

QTL for white mold resistance in 19365-31 dry bean derived from *P. vulgaris* x *P. coccineus*

Phil Miklas, USDA-ARS, Prosser, WA (pmiklas@pars.ars.usda.gov)

Introduction

Few sources of resistance to white mold exist in common bean. Scarlet-runner bean (*Phaseolus coccineus* L.), a representative species of the secondary gene pool of common bean, is a potential source of white mold resistance for improving dry bean. 19365-31 is a black bean line that possesses resistance to white mold putatively derived from scarlet-runner bean (Miklas et al., 1998). This line performed well in the Bean White Mold Nursery in 1997 (Steadman et al., 1998) and in oxalate tests conducted by Kolkman and Kelly (2000).

Objective

Characterize resistance of 19365-31 to white mold in a mapping population tested across multiple field and greenhouse environments.

Material and Methods

Population: Raven/19365-31, consisting of 109 F_{5,8} lines. Raven is a commercial black bean susceptible to white mold.

Two field tests: Field – 1 and Field – 2.
Five greenhouse straw tests: Straw test-1 to -5.

Bulked segregant analysis:

Bulks of RILs for straw test: 5 R and 5 S
Bulks of RILs for field reaction: 6 R and 6 S

Markers screened: 500 decamers for RAPDs,
10 primer pairs for SSRs
8 SCARs (in progress)
4 primer pairs for TRAPs (in progress)

QTL identified by regression (one-way ANOVAs) using ($P < 0.01$)

Partial linkage map constructed with Mapmaker/EXP 3.0

Results and Discussion

Greenhouse resistance. Two major independent QTL conditioning resistance in the greenhouse were stably expressed across five separate straw tests (Table 1, Fig. 1). Phenotypic variation explained by the QTL ranged from 22% to 37%. Both QTL had minor expression in the field (5% to 9%).

The QTL for physiological resistance to white mold as detected by the straw test had less expression in the field than previous QTL identified in other sources (G122, NY6020-4) by the straw test (Miklas et al., 2001; 2003). Less expression of these QTL in the field is likely due to the increased importance of disease avoidance traits in conferring field resistance in this population.

Modeled together the QTL for physiological resistance did not display a fully additive effect either explaining 29% to 42% of disease reaction.

Table1. Two major independent QTL conditioning resistance to white mold across multiple straw tests in the greenhouse.

Trait	Markers			
	A7.1000		J01b	
	R ²	Prob	R ²	Prob
Straw test 1	23.4%	0.0001	23.1%	0.0001
Straw test 2	27.8	0.0001	25.7	0.0001
Straw test 3	34.1	0.0001	28.7	0.0001
Straw test 4	24.6	0.0001	22.0	0.0001
Straw test 5	27.3	0.0001	36.9	0.0001
Field 1	5.9	0.016		
Field 2	5.1	0.027	9.1	0.002
Porosity 1			6.7	0.009
Height 1	6.6	0.011	7.9	0.004

Field resistance. There were four independent QTL identified that conditioned resistance to white mold in the field (Table 2, Fig. 1). All four QTL were expressed (explaining from 9% to 24% of the phenotypic variation for disease score) across multiple environments (two years).

The QTL were associated with disease avoidance traits canopy porosity (7% to 24%) and canopy height (7% to 11%). Taller lines with an open growth habit enable more sunlight and air to penetrate the canopy affecting the microclimate within the canopy to be less conducive to white mold infection.

Multiple regression models indicated the QTL for field resistance detected by A7.800 and AC01.2000 markers in Field-1 and A7.800 and H19.700 in Field-2 explained 29% and 28% of the variation in disease score, respectively. The four QTL do not have a cumulative additive effect on level of field resistance, suggesting that disease avoidance traits alone can only provide for a moderate level of resistance under heavy disease pressure.

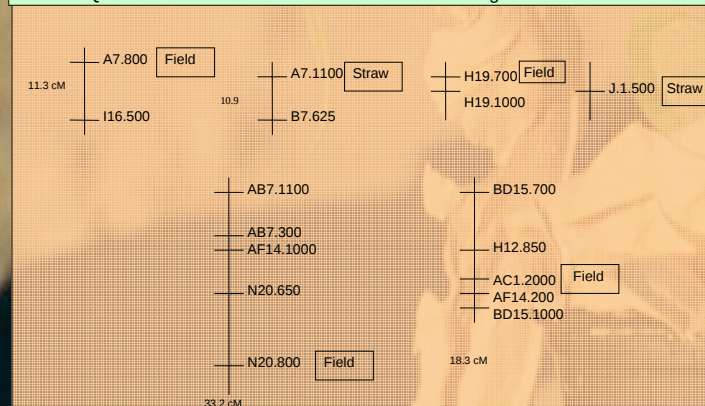
Table 2. Four major independent QTL associated with disease avoidance traits (canopy porosity and height) and field resistance to white mold across two years.

Trait	Markers							
	N20b		AC01		H19b		A7.800	
	R ²	Prob	R ²	Prob	R ²	Prob	R ²	Prob
Field 1	15.9	0.000	14.4	0.000	10.7	0.001	24.2	0.000
Field 2	9.0	0.002	14.1	0.000	15.6	0.000	16.3	0.000
Porosity 1	20.2	0.000	21.6	0.000	24.5	0.000	21.3	0.000
Porosity 2	8.6	0.003	10.1	0.001	7.6	0.007	15.9	0.000
Height 1	6.8	0.008	8.7	0.002	9.1	0.003		
Height 2	9.4	0.002	10.0	0.001	10.9	0.001		
Straw test 2					7.9	0.006		

Literature Cited

- Kolkman, J.M., and J.D. Kelly. 2000. An indirect test using oxalate to determine Physiological resistance to white mold in common bean. *Crop Sci.* 40:281-285.
- Miklas, P.N., R. Delorme, and R. Riley. 2003. Identification of QTL conditioning resistance to white mold in snap bean. *J. Am. Soc. Hort. Sci.* 128:564-570.
- Miklas, P. N., K. F. Grafton, J. D. Kelly, J. R. Steadman, and M. J. Silbernagel. 1998. Registration of four white mold resistant dry bean germplasm lines: 19365-3, 19365-5, 19365-31, and 92BG-7. *Crop Sci.* 38:1728.
- Miklas, P.N., W.C. Johnson, R. Delorme, and P. Gepts. 2001. QTL conditioning physiological resistance and avoidance to white mold in dry bean. *Crop Sci.* 41:309-315.
- Steadman, J., K.F. Grafton, K. Kmiecik, J.M. Kolkman, M. Kyle Jahn, and R. Mainz. 1998. Bean white mold nursery, 1997. *Annu. Rep. Bean Improv. Coop.* 41:173-174.

Figure 1. Partial linkage groups in the Raven/19365-31 population depicting putative QTL for resistance to white mold in the field and greenhouse straw test.



Summary

Resistance of 19365-31 to white mold in the straw test is influenced by two QTL. In combination the QTL have a partially additive effect.

Field reaction in RIL population is influenced by four QTL that are stably expressed across environments and influenced by disease avoidance traits.