

# Quantitative Trait Loci for Resistance to White Mold in Common Bean

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White mold disease of common bean (*Phaseolus vulgaris* L.), caused by *Sclerotinia sclerotiorum* (Lib.) de Bary, is a serious disease and causes annual average yield loss of 20 to 30% worldwide. Development of cultivars with physiological resistance combined with avoidance mechanisms, such as upright plant architecture, is the current strategy to minimize yield losses due to white mold. This research was initiated to verify the effect of a major QTL for resistance found in the Andean bean line G 122 (Miklas et al., 2001), and search for additional resistant QTL. A recombinant inbred line (RIL) population was developed from a cross between adapted pinto line CO72548 and G122 at Colorado State University (CSU RIL). The RIL population was screened in the greenhouse using the straw test (Petzoldt and Dickson, 1996) and a subset of the population was screened in an artificially induced white mold nursery at the Carrington Research and Extension Center, Carrington ND. Field reaction was based on % of plant tissue with mycelial growth. Polymerase chain reactions were conducted on the CSU RIL population to find QTL linked to resistance according to procedures by Kami et al. (1995). Amplified DNA was separated by electrophoresis on either 4% agarose gels or 6% denaturing polyacrylamide gels. All RAPD primers considered for this study were present on the core map developed by Freyre et al. (1998). SSR reactions were performed as described by Blair et al. (2003). AFLP reactions were performed as described by Inventrogen Life Technologies (AFLP analysis system II).

Two RIL had higher resistance than G 122 based on the average of three evaluations using the straw test. CSU RIL lines 31 and 67 had DSI of 3.2 and 3.4, respectively, compared to the resistant parent G 122 with 4.5 (Table 1). Both lines also showed lower levels of disease infection in the field however, the difference was not significant. One hundred twenty four molecular markers were used to map the CSU RIL population based on AFLP, SSR, RAPD and SCAR markers. A significant relationship ( $P < 0.01$ ) was found between the B7 QTL (Miklas et al., 2001) and white mold reaction in both the greenhouse straw test and field. In total, four markers were found to be significantly associated with white mold resistance in the CSU RIL Population using single factor analysis and composite interval mapping (CIM). Based on CIM strong evidence (LOD  $>2.9$ ) indicated that three QTL influenced physiological resistance to white mold (Table 2). The QTL were linked with marker loci a5p4195, ataca300, and *Phs* on linkage groups B2, B6a, and B7, respectively. The ataca300 region of B6a had the largest effect and accounted for 19.3% of the phenotypic variation for white mold reaction in the straw test. The a5p4195 region of the B2 linkage group accounted for 17.6%, and the *Phs* region of the B7 linkage group accounted for 16.3% of the phenotypic variation. A fourth QTL was significant at a genome-wide empirical threshold of LOD = 2.8 at the BM184 region of the B9 linkage group (Table 2). All QTL loci for resistance were contributed from parent G122 in the RIL population.

**Table 1. Entry, phaseolin type and mean straw test DSI among check cultivars and the two most resistant recombinant inbred lines.**

Entry	Phaseolin Type†	Mean DSI
31	T	3.2 a‡
67	T	3.4 a
G 122	T	4.5 bc
CO72548	S	5.8 c
PC-50	T	5.9 c
Montrose	S	8.0 d

† Denotes the seed storage protein type; where T = Tendergreen and S = Sanlic.

‡ Scores followed by the same letter are not significantly different ( $p < 0.05$ ).

**Table 2. Most important QTLs for white mold resistance; location, position, LOD score, estimated effect, nearest marker locus, and source of QTLs for resistance to white mold based on the mean straw test ASI. Results were obtained by composite interval mapping, with genome-wise empirical threshold significance levels.**

Location of QTL	Position	LOD score	R <sup>2</sup>	Nearest Marker	Source	Additive
	--- cM ---	--Score--	----%----	Name		
B2	18	3.63	17.6	a5p4195†	G122	-0.5786
B6a	131	3.83	19.3	ataca300	G122	-0.5530
B7	42	3.59	16.3	<i>Phs</i>	G122	0.5127
B9	28	2.86	9.4	BM184	G122	-0.4015

† a5p4195 and ataca300 are AFLP markers, *Phs* is a SCAR marker, and BM184 is a microsatellite marker

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