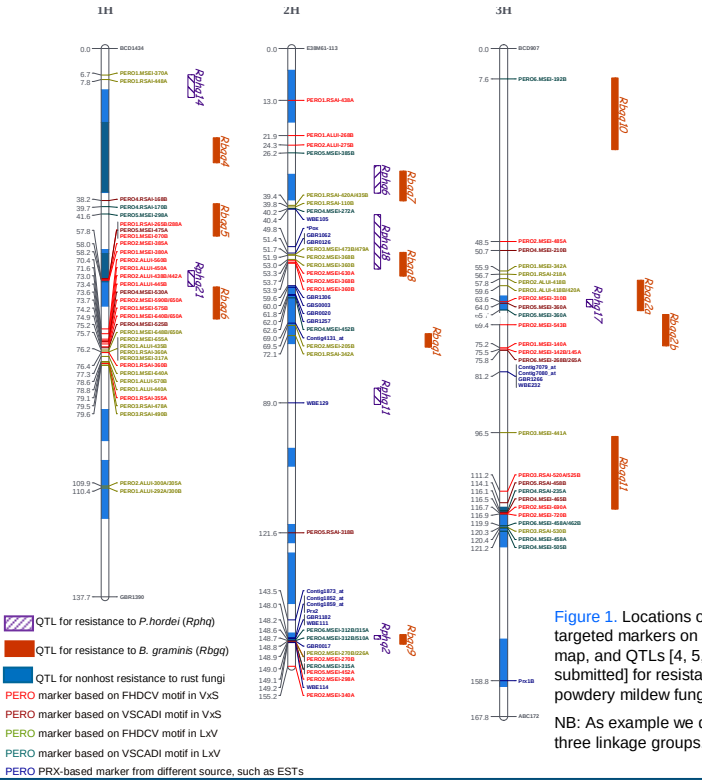

Figure 1. Locations of 200 PRX-targeted markers on barley integrated map, and QTLs [4, 5, Aghnoum et al, submitted] for resistance to rust and powdery mildew fungi.

NB: As example we depict the first three linkage groups.

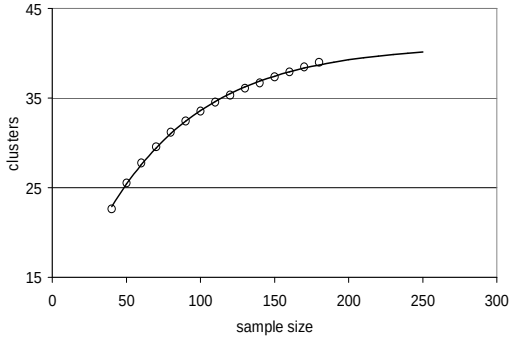

Figure 2. Results of the re-sampling procedure. Each data point represents the mean of 50,000 re-sampling runs. Shown is the relation between sample size and average number of realized clusters in the sample. Curve: exponential curve fitted to the data; the horizontal asymptote equals 40.9.

Association between QTLs for resistance and PRX-targeted markers

63% of the QTLs for partial resistance to *P. hordei*, 59% of the QTLs against *B. graminis* and 51% QTLs for non-host resistance to rust fungi coincided with PRX-targeted markers (Figure 1).

We tested by Chi-square the probability of independent distribution.

The linkage map was divided in BINs of about 5 cM each. We found a statistically significant association between the QTLs and the prx-markers, but not between prx-markers and QTLs for other agronomic traits (Table 1), nor between resistance QTLs and other expressed sequence-derived markers (data not shown).

	PRX	QTL_{ph} [4,5]	QTL_{bg}	QTL_{nh} [5]	QTL_{dh}	QTL_{dp}	QTL_{kw}	QTL_{tw}	QTL_{yi}
BIN no.	**63**	**19**	**23**	**41**	39	9	11	13	23
Marker no.	**200**	**19**	**27**	**41**	52	15	13	18	24
Obs (Exp)		**12 (5.5)**	**16 (6.7)**	**21 (11.9)**	15 (11.5)	3 (2.6)	5 (3.2)	5 (3.8)	9 (6.8)
PRX		**11.85****	**20.38****	**12.09****	1.8	0.2	1.4	0.6	1.1

Table 1. Chi-square values on the probability of independent distribution of Prx markers with barley QTL for resistance:
QTL_{ph}: to *Puccinia hordei*
QTL_{bg}: to *Blumeria graminis*
QTLnh: to rust fungi to which barley is a marginal host
In grey: QTLs for agronomic traits:
dh: days to heading
dp: diastatic power
ph: plant height
kw: kernel weight
tw: test weight

References:

[1] Kristensen et al., 2001. Mol. Plant Pathol. 2: 311–317.

[2] Hückelhoven and Kogel, 2003. Plant J. 36: 589–601.

[3] Van der Linden et al., 2004. Theor. Appl. Genet. 109: 384-393.

[4] Marcel, et al., 2007. Theor. Appl. Genet. 114: 487-500.

[5] Jafary et al., 2008. Genetics. 178: 2327-2339.

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