White Mold

Preamble:
White mold, caused by *Sclerotinia sclerotiorum* is one of the most serious diseases that reduce bean seed yields and quality in Michigan. Breeding for resistance is a major focus of the MSU bean program. Resistance to white mold is complicated by interaction with plant architectural traits and variable environmental conditions. The main focus of the breeding program has been to combine plant architecture avoidance traits with levels of partial physiological resistance available in bean germplasm. Screening for novel sources of resistance, developing mapping populations, dissecting QTLs associated with resistance and marker assisted selection (MAS) have been used to complement this effort (publications cited below). Current research is underway to identify QTL conferring resistance to white mold in two pinto bean RIL populations developed from Buni-derived USPT-WM-1 breeding line crossed to two advanced MSU breeding lines. Recent advances in genomics have facilitated the development of different markers that are very valuable in generating functional maps. These maps are important for the analysis of candidate genes and MAS and exploring syntenic relationships with other species. Common bean is amenable to comparative mapping due to its evolutionary proximity to other legume species like *Lotus japonica*, *Medicago truncatula* and *Glycine max*. The focus of our future work will be to leverage information from BeanCAP on disease resistance from the soybean genome as both species are attacked by the same pathogen.

Field screening is conducted at the Montcalm research farm using natural inoculation, inter-planting with susceptible varieties and overhead sprinkler irrigation. The field is naturally infested with white mold sclerotia from previous crops and irrigation is provided to supplement natural rainfall during flowering when infection occurs. Two types of greenhouse tests are conducted to measure physiological resistance namely the oxalate test and the straw test. The oxalate test is an indirect screening method of plant wilting which gives comparable ratings to field disease scores. The straw test is widely used by bean breeders to detect resistance in the absence of plant architectural traits that provide disease avoidance in the field.

![Figure 1: Screening for reaction to white mold in field using spreader rows under irrigation; lab using oxalate and straw tests.](image-url)
Identification of QTL for agronomic traits and resistance to white mold in wild and landrace germplasm of common bean

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White mold, caused by *Sclerotinia sclerotiorum* (Lib.) De Bary, is a serious yield reducing fungal pathogen of common bean (*Phaseolus vulgaris* L.). Our objective was to identify QTL for resistance to white mold from wild and landrace accessions of common bean using two inbred backcross line (IBL) populations derived from the recurrent black bean parent ‘Tacana’. Selective phenotyping failed to detect QTL for field disease resistance but other agronomic traits less sensitive to environmental conditions or population size were detected. Four novel QTLs for white mold resistance WM3.3\(^{TW}\), WM7.5\(^{TL}\), WM9.2\(^{TW}\) and WM11.1\(^{TL}\) were identified in the greenhouse straw test on linkage groups B3, B7, B9 and B11, respectively and two previously mapped QTL were also validated on B2 and B4. QTL, SY2.1\(^{TL}\) that accounted for 19 to 37% of the variation for yield under white mold pressure over three years, was detected on B2 in the TL population. Enhanced resistance to white mold in common bean could be achieved by combining different QTL associated with physiological resistance with yield under disease pressure.


Previous publications: