A Preliminary Molecular Marker Map for Phaseolus coccineus.
B. Gilmore and J. R. Myers
Department of Horticulture, Oregon State University, Corvallis, OR.

Within Phaseolus, the scarlet runner bean (P. coccineus) has highest levels of white mold resistance. This species is in the secondary gene pool for common bean, and it is possible to introgress genes without using extraordinary measures. Previous researchers have partially transferred resistance, but the resulting germplasm appears not to have been widely used to develop elite common bean cultivars. There are several possible reasons: accessions used were not the most resistant, resistance is quantitatively controlled and not all resistance factors were transferred, and linkage drag hindered transfer. Molecular tools integrated into a breeding program provide new avenues through which the genetic architecture of white mold resistance can be understood and transferred.

Following a screen of the P. coccineus USDA Plant introduction germplasm collection (Gilmore et al., 2002), we focused on a few accessions, including PI 255956. This accession has high levels white mold resistance and has been analyzed for physiological mechanisms of resistance. We crossed PI 255956 to the white mold susceptible ‘Wolven Pole’ P. coccineus parent to examine inheritance in the F2 generation. We intended initially to use bulked segregant analysis to identify molecular markers linked to resistance, but it became apparent from the distribution of progeny (Fig. 1) that resistance was inherited quantitatively. We then created a molecular marker map to place quantitative trait loci (QTL) for resistance.

![Figure 1. Disease reaction of an F2 population of 188 individuals from the cross PI 255956 (R) x Woven Pole (S) when inoculated with white mold in the greenhouse. Scale of 1 to 9 where 1 = immune, and 9 = dead. (A score of 4 or less indicates that Sclerotinia mycelia failed to penetrate a node.)](image)

Resistance of the parents and F2 progeny was assessed using the straw test (Petzoldt & Dickson, 1996) except plants were read after four weeks rather than eight days. Resistant individuals were retested and disease was allowed to progress for another four weeks to identify escapes. DNA was isolated as described by Kobayshi et al., (2000). Random Amplified Polymorphic DNA (RAPD) markers were generated using protocols described by Myers et al. (2004). Bean microsatellite markers (Gaitan-Solis et al., 2002) were also used. Microsatellite primers were synthesized by the MWG-Biotech and PCR amplification protocols of Gaitan-Solis et al. (2002) were used. The scaffold map was constructed in Joinmap (Van Ooijen & Voorrips, 2001) and Windows QTL Cartographer (Basten et al., 2003) was used to place QTL for white mold resistance on the scaffold map.

PI 255956 had a straw test score of 4 while Wolven Pole was 5. The F1 had a straw test score of 4. Forty-eight F2 progeny had scores of 4 or less while 144 F2s had scores greater than 4. The Wolven Pole x PI 255956 map was constructed from an F2 of 188 individuals. From an initial screen of 600 RAPD primers, 111 were used in the total population. Twenty-four of the 111
Groups 1 2 3 3a 4 5 6 7 7a 7b

Figure 2. RAPD and microsatellite based linkage map for *P. coccineus* from the cross Wolven Pole x PI 255956. QTL for white mold resistance are indicated by black bars to right of linkage groups.

Primers were used to screen 188 individuals and the F1 yielded 28 markers. Eighty-seven primers screened with 94 individuals and F1 yielded an additional 92 markers. Three microsatellite marker primers produced polymorphic bands when tested with the two parents, the F2 population of 92 individuals and F1. The map has 102 linked RAPD and microsatellite markers on 14 linkage groups for a total length of 395 cM (Fig. 2). Ten markers are unlinked including one microsatellite. Interval mapping in QTL Cartographer revealed six statistically significant (LOD ≥ 4.0) QTL on linkage groups 3, 7, 8, 11, 12, & 14 (Fig. 2). Percent additive genetic variation explained by QTL individually range from 9 to 12%), while in combination they explain 63%.

The two microsatellites mapped here have been placed on the *P. vulgaris* consensus map with our linkage groups 6 and 7c corresponding to consensus linkage groups 2 and 3, respectively.

**References**


