AN ABSTRACT OF THE DISSERTATION OF

Barbara S. Gilmore for the degree of Doctor of Philosophy in Genetics presented on April 30,2007.
Title: Genetic Resistance to White Mold (*Sclerotinia sclerotiorum* (Lib.) De Bary) in Scarlet Runner Beans (*Phaseolus coccineus* L.)

Abstract approved:

James R. Myers

White mold, caused by *Sclerotinia sclerotiorum* (Lib.) De Bary, is a destructive yield-limiting disease of common bean (*Phaseolus vulgaris* L.). Genetic resistance to this pathogen is limited in common bean. Identification of high levels of partial physiological resistance in a genetically cross compatible species, *Phaseolus coccineus*, is advisable. The objectives of this study were to 1) identify accessions of *P. coccineus* with high levels of partial physiological resistance to *S. sclerotiorum*, 2) create a linkage map in a *P. coccineus* population and 3) identify markers linked to quantitative trait loci (QTL) conferring partial physiological resistance to white mold in this population.

The *P. coccineus* collection of the U.S. Department of Agriculture National Plant Germplasm System (NPGS) Plant Introduction collection maintained at Pullman, WA, consisting of 478 accessions, but only 364 were available to be screened with the pathogen *S. sclerotiorum* to identify partial physiological resistance. 50.1% of the accessions were identified to have high partial physiological

accessions were identified to have high partial physiological resistance using the Petzoldt and Dickson (1996). Accessions were also characterized as to what species they were, based on hilum and seed coat appearance and emergence. Almost 30% of the accessions' seeds were either a mixture of species or labeled the wrong species.

A population of *P. coccineus,* based on the cross Wolven Pole (MS) x PI 255956 (R), segregating for resistance was developed and evaluated for its susceptibility to white mold in the greenhouse. This population was then tested with three polymerase chain reaction (PCR) based markers, random amplified polymorphic DNAs (RAPDs), simple sequence repeats (SSRs), and amplified fragment length polymorphisms (AFLPs). A total of 215 markers were used to create a genetic linkage map with thirteen linkage groups that spanned 797 centimorgans (cM). Four quantative trait loci (QTL) were identified and placed on this map. The two QTL relating to a five week white mold screening explained a total of 89.6% of the phenotypic variation for this trait. The remaining two QTL were for the eight-day straw test results, and were able to explain 13.8% of the phenotypic variation. To our knowledge this is the first genetic linkage map of *P. coccineus*.

Genetic Resistance to White Mold (*Sclerotinia sclerotiorum* (Lib.) De Bary) in Scarlet Runner Beans (*Phaseolus coccineus* L.)

by
Barbara S. Gilmore

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I understand that my dissertation will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my dissertation to any reader upon request.

Barbara S. Gilmore

Barbara S. Gilmore, Author

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DEDICATION

To My Parents

Genetic Resistance to White Mold (*Sclerotinia sclerotiorum* (Lib.) De Bary) in Scarlet Runner Beans (*Phaseolus coccineus* L.)

CHAPTER 1. INTRODUCTION AND LITERATURE REVIEW

Characterization of cultivated *Phaseolus* species

The genus *Phaseolus* is a member of the Fabaceae family and has over 50 annual and perennial herbaceous species. The five cultivated *Phaseolus* species are *P. vulgaris* (common bean), *P. coccineus* (scarlet runner bean), *P. lunatus* (lima bean), *P. dumosus* (formerly *P. polyanthus* or *P. coccineus* subsp. *darwinius* (Freytag and Debouck 2002) or year long bean), and *P. acutifolius* (tepary bean) (Hall 1994). *P. vulgaris* is the most commonly grown species in the Americas, Africa, Asia and Europe (Hall 1994). All five species are diploid; 2n = 2x = 22 (Smartt and Simmonds 1995). The common bean was domesticated 7000 to 8000 years ago in two regions: the Andean region of South America and the Mexican-Guatemalan region of Central America (Mesoamerica). In both areas wild *P. vulgaris* subspecies and other wild relatives still exist (Gepts 1988; Hall 1994; Smartt and Simmonds 1995). Although the archaeological records are few these records indicate that *P. coccineus* and *P. acutifolius* may have been domesticated in Mexico (Smartt and Simmonds 1995; Freytag and Debouck 2002). Recent biochemical evidence indicates that the lima bean had two domestication centers. The small seeded types were probably domesticated in Mesoamerica and large seeded limas in the western Andes (Smartt and Simmonds 1995; Freytag and Debouck 2002). The fifth case of plant

domestication in the genus *Phaseolus* was the domestication of *P. dumosus* possibly in Central America, although it may also have occurred in Mexico (Freytag and Debouck 2002).

Domestication of *Phaseolus* involved altering the plant habit, seed coat permeability, and seed size. Larger, heavier seeds were selected as were smaller more compact plants that aided cultivation. Seed coats more permeable to water, having reduced dormancy, and shorter cooking times were selected (Smartt and Simmonds 1995). Brightly colored seeds seemed to be preferred by early people instead of the wild type, black and brown speckled seeds (Freytag and Debouck 2002). Another highly desirable trait perpetuated by early humans was lower pod wall fiber content and less dehiscent pods, preventing seeds lost due to shattering. Pods that have high wall fiber content allow the pod to easily and forcibly dehisce when dry, throwing seeds up to several meters (Bassett 1986). Beans possess a number of anti-nutritional factors in the seeds, but most of these are detoxified by cooking. The exception is *P. lunatus* where cyanogenic glycosides can be as much as 150 times higher in wild *P. lunatus* than in domesticated types (Lindig-Cisneros et al. 1997). Also as beans moved out of their centers of origin, short day types were unadapted and daylength-insensitive type plants were developed (Gepts 1988; Lindig-Cisneros et al. 1997).

The common bean is a warm season annual that grows in subtropical or temperate areas, at higher elevations or during the cool, dry season in tropical areas. Optimum growing temperatures range from about 24^{o}C to 29^{o}C, with the minimum temperature about 10^{o}C. Soil temperatures should be between 13^{o} to 21^{o}C. All beans are sensitive

to freezing temperatures and because the common bean has epigeal emergence, it is unable to recover from a frost (Bassett 1986; Gepts 1988; Hall 1994).

Beans prefer a well-drained sandy loam, silt loam, or clay loam soil with high organic matter. The pH can ideally range from 5.2 to 6.8. Beans need 46 -52 cm (18-20 inches) of water for optimum growth and under water stress conditions of less than 39 cm, yield is reduced (Hall 1994). In 2004 Michigan dry bean yield trials had results for bush beans as low as 1121 kg ha^{-1} (0.5 T A^{-1}) to as high as 4700 kg ha^{-1} (2.1 T A^{-1}) depending on type and variety (Kelly et al. 2004). Dry bean yield has been increasing 0.6% per year because of genetic improvement (Kelly et al. 1998).

Bean seeds contain about 22% protein of which the majority is phaseolin, accompanied by lesser amounts of lectins. Although the bean protein is incomplete, lacking the sulfur-containing amino acids methionine and cysteine, it is rich in lysine (Gepts 1988; Hall 1994). When beans are combined with maize (*Zea mays*) or other cereals, in an approximate 3:1 cereal:bean ratio, complementation of amino acids produces a nutritionally complete protein. Beans are a low cost, high protein food available to many people in areas of the world that do not have adequate food or use plant proteins as their major source of protein (Young and Pellett 1994). Dry beans are soaked in water overnight and cooked for 45 to 90 min (Iyer et al. 1980).

The scarlet runner bean differs from common bean in that it is a tender perennial with hypogeal emergence (cotyledons stay in the ground during germination). Some *P. coccineus* plants develop large, fleshy, perennial tap roots. It is from these roots that dormant buds sprout each spring to put up that year's vine. The flowers are red or

white and the seeds are usually larger than the common bean (Gepts 1988; Hall 1994). The scarlet runner bean requires longer cooking time than *P. vulgaris*, on average almost an hour, but the digestibility is greater (Carlderon et al. 1992). *P. coccineus* has not had as much breeding work done on it as *P. vulgaris* and the yield reported in Mexico was about 3360 kg ha^{-1} (1.5 T A^{-1}) for type IV (climbing) varieties (Gepts 1988). Santalla et al. (2004) examined thirty one Spanish land races of scarlet runner beans. They found that the premium types yielded between 7850 kg ha^{-1} (3.5 T A^{-1}) to 10090 kg ha^{-1} (4.5 T A^{-1}) for type IV, a tremendous increase over the years past (Santalla et al. 2004).

P. coccineus is an important source of resistance to many pathogens and a few insects. Baggett and Frazier (1959), found resistance to *Pseudomonas phaseolicola* (halo blight), *Uromyces phaseoli* (bean rust), *Colletotrichum lindemuthianum* (anthracnose), Bean Common Mosaic Virus, and Bean Yellow Mosaic Virus. In 1980, Coyne and Schuster found *P. coccineus* types that were resistant to *Xanthomonas axonopodis* pv. *phaseoli* (common bacterial blight) and to *Corynebacterium flaccumfaciens* (bacterial wilt) (Gepts 1988). *P. coccineus* was consistently more resistant to *Sclerotinia sclerotiorum* (white mold) than was *P. vulgaris* (Adams et al. 1973; Abawi et al. 1978; Gilmore and Myers 2000; Gilmore et al. 2002; Schwartz et al. 2006). Resistant accessions exhibit slower mycelial growth and some accessions may show phytoalexin accumulation and/or node enlargement below the infection site (Gilmore, personal observation). While Chipps et al (2005)

implicated oxalic acid tolerance as a resistance mechanism in *P. coccineus*, other mechanisms may be involved (Gilmore et al. 2002; Chipps et al. 2005).

Interspecific hybridization of common and scarlet runner bean

P. coccineus can easily be crossed to *P. vulgaris* if common bean is used as the female parent. *P. coccineus* can be used as the female parent, but embryo rescue is nearly always required. Rarely does the *P.coccineus* x *P.vulgaris* cross produce normal embryos (Smartt 1970), rather, embryos are shrunken and underdeveloped depending on the genotype of the *P. coccineus* parent (Shii et al. 1982; Guo et al. 1989). Even when *P. vulgaris* is the female parent, there are genetic barriers to interspecific hybridization in the F_1, barriers such as dwarfing, leaf abnormalities (curling, rugose texture, chlorosis, necrosis), blocked cotyledon lethals and poor pollen viability (Smartt 1970; Shii et al. 1982; Ferwerda and Bassett 2000).

Ferwerda and Bassett (2000) evaluated blocked cotyledon lethal, crinkle leaf dwarf, and dwarf lethal traits to identify *P. vulgaris* lines that had lower frequency of these abnormalities and would serve as a bridge to bring in valuable characteristics of *P. coccineus*. The three interspecific incompatibility barrier traits are independent of each other and they identified lines suitable *P. vulgaris* bridge lines (Ferwerda and Bassett 2000).

Traits segregating between *P. coccineus* to *P. vulgaris* may be simply inherited (e.g., Bean Yellow Mosaic Virus, BYMV) (Baggett 1956) or quantitatively inherited [e.g. stigma position (Smartt 1970), cotyledon position (Wall and York 1957; Smartt

1970) or fusarium root rot resistance (Hassan et al. 1971)]. Resistance to *S. sclerotiorum* in *P. coccineus* has been reported to be controlled by a single dominant gene (Abawi et al. 1978; Schwartz et al. 2004; Schwartz et al. 2006) or by quantitative trait loci (Gilmore and Myers 2004). Lyons et al (1987) reported using recurrent selection to successfully incorporate white mold resistance from *P. coccineus* into *P. vulgaris* where resistance was treated as a quantitative trait (Lyons et al. 1987).

***Sclerotinia sclerotiorum*, causal agent of white mold disease**

Madame M. A. Libert (1837) described a fungal disease *Peziza sclerotiorum* in Plante Crytogamicae Arduennae (Exsiccati) No. 326, which Leopoldi Fuckel (1870) transferred to the genus *Sclerotinia* in his book, Symbolae Mycologicae. Beiträge zur Kenntniss der Rheinischen Pilze. Jahrbücher des Nassauischen Vereins für Naturkunde. He renamed it *Sclerotinia libertiania* Fuckel in honor of Madame Libert. Wakefield showed this name was inconsistent with the International Rules of Botanical Nomenclature and gave G. E. Massee proper authority for *Sclerotinia sclerotiorum* (Lib.) since Massee had used that binomial in 1895 (Wakefield 1924). But Anton de Bary previously in 1884 used the binomial *Sclerotinia sclerotiorum* in his writings, so the proper name for this fungus became *Sclerotinia sclerotiorum* (Lib.) de Bary (Purdy 1979).

Sclerotinia sclerotiorum is a ubiquitous necrotrophic fungus reported in many countries on six continents (Purdy 1979). It infects more than 400 plant species, including one member of Polypodiaceae, four Gymnosperms of the Pinaceae, almost

30 monocots and numerous herbaceous plants of the Dicotyledoneae (Boland and Hall 1994). It grows at temperatures from 4°C to over 30°C, with optimal range of 20°-25°C (Hall 1994). *S. sclerotiorum* occurs in moist as well as hot arid climates as long as there is sufficient moisture from rainfall or irrigation (Purdy 1979). In North America there are two major variants, one relatively recently evolved that inhabits temperate and subtropical regions and the other an ancestral, strictly temperate population. There is strong evidence that new genotypes are evolving (Hambleton et al. 2002).

S. sclerotiorum is responsible for losses of up to 100% in some crops, with the normal range from 1 to 50% depending on the crop and the environment. The fungus can infect the crop in the field, in transit or in storage (Purdy 1979; Agrios 1997). In green beans when the pod infection rate exceeds 3 - 5%, the processor will reject the field, and refuse to pay the farmer (Stivers 2000).

The pathogen's dormant, over-wintering structures are sclerotia that remain in soil or plant debris until germination conditions are met. Sclerotia are hard structures that consist of a light interior portion called a medulla and a black exterior protective covering called the rind. Melanin pigments in the rind make it highly resistant to degradation, while the medulla is high in glucans and proteins (Nelson 1998). Sclerotia germination occurs with cool temperatures (4°-20°C), adequate moisture and shallow depth (<5 cm) in the soil. For carpogenic germination, sclerotia break dormancy and produce apothecia, which upon maturity produce ascospores from the hymenium (Hall 1994; Agrios 1997). Apothecia remain viable in the field for seven to

nine d (Schwartz and Steadman 1977). The spores are released, or puffed, out into the environment to be carried by the wind. Groups of asci tend to fire their spores almost simultaneously which produce large, visible clouds. This simultaneous puffing also creates air currents that can elevate the spores above the hymenium (Venette 1998). One apothecia can release as many as 3×10^7 ascospores (Abawi and Grogan 1979) that can be viable for up to 21 d under optimum conditions, but for drastically shorter time periods when temperatures are near 25°C (Caesar and Pearson 1983). Spores landing on senescing bean flowers germinate and form mycelia. Senescing tissue provides energy for the mycelia to colonize nearby live tissue. The infection spreads to other bean plants by physical contact with the diseased plant. Mycelia on digested tissue will coalesce into sclerotia. These survival structures either drop to the soil, where they can over winter for as long as eight years, or remain in the plant tissue, to be harvested along with the crop (Adams and Ayers 1979). If the sclerotia are harvested with the crop it may be replanted, thereby spreading inoculum over long distances (Davidson and Byther 1982; Hall 1994; Agrios 1997).

Another means of infection of some crops (mostly members of the Asteraceae family) is mycelial germination of sclerotia in the soil. If the sclerotia are 0.5 to 1.0 cm to the side or up to 2 cm below the germinating seed, infection can occur, but not if the sclerotia are above the seed. Mycelia will grow laterally on the surface from organic debris to infect plant parts near the soil. Thus, mycelial germination tends to produce basal infections whereas carpogenic germination usually causes aerial infections (Huang and Dueck 1980).

Symptoms of *S. sclerotiorum* start with white cottony growth on old, senesced flowers. The white mycelia continue to spread causing water-soaked lesions in advance of mycelial growth. At the field scale, the first symptoms of the pathogen are wilted leaves scattered throughout the field. On closer inspection individual plants have a slimy, watery appearance, and may have developed cottony, mycelial, growths. The lesions on stems and petioles disrupt vascular transport, and along with enforced stomatal opening, causes wilting of the leaves. As infected tissue dies, it appears dry, tattered, and bleached to a pale brown or white color. Stems become friable and easily disintegrate revealing long undigested lignin strands, and often are filled with sclerotia (Steadman 1983; Hall 1994; Agrios 1997).

This organism has become a successful pathogen by several different mechanisms. It releases oxalic acid, which was first observed by De Bary (1886) to kill plant tissues, inactivate defenses, and create a favorable acidic environment for fungal growth (Bateman and Beer 1965). It also has a plethora of enzymes to break down the host structural and storage tissues (Bateman and Beer 1965; Lumsden 1976; Kurian and Stelzig 1979; Favaron et al. 1988).

Pathogenesis mechanisms

Oxalic acid

Oxalic acid occurs extensively in fungi and is important to their ecology and their pathogenicity to plants. The first report of oxalic acid production in fungi was in 1877 by Hamlet and Plowright when they detected oxalic acid in the growing media of 27

species of fungi (Dutton and Evans 1996). Anton de Bary was the first to observe that *S. sclerotiorum* produced oxalic acid as a pathogenicity factor (de Bary 1886). Godoy et al. (1990) developed *S. sclerotiorum* oxalic acid deficient mutants to test the involvement of oxalic acid in pathogenicity. They found that oxalic acid deficient mutants had greatly reduced virulence on beans compared to wild types. Actively growing deficient mutants were unable to infect or cause symptoms on bean leaves, stem or pod, even when the plant was wounded. The mutants produced similar amounts of cellulases and pectinases. Adding one percent exogenous oxalic acid to the medium did not increase pathogenicity, but when the oxalate precursors sodium succinate or calcium oxalate were added to the growth medium, pathogenicity was partially restored. Mycelial strands observed in necrotic lesions were similar to the wild type mycelia in similar lesions. The researchers concluded that oxalic acid and not pathogenic enzymes determined pathogenicity of this fungus (Godoy et al. 1990).

Other researchers have shown that oxalic acid produces conditions favorable for other pathogenic mechanisms to operate. Bateman and Beer (1965) studied the interaction of oxalic acid and polygalacturonase produced by *S. rolfsii*. Infected tissue had a pH of 4.0, oxalic acid production paralleled fungal growth, and it was the low pH that was toxic to the plant. They also determined that oxalate stripped $Ca^{2+}$of calcium pectate from the host cell wall and the pH of 4.0 was optimum for polygalacturonase activity. When the oxalate chelated Ca^{2+}, polygalacturonase could hydrolyze the pectates in the middle lamella. Using young bean hypocotyls, they found that polygalacturonase and oxalic acid had similar devastating effects to

symptoms caused by *S. rolfsii* (Bateman and Beer 1965). Marciano et al. (1989) used two different isolates and several commercial cell wall-like polysaccharides to study the ability of *S. sclerotiorum* to use different carbon sources for growth and oxalic acid synthesis. One isolate was highly virulent and the other was a low virulent type. Both isolates used all carbon sources for mycelial growth, but differed in their ability to use them for oxalate production. Pectic substances and cell wall preparation were the most favorable substrates for oxalate production. These researchers suggested that *S. sclerotiorum* modifies oxalic acid production depending on the carbon source available (Marciano et al. 1989).

Guimarães and Stotz (2004) showed guard cell dysfunction in *Vicia faba* when infected by *S. sclerotiorum*. Oxalate induced stomatal pores to open in the dark and transpiration rates were significantly higher in infected plants. Oxalate deficient *S. sclerotiorum* caused only partial opening of stomata, indicating that oxalic acid caused stomates to open. The open stomata enhanced wilting and permitted the emergence of hyphae for secondary colonization of the fungus (Guimaraes and Stotz 2004).

One of the earliest plant defense responses is the oxidative burst, the controlled release of O_2 and H_2O_2. The oxidative burst is suppressed at low pH and requires an increase in cytosolic Ca^{2+}. Cessna et al (2000) found that oxalic acid suppressed the oxidative burst and depressed H_2O_2 production. Oxalate remained inhibitory even at high pH. Suspension cells remained viable, demonstrating that the oxalate was not suppressing the oxidative burst because of acidic toxicity. Chelation of Ca^{2+} did not inhibit the oxidative burst and although the oxidative burst did require activation of

protein kinases, it probably occurred downstream of the protein phosphorylation. Oxalate did not inhibit superoxide dismutase, because once begun, oxalate failed to inhibit the oxidative burst (Cessna et al. 2000).

The enzyme *o*-diphenol oxidase (*o*-DPO), catalyses the oxidation of *o*-dihydroxy phenols to reactive *o*-quinones, which may act in plant defense to inactivate the pathogen's exoenzymes. The polymerization products (melanins) seal off the site of infection and so stop the pathogens advance. Ferrar and Walker (1993) measured *o*-DPO in apple fruit and bean pods infected with *S. sclerotiorum* and *S. rolfsii*. They discovered that *o*-DPO displayed competitive inhibition and was inactivated when *S. sclerotiorum* was grown on apple fruit. Bean pod tissue pH was reduced to 3.0 by the oxalic acid of *S. rolfsii*, and *o*-DPO displayed no activity, since it was below the pH range of that enzyme (Ferrar and Walker 1993). Sato (1980) found similar inhibition of chloroplast *o*-DPO by oxalate. Oxalate was a potent inhibitor of *o*-DPO in acidic media, but in a neutral environment inhibition was limited (Sato 1980a). *o*-DPO activity could be restored by adding copper, which released the oxalate moiety from the active center of the enzyme as a chelate with copper (Sato 1980b).

Pathogenesis Enzymes

In addition to oxalic acid, *S. sclerotiorum* produces an array of pathogenic enzymes. Callahan and Rowe (1991) demonstrated this production by using dialysis membranes to allow the exudates of *S. trifoliorum* to pass into alfalfa seedling growing media, while excluding mycelial contact. While oxalic acid alone partially inhibited radicle growth, the whole exudate significantly inhibited radicle length.

Oxalic acid was not the sole pathogenic determinant, but the macromolecular components of the exudate were synergistic in inhibiting seedling growth (Callahan and Rowe 1991).

Marciano et al. (1983) found that two *S. sclerotiorum* isolates differing in virulence released cell wall-degrading enzymes, polygalacturonase, cellulase and xylanase in similar quantities on sunflower. Oxalic acid did not directly affect polygalacturonase activity, although this enzyme is very sensitive to pH variation (Marciano et al. 1983). Expression of endopolygalacturonase genes of *S. sclerotiorum* is pH controlled in the host. Cotton et al. extracted RNA from many areas of infection and under a range of pH values, and different amounts endopolygalacturonase RNA were found. The fungus produces pectinases only under pH conditions appropriate for their activity (Cotton et al. 2003).

Lumsden (1976) looked at three pectolytic enzymes, endopolygalacturonase (endo-PG), exopolygalacturonase (exo-PG) and pectin methylesterase (PME) produced by *S. sclerotiorum*. Endo-PG and PME were closely associated with advancing margins of very young lesions. The exo-PG was observed after two d in diseased tissue or three to four d in culture, where level was high and was associated with of rapid tissue maceration. This enzyme was positively associated with mycelial dry weight and was important for releasing hydrolysis products for the nutrition of the rapidly advancing fungus (Lumsden 1976).

Riou et al. (1991) grew *S. sclerotiorum* on media with a variety of carbohydrate growth substrates, and then examined the activity of the pathogen derived enzymes.

Several different enzymes had similar activity, but sometimes had different activities on different substrates, even at the same pH. Pectinolytic enzymes seemed to be produced constitutively. It may be this pathogen's ability to secrete a wide range of polysaccharide degrading enzymes that allows it to infect so many different plant species (Riou et al. 1991).

Five major and several minor polygalacturonases were identified from a *S. sclerotiorum* isolate from *Brassica napus*, but an exhaustive EST search only identified four distinct PG-encoding cDNAs. Li et al (2004) felt it possible that different polygalacturonases were derived from post-translational modifications of a few gene products. Genes appear to be differentially regulated under both saprophytic and parasitic conditions, and the expression of each gene is controlled by a set of environmental, developmental and nutritional factors. Ultimately, this genetic control would allow the pathogen to adapt more easily and quickly to host conditions (Li et al. 2004).

Favaron et al. (1988) examined the role of *S. sclerotiorum* polygalacturonases as elicitors of the soybean phytoalexin, glyceollin I. Three endo-PG isoenzymes (PG-I, PG-II and PG-IV) and one exo-PG (PG-III) were purified from *S. sclerotiorum* infected six day old etiolated soybean hypocotyls. Oxalic acid was an elicitor over a wide range of concentrations, but the PG's concentration range for elicitor activity was limited. Because both oxalic acid and PGs are important factors of pathogenesis, changes in synthesis rate and accumulation may prevent phytoalexin production by rapid cell destruction (Favaron et al. 1988).

Soledade et al. (2004) discovered that *S. sclerotiorum* has the ability to detoxify bassinin, a cruciferous phytoalexin, into glucosyl derivatives that have no detectable antifungal activity. The deactivation of the phytoalexins occurred at different rates depending upon organic structure, and was due to the release of different fungal enzymes (Soledade et al. 2004).

Because as much as 10% of the cell wall of a plant can be comprised of proteins, Poussereau et al. (2001) examined the acid proteases of *S. sclerotiorum*, discovering that acid protease (*acp 1*) exhibited 50% to 62% sequence identity with proteases of three other filamentous fungi. The expression of this gene was very tightly regulated by the environment (Poussereau et al. 2001).

Girard et al. (2004) found that in *S. sclerotiorum acp1* expression was increased if gelatin was added to nitrogen-free medium. Exogenous cAMP and caffeine triggered expression, but the gene was not triggered in a neutral pH medium or if ammonium was added to the medium, preventing export into the environment. They concluded that cAMP is a likely intermediate in the cellular cascade leading to *acp1* production (Girard et al. 2004).

Martel et al. (2002) purified and characterized a glucoamylase secreted by *S. sclerotiorum*. This amylase had enzymatic parameters (pH 3.5-4 and 50^{o}) that were typical of the fungal glucoamylases specifically and starch-hydrolyzing enzymes in general. The enzyme hydrolyzed starch from macerated plant cells and released glucose to provide energy for the growing fungus (Martel et al. 2002).

In summary, *S. sclerotiorum* uses oxalic acid to damage host cells and create an optimal environment for growth. On a whole plant level, oxalic acid maintains stomatal opening, causing wilting and additional secondary invasion points. It is able to tailor gene expression of degradative pectinases, amylases and proteases to adapt to different substrates found in a wide range plant species. The ability to inactivate, delay or manipulate the hosts' defense mechanisms and modify pathogenic products to changing environments leaves most hosts virtually defenseless.

Host resistance to white mold

S. sclerotiorum has effective measures to attack, kill and consume its host, but as with all diseases there is never complete host susceptibility. Mechanisms to mitigate attack by *S. sclerotiorum* include avoidance and resistance. Avoidance in general, operates before contact between host and pathogen is established and decreases disease because the host and pathogen never meet (Do Vale et al. 2001). Avoidance can be the result of a morphological trait, or by avoiding the environment that favors the pathogen. Varieties that have large dense canopies, holding moisture and creating a more favorable environment for the pathogen to grow in are more likely to become infected. Bean cultivars with upright architecture and porous canopy structure have little disease in all but the most conducive environments (Schwartz et al. 1978; Abawi and Hunter 1979; Schwartz et al. 1987). Early flowering and maturity may allow bean plants to evade ascospore dissemination (Boland and Hall 1987). Avoidance will not

be effective when the environment is highly conducive to disease, necessitating the use of resistance.

Physiological resistance results from some functioning mechanism of the plant that excludes or overcomes, completely or in some degree, the effect of a pathogen (Agrios 1997). A morphological mechanism in beans, such as a thick cuticle, serves as a physical barrier to infection. Resistance to *S. sclerotiorum* in *P. vulgaris* is low and may be controlled by several genes (Grafton 1998). Avoidance may be necessary for expression of partial physiological resistance, because an increase in relative humidity within the canopy is otherwise more likely, allowing the pathogen to overcome physiological resistance mechanisms of the host. Even the most resistant genotypes will become infected if wet conditions exist for prolonged periods. Partial physiological resistance may be most valuable when combined with cultural controls and/or avoidance mechanisms that create environmental conditions less favorable to the pathogen (Schwartz et al. 1987; Miklas et al. 1992).

Abawi et al. (1978) incubated ascospores on blossoms of a *P. coccineus* line for one week in a mist chamber. *P. coccineus* had none to very small lesions, and this lack of infections was credited to an unknown factor in the blossoms (Abawi et al. 1978).

Bateman and Beer (1965) noted that young bean plants are more susceptible to attack than older plants. Susceptibility of the bean hypocotyls of different ages to *Rhizoctonia solani* attack was inversely related to the calcium content of the tissue. While *R. solani* polygalacturonases cannot easily hydrolyze calcium pectate, those of

S. rolfsii and *S. sclerotiorum* can because of reduced pH by oxalic acid, and so have the ability to infect older tissue (Bateman and Beer 1965).

Sutton and Deverall (1984) found that common bean 'Redlands Pioneer' and soybean 'Lee' developed different phytoalexins in different concentrations depending on location and the type of infection. When infected by ascospores, the bean leaves produced high concentrations of phaseollin and phaseollidin, but bean hypocotyls yielded kievitone. The soybean leaves contained no glyceollin, but the hypocotyls did. When plants were infected with mycelia, bean leaves produced no detectable phytoalexins while hypocotyls had kievitone as before. The soybean leaves contained glyceollin, (hypocotyls were not tested). The effects of phytoalexins on ascospore germination and hyphal growth in vitro were also examined. Phaseollin was the most inhibiting, followed by kievitone and glyceollin (Sutton and Deverall 1984).

Beckman et al. (1974) found that artificial cell wall membranes were quickly disintegrated by oxalate and pectinase by *Fusarium oxysporum*. By infusing these membranes with the phenolic compounds polyphenoloxidase and hydroxytyramine, the membranes became highly resistant to disintegration. Cortical tissues of banana root, although not affected by oxalate and pectinase of *F. oxysporum*, became very fragile when exposed to low and high pH cycles plus oxalate. As before, the phenolic infusion prevented damage to these tissues. The researchers postulated that release of phenolics may serve to insulate the infection from healthy tissue and so turn off host defense responses. But they felt that timing was a critical factor, too early and other

defenses would fail to happen, and too late the pathogen could degrade the sealing-off structures and systemic infection would occur (Beckman et al. 1974).

Polygalacturonase inhibitor proteins (PGIPs) have been shown to inhibit some fungal endopolygalacturonases (PGs) in vitro. PGIPs have a structural motif, the leucine-rich repeat, a component of many plant resistance gene products. Powell et al. (2000) expressed apple PGIP in a transgenic tomato with a 20- to 25-fold increase in inhibitor activity. Tomato plants inoculated with *Botrytis cinerea* became infected but symptoms were reduced (Powell et al. 2000).

Tu (1985) noticed that the water soaked zone around *Sclerotinia* infected tissue was smaller in Ex Rico 23 than in susceptible Kentwood and Seafarer, all common bean varieties. Susceptible types quickly showed infection, and total collapse happened by the seventh or eighth day, but Ex Rico 23 developed less severe symptoms and the disease progressed about one third slower than in susceptible lines. This could indicate possible cellular impedance to disease progression. When excised leaves were placed in oxalic acid, there were more symptoms on Kentwood and Seafarer than on Ex Rico 23. Using ^{14}C labeled oxalic acid he showed that the susceptible beans absorbed three times more oxalic acid than did Ex Rico 23. The ^{14}C was found throughout the susceptible bean leaves, but only near veins in Ex Rico leaves (Tu 1985). Tu (1989) found visible differences with the electron microscope when observing the cell cytoplasm of Ex Rico 23 and Fleetwood. Plasma membranes and cellular organelles were more severely disrupted by the oxalic acid in Fleetwood than in Ex Rico 23. In both varieties oxalic acid had to alter all of the cell's

membranes, including the chloroplast membrane, before it could enter the cell or the cell's organelles. The plasma membrane was also more stable in Ex Rico 23, leading Tu to the conclusion that tolerance of the plasma membrane to oxalic acid might be an important factor determining the rate of disease progression (Tu 1989).

Because certain lines of *P. coccineus* have high levels of resistance to white mold (Gilmore and Myers 2000; Gilmore et al. 2002), Chipps et al. (2005) tested two accessions and one cultivar of *P. coccineus* and three cultivars of *P. vulgaris* for tolerance to oxalic acid. Cuttings were subjected to an oxalate solution where wilting was observed. The two partially resistant accessions of *P. coccineus* had low wilting levels compared to the susceptible *P. coccineus* accession. One partially resistant accession produced a purple pigment at the site of infection which may have been a phytoalexin or polyphenol response in addition to oxalic acid tolerance. The *P. coccineus* accessions showed much greater oxalate tolerance than any of the *P. vulgaris* accessions (Chipps et al. 2005).

Jasmonic acid (JA) and ethylene signaling are necessary components of induced systemic resistance in plants in many host-pathogen systems. Guo and Stotz (2007) used *Arabidopsis thaliana* mutants to determine if the JA pathway influenced resistance to *S. sclerotiorum*. They found *coi-1*, and *coi-2* mutants (both involved in jasmonate signaling), were hyper-susceptible to *S. sclerotiorum* compared to wild type *A. thaliana*. These mutants displayed lesions even when an oxalate-deficient *S. sclerotiorum* strain (Godoy et al. 1990) was used. This suggested that the JA-dependent resistance was independent of oxalic acid exposure. The mutant, *jin1*, also

involved in jasmonate signaling but at a different point in the pathway than *coi-1*, and *coi-2*, had the same susceptibility as the wild type, indicating that transcription factors other than JIN1 were involved in increased wild-type plant resistance. Two mutants, *npr1* and *ein2*, involved in non-JA resistance pathways were hyper-susceptible when inoculated with *S. sclerotiorum*. Because both *npr1* and *ein2* mutants showed susceptibility this suggests that salicylic acid and ethylene pathways are also involved in resistance (Guo and Stotz 2007).

Research on determining mechanisms of resistance to *Sclerotinia* has begun to increase, in part fueled by increased access to genomic data and the understanding of resistance mechanisms in other host-pathogen systems. The advent of the National Sclerotinia Initiative (http://www.whitemoldresearch.com/) has also increased funding for this area of research. As such, there is a tremendous amount of interest in locating resistance to be used in breeding programs. As resistant lines and cultivars are discovered, their DNA is being scrutinized for information that will allow researchers to help identify these same resistant mechanisms in their progeny. Molecular markers will be the tools that will enable us to expand our knowledge in this capacity.

PCR based markers

With the invention of molecular markers in genetic research it was no longer necessary for a gene to cause a discrete and visible change in an organism's phenotype in order to study that gene (Tanksley 1993). The earliest molecular markers were allozymes or isozymes, which are allelic forms of enzymes that can be separated on

electrophoretic gels and then detected with histochemical activity stains. Although limited by the number of enzymes available, researchers began to create linkage maps in many plant species, and locate qualitative and quantitative traits on these maps. (Prior to the molecular era, only four crop species – maize, tomato, pea and barley – had substantial linkage maps.) DNA-based genetic markers, the first being RFLPs or restriction fragment length polymorphisms were soon introduced. With the discovery of Taq polymerase, genetic markers based on the polymerase chain reaction (PCR) were developed (Tanksley 1993; Griffiths et al. 1996).

Markers are invaluable tools for genetic analysis, and the use of PCR-based markers revolutionized plant research and breeding. They require very small amounts of efficiently obtained DNA, are relatively inexpensive, are fast, plentiful, and are highly reproducible. Marker assisted selection became possible for breeders when molecular markers closely linked to traits of interest were identified. This permitted selection for the trait of interest without having to know the phenotype (Lorz and Wenzel 2005). RAPDs (random amplified polymorphic DNAs) and AFLPs (amplified fragment length polymorphisms) require no prior sequence analysis, primer synthesis or characterization of DNA probes. These two methods amplify random genomic DNA fragments by arbitrarily selected PCR primers (Vos et al. 1995; Jones et al. 1997). SSRs (simple sequence repeats) and VNTRs (variable number tandem repeats) do require knowledge of sequence and specialized primer development (Nakamura et al. 1987; Vos et al. 1995; Jones et al. 1997). The fragments generated by the following methods depend on the sequence of the PCR primers, the nature of

the template DNA, presence of polymerase, and a machine to precisely control a sequence of repeated temperature cycles (thermocycler).

RAPDs were first described by Welsh and McClelland (1990) and Williams et al. (1990). These markers use single arbitrary primers, usually ten-base oligomers of varying GC content, included in a PCR mixture that is amplified in a thermocycler (Jones et al. 1997). A low temperature is used to allow the primer to anneal to multiple locations in the DNA (Vos et al. 1995). Each product is derived from a region of the genome that contains two short segments in inverted orientation on opposite DNA strands that are complementary to the 5' and 3' strands of the primer and sufficiently close together for amplification to work. Amplification products are separated on agarose gels and stained with ethidium bromide, then visualized under ultraviolet light. The brightest bands obtained with RAPDs are reproducible across laboratories when protocols are standardized and strictly adhered to, but fainter bands are more problematic. The final results may be affected by type of Taq polymerase and thermocycler used. RAPDs are dominant markers (Jones et al. 1997; Lorz and Wenzel 2005). RAPDs have been criticized for lack of reproducibility and because bands of similar molecular weight from different genotypes may not possess the same DNA sequence (Roberds et al. 1997), however in common bean, they have been used quite successfully.

A more robust marker is the AFLP based on selective PCR amplification of the restriction fragments from a total double-digest of the genomic DNA. The DNA is cut with two restriction enzymes and double-stranded adapters are ligated to the ends of

the enzyme created DNA fragments generating the template DNA. The adapter's sequence and adjacent restriction site serve as primer binding sites for the amplification of the restriction fragments. Selective nucleotides are included at the primer 3' end, which can only prime DNA synthesis from the restriction sites. Only restriction fragments that have the matching flanking nucleotides to the selective nucleotides are amplified (Vos et al. 1995; Lorz and Wenzel 2005).

Two restriction enzymes, a rare cutter and a frequent cutter, are used to create the restriction fragments. The frequent cutter generates small DNA fragments that amplify well and are of the size range for separation on gels. The use of a rare cutter reduces the number of fragments because only the fragments cut by both enzymes are amplified. Using the two restriction enzymes allows labeling one strand of the double stranded PCR products, preventing 'doublets' on the gel caused by the separate strands having unequal mobility. The two enzyme system generates large numbers of bands using only a few primers in various combinations (Vos et al. 1995).

With complex genomes, a pre-selective PCR reaction is used. This step ligates a single nucleotide to the fragment and is used as the template in the next PCR step. The AFLP selective primers consist of three parts, a core sequence, an enzyme specific sequence and a selective extension. The enzyme specific sequence varies depending upon the cutters used. The usual selective extensions are eight base pairs for EcoRI and eight for the MseI, and when used in combination give the option of 64 different primer pairs. The fragments are separated on a sequencing gel and can be

visualized using radioactivity, silver staining, or fluorescent labeling (Vos et al. 1995; Jones et al. 1997; Lorz and Wenzel 2005).

AFLPs are dominant markers and are very reproducible when the same protocol is used across labs. AFLPs have the ability to generate many markers, and this feature allows saturation of an existing linkage map (Vos et al. 1995; Jones et al. 1997; Arcade et al. 2000; Hayashi et al. 2005).

Microsatellites or SSRs are loci consisting of variable number repeats that are highly mutable and present at many sites in a genome. Primers are designed to the unique flanking sequences around the repeats. Primers usually amplify a single locus which is often multi-allelic due to the high mutation rate of the SSR region. Alleles may differ by a single base pair to many base pairs in length. Sequencing gels are required to detect small size differences in SSRs and are highly reproducible between laboratories. The accuracy of size estimation is influenced by the amount of stutter - a phenomenon that develops during PCR amplification where fragments are produced that are shorter and longer than the target fragment (Hongtrakul et al. 1998), the choice of the band selected as the allele, and the distance of the allele from the sequence that is used as the standard. Methods used to visualize the bands, silver staining or electropherograms, have some effect on the size of the fragment and may vary by as much as two base pairs, but the relative fragment sizes are consistent throughout the different methods (Jones et al. 1997).

These molecular markers discussed above are mostly phenotypically neutral, with alternate alleles causing no obvious changes in the phenotype of the organism. This

provides an unbiased way to estimate the phenotypic effect of polygenes without interference by the marker locus (Tanksley 1993).

The molecular linkage map

A linkage map is an abstract depiction of chromosomal loci created by using the percent chromosome recombination as a quantitative index of the linear distance between two markers or genes. Each linkage group is a group of genes or markers known to be linked, and correspond to a physical chromosome (Griffiths et al. 1996). Quantitative traits are thought to be under the control of polygenes or several genes with small effects. The phenotypes of quantitative traits are characterized by continuous variation (Kang 2002; Irzykowska and Wolko 2004). These can be located on linkage maps by association with individual marker genes and are given the name quantitative trait locus or loci (QTL) (Tanksley 1993).

Many of the more important agronomic traits are controlled by quantitative trait loci (Li et al. 2005). In the past, although quantitative genetics had made many important contributions to basic genetics and to animal and plant breeding, the inability to describe, study and ultimately clone individual genes affecting the quantitative traits had delayed the study of natural variation at loci for which macromutations did not exist (Tanksley 1993). The first step of QTL analysis is development of molecular markers, then creating the population with which to build a linkage map characterizing the population for the quantitative trait and finally analyzing the QTLs. Single marker analysis and interval mapping are performed to

identify the location of each QTL (Coffman et al. 2003; Li et al. 2005). The basis of interval mapping is that sets of linked markers are analyzed simultaneously with respect to their effects on quantitative traits (Tanksley 1993). By using linked markers for analysis, this linkage allows compensation for recombination between the markers and the QTL and provides an unbiased estimate of the QTL effect on the trait. The greatest benefit of interval mapping is that it makes possible the use of linked markers that are over 20cM apart, where it would be expected to have a high amount of crossovers between the markers and the QTL. When linked markers are closer together interval mapping gives nearly identical results to single marker analysis, but for distances greater than 35cM interval mapping becomes inefficient in detecting QTLs (Tanksley 1993).

In organisms, other than haploids, the alleles at a genetic locus can interact in several ways to produce the phenotype of the individual (Tanksley 1993). These interactions of gene loci and quantitative traits (termed gene action) are tied to the magnitude of the effects of the different allelic substitutions, the degree of dominance of alleles at each locus and the amount of epistasis among the loci (Griffiths et al. 1996). In classical genetics, alleles are normally dominant, recessive, co-dominant, incompletely dominant or overdominant, but natural systems encompass these categories and more. Because of this situation quantitative geneticists have developed guidelines to describe continuous gene action (Tanksley 1993).

Genetic mapping of white mold resistance in common bean

In the past, only limited levels of resistance to white mold that was quantitatively inherited with low to moderate heritability had been found in common bean, *P. vulgaris*. Miklas et al. (1999) and Gilmore et al. (2002) identified *P. vulgaris* accessions that had moderately high to high levels of resistance, but even these accessions were much lower than the levels of resistance found in *P. coccineus* (Miklas et al. 1999; Gilmore et al. 2002).

Molecular mapping and genetic analysis of beans have increased our knowledge and our ability to use that knowledge in many areas. White mold resistance QTL from five common bean mapping populations map to eight linkage groups. Some QTL linked to white mold resistance consistently appear in more than one bean population (Table 1.1).

Table 1.1 Mapped resistance to white mold in *Phaseolus vulgaris.*

Population	Bean Type	Linkage Group[y]	R^2 (%)[z]	Test Type/Trait	Reference
Bunsi /Newport	Small white	B2	12	Field	(Kolkman and Kelly 2003)
		B7	17	Field	
		B7	16	Oxalate resistance	
Bunsi/Raven	Small white	B2	9-10	Field	(Ender and Kelly 2005)
		B5	11	Field	
		B7b	14-15	Field	
		B8	9	Field	
A55/G122	Cranberry	B1	18	Field	(Miklas et al. 2001)
		B1	34	Canopy porosity	
		B7	38	Straw Test	
		B7	26	Field	
PC50 /XAN-159	Red mottled	B4a	5	Greenhouse	(Park et al. 2001)
		B7	5-9	Greenhouse	
		B7	16	Field	
		B7	10	Plant height	
		B8	9	Field	
		B8	11	Canopy porosity	
		B8	15	Plant height	
		B8	12-24	Greenhouse	
		B5	11	Greenhouse	
		B2	7	Greenhouse	
Benton/ NY-6020-4	Snap	B6	12	Straw Test	(Miklas and Delorme 2003)
		B6	13	Field	
		B8	38	Straw Test	
		B8	26	Field	
Tacana/ PI318695	Black	B9	?	Straw Test	(Terpstra and Kelly 2006)
		LG A	17-47	Field	
CO72548/ G122	Pinto /cranbery	B6a	19	Straw Test	(Maxwell et al. 2006)
		B2	18	Straw Test	

Table 1.1 (Continued)

Population	Bean Type	Linkage Group[y]	R^2 (%)[z]	Test Type/Trait	Reference
		B7	16	Straw Test	
		B9	9	Straw Test	
Bunsi/navy (Aztec/ ND88-106-04)	Pinto/navy	B2	9-25	Field/Stay green trait	(Miklas et al. 2007)
		B3	6-16	Canopy porosity	

[z]Percent phenotypic variation explained by QTL. [y]LG = linkage group.

Miklas et al. (2001) located four QTL on two linkage groups of a map of G122/A55, with both of the agronomic traits on linkage group B1. The QTL on B7 explained 38% of the straw test and 26% of the field test phenotypic variance. But they noted that both of the parents expressed field resistance and this was related to avoidance conferred by the type II growth habit of A55, the susceptible parent. The traits related to field resistance on B1 were canopy porosity and plant height, which may be related to the location of fin (the determinancy/indeterminancy locus) because the resistant parent was determinant, whereas the indeterminant parent was susceptible (Miklas et al. 2001).

Miklas and Delorme (2003) identified four QTL, from the snap bean NY6020-4 on B6 and B8 related to white mold resistance. The two QTL for the straw test were in the same region as the QTL for the field disease score. The percent variance explained was higher for the field results than the straw test, but both were highly significant (Miklas and Delorme 2003).

Park et al. (2001) used RAPDs to map a PC-50 (resistant) x XAN 159 (susceptible) population, and found nine QTL affecting partial physiological

resistance. Composite interval mapping presented strong evidence for QTL on linkage groups on 4a, 7 and 8, but evidence was weaker for the other six. They found that three of the most significant regions accounted for 39% of the phenotypic variation (Park et al. 2001).

Kolkman and Kelly (2003) used Bunsi as the resistant parent to find QTL that were linked to resistance and agronomic traits that could influence white mold severity. Both physiological resistance and avoidance mechanisms were located on B7, suggesting linkage or pleiotropy. Interestingly, the physiological traits that influenced the field resistance QTL on B2 were derived from the susceptible parent (Kolkman and Kelly 2003). Ender and Kelly (2005) developed 98 F_4 recombinant inbred lines that had Bunsi as the white mold resistance donor. They found two QTL on B2, one on B5, one on B8 and two on B7 all relating to white mold resistance. The authors felt that the QTL on B7 was different than the QTL found in G122 by Miklas et al. (2001) and in PC-50 by Park et al. (2001). The second QTL on B7 was not verified by composite interval mapping (Ender et al. 2003; Ender and Kelly 2005).

Terpstra and Kelly (2006) developed and tested a black x wild bean population for white mold resistance. While the population was not specifically created to study white mold resistance, both parents had moderate levels of resistance. They found a QTL related to straw test resistance on B9, and another QTL related to field resistance that was located on an unlinked fragment. The latter QTL was felt to be important because it explained 17% and 47% of phenotypic variance in two different seasons (Terpstra and Kelly 2006).

Maxwell et al. (2006) using a population with G122 as the resistant parent found four QTL with G122 as their source. The QTL were on linkage groups B2, B6a, B7 and B9, but these QTL only explained moderate levels of phenotypic variance with moderate LOD scores (highest was 3.83). The B7 QTL showed a significant relationship in both field and straw tests, but had a lower percent phenotypic variance than that found by Miklas et al. (2001).

Miklas et al. (2007) found two QTL for resistance to white mold using a pinto (Bunsi) X navy bean (Aztec/ND88-106-04) cross. The QTL for partial resistance to white mold was located on linkage group B2 and accounted for 24.7% of the phenotypic variation in 2001 and 9.0% variation in 2002. The other QTL was placed on linkage group B3 and in one location in 2001 accounted for 5.3%, but at their other location this QTL accounted for 15.7% of the phenotypic variation. Besides physiological resistance mechanisms, disease avoidance was probably responsible for this QTL (Miklas et al. 2007).

The most significant QTL are on B7 from G122, B8 from NY-6020-4, and B2 from Bunsi. The phenotypic variance explained for G122 on B7 is 38% and 16% for the two different populations, measured with the straw test. This agrees with the observed field variance of 26%. The fact that the G122 QTL was observed in two populations provides validation of this QTL, although the authors felt these QTL may be dissimilar. Miklas (2006) introgressed the B7 QTL from G122 using marker-assisted selection (MAS). The introgression was successful at transferring the white

mold resistance, but found linkage drag for reduced yield. He is also attempting to increase resistance by pyramiding the NY-6020-4 B8 QTL (Miklas 2006).

As shown by the discussion above and in Table 1.1, white mold resistance is predominantly inherited quantitatively. Individual QTL generally account for low percent phenotypic variance. To achieve high levels of resistance, several QTL must be combined. While more than eight putative QTL have been identified in common bean, there are probably many more to be found in the cultivated species and its relatives. In soybean for example, more than 30 QTL for Sclerotinia stem rot resistance have been identified (G. Graef, personal communication). Because of the need to accumulate many loci with small individual effect into a common background, it will be necessary to use techniques that allow simultaneous and efficient transfer of markers. This will most easily be accomplished with a high throughput, low cost system that could screen seedlings for several markers at once.

White mold, with its overwhelmingly effective use of oxalate, has been decimating bean fields and reducing bean yields for many years. Recent interest in the mechanisms of pathogenesis of *S. sclerotiorum* and possible factors involved in resistance to the pathogen has begun to produce insight into how to develop genetic control mechanisms for this disease. The resistance found in *P. coccineus* as characterized with molecular markers may assist in implementing a non-chemical solution to this devastating disease.

In the present work, I describe the screening of the *P. coccineus* germplasm collection held by the USDA National Plant Germplasm System to identify accessions

with the highest levels of resistance. I also created the first *P. coccineus* linkage map, and on it I placed novel QTL for white mold resistance.

CHAPTER 2. SCREENING THE *PHASEOLUS COCCINEUS* PLANT INTRODUCTION COLLECTION FOR RESISTANCE TO *SCLEROTINIA SCLEROTIORUM*

Introduction

The common bean (*Phaseolus vulgaris* L.) is a warm season annual that grows in subtropical or temperate areas, and at higher elevations or during the cool dry season in tropical areas (Bassett 1986; Gepts 1988; Hall 1994). Beans are a nutritious and cheap source of approximately 22% protein. Beans supply protein and carbohydrates to many people of the world that do not have adequate food or use plant proteins as their major source of protein (Gepts 1988; Young and Pellett 1994).

White mold caused by *Sclerotinia sclerotiorum* (Lib) de Bary causes widespread loss of yield and quality in both snap and dry beans. In some extreme instances, there can be a one hundred percent yield loss under irrigated situations (Hall 1994). In green beans when the pod infection incidence exceeds 3 - 5%, the processor will reject the field (Stivers 2000). Foliar applications of fungicides applied prophylactically can control white mold. Timing is critical, and two applications may be needed. Fungicides currently available are expensive and may eliminate any net profit realized by the grower when their crop is sold to the processor. No fungicide currently exists that effectively controls white mold after the disease is widespread in the field (Hall 1994; du Toit et al. 2006). The environmental and human health impacts are concerns

as well. In 2005, Ronalin, the most effective fungicide registered for white mold control was removed from the market by EPA because of health and environmental concerns (Pscheidt 2006).

Sclerotinia sclerotiorum is a ubiquitous necrotrophic fungus that has been reported in many countries on six continents (Purdy 1979). It has the ability to infect more than 400 plant species, including one member of the Polypodiaceae family, four Gymnosperms of the family Pinaceae, almost 30 monocots and the rest usually being herbaceous plants of the subclass Dicotyledoneae (Boland and Hall 1994). It grows at temperatures from 4^{o}C to over 30^{o}C, although 20^{o}-25^{o}C is considered optimum (Hall 1994). *S. sclerotiorum* is favored by moisture from rainfall or irrigation (Purdy 1979).

This organism had become a successful pathogen by employing a combination of oxalic acid and proteolytic enzymes. Oxalic acid is released into living tissue ahead of mycelial growth. It signals stomata to open, causing the plant to wilt and allowing secondary penetration by mycelia (Guimaraes and Stotz 2004). It depresses cellular pH, which disrupts pathogen defenses and kills plant tissues. The lower pH appropriates Ca^{2+} from cell walls and creates an optimal environment for polygalacturonase activity to break down cell walls (Bateman and Beer 1965). Oxalate can suppress polyphenol oxidase (Kurian and Stelzig 1979; Sato 1980a; Sato 1980b; Marciano et al. 1983; Tu 1989; Ferrar and Walker 1993), related phytoalexins (Favaron et al. 1988), and the oxidative burst (Cessna et al. 2000).

P. coccineus is an important source of resistance to many pathogens and a few insects. Baggett and Frazier (1959) found resistance to *Pseudomonas phaseolicola*

(halo blight), *Uromyces phaseoli* (bean rust), *Colletotrichum lindemuthianum* (anthracnose), Bean Common Mosaic Virus, and Bean Yellow Mosaic Virus (Gepts 1988). Coyne and Schuster (1980) found *P. coccineus* types that were resistant to *Xanthomonas axonopodis* pv. *phaseoli* (common bacterial blight) and to *Corynebacterium flaccumfaciens* (bacterial wilt) (Gepts 1988). *P. coccineus* and *P. polyanthus* (*P. dumosus*) have been found to have several sources of resistance to angular leaf spot, *Phaeoisariopsis griseola* (Mahunku et al. 2003). Resistance to bean golden yellow mosaic virus, (BGYMV) has been found in *P. coccineus* (Osorno et al. 2003). *P. coccineus* has been tested with white mold mycelium and ascospores and has been found to be consistently more resistant to *S. sclerotiorum* (white mold) than *P. vulgaris* (Adams et al. 1973; Abawi et al. 1978; Gilmore and Myers 2000; Gilmore et al. 2002; Schwartz et al. 2006). Resistant accessions exhibit slower mycelial growth and some accessions may show phytoalexin accumulation and/or node enlargement below the infection site (Gilmore, personal observation). While Chipps et al. (2005) implicated oxalic acid tolerance as a resistance mechanism in *P. coccineus* (Chipps et al. 2005), other mechanisms may be involved (Gilmore and Myers 2000).

Genetic resistance in common bean is limited and often leaves fields at risk of total infection (Hall 1994). Moderately high resistance is beginning to be found in *P. vulgaris* and used in breeding. Lines such as G122 (Miklas et al. 2001), PC 50 (Park et al. 2001), and NY6040-4 (Miklas and Delorme 2003) are considered some of the most resistant cultivars available. The resistance of these lines is quantitatively

inherited, and QTL have been located. Miklas (2006) using two moderately resistant lines with marker assisted selection white mold resistance was increased. He found that due to linkage drag that yield reduced (Miklas 2006). However, even the most resistant *P. vulgaris* line is not as resistant as certain accessions of *P. coccineus*.

Another species of interest is *P. dumosus*. Formerly known as *P. polyanthus* or *P. coccineus* subsp. *darwininus*, it represents the fifth domesticate of the genus *Phaseolus* (Freytag and Debouck 2002). In many respects, it closely resembles and is easily confused with, *P. coccineus*, but has epigeal emergence, fibrous roots, and white or purple flowers (never red). It shares many traits and has a closer phylogenetic relationship to *P. vulgaris* than *P. coccineus* has with *P. vulgaris*. Its resistance to various diseases and insects has not been well studied. It is found in similar habitats to that of *P. coccineus* and may have undergone similar selection pressures for diseases and insects.

Traits segregating between *P. coccineus* and *P. vulgaris* may be simply inherited (e.g., Bean Yellow Mosaic Virus, BYMV) (Baggett 1956) or quantitatively inherited [e.g. stigma position (Smartt 1970), cotyledon position (Wall and York 1957; Smartt 1970) or fusarium root rot resistance (Hassan et al. 1971)]. Resistance to *Sclerotinia* in *P. coccineus* has been reported to be controlled by a single dominant gene (Abawi et al. 1978; Schwartz et al. 2004; Schwartz et al. 2006) or by quantitative trait loci (Gilmore and Myers 2004). Lyons et al. (1987) reported using recurrent selection to successfully incorporate white mold resistance from *P. coccineus* into *P. vulgaris* where resistance was treated as a quantitative trait (Lyons et al. 1987). The rather

scanty knowledge that higher levels of resistance to white mold were found in *P. coccineus* prompted our group to examine the entire collection of *P. coccineus* available from the USDA Western Region National Plant Germplasm Repository for resistance to white mold. Until our work the *P. coccineus* collection had not previously been examined for resistance to this pathogen.

Methods and materials

Source of plant materials

In 1999, eighty-one accessions of *P. coccineus* were requested and tested with the pathogen *S. sclerotiorum*, and in 2001 the rest of the 478 accessions were obtained from the U.S. Department of Agriculture National Plant Germplasm System Plant Introduction Collection maintained at Pullman, WA. Appendix 1.1. has the available passport data for accessions. The eighty-one accessions tested in 1999 included six accessions labeled as *P. coccineus* subspecies darwininus, and four accessions labeled *P. coccineus* subspecies *coccineus* (Table 2.1). In 2001 forty-four of the *P. coccineus*, four accessions of the *P. coccineus* subspecies darwininus, and two *P. coccineus* subspecies *coccineus* were retested. Two hundred eighty-three accessions were examined in 2001, including seven accessions labeled *P. coccineus* subspecies darwininus and fourteen accessions labeled *P. coccineus* subspecies *coccineus*.

Table 2. 1 Number of *Phaseolus coccineus* accessions tested or retested for resistance to white mold**.**

Subspecies	Total Requested	Tested or retested 1999	Tested or retested 2001	Not Avail.
P. coccineus	411	72	264 (44)[z]	75
P. coccineus subsp. *darwininus*	27	6	14 (4)	7
P. coccineus subsp. *coccineus*	22	3	5 (2)	14
P. coccineus subsp. *obvallatus*	2	0	0	2
P. coccineus subsp. *formosus*	16	0	0	16
Total	478	81	283 (50)	114

[z]Number of accessions tested in1999 and retested in 2001 shown in ().

Figure 2. 1. Seeds of the three *Phaseolus* species found in accessions obtained from the USDA-NPGS germplasm *P. coccineus* collection. Top: *P. coccineus*, Middle: *P. dumosus*, and bottom *P. vulgaris* showing Andean (left) and Mesoamerican (right) types.

Seeds of some accessions were uniform in appearance while others showed mixtures of seed testa colors and patterns and in some cases, mixtures of *Phaseolus* species. The three *Phaseolus* species found were *P. coccineus* (including subsp

coccineus), *P. dumosus* (formerly *P. polyanthus* or *P. coccineus* subsp. *darwininus*), and *P. vulgaris* (Fig 2.1). Interspecies mixtures were most commonly *P. coccineus* with *P. dumosus* or *P. coccineus* with *P. vulgaris*. Occasionally an accession would be a mixture of all three species. Species were identified by seed size, shape, pattern, and hilum characteristics (Fig 2.1). *P. coccineus* seed were generally the largest, although some were similar in size to *P. dumosus*. *P. dumosus* seeds were typically uniform in color and had a large oval hilum often with a split membrane. *P. vulgaris* seeds were usually smallest. Seeds sorted by color and by species were tested separately. Only 30 seeds per accession were received, which after sorting produced some classes with only limited numbers for testing, and causing unequal numbers of seeds per accession type. In 2001 prior to testing, the seeds were scanned to produce a visual record of the accession.

Fungal maintenance

In October, 1998 *S. sclerotiorum* sclerotia were collected from the green bean white mold nursery at the Oregon State University Vegetable Research Farm. The sclerotia were stored at 4.0^{o}C for the duration of the project. To prepare each field collected sclerotium for culture, sclerotia were placed into a 20% bleach solution for 20 min, rinsed with distilled water, placed in 95% ethanol for five min, removed and immediately flamed. In a laminar hood, each surfaced sterilized sclerotium was plated onto sterile potato dextrose agar, seven mm thick, in a 15 mm x 100mm Petri dish. Difco potato dextrose agar, 3.9% solution, was made by adding thirty-nine grams of dry media to one liter of water, stirring and then autoclaving the solution at 121^{o}C for

15 min. The plates were set on a laboratory shelf with daytime temperature of approximately 21°C with overhead fluorescent lighting. The mycelia were allowed to grow until new sclerotia formed on the outer edges of the plate. These primary plates produced enough sclerotia to inoculate 30 PDA plates which were then used for the white mold screening. These secondary sclerotia were placed on a PDA plate and allowed to grow for five d.

Bean plant growth

The planting mix was Sunshine brand SB-40 professional growing mix and a dry volume of 10 ml of Scotts brand Osmocote fertilizer was added. The minimum daytime temperature was 21°C and minimum nighttime temperature was 16°C. The pots were watered initially when planted, but not again until the first true leaves emerged from the soil. The maturing plants were then watered on an as needed schedule.

Seeds of each accession were planted in two 3.8 liter pots, each pot with approximately eight seeds. Twenty-two accessions required three pots each due to the extreme variability of the accessions. Seeds were examined and then categorized into different suspected species. The average number of seeds tested per accession was fourteen. At two weeks after planting, emergence was recorded as hypogeal (typical of *P. coccineus*, epigeal (typical of *P. vulgaris* and *P. dumosus*, or intermediate (atypically found with *P. coccineus*).

Inoculations

The conventional straw test procedure was used (Petzoldt and Dickson 1996). A straw segment three - four cm long and stapled at one end was used to extract a plug of agar with the growing edge of the mycelium. The plant's growing terminal was removed leaving ten centimeters of stem above the third node of the plant. The mycelial plug and straw were placed on this trimmed tip and the disease was allowed to progress. The scale of the Petzoldt and Dickson (1996) straw test result scale was modified due to the higher resistance of *P. coccineus* (Table 2.2).

Table 2. 2 Modified straw test scale used to rate disease progression in test of *P. coccineus* USDA Plant Introduction accessions (oringinal scale by Petzoldt and Dickson (1996).

Score	Lesion Size
1	1 to 3 cm.
2	Approximately 4 cm.
3	Lesion past the end of the straw, but not to the first node.
4	Lesion at the first node.
5	Lesion past the first node, but not to the second node.
6	Lesion to the second node.
7	Lesion past the second node, but not to the third node.
8	Lesion to the third node.
9	Lesion past the third node or the plant has died.

Screening for Sclerotina resistance

Seedlings were inoculated 23 to 25 d after planting and evaluated for disease eight d later. Although the standard time for inoculation is 28 d after planting, *P. coccineus*

has such a vigorous indeterminate plant with long internodes, inoculation time was earlier than with *P. vulgaris*. Plants that appeared resistant at the first reading at eight d were re-inoculated after thirteen to fifteen d, depending on the plant's growth, and the new lesions were again read eight d later. The controls OR 91G, a susceptible bush blue lake snap bean, and M0162, a partially resistant yellow-brown seeded dry bean, were inoculated at 32 d, which was better synchronized with the weekly planting schedule. Because the control lines had determinate habit and short internodes, they required extra time to obtain sufficient growth for testing and so were planted earlier.

Most of the accessions were screened during the high light, warm temperature and low humidity months of summer. These conditions were less favorable for the pathogen, but more favorable for the host. Consequently, our susceptible control has a lower rating (less disease) than normally observed during the winter months. An exception to the uniformly warm conditions found through much of this screening occurred on July 4th and 5th, 2000 in Corvallis, OR the weather was cool (19.4^{o}C day and 8.3 ^{o}C night) and precipatation of approximately 3.75 mm. The rest of the month averaged normal daytime highs around 26.8 ^{o}C and night time lows of 10.2 ^{o}C.

Statistical Analysis

Averages and standard deviations were calculated using Microsoft® Office Excel 2003 SP2, Microsoft Corporation, USA.

An augmented design (Federer et al. 2001) was used to analyze tests performed over time. In this procedure, means of experimental entries are adjusted based on the means of checks common to each individual trial. PROC GLM of the statistical

program SAS®9.1.3., SAS Institute Inc., Cary, NC 2004 was used to analyze data, calculate least square (LS) means and test for significance of the experimental lines compared to the check lines.

SAS Model Statement:

```
PROC GLM [DATA=WORK.file];
  CLASS DATE X C;
  MODEL WM_SCORE = DATE C X(C);
  RANDOM DATE/TEST;
  LSMEANS C X(C)/PDIFF;
```

Two columns of dummy variables were created: X with sequential numeric values for experimental accessions, while checks are held at zero, and C, with unique numeric values for checks while experimental accessions are held to zero. The model statement partitions by date, check and experimental accession nested within checks. A mixed model was used where dates were random and accessions and checks were fixed effects. The PDIFF function was used to conduct multi-way t-tests to determine whether significant differences existed among checks and accessions.

Results

Considerable genetic variation was observed in the *P. coccineus* plant introduction collection. Not only is *P. coccineus* a highly variable species, but other species, most notably *P. dumosus* and *P. vulgaris* were also found. In some cases, the accession appears to have been misclassified, whereas in other cases, the accession was a mixture of species. Mixtures most likely happened during the collection process as it has been a common practice by plant collectors to take a “market sample” when

visiting a village market. Mixtures may also be deliberately cultivated in farmers' fields, or the harvest may contain a mixture. When increased by the germplasm curator, it has been standard procedure to maintain the visible components in a mixture in roughly the same proportion. Nearly all accessions showed characteristics of the cultivated type, and we do not believe that we evaluated any wild accessions. A few accessions were of the genus *Phaseolus*, but they were not of the three predominant species in this survey. These accessions failed to flower, so lacked reproductive structures that would have aided accurate identification.

Table 2.3 *P. coccineus* accessions from the USDA National Plant Germplasm System Plant Introduction Collection tested for white mold resistance in 1999. Means are based on 3 to 13 plants per accession.

Plant Introduction Number	Cotyledon position at emergence[y]	Straw Test Score[z]		Plants Tested
Phaseolus coccineus		Mean	S.D.	No.
PI 150932	hypogeal	4.3	1.0	9
PI 175858	epigeal	4.2	1.0	10
PI 176675	hypogeal	3.5	0.9	11
PI 181790	hypogeal	5.2	1.1	11
PI 183412	epigeal	5.2	1.8	5
PI 189023	hypogeal	3.2	1.4	9
PI 194575	epigeal	4.5	0.9	11
PI 195336	epigeal	3.3	1.5	3
PI 195363	epigeal	4.1	1.1	9
PI 195388	epigeal	3.8	1.0	12
PI 201290	epigeal	4.0	1.2	9
PI 201299	hypogeal	4.3	1.1	12
PI 201305	hypogeal	4.7	0.8	6
PI 201312	hypogeal	3.7	1.0	13
PI 201352	hypogeal	4.2	1.0	10
PI 203931	mixed	3.8	1.2	10
PI 209663	hypogeal	4.1	0.9	10

Table 2.3. (Continued)

Plant Introduction Number	Cotyledon position at emergence[y]	Straw Test Score[z]		Seeds Tested
		Mean	S.D.	No.
PI 223803	hypogeal	3.9	1.2	11
PI 226594	epigeal	3.9	1.3	11
PI 229618	hypogeal	3.8	1.2	9
PI 247303	hypogeal	4.2	1.0	10
PI 255573	hypogeal	3.1	0.7	10
PI 255956	hypogeal	3.1	1.4	10
PI 255957	hypogeal	4.0	1.7	11
PI 257221	epigeal	4.5	0.8	11
PI 257222	epigeal	4.8	2.0	8
PI 273448	hypogeal	4.0	1.0	9
PI 273666	hypogeal	3.4	0.5	9
PI 273667	hypogeal	4.1	1.0	10
PI 307664	hypogeal	3.9	1.8	8
PI 307778	epigeal	3.1	0.9	7
PI 311186	epigeal	3.6	1.2	12
PI 311196	epigeal	3.4	1.6	9
PI 311202	hypogeal	3.3	1.2	8
PI 311210	hypogeal	2.8	1.5	8
PI 311218	hypogeal	2.8	0.7	8
PI 311879	epigeal	3.8	1.2	8
PI 311953	hypogeal	2.3	1.3	9
PI 312035	hypogeal	4.0	0.9	8
PI 313221	hypogeal	2.0	1.3	9
PI 313500	hypogeal	3.0	1.2	10
PI 317550	epigeal	3.6	1.4	8
PI 317571	epigeal	3.4	1.5	10
PI 321088	hypogeal	2.8	0.7	9
PI 325584	hypogeal	3.9	1.1	9
PI 325596	hypogeal	3.9	1.2	12
PI 325604	epigeal	3.4	1.6	10
PI 355423	epigeal	4.2	1.0	9
PI 358087	epigeal	4.1	1.0	8
PI 361302	hypogeal	2.6	1.2	11
PI 361328	hypogeal	3.5	1.2	13
PI 361361	hypogeal	2.4	1.2	10
PI 361372	hypogeal	2.2	0.8	10

Table 2.3. (Continued)

Plant Introduction Number	Cotyledon position at emergence[y]	Straw Test Score[z]		Seeds Tested
		Mean	S.D.	No.
PI 361451	hypogeal	3.3	1.0	9
PI 361539	hypogeal	1.8	1.6	7
PI 370507	hypogeal	3.3	1.1	12
PI 390414	epigeal	3.7	1.1	9
PI 406936	hypogeal	3.6	1.4	13
PI 406938	hypogeal	3.2	0.9	13
PI 407387	hypogeal	3.6	1.4	13
PI 417592	hypogeal	5.5	1.0	4
PI 417605	hypogeal	4.3	0.8	6
PI 420322	hypogeal	3.1	0.8	13
PI 432581	hypogeal	4.0	0.9	10
PI 432583	hypogeal	3.7	0.9	10
PI 433253	hypogeal	3.2	1.2	6
PI 433927	epigeal	7.4	0.8	11
PI 438910	mixed	4.1	1.2	13
PI 442540	hypogeal	2.2	1.0	10
PI 476704	epigeal	5.3	1.1	11
PI 549449	hypogeal	2.6	1.4	10
PI 583553	hypogeal	1.4	0.7	13
Phaseolus coccineus subsp. darwininus[x]				
PI 201347	epigeal	3.6	0.8	10
PI 209502	epigeal	4.6	1.7	9
PI 311179	epigeal	3.6	1.1	13
PI 311201	epigeal	3.7	0.8	7
PI 311216	epigeal	4.5	0.8	6
PI 313417	epigeal	2.3	0.9	9
Phaseolus coccineus subs*P. coccineus*				
PI 535278	hypogeal	3.8	1.4	11
PI 535281	hypogeal	3.0	2.0	3
PI 535287	hypogeal	4.3	1.0	4

[z]Based on a scale of 1 – 9 where 1 is immune and 9 is dead. Accessions with a score of 4 or less were considered resistant. [y] *P. coccineus* has hypogeal emergence. [x] name changed to *P. dumosus*.

In 2001, a subset of forty-four accessions was retested for white mold resistance, along with additional accessions from the PI collection (Table 2.4). Not all accessions were retested in 2001 and retesting hinged on seed availability and if the accession had shown any resistance when first tested in 1999. Morphological characters evaluated in this material included root type in addition to cotyledon position. We also made a tentative assignment of species based on seed and initial morphological characteristics. Average scores were higher in the second test (mean scores of 3.3 in the first test versus 4.3 in the second test). The two tests show significant association but the regression coefficient was low ($R^2 = 0.10$*). Checks used in this test were M0162 and OR 91G with scores of 4.7 and 5.5, respectively.

Table 2. 4 *Phaseolus coccineus* Group 1 accessions retested in 2001 for white mold resistance.

Date Planted	PI Number	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
Phaseolus coccineus					Mean	SD[y]	No.
Oct.	176675	hypogeal		tuber	4.7	0.6	15
Oct.	189023	hypogeal		tuber	2.7	1.2	12
Oct.	195336	epigeal	*P.d.*	fibrous	5.4	1.2	15
Oct.	195388	epigeal	*P.d.*	fibrous	4.9	0.5	14
Oct.	201312	hypogeal		tuber	3.8	1.3	13
Oct.	203931	hypogeal		tuber	4.0	1.3	15
Oct.	223803	hypogeal		tuber	4.4	0.6	14
Oct.	226594	epigeal	*P.d.* & ?	fibrous	4.7	0.8	11
Oct.	229618	hypogeal		tuber	5.7	1.0	9
Oct.	255573	hypogeal		tuber	3.9	1.4	12
Oct.	255956	hypogeal		tuber	3.8	0.9	12
Oct.	273666	mixed		fibrous	4.2	1.1	14
Oct.	307664	hypogeal		mixed	3.8	1.4	14
Oct.	307778	epigeal	*P.l.*	fibrous	5.1	0.5	14
Oct.	311186	epigeal	*P.d.*	fibrous	5.0	0.4	16

Table 2.4 (Continued) Group 1 accessions retested in 2001.

Date Planted	PI Number	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
Oct.	311196	epigeal	*P.d.*	fibrous	4.6	1.3	9
Oct.	311202	mixed	*P.d.*	fibrous	5.3	1.3	11
Oct.	311210	hypogeal		tuber	3.2	1.4	13
Oct.	311218	hypogeal		mixed	4.2	1.4	15
Oct.	311879	hypogeal		tuber	3.5	1.4	11
Oct.	311953	hypogeal		mixed	4.6	0.6	14
Oct.	313221	hypogeal		fibrous	4.4	1.0	13
Oct.	313500	hypogeal		mixed	4.4	1.0	19
Oct.	317550	Epigeal	*P.d.*	fibrous	4.1	1.1	14
Oct.	317571	epigeal	*P.d.*	fibrous	4.5	1.2	16
Oct.	321088	mixed		tuber	4.6	0.5	8
Oct.	325584	hypogeal		mixed	4.6	0.9	14
Oct.	325596	mixed	*P.c.,P.v.*	mixed	4.4	1.1	16
Oct.	325604	epigeal		fibrous	5.3	0.9	16
Oct.	361302	hypogeal		tuber	3.0	0.6	12
Oct.	361328	hypogeal		mixed	3.8	0.9	12
Oct.	361361	hypogeal		tuber	3.2	0.4	13
Oct.	361372	hypogeal		fibrous	3.2	0.4	13
Oct.	361451	hypogeal		mixed	3.9	0.7	15
Oct.	361539	hypogeal		mixed	3.8	1.0	11
Oct.	370507	hypogeal		tuber	5.0	0.9	13
Oct.	390414	epigeal	*P.d.*	fibrous	5.6	0.5	15
Oct.	406936	hypogeal		fibrous	4.0	1.8	13
Oct.	406938	hypogeal		fibrous	3.5	1.0	15
Oct.	407387	hypogeal		tuber	3.9	1.0	10
Oct.	420322	hypogeal		tuber	3.7	1.0	6
Oct.	432583	hypogeal		tuber	3.6	0.7	14
Oct.	433253	hypogeal		tuber	3.3	1.4	15
Oct.	442540	hypogeal		tuber	4.8	0.5	16
Phaseolus coccineus subsp. *darwininus*[x]							
Oct.	201347	epigeal		fibrous	5.6	0.8	15
Oct.	311179	epigeal		fibrous	4.9	0.5	14
Oct.	311201	epigeal	*P.v.*	fibrous	5.3	0.7	17
Oct.	313417	hypogeal		mixed	3.1	1.0	22

Table 2.4 (Continued) Group 1 accessions retested in 2001.

Date Planted	PI Number	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
Phaseolus coccineus subs*P. coccineus*							
Oct.	535278	hypogeal		fibrous	4.6	1.3	5
Oct.	535281	hypogeal		fibrous	4.4	1.3	5

[z]: ? = species unknown, P.c. = *P. coccineus*, P.d. = *P. dumosus*, P.v. = *P. vulgaris*, P.l. = P.lunatus. A blank indicates that we agree with the species classification. [y]SD: Standard Deviation [x]*P. dumosus*.

Table 2.5 shows results for the 283 accessions tested for the first time in 2001. Straw tests were conducted over a five month period from May to October. Thus, testing was performed under conditions of moderate warmth and relatively high light intensity. Conditions were optimal for plant growth and temperatures were within the range for normal growth of the pathogen ($15^{o} – 28^{o}C$).

We observed cotyledon position at emergence, and whether the root system was tuberous or fibrous. These along with seed characteristics were important in determining species. We again noted deviations from species classification, with *P. coccineus* being misclassified as *P. vulgaris* (13 times) or more commonly, as *P. dumosus* (56 times). The most common multiple mix of species was *P. coccineus* with *P. dumosus* (14 times) followed by *P. coccineus* and *P. vulgaris* (6 times), *P. coccineus* with both *P. dumosus* and *P. vulgaris* (5 times) and finally, one *P. dumosus* with *P. vulgaris* mix. Some of the *P. dumosus* accessions were misclassified, with two being *P. coccineus – P. dumosus* mixes, and one each of *P. coccineus*, *P. vulgaris*, and

a three-species mix. When an accession was a composite of more than one species, the different species were evaluated separately.

The average straw test score was based on the white mold score rating of the plants sampled. For accessions of mixed species, scores were averaged across species. Because testing was done on different dates on different numbers of lines per accession, we report average straw test scores with standard deviation only to provide a sense of the variability in the data.

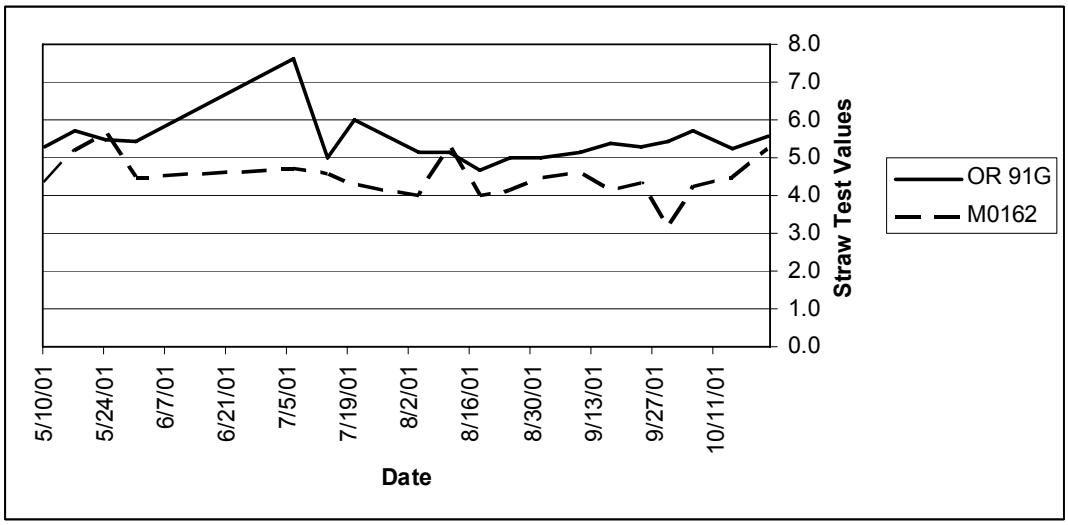


Figure 2. 2 Performance of checks, OR 91G and M0162, for white mold resistance in a test of the *P. coccineus* plant introduction collection performed over a period of five months.

The checks common to all tests (M0162 and OR 91G) varied in response from date to date, but in nearly every case, M0162 had a lower score than OR 91G, and both checks scored higher than most *P. coccineus* accessions. During the cooler temperatures of July 4 - 5th OR 91G exhibited significantly longer lesion development than during other periods of testing.

Table 2. 5 *Phaseolus coccineus* accessions (Group 2) tested for white mold resistance in 2001.

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
Phaseolus coccineus							
11 Aug	165421	hypogeal		tuber	3.4	1.0	14
11 Aug	165436	hypogeal		mixed	3.7	1.3	13
11 Aug	175829	mixed	*P.c., P.v.*	mixed	4.8	0.8	13
11 Aug	175855	hypogeal		tuber	4.0	0.7	14
11 Aug	175860	hypogeal		tuber	4.5	0.5	11
11 Aug	176672	hypogeal		tuber	4.6	0.5	13
11 Aug	176695	hypogeal		fibrous	3.5	1.1	13
11 Aug	183464	epigeal	*P.d.*	fibrous	4.9	0.7	12
6-Jul	190074	epigeal	*P.d.*	fibrous	4.5	0.6	22
6-Jul	193045	hypogeal		tuber	3.4	1.2	12
6-Jul	194585	epigeal	*P.d.*	fibrous	5.0	0.4	24
6-Jul	194586	epigeal	*P.d.*	fibrous	4.9	0.7	14
4-Aug	195337	epigeal	?	fibrous	4.9	0.3	9
20-Jul	195338	mixed	*P.c., P.d.*	mixed	4.1	1.0	15
20-Jul	195352	epigeal	*P.d.*	fibrous	4.6	0.5	11
20-Jul	195353	epigeal	*P.d.*	fibrous	4.5	0.7	14
6-Jul	195359	epigeal	*P.d.*	fibrous	4.7	0.6	15
6-Jul	195372	hypogeal		tuber	4.0	1.0	15
6-Jul	195381	epigeal	*P.d.*	fibrous	4.4	0.5	16
6-Jul	195389	epigeal	*P.d.*	fibrous	4.6	0.5	13
14-Jul	195395	epigeal	*P.d., P.v.*	fibrous	4.3	0.6	12
14-Jul	195399	epigeal	*P.d.*	fibrous	4.7	0.7	14
14-Jul	196413	epigeal	*P.v.*	fibrous	4.1	0.7	14
14-Jul	201295	hypogeal		mixed	3.9	1.3	20
14-Jul	201297	hypogeal		tuber	3.6	1.1	13
14-Jul	201300	hypogeal		mixed	4.0	1.2	14
14-Jul	201301	hypogeal		tuber	3.4	1.0	13
14-Jul	201304	hypogeal		mixed	3.0	0.9	21
11-Aug	201306	mixed	*P.c., P.d.*	fibrous	4.6	1.1	11
11-Aug	201309	hypogeal		mixed	3.9	1.1	15
11-Aug	201310	hypogeal		mixed	4.1	1.2	12

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
11-Aug	201320	hypogeal		mixed	3.7	1.1	15
14-Jul	201323	epigeal	*P.d.*	fibrous	4.8	0.4	13
14-Jul	201328	mixed		tuber	3.7	1.1	13
14-Jul	201335	epigeal	*P.d.*	fibrous	4.7	0.9	11
14-Jul	201336	hypogeal		tuber	4.1	0.7	12
28-Jul	201337	epigeal	*P.d.*	fibrous	4.6	0.8	15
28-Jul	201338	epigeal	*P.d.*	fibrous	5.2	0.8	11
28-Jul	201356	hypogeal		tuber	4.3	1.1	22
28-Jul	201366	hypogeal		tuber	3.8	1.2	13
20-Jul	201389	hypogeal		fibrous	3.9	1.4	14
20-Jul	201477	hypogeal		tuber	3.8	1.3	13
20-Jul	202129	epigeal	*P.d.*	fibrous	5.4	0.7	11
20-Jul	205360	hypogeal		tuber	4.5	0.9	12
11-Aug	209664	hypogeal		mixed	4.0	1.0	20
11-Aug	209665	hypogeal		tuber	4.3	1.1	12
14-Jul	209666	hypogeal		tuber	4.5	0.8	10
4-Aug	209667	hypogeal		mixed	4.3	1.1	12
4-Aug	209669	hypogeal		mixed	3.5	1.3	11
4-Aug	224711	hypogeal		tuber	4.1	1.7	12
4-Aug	224784	epigeal	*P.d.*	fibrous	5.0	0.0	11
4-Aug	273449	hypogeal		mixed	3.8	1.1	19
4-Aug	277802	hypogeal		tuber	4.7	0.8	11
4-Aug	282119	mixed		mixed	5.0	0.6	16
4-Aug	304749	hypogeal		tuber	4.4	1.0	12
4-Aug	307663	hypogeal		mixed	4.2	1.1	20
4-Aug	307665	hypogeal		tuber	5.5	1.4	12
4-Aug	309694	hypogeal		tuber	4.5	1.0	13
May[w]	309888	hypogeal		tuber	5.3	0.8	14
May[w]	309889	hypogeal		mixed	4.7	1.3	15
May[w]	311168	epigeal	*P.d.*	fibrous	5.2	0.6	12
May[w]	311176	mixed	*P.c., P.d.*	mixed	4.5	1.0	16
May[w]	311180	hypogeal		mixed	4.5	1.3	22
May[w]	311185	hypogeal		tuber	4.5	1.1	17
May[w]	311188	epigeal	*P.d.*	fibrous	4.7	0.8	14
May[w]	311194	mixed	*P.c., P.d., P.v.*	mixed	4.0	1.0	28

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
May[w]	311198	epigeal	*P.d.*	fibrous	4.6	0.7	18
May[w]	311199	epigeal	*P.d.*	fibrous	4.9	0.4	14
May[w]	311203	epigeal	*P.d.*	fibrous	5.0	0.0	14
May[w]	311204	mixed	*P.c., P.d.*	mixed	4.7	0.9	17
May[w]	311207	epigeal	*P.d.*	fibrous	5.1	0.3	15
May[w]	311209	mixed	*P.c., P.d.*	mixed	4.9	0.3	15
May[w]	311211	mixed	*P.c., P.d.*	mixed	5.5	1.7	20
May[w]	311212	epigeal	*P.d.*	fibrous	4.7	1.0	13
May[w]	311214	hypogeal		tuber	3.7	1.4	14
4-Aug	311217	epigeal	*P.d.*	fibrous	4.3	1.1	10
4-Aug	311219	epigeal	*P.d.*	fibrous	4.8	0.4	11
4-Aug	311220	epigeal	*P.v.*	fibrous	4.4	0.6	14
4-Aug	311819	hypogeal		mixed	3.7	0.9	13
May[w]	311826	hypogeal		tuber	5.0	1.0	16
May[w]	311827	hypogeal		mixed	4.9	1.1	18
May[w]	311833	epigeal	*P.d.*	fibrous	4.8	0.6	12
May[w]	311850	epigeal	*P.d.*	fibrous	4.6	0.5	13
May[w]	311855	epigeal	*P.d.*	fibrous	5.0	0.4	13
May[w]	311859	epigeal	*P.v.*	fibrous	3.7	0.9	15
May[w]	311880	hypogeal		tuber	4.9	1.2	14
May[w]	311882	hypogeal		tuber	4.0	1.2	18
20-Jul	311920	hypogeal		mixed	3.8	1.5	14
20-Jul	311939	hypogeal		mixed	3.1	1.1	20
28-Jul	311950	hypogeal		tuber	4.1	1.2	22
28-Jul	311977	hypogeal		tuber	4.4	1.2	14
May[w]	311981	hypogeal		tuber	3.9	1.4	14
May[w]	311985	hypogeal		tuber	3.5	1.5	13
May[w]	312009	hypogeal		tuber	3.5	1.2	14
May[w]	312013	hypogeal		tuber	4.3	1.0	16
May[w]	312076	hypogeal		tuber	4.6	1.0	14
May[w]	312080	hypogeal		mixed	3.8	1.1	26
May[w]	313268	hypogeal		tuber	4.2	1.3	15
May[w]	313310	epigeal	*P.d.*	fibrous	3.9	1.0	17
May[w]	313313	epigeal	*P.d.*	fibrous	4.6	0.6	17
May[w]	313455	hypogeal		tuber	4.3	1.2	21

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
May[w]	313496	hypogeal		mixed	4.5	1.1	22
20-Jul	313497	hypogeal		mixed	4.6	0.9	20
20-Jul	313503	hypogeal		mixed	4.0	1.1	12
20-Jul	313506	hypogeal		fibrous	4.2	0.6	13
20-Jul	313573	epigeal	*P.v.*	fibrous	4.8	1.0	12
14-Jul	317551	hypogeal		tuber	2.9	0.9	13
6-Jul	317552	epigeal	*P.v.*	fibrous	4.8	0.4	23
6-Jul	317554	epigeal	*P.d.*	fibrous	4.7	0.5	15
6-Jul	317562	epigeal	*P.d.*	fibrous	4.8	0.4	12
28-Jul	317563	epigeal	*P.d.*	fibrous	4.9	0.5	21
May[w]	317572	mixed	*P.c., P.d.*	mixed	4.3	1.2	18
28-Jul	317573	epigeal	*P.d.*	fibrous	4.8	0.6	16
28-Jul	317574	epigeal	*P.d.*	fibrous	4.7	0.5	15
28-Jul	317575	epigeal	*P.d.*	fibrous	4.3	0.8	12
6-Jul	317576	epigeal	*P.d.*	fibrous	4.4	0.9	16
6-Jul	317577	epigeal	*P.d.*	fibrous	4.7	0.6	23
6-Jul	317580	hypogeal		tuber	4.8	0.6	14
6-Jul	317582	epigeal	*P.d.*	fibrous	4.5	0.7	15
6-Jul	317583	epigeal	*P.d.*	fibrous	4.6	0.6	14
May[w]	317584	epigeal	*P.d.*	fibrous	4.8	0.6	15
May[w]	317585	epigeal	*P.d.*	fibrous	4.8	0.7	17
May[w]	317596	hypogeal		tuber	4.4	1.2	14
May[w]	319449	mixed	*P.c., P.v.*	mixed	4.7	1.0	23
May[w]	325588	hypogeal		tuber	4.0	1.2	15
May[w]	325589	hypogeal		tuber	4.9	1.2	21
May[w]	325590	hypogeal		tuber	4.2	1.0	20
May[w]	325591	hypogeal		tuber	4.3	1.0	23
May[w]	325592	hypogeal		tuber	4.3	1.2	16
May[w]	325593	mixed	*P.c., P.d., P.v.*	mixed	4.6	1.1	19
May[w]	325594	hypogeal		tuber	4.1	1.2	24
May[w]	325595	mixed	*P.c., P.d., P.v.*	mixed	4.2	1.0	17
May[w]	325597	hypogeal		tuber	4.2	1.3	21
May[w]	325598	mixed	*P.c., P.v.*	mixed	4.9	0.5	14
May[w]	325599	hypogeal		tuber	3.7	1.4	15
May[w]	325600	hypogeal		tuber	4.2	1.3	23
May[w]	325601	epigeal	*P.d.*	fibrous	5.2	0.6	12

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
May[w]	325602	epigeal	*P.d.*	fibrous	5.1	0.6	16
May[w]	325603	hypogeal		tuber	3.9	1.9	10
May[w]	325605	epigeal	*P.d.*	fibrous	5.1	0.5	14
May[w]	325606	epigeal	*P.d.*	fibrous	4.8	0.6	13
24-Sep	325607	epigeal	*P.d.*	fibrous	5.0	0.8	15
24-Sep	325608	epigeal	*P.d.*	fibrous	4.8	0.4	11
24-Sep	346950	mixed		mixed	4.1	0.8	13
24-Sep	346951	hypogeal		fibrous	4.4	1.1	24
24-Sep	358087	epigeal	*P.v.*	fibrous	5.0	0.0	13
24-Sep	358088	hypogeal		tuber	4.1	0.8	12
24-Sep	358089	hypogeal		tuber	4.3	1.0	11
24-Sep	358090	hypogeal		tuber	4.3	0.9	12
24-Sep	358091	hypogeal		tuber	4.1	1.0	14
24-Sep	358092	mixed	*P.c., P.v.*	mixed	4.1	0.9	11
24-Sep	358093	hypogeal		tuber	4.3	0.7	14
24-Sep	358094	epigeal	*P.v.*	fibrous	4.9	0.3	14
24-Sep	361310	hypogeal		tuber	3.9	0.9	13
24-Sep	361327	hypogeal		fibrous	3.5	0.7	13
24-Sep	361351	hypogeal		fibrous	4.1	1.0	15
24-Sep	361354	hypogeal		tuber	3.4	0.9	9
24-Sep	361355	hypogeal		fibrous	3.6	0.9	14
30-Sep	361356	hypogeal		tuber	3.5	0.7	14
30-Sep	361357	hypogeal		fibrous	3.3	0.9	13
30-Sep	361358	hypogeal		fibrous	3.5	1.0	13
30-Sep	361359	hypogeal		tuber	3.8	0.8	12
17-Sep	361360	hypogeal		fibrous	3.9	0.7	14
17-Sep	361370	hypogeal		tuber	3.7	1.1	21
17-Sep	361371	hypogeal		fibrous	3.5	1.2	15
17-Sep	361480	hypogeal		fibrous	3.4	1.0	12
17-Sep	361509	hypogeal		mixed	3.6	1.3	14
17-Sep	361510	hypogeal		fibrous	3.6	0.5	13
17-Sep	361511	hypogeal		mixed	4.5	1.4	15
17-Sep	361512	hypogeal		tuber	3.8	1.3	13
17-Sep	361514	hypogeal		fibrous	3.6	0.6	13
17-Sep	361519	hypogeal		tuber	3.9	0.6	13
17-Sep	361520	hypogeal		tuber	4.1	1.9	13
17-Sep	361538	hypogeal		fibrous	3.9	0.5	13

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
17-Sep	361551	hypogeal		tuber	3.4	0.6	14
17-Sep	361553	hypogeal		fibrous	3.3	0.7	14
17-Sep	361578	hypogeal		tuber	3.6	0.8	12
17-Sep	367903	hypogeal		mixed	4.1	1.0	21
17-Sep	368709	hypogeal		tuber	3.5	0.8	11
30-Sep	368710	hypogeal		tuber	4.0	1.1	13
30-Sep	368711	hypogeal		tuber	3.7	0.6	13
30-Sep	368714	hypogeal		tuber	3.8	0.8	13
30-Sep	370508	hypogeal		tuber	3.6	1.1	14
30-Sep	370509	hypogeal		tuber	3.4	0.9	14
30-Sep	370510	hypogeal		mixed	3.6	0.8	14
6-Oct	370511	hypogeal		tuber	3.6	1.1	14
6-Oct	370512	hypogeal		tuber	4.1	0.8	11
30-Sep	370534	hypogeal		tuber	3.2	1.0	13
30-Sep	370550	hypogeal		tuber	3.4	1.2	14
30-Sep	379426	hypogeal		tuber	4.0	1.0	11
30-Sep	379427	hypogeal		tuber	3.7	0.9	13
30-Sep	406785	hypogeal		fibrous	4.4	1.4	13
25-Aug	417585	hypogeal		fibrous	4.3	1.1	9
25-Aug	417586	hypogeal		tuber	3.2	1.3	12
25-Aug	417587	hypogeal		tuber	3.1	1.0	14
25-Aug	417588	hypogeal		tuber	3.9	1.0	14
18-Aug	417593	hypogeal		tuber	5.0	0.0	12
18-Aug	417594	hypogeal		tuber	5.1	0.3	14
18-Aug	417602	hypogeal		tuber	3.2	1.1	9
18-Aug	417603	hypogeal		tuber	5.0	1.4	14
18-Aug	417604	hypogeal		tuber	4.0	1.5	8
18-Aug	417607	hypogeal		tuber	3.8	1.2	9
18-Aug	417608	hypogeal		tuber	4.3	0.9	10
18-Aug	417610	hypogeal		tuber	4.9	1.0	15
18-Aug	417611	hypogeal		tuber	4.6	0.7	10
18-Aug	417755	mixed	*P.c.*	mixed	4.4	1.0	19
18-Aug	430174	epigeal	*P.v.*	fibrous	4.6	0.9	14
18-Aug	430178	hypogeal		tuber	4.2	1.8	5
18-Aug	430179	hypogeal		tuber	4.8	0.6	13
18-Aug	430180	hypogeal		tuber	4.1	1.2	11
18-Aug	430182	hypogeal		tuber	4.4	1.0	12

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
18-Aug	430183	hypogeal		tuber	3.6	1.8	5
25-Aug	430185	hypogeal		tuber	4.1	1.0	12
25-Aug	430187	hypogeal		tuber	3.9	1.4	11
25-Aug	430188	hypogeal		tuber	3.7	1.0	14
25-Aug	430189	hypogeal		fibrous	3.7	1.1	7
25-Aug	430190	hypogeal		tuber	4.0	1.1	12
25-Aug	430191	hypogeal		tuber	3.1	1.4	11
25-Aug	430192	hypogeal		tuber	3.2	1.3	15
25-Aug	433235	epigeal	*P.d.*	fibrous	4.4	0.7	11
25-Aug	433236	hypogeal		fibrous	2.7	1.2	1.2
25-Aug	433237	hypogeal		tuber	3.5	1.3	13
25-Aug	433238	hypogeal		tuber	3.0	0.9	15
25-Aug	433239	hypogeal		tuber	3.2	1.2	22
1-Sep	433242	hypogeal		mixed	3.3	1.3	14
1-Sep	433243	hypogeal		mixed	3.7	1.3	15
1-Sep	433244	hypogeal		tuber	4.3	1.1	10
1-Sep	433245	hypogeal		tuber	3.4	1.1	21
1-Sep	433246	hypogeal		tuber	2.4	1.3	7
1-Sep	433247	hypogeal		tuber	3.5	1.2	20
1-Sep	433248	hypogeal		tuber	3.9	1.3	23
1-Sep	433249	hypogeal		tuber	3.8	1.1	14
1-Sep	433250	hypogeal		tuber	3.7	1.2	13
1-Sep	433251	hypogeal		tuber	3.3	1.8	12
1-Sep	433252	hypogeal		tuber	4.0	1.2	14
1-Sep	433254	hypogeal		tuber	4.4	1.2	14
1-Sep	433627	hypogeal		tuber	3.7	0.8	11
1-Sep	438597	hypogeal		mixed	4.0	1.5	13
1-Sep	438598	epigeal	*P.d.*	fibrous	4.4	1.1	10
1-Sep	439534	hypogeal		tuber	3.1	0.9	14
30-Sep	439535	hypogeal		tuber	3.9	0.7	10
6-Oct	439536	hypogeal		mixed	4.1	1.0	14
10-Sep	449381	epigeal	*P.v.*	fibrous	6.5	0.8	12
10-Sep	451862	hypogeal		tuber	3.3	1.6	11
10-Sep	451863	hypogeal		tuber	3.0	1.3	12
10-Sep	451866	hypogeal		tuber	4.5	0.9	12
10-Sep	451867	hypogeal		tuber	4.0	1.6	12

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
10-Sep	451868	epigeal	*P.v.*	fibrous	3.6	1.1	14
10-Sep	451869	hypogeal		tuber	3.7	1.5	15
10-Sep	451870	hypogeal		tuber	4.1	1.1	22
10-Sep	451871	hypogeal		mixed	3.6	1.3	14
10-Sep	451872	hypogeal		tuber	4.3	1.4	15
10-Sep	451873	mixed	*P.c., P.d., P.v.*	mixed	4.1	1.2	10
20-Nov	451874	mixed	*P.c., P.v.*	mixed	3.7	1.2	21
10-Sep	451883	epigeal	*P.d.*	fibrous	4.5	0.9	7
10-Sep	458561	hypogeal		tuber	3.2	1.3	20
10-Sep	458562	hypogeal		tuber	4.0	1.0	23
10-Sep	475745	hypogeal		tuber	3.0	1.2	13
30-Sep	477015	hypogeal		tuber	3.7	0.7	14
30-Sep	494068	hypogeal		tuber	4.5	0.8	13
30-Sep	510637	hypogeal		tuber	3.8	1.2	15
30-Sep	583554	hypogeal		tuber	3.1	0.9	12
30-Sep	583555	hypogeal		tuber	4.1	0.7	11
24-Sep	W6 10126	hypogeal		tuber	4.1	0.7	10
Phaseolus coccineus subsp. darwininus[x]							
6-Oct	201340	epigeal		fibrous	*4.5*	1.0	13
6-Oct	311165	epigeal		fibrous	4.5	0.8	13
6-Oct	311171	epigeal		fibrous	4.3	0.6	13
6-Oct	311174	epigeal		fibrous	4.4	0.9	14
6-Oct	311178	epigeal		fibrous	4.2	1.0	14
6-Oct	311182	epigeal		fibrous	5.0	0.6	7
6-Oct	311183	epigeal		fibrous	4.9	0.5	14
6-Oct	311184	epigeal		fibrous	4.0	1.0	15
6-Oct	311205	mixed	*P.c., P.d., P.v.*	mixed	3.7	1.1	11
6-Oct	311206	mixed	*P.c., P.d.*	mixed	5.3	1.1	19
6-Oct	311208	epigeal		fibrous	5.1	1.1	13
6-Oct	311213	hypogeal	*P.c.*	mixed	4.8	1.7	13
6-Oct	311215	mixed	*P.c., P.d.*	fibrous	4.1	2.0	14
6-Oct	311847	epigeal		fibrous	4.5	0.9	11
Phaseolus coccineus subs*P. coccineus*							
15-Oct	535279	hypogeal		tuber	6.0	1.0	5

Table 2.5. (Continued)

Date Lesion Read	PI No.	Cotyledon position at emergence	Suspected species[z]	Root type	Straw Test Score		Seeds Tested
					Mean	SD[y]	No.
15-Oct	535280	hypogeal		tuber	5.3	1.8	7
15-Oct	535283	hypogeal		fibrous	3.5	0.9	12
15-Oct	535284	hypogeal		tuber	4.8	1.6	12
15-Oct	535286	hypogeal		tuber	5.0	1.6	12

[z]: *P.c.* = *P. coccineus*, *P.d.* = *P. dumosus*, *P.v.* = *P. vulgaris*. A blank indicates that we agree with the species classification. [y]: Standard Deviation [x]*P. dumosus*. [w] :exact date in May unknown.

To develop a means to compare accessions tested at different times, we applied an augmented analysis to the data. This method adjusts means of experimental entries based on the means of check entries common to the entire trial. Because of the unbalanced nature of the experiment, individual mean comparisons were performed to determine statistical significance. In table 2.6, we report adjusted (LS) means with two columns, each being the probability associated with the accession mean being significantly greater or smaller than OR 91G and M0162, respectively. There were 314 entrys, but only 292 accessions, since some accessions consisted of two or more species. In table 2.6, two accessions had an LS mean that was significantly larger than the LS means value of 5.39 for OR91G, and eight accessions had LS means significantly greater than 4.43 for M0162. At the $p \leq 0.01$ level, one hundred accessions had an LS means that was not significantly different from OR 91G or 31.8%. At the $p \leq 0.01$ level, two hundred sixty-five accessions, or 84.4%, had an LS means that was not significantly different from MO162. Two hundred twelve accessions, or 67.5%, were significantly lower than OR 91G at $p \leq 0.01$ and forty-one

accessions, or 13.1%, were significantly lower than M0162 at $p \leq 0.01$. Table 2.6. includes all three species (*P. coccineus*, *P. vulgaris* and *P. dumosus*) and accessions that are mixtures of either two or three species are separated as to which species is being analyzed.

Table 2. 6. Adjusted least square means for *Phaseolus coccineus* accessions grown in an augmented design in 2001 and tested for resistance to white mold. Ranked from lowest to highest score.

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y]	
			91G	M0162
193045	pc	2.32	<.0001	<.0001
311205	pv	2.50	0.0001	0.0101
433246	pc	2.51	<.0001	<.0001
311215	pc	2.83	<.0001	0.0009
311939	pc	2.87	<.0001	<.0001
195372	pc	2.91	<.0001	0.0001
361302	pc	2.95	<.0001	<.0001
195338	pc	2.97	<.0001	0.0023
317551	pc	2.97	<.0001	0.0004
433236	pc	2.99	<.0001	0.0006
451863	pc	3.00	<.0001	0.0003
475745	pc	3.00	<.0001	0.0002
201304	pc	3.05	<.0001	0.0002
165421	pc	3.06	<.0001	0.0005
312009	pc	3.08	<.0001	<.0001
313417	pc	3.09	<.0001	<.0001
361372	pc	3.10	<.0001	0.0002
311985	pc	3.12	<.0001	<.0001
439534	pc	3.15	<.0001	0.003
458561	pc	3.16	<.0001	0.001
176695	pc	3.17	<.0001	0.0017
361361	pc	3.18	<.0001	0.0004
311194	pv	3.19	<.0001	0.0001
325593	pv	3.20	<.0001	0.0016
311194	pc	3.25	<.0001	0.0069
311859	pv	3.25	<.0001	<.0001
325599	pc	3.25	<.0001	<.0001

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
451862	pc	3.28	<.0001	0.0043
317576	pd	3.28	<.0001	0.0031
433253	pc	3.28	<.0001	0.0007
311214	pc	3.29	<.0001	0.0002
433238	pc	3.32	<.0001	0.0057
433251	pc	3.33	<.0001	0.0133
165436	pc	3.33	<.0001	0.0058
325595	pd	3.33	<.0001	0.0363
195381	pd	3.34	<.0001	0.0052
433242	pc	3.36	<.0001	0.0135
201320	pc	3.37	<.0001	0.006
417587	pc	3.39	<.0001	0.0109
190074	pd	3.41	<.0001	0.0051
430191	pc	3.41	<.0001	0.0181
406938	pc	3.42	<.0001	0.0028
312080	pc	3.43	<.0001	<.0001
201301	pc	3.43	<.0001	0.016
311176	pc	3.44	<.0001	0.0154
311981	pc	3.44	<.0001	0.0013
317582	pd	3.44	<.0001	0.0119
361553	pc	3.46	<.0001	0.0134
325603	pc	3.48	<.0001	0.0072
417586	pc	3.49	<.0001	0.0256
311879	pc	3.49	<.0001	0.0122
311205	pc	3.50	0.0008	0.0961
201309	pc	3.50	<.0001	0.0164
433239	pc	3.50	<.0001	0.0131
433245	pc	3.51	<.0001	0.0219
313310	pd	3.52	<.0001	0.0016
430192	pc	3.52	<.0001	0.0236
195389	pd	3.52	<.0001	0.0256
361354	pc	3.54	<.0001	0.0439
317583	pd	3.55	<.0001	0.0277
361327	pc	3.56	<.0001	0.0294

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
370511	pc	3.57	<.0001	0.0188
195359	pd	3.57	<.0001	0.0297
311211	pc	3.58	<.0001	0.0162
311882	pc	3.58	<.0001	0.0027
325588	pc	3.58	<.0001	0.0049
432583	pc	3.59	<.0001	0.0155
201477	pc	3.59	<.0001	0.0396
361480	pc	3.59	<.0001	0.0397
317577	pd	3.60	<.0001	0.0226
361551	pc	3.61	<.0001	0.0352
311920	pc	3.61	<.0001	0.0402
433247	pc	3.62	<.0001	0.0635
420322	pc	3.62	0.0001	0.0801
368709	pc	3.63	<.0001	0.055
175855	pc	3.64	<.0001	0.0432
209664	pc	3.64	<.0001	0.0292
583554	pc	3.64	<.0001	0.0534
317554	pd	3.64	<.0001	0.0451
311210	pc	3.64	<.0001	0.026
451868	pv	3.65	<.0001	0.0393
451871	pc	3.65	<.0001	0.0393
201297	pc	3.66	<.0001	0.0642
361355	pc	3.67	<.0001	0.0527
317580	pc	3.69	<.0001	0.0655
451869	pc	3.70	<.0001	0.0582
255956	pc	3.70	<.0001	0.0444
361328	pc	3.70	<.0001	0.0444
325594	pc	3.70	<.0001	0.0048
361371	pc	3.71	<.0001	0.062
201310	pc	3.72	<.0001	0.0816
325590	pc	3.73	<.0001	0.0103
317552	pd	3.73	<.0001	0.0551
417602	pc	3.73	0.0004	0.1344
307664	pc	3.73	<.0001	0.0449
201328	pc	3.74	<.0001	0.096

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
317562	pd	3.74	<.0001	0.0967
433243	pc	3.74	0.0001	0.1084
325595	pv	3.75	0.0002	0.1196
361509	pc	3.75	<.0001	0.0821
201389	pc	3.75	<.0001	0.0906
361578	pc	3.76	<.0001	0.1001
194586	pd	3.76	<.0001	0.0964
313268	pc	3.78	<.0001	0.0316
361357	pc	3.79	<.0001	0.1095
370534	pc	3.79	<.0001	0.1095
433249	pc	3.79	0.0003	0.1405
361510	pc	3.79	<.0001	0.1103
361514	pc	3.79	<.0001	0.1103
433627	pc	3.80	0.0006	0.1697
325597	pc	3.82	<.0001	0.0228
313503	pc	3.82	0.0002	0.1446
312013	pc	3.83	<.0001	0.0423
451873	pv	3.84	0.0016	0.2285
325591	pc	3.84	<.0001	0.0239
358092	pc	3.84	0.0007	0.202
407387	pc	3.85	<.0001	0.1332
317572	pd	3.86	<.0001	0.0435
433237	pc	3.86	0.0003	0.1703
313455	pc	3.86	<.0001	0.0359
194585	pd	3.86	<.0001	0.1181
255573	pc	3.87	<.0001	0.1214
209669	pc	3.87	0.0003	0.1826
209665	pc	3.89	0.0002	0.1834
317596	pc	3.89	<.0001	0.0897
319449	pv	3.89	<.0001	0.0897
361370	pc	3.89	<.0001	0.1352
325592	pc	3.89	<.0001	0.0692
201295	pc	3.90	0.0001	0.1622
195395	pv	3.90	0.0026	0.2827
325600	pc	3.91	<.0001	0.0414

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
370550	pc	3.91	0.0002	0.1914
433250	pc	3.92	0.001	0.25
361512	pc	3.95	0.0003	0.227
406936	pc	3.95	<.0001	0.1765
311204	pd	3.95	0.0002	0.2222
370509	pc	3.98	0.0003	0.2608
311184	pd	4.00	0.0001	0.2311
451867	pc	4.00	0.0005	0.2844
451873	pc	4.00	0.0048	0.3885
458562	pc	4.00	0.0005	0.2844
311819	pc	4.02	0.0006	0.3067
361310	pc	4.02	0.0006	0.3067
361358	pc	4.02	0.0006	0.3067
317550	pd	4.02	<.0001	0.24
430188	pc	4.04	0.0012	0.3372
430189	pc	4.04	0.0064	0.4232
201300	pc	4.05	0.0012	0.3501
313506	pc	4.05	0.0012	0.3594
361356	pc	4.06	0.0007	0.3461
439536	pc	4.07	0.0004	0.3268
433252	pc	4.08	0.0028	0.4184
438597	pc	4.08	0.0032	0.4252
311180	pc	4.08	<.0001	0.1883
311209	pc	4.08	0.0717	0.6331
451870	pc	4.08	0.0008	0.3717
370512	pc	4.09	0.001	0.3865
361519	pc	4.10	0.0014	0.4125
361538	pc	4.10	0.0014	0.4125
361360	pc	4.11	0.0012	0.4121
311185	pc	4.11	<.0001	0.2707
313496	pc	4.11	<.0001	0.2707
430183	pc	4.11	0.0224	0.5689
433248	pc	4.12	0.0019	0.4479
370508	pc	4.13	0.0013	0.4472
201336	pc	4.13	0.0033	0.4814

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
311198	pd	4.13	<.0001	0.3025
201306	pd	4.14	0.0125	0.5611
361351	pc	4.16	0.0015	0.4935
273666	pc	4.16	0.0004	0.4475
358091	pc	4.17	0.0018	0.508
273449	pc	4.17	0.0009	0.4823
313313	pd	4.17	<.0001	0.37
346950	pc	4.17	0.0023	0.5244
358088	pc	4.18	0.003	0.5429
417588	pc	4.18	0.0038	0.544
175860	pc	4.18	0.0039	0.5565
196413	pv	4.19	0.0038	0.5602
W6 10126	pc	4.19	0.0052	0.5886
311850	pd	4.19	0.0002	0.4678
370510	pc	4.20	0.0024	0.5634
311178	pd	4.21	0.0015	0.5556
312076	pc	4.22	0.0002	0.5108
430187	pc	4.23	0.0086	0.6511
368711	pc	4.25	0.0043	0.6572
379427	pc	4.25	0.0043	0.6572
176672	pc	4.25	0.0046	0.6618
361520	pc	4.25	0.005	0.6667
477015	pc	4.27	0.0044	0.6924
311212	pd	4.27	0.0004	0.6289
367903	pc	4.27	0.0022	0.6698
417607	pc	4.29	0.02	0.7695
451872	pc	4.29	0.004	0.7214
311188	pd	4.29	0.0004	0.6703
311171	pd	4.30	0.0042	0.7437
361359	pc	4.31	0.0079	0.7692
309889	pc	4.31	0.0003	0.7089
313500	pc	4.32	0.0007	0.7342
430190	pc	4.32	0.0135	0.8065
195353	pd	4.32	0.0084	0.7988

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y]	
			91G	M0162
205360	pc	4.32	0.011	0.8058
368714	pc	4.32	0.0078	0.8018
311833	pd	4.33	0.0012	0.7703
313221	pc	4.33	0.0028	0.7962
325589	pc	4.34	<.0001	0.754
317585	pd	4.34	0.0003	0.7784
535281	pc	4.35	0.0374	0.8792
311174	pd	4.35	0.0054	0.8429
510637	pc	4.36	0.0076	0.8573
311194	pd	4.36	0.0051	0.8537
325595	pc	4.36	0.0126	0.8786
175829	pv	4.36	0.0144	0.8813
358089	pc	4.37	0.0144	0.8888
433244	pc	4.38	0.032	0.9177
317584	pd	4.38	0.0008	0.8797
358093	pc	4.38	0.0103	0.9082
311205	pd	4.40	0.0555	0.954
430185	pc	4.41	0.0229	0.9632
224711	pc	4.41	0.0163	0.967
195352	pd	4.42	0.0278	0.9976
313497	pc	4.42	0.0104	0.9972
325606	pd	4.43	0.0024	0.9982
358090	pc	4.43	0.0185	0.9953
451873	pd	4.43	0.0408	0.9854
201306	pc	4.44	0.075	0.9837
311199	pd	4.44	0.002	0.9697
311880	pc	4.44	0.002	0.9697
439535	pc	4.46	0.0295	0.9428
325598	pc	4.46	0.0025	0.9007
307663	pc	4.47	0.0122	0.891
438598	pd	4.48	0.0534	0.9098
451866	pc	4.50	0.0261	0.8387
451883	pd	4.50	0.0206	0.8322
311196	pd	4.50	0.0269	0.8403
433254	pc	4.51	0.0449	0.8507

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y]	
			91G	M0162
346951	pc	4.51	0.0128	0.8076
417604	pc	4.51	0.0722	0.8549
311827	pc	4.52	0.0021	0.7248
201340	pd	4.53	0.0245	0.7701
311165	pd	4.53	0.0245	0.7701
311847	pd	4.54	0.0333	0.7669
209666	pc	4.55	0.0605	0.7838
535278	pc	4.55	0.0932	0.8021
183464	pd	4.55	0.0416	0.753
368710	pc	4.56	0.0376	0.7434
379426	pc	4.56	0.0462	0.7536
313573	pv	4.57	0.052	0.7183
209667	pc	4.57	0.0465	0.7127
311176	pd	4.58	0.0282	0.6736
311203	pd	4.58	0.0088	0.6159
311204	pc	4.58	0.0282	0.6736
311209	pd	4.58	0.0109	0.6258
311826	pc	4.58	0.0059	0.5982
311855	pd	4.58	0.0109	0.6258
430180	pc	4.60	0.0815	0.6851
311217	pd	4.62	0.0751	0.6397
361511	pc	4.64	0.0574	0.5664
311207	pd	4.65	0.0137	0.4613
583555	pc	4.65	0.0761	0.5945
417585	pc	4.66	0.1146	0.6091
319449	pc	4.68	0.0448	0.4689
311220	pv	4.68	0.0729	0.5121
433235	pd	4.69	0.1118	0.5421
195338	pd	4.70	0.1403	0.5518
325602	pd	4.70	0.0201	0.3405
430178	pc	4.71	0.2283	0.6013
325605	pd	4.72	0.0314	0.3344
304749	pc	4.74	0.1141	0.4367
311168	pd	4.75	0.0506	0.3257
325601	pd	4.75	0.0506	0.3257

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y]	
			91G	M0162
195399	pd	4.76	0.1313	0.4093
201335	pd	4.77	0.1616	0.4176
309694	pc	4.79	0.1339	0.3651
417608	pc	4.81	0.2126	0.3888
311213	pc	4.84	0.1519	0.2636
195395	pd	4.85	0.3263	0.4374
311183	pd	4.85	0.1522	0.2417
309888	pc	4.86	0.0917	0.1531
201323	pd	4.89	0.2418	0.258
325608	pd	4.91	0.2572	0.2417
430182	pc	4.93	0.3015	0.2416
417755	pc	4.93	0.2643	0.1959
406785	pc	4.94	0.2662	0.1966
226594	pd	4.95	0.6725	0.6082
325593	pd	4.95	0.2657	0.1694
311182	pd	5.00	0.3969	0.2075
494068	pc	5.02	0.3586	0.1378
358094	pv	5.02	0.3573	0.1274
277802	pc	5.05	0.4263	0.1319
311208	pd	5.07	0.4117	0.0824
430174	pv	5.08	0.4824	0.1136
325607	pd	5.09	0.4537	0.083
358087	pv	5.09	0.4688	0.0936
358092	pv	5.09	0.6548	0.2994
417611	pc	5.11	0.5551	0.1261
311215	pd	5.12	0.5489	0.1078
175829	pc	5.14	0.7472	0.351
311219	pd	5.14	0.5644	0.0845
325593	pc	5.16	0.7112	0.222
202129	pd	5.19	0.647	0.0704
311206	pd	5.22	0.6958	0.0568
224784	pd	5.32	0.8906	0.0306
282119	pc	5.32	0.8803	0.0181
195336	pd	5.35	0.9232	0.0061
430179	pc	5.36	0.9563	0.0273
417610	pc	5.45	0.8795	0.0129

Table. 2.6. (Continued).

PI No.	Species[z]	Adjusted White mold score	Probability of statistically sign. difference compared to checks[y] 91G	M0162
417593	pc	5.51	0.7665	0.0115
417603	pc	5.51	0.7592	0.009
201347	pd	5.55	0.617	0.0008
417594	pc	5.58	0.635	0.0054
311206	pc	5.70	0.4403	0.0016
307665	pc	5.82	0.2743	0.0006
449381	pv	6.50	0.0044	<.0001
311211	pd	6.58	0.0006	<.0001
Checks				
OR 91g	pv	5.38	-------	<.0001
M0162	pv	4.42	<.0001	-------

[z] pc = *P. coccineus,* pv = *P. vulgaris,* pd = *P. dumosus*

[y] Prob. > |t| for H0: LSMean of OR 91G or M0162 = LSMean accession.

To further compare the results produced from the two separate analyses means adjusted using the augmented method were regressed on unadjusted means. The two methods generally showed good agreement (Fig. 2.3) with a moderate degree of correlation ($R^2 = 0.68$). One set of points above and to the left of the regression line was outside of the 95% confidence ellipse. These points are all associated with the July 6 test, where means were adjusted to a greater degree than observed with other data points. On this date, OR 91G had an average score of 7.6. This was associated a two day period when the weather was cool (19.4^{o}C day and 8.3 ^{o}C night) and a rare summer rain (3.75 mm) fell. The rest of the month averaged normal daytime highs around 26.8 ^{o}C and night time lows of 10.2 ^{o}C. During the cooler temperatures of July 4 - 5th, OR 91G exhibited significantly longer lesion development than during other periods of testing. The significantly higher score was sufficient to cause a greater

adjustment in mean scores for all accessions included in that trial. We examined the effect of omitting the July 6 test from the analysis, and replacing OR 91G July 6 test mean with the mean for the entire trial (Table 2.7). We found that these modifications had little effect on trial means by species. In both cases, all three species means were significantly lower than OR 91G (Table 2.7). Likewise, M0162 had a significantly higher score than *P. coccineus*, but was not significantly different from *P. dumosus* and *P. vulgaris*.

Figure 2. 3 Comparion of unadjusted straw test scores of *Phaseolus coccineus* accessions tested over five months compared to scores adjusted based on performance of common checks.

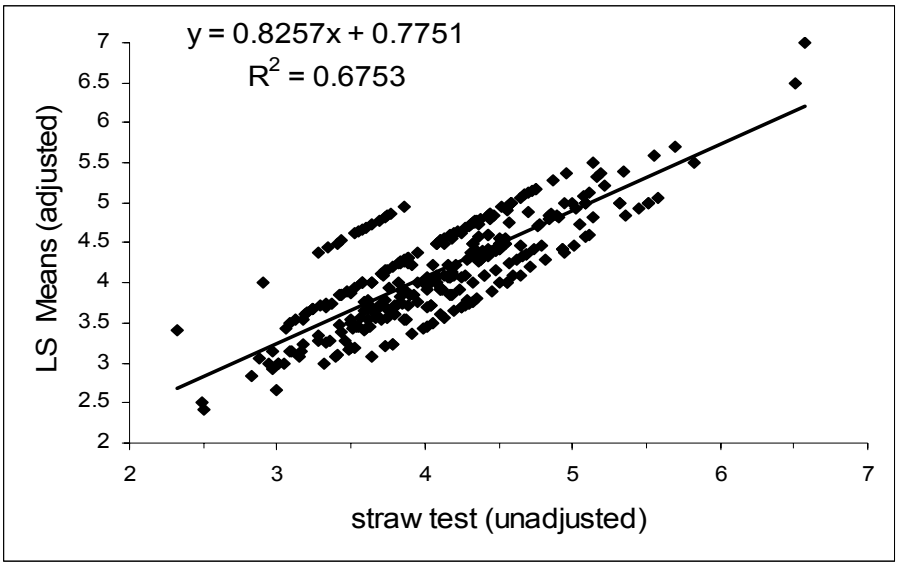


Table 2.7. shows that adjusted means by species ranked with *P. coccineus* having the lowest mean score, followed by *P. vulgaris* and last by *P. dumosus*. Based on comparison to the checks, *P. vulgaris* and *P. dumosus* do not differ significantly, but *P. coccineus* is significantly more resistant. However, the *P. dumosus* and *P. vulgaris* accessions included in this study did appear to have significantly better

resistance than the highly susceptible OR 91G. This confirms our hypothesis that there is greater resistance in the samples of *P. coccineus* than in the accessions of the other two species.

Table 2. 7 Comparison of mean straw test score for the three species found in the *P. coccineus* screen of plant introduction selections and comparison to performance of the checks OR 91G (susceptible) and M0162 (moderately resistant).

		LS Means without July 4th OR 91G Data[y]			LS Means with Modified July 4th OR 91G Score[x]		
	Straw test	LS	Sign. diff. from:			Sign. diff. from:	
Species	Ave.[z]	Mean	91G	MO162	LSMean	91G	MO162
P. coccineus	4.0	4.0	<.0001	<.0001	3.9	<.0001	<.0001
P. vulgaris	4.4	4.2	<.0001	0.1152	4.2	<.0001	0.0889
P. dumosus	4.8	4.5	<.0001	0.7057	4.6	<.0001	0.1087

[z]All accessions included, and straw test average without adjustment. [y]LS Means calculated with July 6th data omitted. [x]LS Means calculated using the experiment-wide OR 91G straw test average for the July 6th value.

Based on adjusted means, forty-one of the most resistant 50 accessions were *P. coccineus,* four were *P. vulgaris* and five were *P. dumosus*. Using the unadjusted means of the top 50 accessions, forty-nine accessions were *P. coccineus* and one was *P. vulgaris*. The unadjusted score of the one *P. vulgaris* accession, PI 311205, only consisted of two plants, that when retested did not perform as well (straw test score of 5.5). The other three accessions, PI 311859, PI 311194, and PI 325593, in the top 50 adjusted means performed much better. The seed sample was larger and the unadjusted means were in the resistant range (≤ 4) and accessions, PI 311859 and PI 311194, had almost the same retest value. The one of the *P. dumosus* accessions, PI 325595, was represented by four seeds and had a score of 5.5 for its retest. These

accessions had an eight day straw test result indicating that the lesion had moved less than 10 cm on most of the plants.

Of the top 100 adjusted accessions 81 were *P. coccineus,* six were *P. vulgaris*, and thirteen were *P. dumosus*. Using the unadjusted means the top 100 accessions were 94 *P. coccineus,* five were *P. vulgaris* and one was *P. dumosus.* The five most resistant *P. vulgaris* ranked 2nd, 61st, 65th, 67th, and 71st on the straw test score average, and 2nd, 23rd, 24th, 26th and 81st based on adjusted means. Thefive most resistant *P. dumosus* ranked 194th, 90th, 207th, 211th and 223rd on straw test score averages, and 29th, 35th, 36th, 40th and 47th based on the adjusted means.

Table 2. 8 Most resistant 50 *Phaseolus* accessions based on adjusted straw test mean for white mold resistance.

PI No.	Species[z]	Adjusted straw test mean	Rank, Adjusted Straw Test	Unadjusted straw test mean	Rank Unadjusted straw test
193045	pc	2.32	1st	3.42	34th
311205	pv	2.50	2nd	2.50	2nd
433246	pc	2.51	3rd	2.43	1st
311215	pc	2.83	4th	2.83	4th
311939	pc	2.87	5th	3.05	11th
195372	pc	2.91	6th	4.00	124th
361302	pc	2.95	7th	3.00	6th
195338	pc	2.97	8th	3.14	17th
317551	pc	2.97	9th	2.92	5th
433236	pc	2.99	10th	2.67	3rd
451863	pc	3.00	11th	3.00	7th
475745	pc	3.00	12th	3.00	8th
201304	pc	3.05	13th	3.00	9th
165421	pc	3.06	14th	3.43	36th
312009	pc	3.08	15th	3.50	45th
313417	pc	3.09	16th	3.14	16th
361372	pc	3.10	17th	3.15	18th
311985	pc	3.12	18th	3.54	49th
439534	pc	3.15	19th	3.07	12th

Table. 2.8. (Continued)

PI No.	Species[z]	Adjusted straw test mean	Rank, Adjusted Straw Test	Unadjusted straw test mean	Rank Unadjusted straw test
458561	pc	3.16	20th	3.15	19th
176695	pc	3.17	21st	3.54	50th
361361	pc	3.18	22nd	3.23	24th
311194	pv	3.19	23rd	3.62	61st
325593	pv	3.20	24th	3.63	65th
311194	pc	3.25	25th	3.67	70th
311859	pv	3.25	26th	3.67	71st
325599	pc	3.25	27th	3.67	72nd
451862	pc	3.28	28th	3.27	28th
317576	pd	3.28	29th	4.38	194th
433253	pc	3.28	30th	3.33	31st
311214	pc	3.29	31st	3.71	82nd
433238	pc	3.32	32nd	3.00	10th
433251	pc	3.33	33rd	3.25	27th
165436	pc	3.33	34th	3.69	75th
325595	pd	3.33	35th	3.75	90th
195381	pd	3.34	36th	4.44	207th
433242	pc	3.36	37th	3.29	29th
201320	pc	3.37	38th	3.73	89th
417587	pc	3.39	39th	3.07	13th
190074	pd	3.41	40th	4.50	211th
430191	pc	3.41	41st	3.09	15th
406938	pc	3.42	42nd	3.47	44th
312080	pc	3.43	43rd	3.85	104th
201301	pc	3.43	44th	3.38	33rd
311176	pc	3.44	45th	3.86	107th
311981	pc	3.44	46th	3.86	108th
317582	pd	3.44	47th	4.53	223rd
361553	pc	3.46	48th	3.29	30th
325603	pc	3.48	49th	3.90	112th
417586	pc	3.49	50th	3.17	20th

[z] pc = *P. coccineus,* pv = *P. vulgaris,* pd = *P. dumosus*

Discussion

Examining the core collection of *P. coccineus* from the U.S. Department of Agriculture National Plant Germplasm System Plant Introduction Collection was a

fascinating exercise from two standpoints. One was the amazing array of genetic variation contained in the collection; the other was the relatively high degree of resistance within the collection compared to *P. vulgaris*.

Correlation between the 1999 and 2001 tests was significant but relatively low. Differences in environmental conditions may have increased variation in genotypic response. In addition, we were still in a learning phase with regard to conducting the straw test in 1999, so the results may not be as accurate as that obtained from the 2001 tests. In 1999 we had expected all the accessions to be of the same species and as a result, pooled the results across species within an accession. By 2001, we recognized that mixed accessions were present.

In the past, selected *P. coccineus* accessions were screened for white mold resistance (Abawi et al., 1978; Adams et al., 1973; Lyons et al., 1983), but the results presented here represent the first time that the entire available *P. coccineus* collection was tested with the pathogen *S. sclerotiorum* and was systematically characterized for species composition.

The two controls chosen for our testing were OR 91G, the main commercial snap bean in Oregon and M0162, a bean that we had observed to have moderately high resistance. We hypothesize that M0162 has resistance derived from *P. coccineus* as described by Haggard and Myers (2007). Apart from resistance to white mold, M0162 has entirely *P. vulgaris* characteristics. Steadman et al. (2002) found no significant difference for reaction to *S. sclerotiorum* between M0162 and G122, PC-50 and NY6020-5 (three lines currently recognized as having moderately high resistance to

white mold). Steadman's National Trial, 2002, evaluation consisted of three field trials, located in Michigan, Washington and Wisconsin, and three straw test evaluations performed in Oregon, Washington and Wisconsin (Steadman et al. 2002). We have observed in the field and greenhouse that OR 91G is highly susceptible to white mold in line with empirical observations of processing industry fieldmen. In this study OR 91G was a highly susceptible entry, but not the highest, and significantly more susceptible than M0162. Based on adjusted means, *P. coccineus* accessions as a whole were significantly more resistant than the checks. There was variation within *P. coccineus*, with the most resistant lines being significantly more resistant than the least resistant (data not shown). In addition to showing consistent resistance in retests, we observed that P.*coccineus* was able to slow the progress of the pathogen. The greatest drawback to working with the resistance of *P. coccineus* is that it is interspecific transfer will be necessary if the resistance is to be of utility in a *P. vulgaris* background. Most cultivated scarlet runner bean varieties have long vines (easily growing to five meters), long internode length, and are cross pollinated. The latter trait means that unlike *P. vulgaris*, considerable heterogeneity among individuals in a population exists. In the absence of insect pollinators, *P. coccineus* flowers must be tripped or hand fertilized to ensure seed set. Although it is possible to bring *P. coccineus* traits into *P. vulgaris*, there are barriers to crossing of the two species (Shii et al. 1982; Guo et al. 1989), genetic barriers to interspecific hybridization (Smartt 1970; Ferwerda and Bassett 2000), and the desired resistance has a tendency to be lost.

In addition, use of *P. coccineus* as a female, and further backcrossing of the progeny to the *P. coccineus* parent involves embryo rescue (Shii et al. 1982).

Despite the barriers to crossing, it appears worthwhile to tackle this problem because the resistance to white mold observed in some accessions is the best available within the genus *Phaseolus*. More than one mechanism may be involved in resistance (Chipps et al. 2005), and systematic study will facilitate identifying underlying biochemical basis of resistance, and the genetic control.

The results reported here along with scanned images of the seeds have been deposited in the Germplasm Resource Information Network database, and are in searchable form for other researchers interested in accessing *P. coccineus* germplasm as a source of white mold resistance. In addition, the classification of accessions has been confirmed, or in some cases, reclassified into other species categories (Appendix 1.1). The results reported here have been essential to designing intra- and interspecific crossing populations for the study of the inheritance and interspecific transfer of white mold resistance.

CHAPTER 3. MOLECULAR MARKER DISSECTION OF QTL CONFERRING RESISTANCE TO WHITE MOLD DISEASE IN *PHASEOLUS COCCINEUS*

Introduction

The common bean (*Phaseolus vulgaris*) is a warm season annual that grows in subtropical or temperate areas, and at higher elevations or during the cool, dry season in tropical areas (Bassett 1986; Gepts 1988; Hall 1994). Beans are a low cost, high protein and carbohydrate food available to many people in areas of the world that do not have easy access to animal proteins in their diet (Gepts 1988; Young and Pellett 1994). Common bean is the most widely grown of the grain legumes, both for dry seed consumption as well as vegetable uses.

Scarlet runner bean (*P. coccineus*) has not received the same attention to breeding and genetics that *P. vulgaris* has. Except for a few local regions, it has generally been regarded as a minor vegetable or grain legume crop. Most of what we know of the genetics of *P. coccineus* has come from interspecific crosses to common bean in the attempt to transfer various traits. Lamprecht (1945, 1948, 1957) formulated a theory of species-specific gene blocks based on such crosses (Lamprecht 1945; Lamprecht 1948; Lamprecht 1957). He and others studied transfer epigeal emergence and extrose stigma position, but found that populations selected for these traits reverted to the *P. coccineus* phenotype (Lamprecht 1957; Wall and York 1957; Manshardht and Bassett 1984). Bassett (1993, 2003) studied the inheritance of flower color transferred from *P. coccineus* into *P. vulgaris*. Researchers have established that genes for flower and

seed coat color, and growth habit are homologous with common bean (Bassett 1993; Bassett 2003). Virtually no molecular studies apart from those dealing with phylogenetic relationships in the genus *Phaseolus* have been done (Lioi et al. 2006).

P. coccineus is an important source of resistance to many pathogens and a few insects. Baggett and Frazier (1959), found resistance to *Pseudomonas phaseolicola* (halo blight), *Uromyces phaseoli* (bean rust), *Colletotrichum lindemuthianum* (anthracnose), Bean Common Mosaic Virus, and Bean Yellow Mosaic Virus (Gepts 1988). In 1980, Coyne and Schuster found *P. coccineus* types that were resistant to *Xanthomonas axonopodis* pv. *phaseoli* (common bacterial blight) and to *Corynebacterium flaccumfaciens* (bacterial wilt) (Gepts 1988). *P. coccineus* and *P. polyanthus* (*P. dumosus*) have been identified as sources of resistance to angular leaf spot, *Phaeoisariopsis griseola* (Mahunku et al. 2003). Osorno et al. (2003) found resistance to bean golden yellow mosaic virus, (BGYMV) in *P. coccineus* (Osorno et al. 2003).

The consensus has been that common bean had limited levels of resistance to white mold and this resistance was quantitatively inherited with low to moderate heritability (Fuller et al. 1984). *P. coccineus* shows consistently greater resistance to *S. sclerotiorum* than does *P. vulgaris* (Adams et al. 1973; Abawi et al. 1978).

White mold, caused by *S. sclerotiorum* (Lib.) de Bary, causes widespread loss of yield and quality in both snap and dry beans (*Phaseolus vulgaris* L). In some extreme instances, there can be a one hundred percent loss in bean yield under irrigated

situations (Hall 1994). In green beans, even a 3 - 5% pod infection rate can result in refusal of the field by the processor (Stivers 2000).

S. sclerotiorum is a ubiquitous necrotrophic fungus that has been reported in many countries on six continents (Purdy 1979). It has the ability to infect more than 400 plant species (Boland and Hall 1994). It occurs in a range of temperatures from 4^{o}C to over 30^{o}C, although the most common range is a relatively cool, 20^{o}-25^{o}C (Hall 1994). *S. sclerotiorum* occurs in moist areas, due either to rainfall or irrigation, but may be found in hot arid areas as well (Purdy 1979).

Before the advent of molecular markers, slow progress in breeding for white mold resistance was made in common bean. Only limited genetic variation was known, and that was inherited quantitatively. The onset of molecular mapping and its application to quantitative genetics to place quantitative trait loci (QTL) on linkage maps has transformed breeding for disease resistance. Several groups have found QTL from five common bean sources that map to eight linkage groups (Miklas et al. 2001; Park et al. 2001; Kolkman and Kelly 2003; Miklas and Delorme 2003; Ender and Kelly 2005; Maxwell et al. 2006; Miklas et al. 2006; Miklas et al. 2007). While this effort is in its infancy a picture of the genetic architecture of white mold resistance in common bean is beginning to emerge where QTL are found in more than one bean population, and some QTL may map to similar locations in different populations. Most QTL have small effect, implying that many will need to be pyramided into a common background to achieve high levels of resistance. This strategy is based on the assumption that white mold QTL are additive. To implement this strategy, new and

novel sources of resistance are needed, and *P. coccineus* is a prime candidate for novel forms of resistance.

The utility of white mold resistant QTL for marker assisted selection (MAS) will increase as more populations are examined and QTL are validated. Knowing that high levels resistance to white mold are found in *P. coccineus* (Gilmore et al. 2002) we set out to create a linkage map of this species and identify resistance QTL. Using a very resistant accession, PI255956, crossed to a moderately resistant cultivar, Wolven Pole, (Chipps et al. 2005) we created an F_2 population and linkage map with QTL for white mold resistance.

Methods and materials

Plant materials and development of genetic populations

PI 255956 was among seven highly resistant lines that we identified from a greenhouse screen in 1999 of eighty-one accessions of *P. coccineus* requested from the U.S. Department of Agriculture National Plant Germplasm System (NPGS) Plant Introduction Collection maintained at Pullman, WA. PI255956 (G 6753) is a white-flowered and -seeded cultivated climber originally collected in Guatemala. The moderately susceptible 'Wolven Pole' heirloom variety was identified in the same screen. It is a climbing white–flowered and -seeded type originally provided by Dr. Ken Kmiecik, Seminis Vegetable Seeds, DeForest, Wisconsin. This cross was one of several made following the 1999 screen (Table 3.1) and was the one used for mapping since large quantities of seed could be obtained. Another consideration was that PI

255956 combined well with common bean cultivar OR 91G. One hundred eighty-eight F_2 progeny of the Wolven Pole/PI 255956 were used for creating the linkage map.

Bean plant growth

The planting mix used was Sunshine brand SB-40 professional growing mix and a dry volume of 10 ml of Scotts brand Osmocote fertilizer was added. The minimum daytime temperature was 21°C and minimum nighttime temperature was 16°C. The pots were watered initially when planted, but not again until the first true leaves emerged from the soil. The maturing plants were then watered on an as needed schedule.

Table 3.1. *Phaseolus coccineus* plant introduction accessions with high levels of white mold resistance retained for genetic analysis in the Vegetable Breeding Program at Oregon State University.

PI No.	Crossed with PI 150932	Crossed with Wolven Pole	Crossed with OR 91G	Crossed with 5-593
201299	No Viable seed	Viable Seed	50:50 dwarf: normal	50:50 normal: lacking terminal buds
255956	No Viable seed	Viable Seed	All normal	Did not set seed
361302	Viable Seed	Viable Seed	No germination	All healthy
361372	Viable Seed	Viable Seed	Germination, then seedling death	Did not set seed
535278	Viable Seed	Viable Seed	50:50 dwarf: normal	All healthy

Fungal maintenance

In October, 1998 wild-type *S. sclerotiorum* sclerotia were collected from the white mold nursery grown at the Oregon State University Vegetable Farm, Corvallis. The sclerotia were stored at 0^{o}C for the duration of the project. To prepare them for culture, sclerotia were placed into a 20% bleach solution for 20 min, rinsed with distilled water, placed in 95% ethanol for five minutes, removed and immediately flamed. In a laminar hood, each surfaced sterilized sclerotium was plated onto sterile potato dextrose agar (PDA), seven mm thick, in a 15 x 100 mm Petri dish. Difco potato dextrose agar, 3.9% solution, was made by adding 39 g of dry media to one liter water, stirring and then autoclaving the solution at 121^{o}C for 15 minutes. The plate was set on a lab shelf with daytime temperatures approximately 21^{o}C and overhead fluorescent lighting providing about 10 h of light daily. The mycelia were allowed to grow until new sclerotia formed on the outer edges of the plate. These primary plates produced enough sclerotia to inoculate 30 PDA plates, which were then used for the white mold screen. The secondary sclerotia were placed on a PDA plate and allowed to grow for five days under the conditions described above prior to use.

Inoculations

The conventional straw test procedure was used (Petzoldt and Dickson 1996). Briefly, a hollow straw segment three to four cm in length with one end stapled, was used to remove a plug of the growing edge of the mycelium and agar. The terminal growing point of the plant was removed, leaving ten centimeters of internode above the third node. The straw with a mycelial plug was placed on the trimmed tip and the

disease was allowed to progress. Growing conditions in the greenhouse were as described above. The Petzoldt and Dickson straw test scale was modified (Table 3.2) because of the higher levels of resistance of *P. coccineus,* (modifications to scores 1, 2, and 3).

Table 3.2. Modified straw test scale used to rate white mold disease progression in *Phaseolus coccineus* accessions grown in the Vegetable Breeding Program at Oregon State University.

Score	Lesion Size
1	1 to 3 cm.
2	Approximately 4 cm.
3	Past the end of the straw, but not to the first node.
4	At the first node.
5	Past the first node, but not to the second node.
6	To the second node.
7	Past the second node, but not to the third node.
8	To the third node.
9	Past the third node or the plant has died.

Eight days after inoculation, if the mold infection was scored seven or above, then the infection site was removed to preserve the plant, and it was assigned a score of 9, meaning that the plant would have ultimately died. If the plant received a score of six or less than it was evaluated the following week. The lesions were read every week for five weeks, after which all lesions were removed so plants could be kept for other observations. Thus, while the standard straw test for *P. vulgaris* calls for reading after only eight days, readings were conducted over five weeks for the *P. coccineus* materials because the high partial physiological resistance delayed growth of the pathogen.

Phaseolus DNA Extraction Protocol

Young leaves were collected in greenhouse, before the white mold inoculation, and taken to lab. Approximately one gram leaf tissue was ground using a tissue homogenizer with extraction buffer. About 1.5 ml of homogenized tissue was collected into a microfuge tube and immediately placed on ice. The tube was centrifuged for five minutes at 10,000 xg. The supernatant was poured off and excess residual liquid was removed with pipette. One milliliter of lysing solution with proteinase K was added, and then the pellet was resuspended using a pipette tip. The tube was vortexed briefly, and then incubated at 37^{o}C for about one hour. Tubes were then centrifuged for 10 minutes at 13,000 xg. 700 µl of lysing solution and supernatant was moved to a new microfuge tube and 700 µl isopropanol was added. The solution was mixed well by inverting the tube several times and the tubes then stored overnight at -20^{o}C. The next morning the tube was centrifuged for ten min at 13,000 xg. The supernatant was poured off and excess residual liquid was removed with a pipette. 300 µl Tris-EDTA (TE) buffer, pH 8.0, was added and the pellet was re-suspended using a pipette tip to dislodge and mix the suspension. The tube was vortexed briefly and the tubes were stored overnight at 4^{o}C. 300 µl phenol:chloroform was added to the tube, and then vigorously shaken for one to two minutes. The tube was centrifuged for ten minutes at 13,000 xg, and 200 µl of the upper aqueous layer was transferred to a new tube. The DNA was precipitated out by adding 400 µl 95% ethanol. The content of the tube was mixed well by inverting the tube several times. The tube was stored at -20^{o}C overnight. The following morning the tube was

centrifuged for ten minutes at 12,000xg. The supernatant was poured off and the residual liquid was removed with a pipette and placed in a vacuum desicator for 30 minutes. The pellet was dissolved by adding 100 µl TE buffer, and stored overnight at 4^{o}C (Kobayashi et al. 2000). The concentration was determined using a DyNAQuant 200 flourometer and then templates were diluted to 10 ng/µl for RAPDs and 3 ng/µl for SSRs.

Molecular Markers

RAPDs

Random amplified polymorphic DNA (RAPD) ten-base oligomer primers were purchased from Operon Biotechnologies, Inc., Huntsville, Alabama. The RAPD PCR primer reactions were performed with 15 µL volumes containing 1.5 µl 1X reaction buffer, 0.45 µl 50 mM $MgCl_2$, 0.9 µl 2.5 mM dNTPs, 0.24 µl 10 µM of the forward and reverse primers, 0.1µl 5 units/ul of Biolase Taq DNA polymerase (Bioline USA Inc., MA), and 1.2 µl of 10 ng genomic DNA. This was amplified in a Dual 96-Well GeneAmp® PCR System 9700 or a 96-Well GeneAmp® PCR System 9700 (Applied Biosystems, CA), programmed for an initial denaturation step of 94° C for one minute, then 45 cycles of a 60 seconds denaturation step at 94° C, a 90 seconds annealing step at 37° C and a 120 seconds extension step at 72° C. A final fifteen minute step at 72° C finished the program. PCR products were separated on a 1.5% agarose gel. The agarose gels were stained with ethidium bromide and visualized on a UV trans-illuminator UVP Darkroom, (UVP, Inc. Upland, CA) system. Primers were scored by

amplification product matching the expected size bands observed in the parents. RAPD bands were scored either the same as PI255956 (a) or the same as Wolven Pole (b).

SSRs

The SSRs were designed and tested in *P. vulgaris* by Gaitan-Solis et al. (2002) and ordered from MWG Biotech, Ag., High Point, NC (Gaitan-Solis et al. 2002; Blair et al. 2003). The SSR PCR primer reactions were performed with 10 µL volumes containing 1.0 µl 1X reaction buffer, 0.4 µl 50 mM $MgCl_2$, 0.8 µl 2.5 mM dNTPs, 0.3 µl 10 µM of the forward and reverse primers, 0.05 µl 0.25 units of Biolase Taq DNA polymerase (Bioline USA Inc., MA), and 1 µl of 3 ng genomic DNA. The optimum annealing temperature for each primer pair was determined by gradient PCR using two programs: The first program was run from 55° C to 65° C and if unsuccessful, followed by a 45° C to 55° C program, depending on the recommended annealing temperature. After the optimum annealing temperature was obtained DNA was amplified in an Eppendorf Gradient thermocycler (Brinkmann Instruments Inc., NY) or an MJ Research Tetrad thermocycler (MJ Research, Inc., MA) programmed for 35 cycles of a 40 s denaturation step at 94° C, a 40 s annealing step at the optimum annealing temperature of the primer pair, and a 40 s extension step at 72° C. PCR products were separated on a 2.75% agarose gel stained with ethidium bromide and visualized on a UV transilluminator using a Bio-Rad GelDoc 2000 digital imaging system (Bio-Rad laboratories, CA). Primer pairs were scored by amplification of products matching the expected size bands observed in parent. SSR bands were

scored either the same as PI255956 (a) or the same as Wolven Pole (b), or with eight primer sets the heterozygous condition (h) was observable.

AFLPs

Genomic DNA was first re-cleaned with a phenol-choloroform purification step. The product and lamda DNA were separated on a 1.25% agarose gel, stained with ethidium bromide and visualized on a UV transilluminator using a Bio-Rad GelDoc 2000 digital imaging system (Bio-Rad laboratories, CA). The genomic DNA was quantified using three quantities of lamda DNA to estimate values.

Using the AFLP® Core Reagent Kit, (Invitrogen Life Technologies, Carlsbad, CA) genomic DNA (100 to 500 ng) was cut with restriction enzymes EcoR I, a six base cutter, and MseI, a four base cutter, at 37 °C for three hours using 2 µL of EcoRI/Mse I and 5 µL of 5X restriction buffer [50 mM Tris-HCl (pH 7.5), 50 mM Mg-acetate, 250 mM K-acetate] in a final volume of 25 µL. The temperature of the mixture was raised to 70^{o} C for 15 minutes to inactivate the restriction endonucleases and then placed on ice. Adaptor ligation followed by adding 24 µL of adapter/ligation solution [EcoR I/Mse I adapters, 0.4 mM ATP, 10 mM Tris-HCl (pH 7.5), 10 mM Mg-acetate, 50 mM K-acetate], 1 µL T4 DNA Ligase [1 unit/µl in 10 mM Tris-HCL (pH 7.5), 1mM DTT, 50 mM KCl, 50% (v/v) glycerol] to 24 µL of each double-digested DNA samples (49 µL final volume) and incubating at 16 °C overnight. A 1:10 dilution was performed, taking 10 µL of the reaction mixture and adding 90 µL TE buffer. A pre-amplification step was then performed with primers complementary to the adapter sequences and carrying an additional selective

nucleotide, (EcoR I+ A and Mse I + C). The pre-amplification PCR mixture, total volume of 25 µL, contained 2.5 µL of 10X Biolase buffer, 0.75 µL (50 mM) $MgCl_2$, 2 µL (2.5 mM of each) dNTP's, 0.75 µL of (10 µM) of primer E, EcoRI+ A, and primer M, MseI+ C, 0.125 µL of (5 U) Biolase Taq DNA polymerase (Bioline USA Inc., Randolph, MA) and 5 µL of diluted restricted/ligated DNA. The MJ thermocycler (MJ Research Inc., Reno, Nev.) was used with the following cycling parameters: 72° C for 2 min, 20 cycles of 94 ˚ C for 20 seconds, 56 °C for 30 seconds and 72 °C for 120 seconds, then 72° C for 120 seconds and 60° C for 30 minutes. Seven µL of each sample were checked on a thin 1.5% agarose gel to visualize a smear. For selective amplification the pre-selective product was diluted 1:40, 5 µl pre-selective product with 195 µl TE (pH 8.0), and used as template DNA. EcoR I and Mse I primers with three selective bases at the 3' end were used for selective amplification. Eight primers and 64 primer pairs were initially tested to select for the most polymorphic set of primer pairs. For detection, the EcoRI-based primers were fluorescently labeled with FAM (Sigma Aldrich Co., Mo.) fluorescent dye. The Mse I primer was the unlabeled reverse primer. The selective amplification PCR mixture (15 µL final volume) consisted of 1.5 µL of 10X PCR buffer, 1.2 µL of 25 mM $MgCl_2$, 0.72 µL of 2.5 mM of each dNTP's, 0.06 µL of labeled 10 µM EcoRI+ 3 primer, 0.3 µL of unlabeled 10 µM MseI+ 3 primer, 0.12 µL of BSA (1 mg/ml), 0.15 µL of 0.75U AmpliTaq Gold DNA polymerase (Applied Biosystems, CA.) and 3 µL of diluted pre-selective template. Selective amplification was carried out in an MJ thermocycler using the following temperature profile: an initial denaturation step of 94 °C for 2 minutes; 10

cycles of 94 °C for 30 seconds, 65 °C (decreasing by 0.7°C /cycle) for 30 seconds and 72°C for 2 minutes followed by 24 cycles of 94 °C for 30 seconds, 56 °C for 30 seconds and 72 °C for 2 minutes, with a final cycle of 72 °C for 10 minutes. The sizes of the AFLP fragments were determined after separation on an ABI 3100 capillary sequencer at the Central Services Laboratory (Oregon State University). GeneScan (version 2.1) and Genotyper (version 2.0) were used for automated data collection and computation of allele size and accurate visualization of the alleles, respectively. Those six primer pairs were tested with DNA from 14 F_2 individuals and the two parents on the CEQ 8000 Genetic Analyzer (Beckman Coulter, Fullerton, CA). For detection, the EcoRI-based primers were fluorescently labeled with a D4 WellRed fluorescent dye (Sigma Aldrich Co., Mo.). The selective amplification PCR mixture (15 µL final volume) consisted of 1.5 µL of 10X PCR buffer, 1.2 µL of 25 mM $MgCl_2$, 1.2 µL of 2.5 mM of each dNTP, 0.9 µL of labeled 10 µM EcoRI+ 3 primer, 0.9 µL of unlabeled 10 µM MseI+ 3 primer, 0.2 µL of 0.75 U Platinum Taq DNA Polymerase (Invitrogen, Co., CA) and 3.8 µL of the diluted preselective template. Selective amplification was carried out in an MJ thermocycler using the following temperature profile: an initial denaturation step of 94 °C for 2 minutes; 10 cycles of 94 °C for 20 seconds, 66 °C (decreasing by 1°C /cycle) for 30 seconds and 72°C for 2 minutes followed by 25 cycles of 94 °C for 30 seconds, 56 °C for 30 seconds and 72 °C for 2 minutes, with a cycle of 72 °C for 3 minutes followed by a final cycle of 60^{o} C for 30 minutes. Nine µL of the selective amplification product was run on a thin 1.5% agarose gel to confirm amplification success.

The fluorescently labeled amplified fragments were analyzed by capillary gel electrophoresis using the CEQ 8000 Genetic Analyzer (Beckman Coulter, CA). One µL of the selective amplification PCR product, 35 µL of the sample loading solution (Beckman Coulter, Inc., Fullerton, CA) and 0.66 µL of DNA size standard (600) were added into each well of the sample plate. Inclusion of internal size CEQ-600 size standard enabled accurate sizing and scoring (presence/absence) of DNA fragments between 60-500 base pairs. The acceptable range of bands for each primer pair was determined using two size standard bands preceding the first recorded band and two size standard bands following the last recorded band (Hayashi et al. 2005). AFLP products were scored as present (1) or absent (0) to create a binary matrix.

Qualitative traits versus quantitative traits

The two traits, eight day straw test results and five week straw test results were first analyzed as qualitative traits. Any score greater than four was rated suspectible, and any score four and below was rated as resistant. JoinMap® was unable to link these two traits to any other markers, so then actual values were used changing the two disease qualitative traits into quantitative traits.

Statistical Analysis of SSR and AFLP Data

Microsoft® Office Excel 2003 was used to record data, check for Chi-Square values, and manipulate data for use by genetic programs creating the linkage map and QTL relationships. The CEQ 8000 Genetic Analyzer (Beckman Coulter, CA) software was used for band detection and identification.

Genetic Linkage Map

Linkage groups were identified using JoinMap® 4, Plant Research International B.V. and Kyazma B.V. (Van Ooijen 2006). A partial linkage map of the selectively mapped markers was constructed using JoinMap.

MapQTL®5 (Plant Research International B.V. and Kyazma B.V., 2006) was used as a preliminary QTL mapping tool to locate QTL, LOD scores and phenotypic variances. Windows QTL Cartographer Version 2.5, Statistical Genetics, North Carolina State University, NC (Wang et al. 2006) was used as the defining source of the QTL information. The linkage map was drawn by MapChart 2.1 (Plant Research International) (Voorrips 2002) .

Results

Six-hundred ten RAPD primers were screened against the two parents to identify primers that amplified and produced bands. The two parents and six progeny were then screened for polymorphism. Finally, primers polymorphic in the parents and six progeny were amplified in the total population of one hundred eighty-eight F_2 progeny. Fifty-one primer pairs failed to amplify and 471 primer pairs were monomorphic (Table 3.3). Eighty-eight RAPD primers were used for mapping, with six primers contributing three bands, twenty-nine primers contributing two bands, and the remaining fifty-three contributing a single polymorphic band for a total of 129 polymorphic markers. Thirty-four markers were scored in the full population of 188 individuals; the remaining ninety-five markers were scored in ninety-four F_2 progeny.

Table 3 3 Summary of molecular markers used to create a linkage map for the *P. coccineus* cross Wolven Pole x PI255956.

	Primers					
Type of Marker	Tested	Failed	Monomorphic	Polymorphic	Used	Total Bands
	(No.)					
RAPD	610	51	471	88	88	129
SSR	76	12	46	18	11	11
AFLP	64	0	0	64	4	100
Total	750	63	517	170	103	240

Seventy-six SSR primer pairs were screened for amplification and polymorphism in PI255956, Wolven Pole and six progeny. Twelve primer pairs failed to amplify, forty-six were monomorphic and eighteen primer pairs were polymorphic (but had nulls or were too close to call on agarose gels), and eleven primer pairs were polymorphic (Table 3.3). SSR primers were amplified in the full population of 188 individuals.

For AFLPs, DNA from Wolven Pole and PI 255956, the two parent plants, was amplified using 64 primer pairs. All primer pairs were polymorphic, so the six most polymorphic pairs were further evaluated. These six primer pairs chosen were re-run with the parents and fourteen progeny. The four most promising pairs were run with the entire population of 188 progeny and yielded 100 polymorphic bands (Table 3.3).

Because *P. coccineus* is an out-crossing species we expected fairly high levels of polymorphism, especially for the AFLPs. Phenotypically the two parents were very similar in appearance and growth habit. PI 255956 showed greater vigor and larger, longer pods, whereas Wolven Pole was shorter in stature, had shorter pods, and was

able to set selfed seed more readily. They have different origins as well; PI 255956 was collected in Guatemala, whereas Wolven Pole was received from Wisconsin, and appeared better adapted to the shorter cool seasons found at higher latitudes. About 14% of RAPD and the SSRs primers were polymorphic within our population. AFLPs provided higher levels of polymorphism than other markers. The number of bands observed with the initial screening of 64 primer pairs was 1,552 of which 60% were monomorphic and 40% were polymorphic. The second screen of six most polymorphic primer pairs produced 257 bands, of which 59.5% were monomorphic and 40.5% were polymorphic. The final four primer pairs chosen for the map generated 198 bands with 50.5% polymorphism.

Linkage Map

Linkage map construction placed 215 markers in 13 linkage groups (LGs) that spanned 797 cM. A pairwise linkage analysis of the marker data, imposing a minimum LOD score of 4.0 and a maximum distance of 30 centimorgan (cM) was used to establish the linkage groups. Eight markers were linked on various LGs, but could not be located with precision. Nineteen markers were not able to be linked, including the straw test five weeks results and the straw test eight days results.

For the straw test reading at eight days of the 188 progeny, there were 166 progeny with a score of four or less and only 22 progeny with a score of above four. If the scale is converted to a qualitative rating, where four and less is considered resistant, and anything greater is susceptible, then the data do not fit a 3:1 ratio as

would be expected for a single dominant gene ($\chi^2 = 17.7$, Prob. ≤ 0.0001), or a 15:1 ratio for a two gene model ($\chi^2 = 9.5$, Prob. ≤ 0.002). Thus, it appears that a quantitative approach to analyzing resistance was justified. The two QTL for this trait were located on LG1a and LG5 and accounted for about 14% of the observed phenotypic variation.

For the straw test results at five weeks 49 individuals were rated resistant and 139 individuals were rated susceptible, which fits a 1:3 (R:S) ratio ($\chi^2 = 0.113$, Prob.=.74,). Yet during analysis, JoinMap® was unable to link this trait to any other marker. We converted this trait to a quantitative trait by using actual values instead of resistant or susceptible. Two QTL were located on LG 1c and LG C and accounted for 82% of the observed phenotypic variation.

The two QTL for physiological resistance from straw test readings taken over five weeks were placed on the map. The QTL on LG 1c and LG C were in repulsion phase. There were two QTL for the straw test results at eight days; the first located on LG 1a in repulsion phase, as was the other on LG5.

Linkage Group 1 (1a) Linked Groups of 1 (1b)

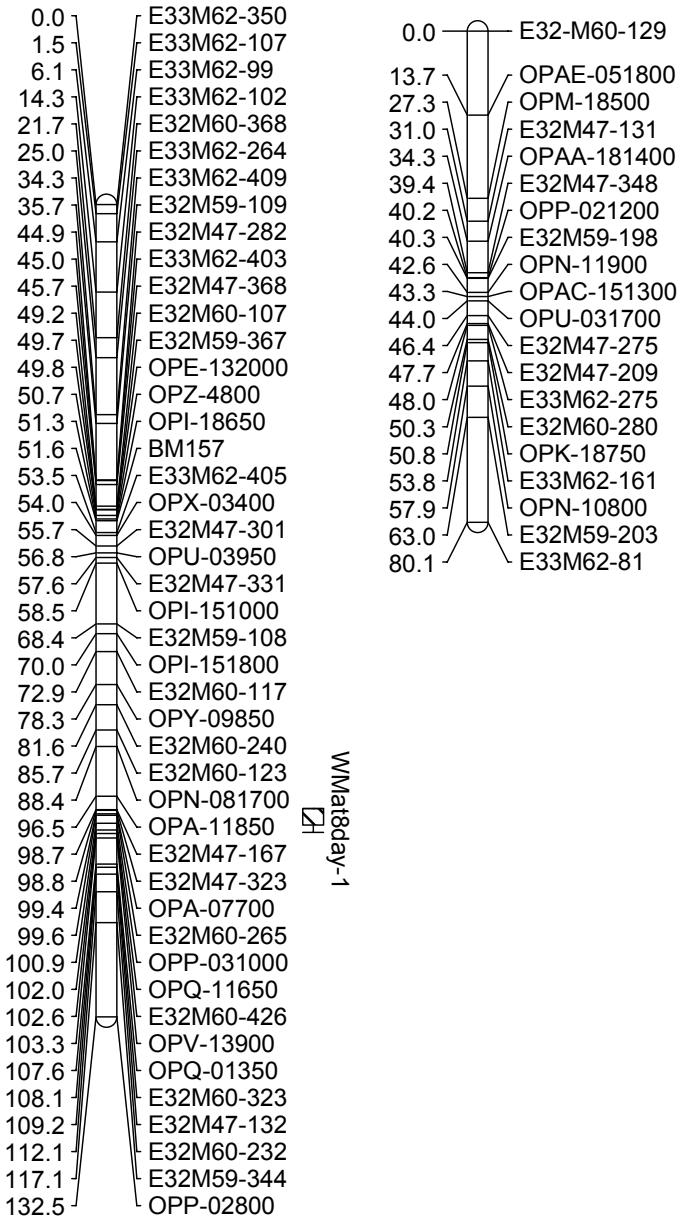


Figure 3. 1. Linkage map created with RAPDs, SSRs and AFLPs from 188 individuals in a Wolven Pole/PI 255956 F_2 population. Distance in cM shown to left of LG with marker name to right. QTL are shown as bars to right of LG, with crosshatched bars QTL for eight day resistance, and solid bars QTL for five week resistance.

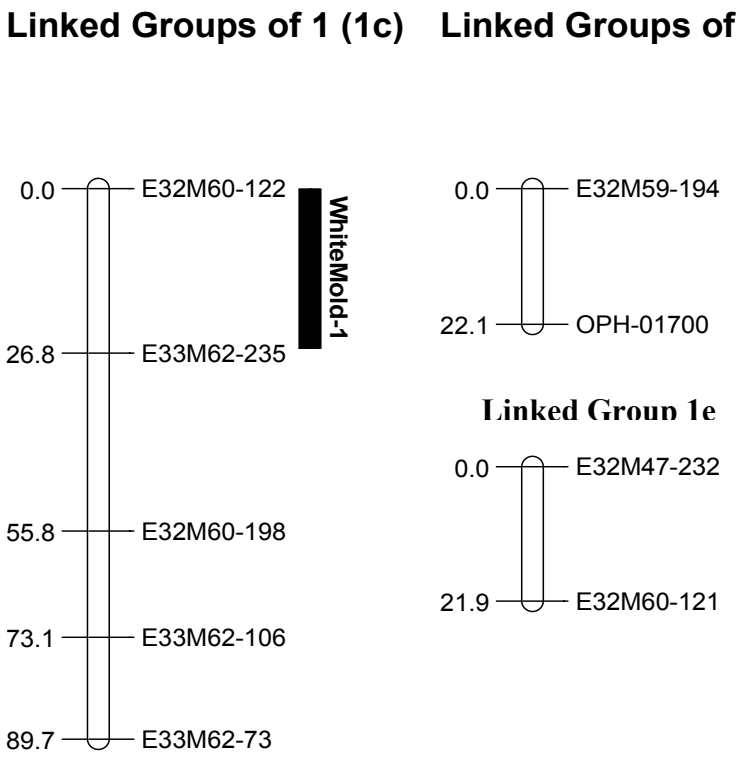
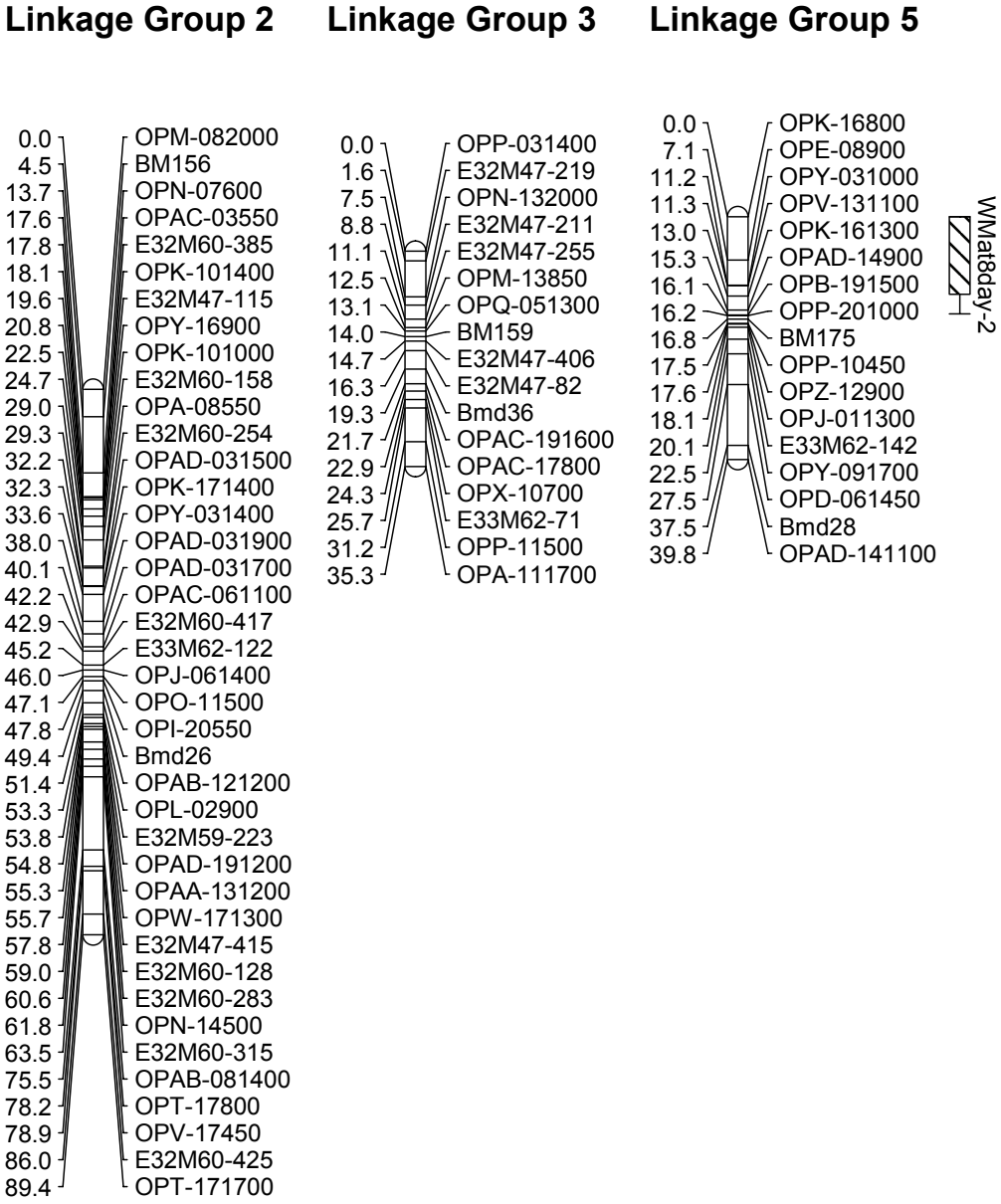


Figure 3.1. (Continued)



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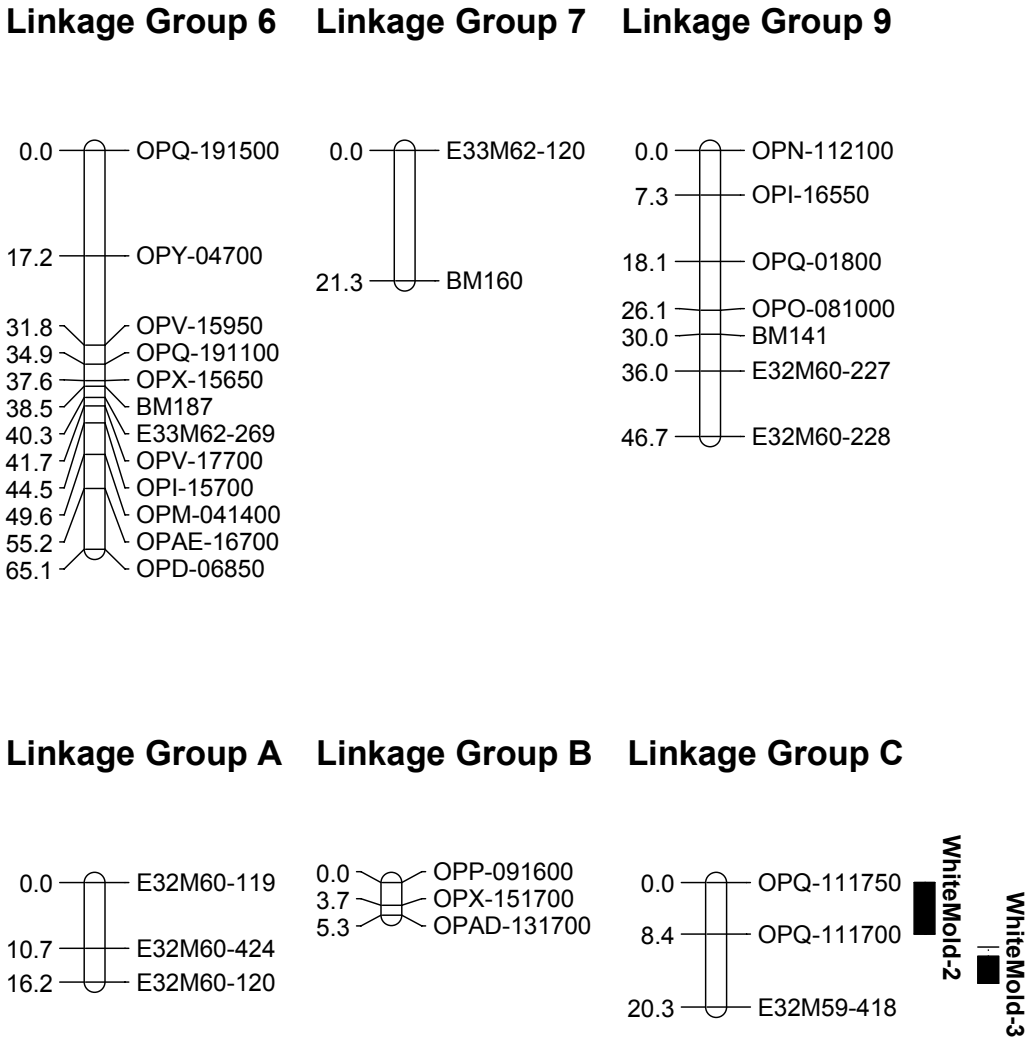


Figure 3.1. (Continued)

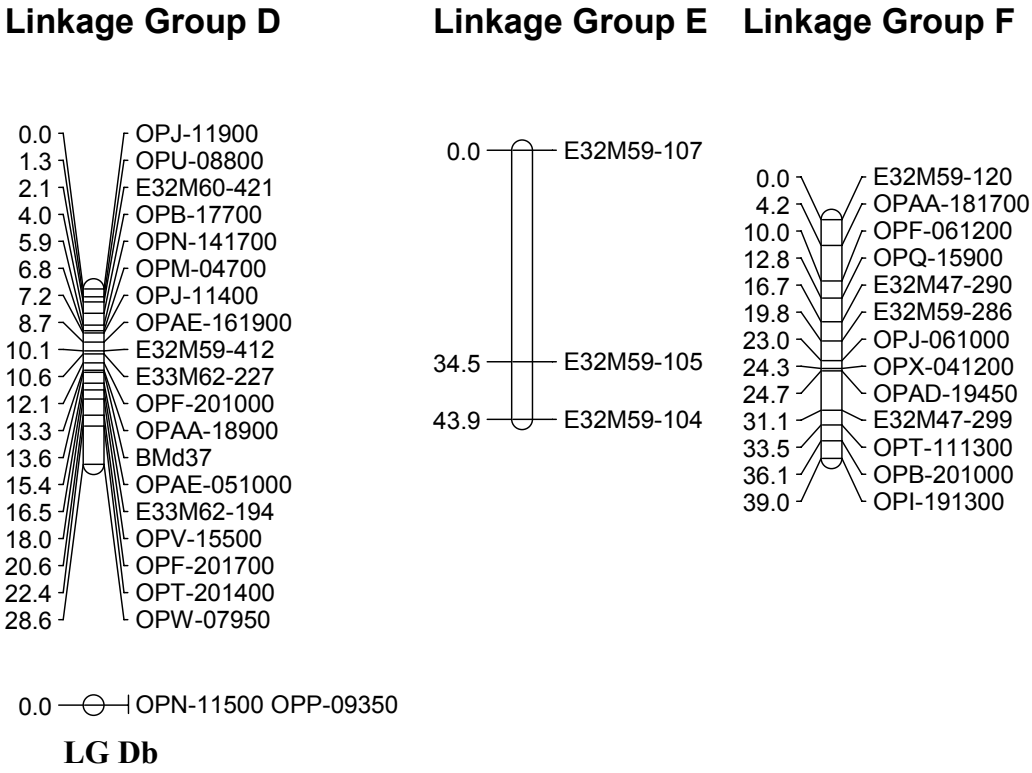


Figure 3.1. (Continued)

Distortion

Thirty markers segregated significantly different from a 3:1 expected model. Overall, 11% of markers showed distorted segregation. Most distorted groups were composed of short segments of 2 - 5 markers. Of the longer groups, LG 1a had 27% and LG 1c had 80% segregation distorted markers (Table 3.4, Figure 3.2 and 3.3). The other linkage groups had only one or two markers with distorted segregation ratios and seemed to be largely unaffected by it.

Table 3.4 Number of markers by linkage group showing segregation distortion from the cross Wolven Pole/PI 255956.

Linkage Group	Markers in Linkage Group	Distorted Markers	
	Total no.		%
1a	45	12	27
1b	20	1	5
1c	5	4	80
1d	2	1	50
1e	2	1	50
2	40	0	0
3	17	2	12
5	17	0	0
6	12	1	8
7	2	0	0
9	7	1	14
A	3	3	100
B	3	0	0
C	3	0	0
D	19	0	0
Db	2	0	0
E	3	3	100
F	13	1	8

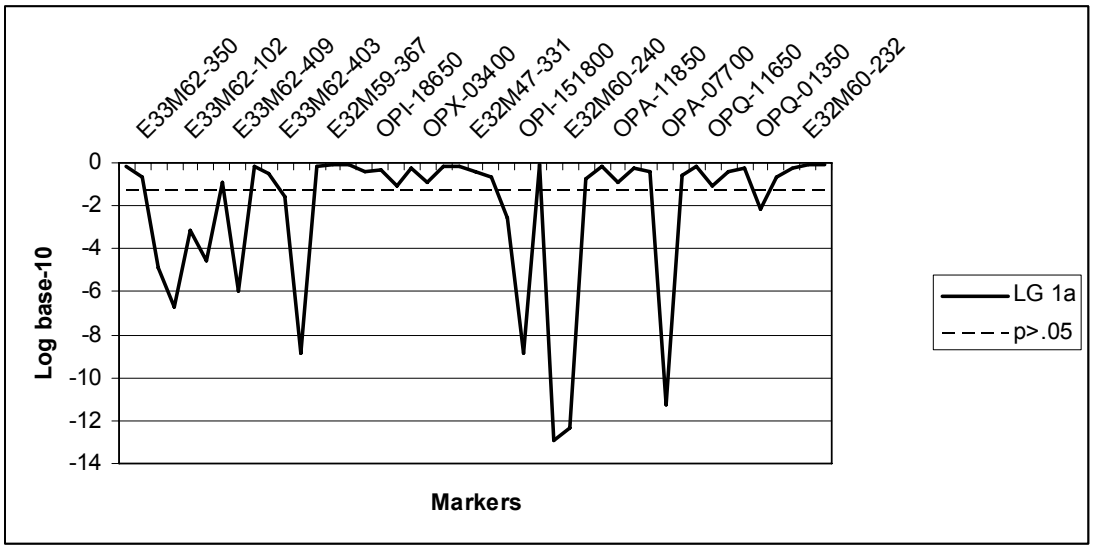


Figure 3.2. AFLP and RAPD markers showing segregation distortion in LG 1a from the Wolven Pole/PI 255956 F_2 population. The probability significance values for the χ^2 of each marker transformed with Log base-10.

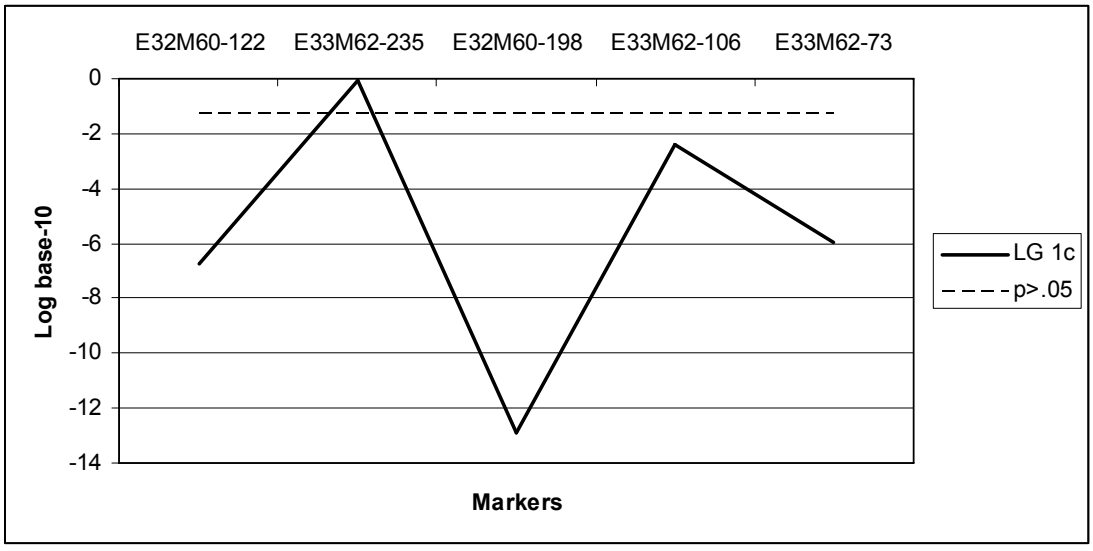


Figure 3.3. AFLP and RAPD markers showing segregation distortion in LG 1c from the Wolven Pole/PI 255956 F_2 population. The probability significance values for the χ^2 of each marker transformed with Log base-10.

Linkage distortion was observed primarily with AFLP markers, where 37% were affected. Only 1.5% of RAPD markers and 9.1% of the SSRs showed distortion.

When distorted markers were removed from the linkage map, we found little difference in the two linkage maps. The linkage map that included distorted markers had greater length because more markers were placed by JoinMap® 4 and the number of small linkage groups was reduced (Table 3.5). Inclusion of distorted markers was necessary for two separate groups to join to form LG1a. There were slight changes in marker order in all groups except for LG 9, LG B, and LG C.

Table 3.5 Comparison of linkage maps created with and without segregation distorted markers for a Wolven Pole/PI 255056 F_2 population.

Linkage Group	Total Markers	Markers removed	LGs w/o Distortion	Markers in both LGs	Markers unmatched in both LGs
			No.		
LG 1a	45	12	29	All 29	4
LG 1b	20	1	19	all 19	0
LG 1c	5	4		No Group	
LG 1d	2	1		No Group	
LG 1e	2	1		No Group	
LG 2	40	0	40	All 40	0
LG 3	17	2	15	All 15	0
LG 5	17	0	17	All 17	0
LG 6	12	1	10	All 10	1
LG 7	2	0	2	All 2	0
LG 9	7	0	6	All 6	1
LG A	3	3		No Group	
LG B	3	0	3	All 3	0
LG C	3	0	3	All 3	0
LG D	19	0	19	All 19	0
LG Db	2	0	2	All 2	0
LG E	3	3		No Group	
LG F	13	1	12	All 12	0

Table 3.6 SSR markers placed on Wolven Pole X PI255956 linkage map.

Marker	Tm (°C)	Predicted size (bp)	Actual Size (bp)	Genotypic Class[z]	Source of Primer
BM141	59	218	160-220	a,b,h	(Gaitan-Solis et al. 2002)
BM156	52	267	200-280	a,b,h	(Gaitan-Solis et al. 2002)
BM157	54	113	90-150	a,b,h	(Gaitan-Solis et al. 2002)
BM159	52	198	190-270	a,c	(Gaitan-Solis et al. 2002)
BM160	52	160	180-290	a,b,h	(Gaitan-Solis et al. 2002)
BM175	59	170	120-180	a,b,h	(Gaitan-Solis et al. 2002)
BM187	56	191	150-200	a,b,h	(Gaitan-Solis et al. 2002)
BMd26	59	141	110-190	a,b,h	(Blair et al. 2003)
BMd28	59	151	100-140	b,d	(Blair et al. 2003)
BMd36	56	164	150-240	a,b,h	(Blair et al. 2003)
BMd37	47	134	550	a,c	(Blair et al. 2003)

[z]JoinMap® Symbol--a for homozygous recessive PI255659, b for homozygous recessive Wolven Pole, h for known heterozygotes, c not genotype PI255659 (the Wolven Pole allele is dominant), d not genotype Wolven Pole (the PI255659 allele is dominant).

In Table 3.6, the SSRs located on the linkage map Wolven Pole/PI 255956 are shown with expected sizes and range in actual size. Eleven markers were placed, and all but BMd37 had actual size range similar to predicted size range. BM160 appears to be slightly higher than expected, but this is most likely due to our inability to accurately size these bands on agarose. Also since our population is is *P. coccineus* these may be different alleles. The fragment amplified by the BMd37 primers was four times expected size, suggesting that the locus amplified by these primers was not the one for which it was designed. BMd37 segregated in the expected 3:1 ratio (Prob. = 0.39), so although not the expected locus, this should be an acceptable marker to place on the map.

Table 3.7 SSR Markers placed on the Wolven Pole/PI 255956 *P. coccineus* map that have been mapped to other microsatellite or consensus maps in *P. vulgaris.* Anchoring the Wolven Pole/PI 255956 map to the *P. vulgaris* consensus map.

Wolven Pole/ PI 255956 Linkage Groups	SSR Markers	Chromosome Name	Reference Map Source
LG 1a	BM157	b01	(Blair et al. 2003)
LG 2	BM156[z]	b02d	(Freyre et al. 1998)
LG 2	Bmd26[z]	b04b	(Freyre et al. 1998)
LG 3	BM159	b03c	(Freyre et al. 1998)
LG 3	Bmd36	b03c	(Freyre et al. 1998)
LG 5	BM175	b05e	(Freyre et al. 1998)
LG 5	Bmd28	b05e	(Freyre et al. 1998)
LG D	BMd37[y]	b06g	(Freyre et al. 1998)
LG 7	BM160	b07a	(Freyre et al. 1998)
LG 9	BM141	b09k	(Freyre et al. 1998)
LG 6	BM187[y]	b06	(Blair et al. 2006)

[z]JoinMap® places these to markers on the same linkage group up to LOD 8. [y]On consensus map these are both on group b06 but according to JoinMap® they are linked only at LOD 2.

Eleven microsatellite markers allowed us to anchor some LGs from the *P. coccineus* map to the *P. vulgaris* map. Where more than one marker was in the same LG, it generally matched the placement on the consensus map (Figure 3.4). There were two exceptions, however. BMd37 and BM187 have been placed on LG b06 on the consensus map, but BMd 37 was associated with a different LG in our Wolven Pole/PI255956 map (Table 3.7). This may be explained by the fact that while the expected fragment size for BMd37 is 134 bp, the band actual size we observed was 550 bp, and probably represents a different locus (Table 3.6). While BM156 and BMd26 were tightly linked at LOD 8 on the *P. coccineus* map, these were placed on different LGs of the consensus map. This could be due to a data entry mistake, an inter-species chromosomal rearrangement, or a difference in locus identified. The last

explanation would appear to be remote since the bands seen are the expected size. We chose to place BM156 and Bmd26 on LG 02 although we might have easily placed the two markers on LG 04. In other mapping studies most microsatellites map where originally published, but a few mapped to other locations. This is true for BM189, which Blair et al. (2003) mapped to LG b08 but was found by Haggard and Myers, and Terpstera and Kelly (unpublished data) to map to LG 03.

In two cases, we found that markers reported to be linked on the consensus map were linked in the *P. coccineus* map. On LG 3 of the *P. coccineus* map, BM159 and BMd36, were 5.4 cM apart, but on the consensus map the same two markers are approximately 33 cM apart. Similarly, BM175 and BMd28, are 20.7 cM apart on LG 5 whereas on the consensus map, these markers are separated by 62 cM. With the exception of BM156 and BMd26, other SSR markers were unlinked. Differences in linkage distances between the two species were observed. Reduced linkage distance may be related to differences in recombination frequency, or differences in marker saturation on the maps.

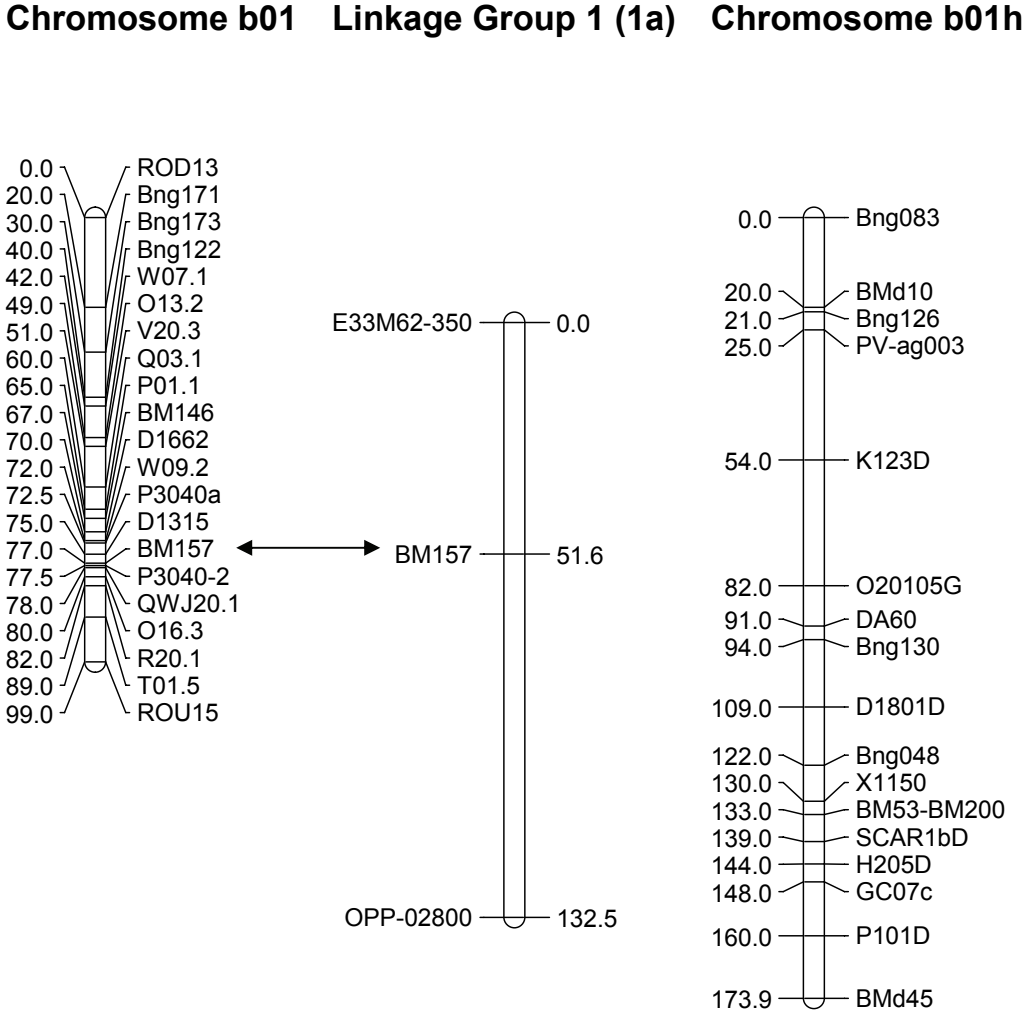


Figure 3. 4 Alignment of the Wolven Pole/PI 255956 *P. coccineus* map with the Blair et al., 2003 *P.* vulgaris microsatellite map. Blair linkage groups are indicated by "b" followed by a number and letter; the *P. coccineus* linkage groups have just numbers followed in some cases by a letter. Only the terminal markers and microsetellites used to align the *P. coccineus* linkage groups are shown. Arrows indicate markers anchored to the consensus map.

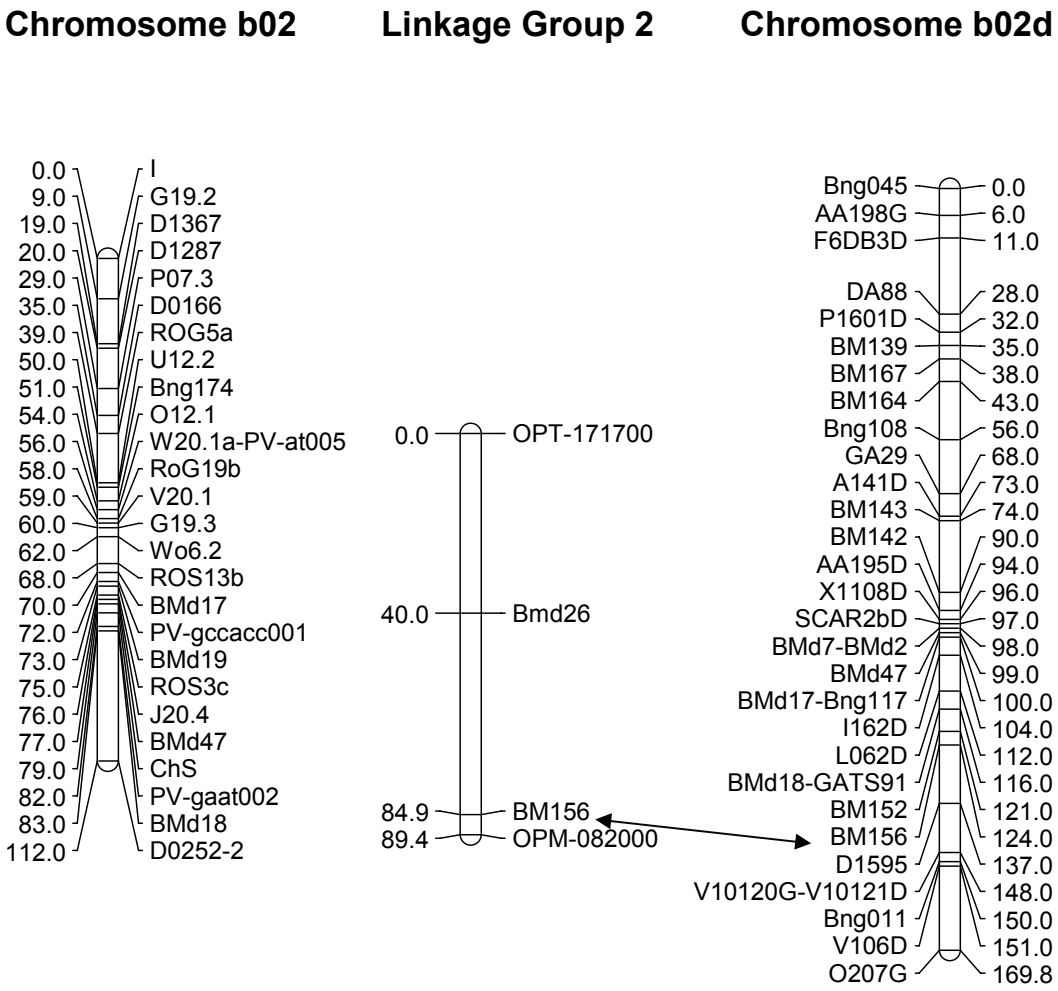


Figure 3.4 (Continued)

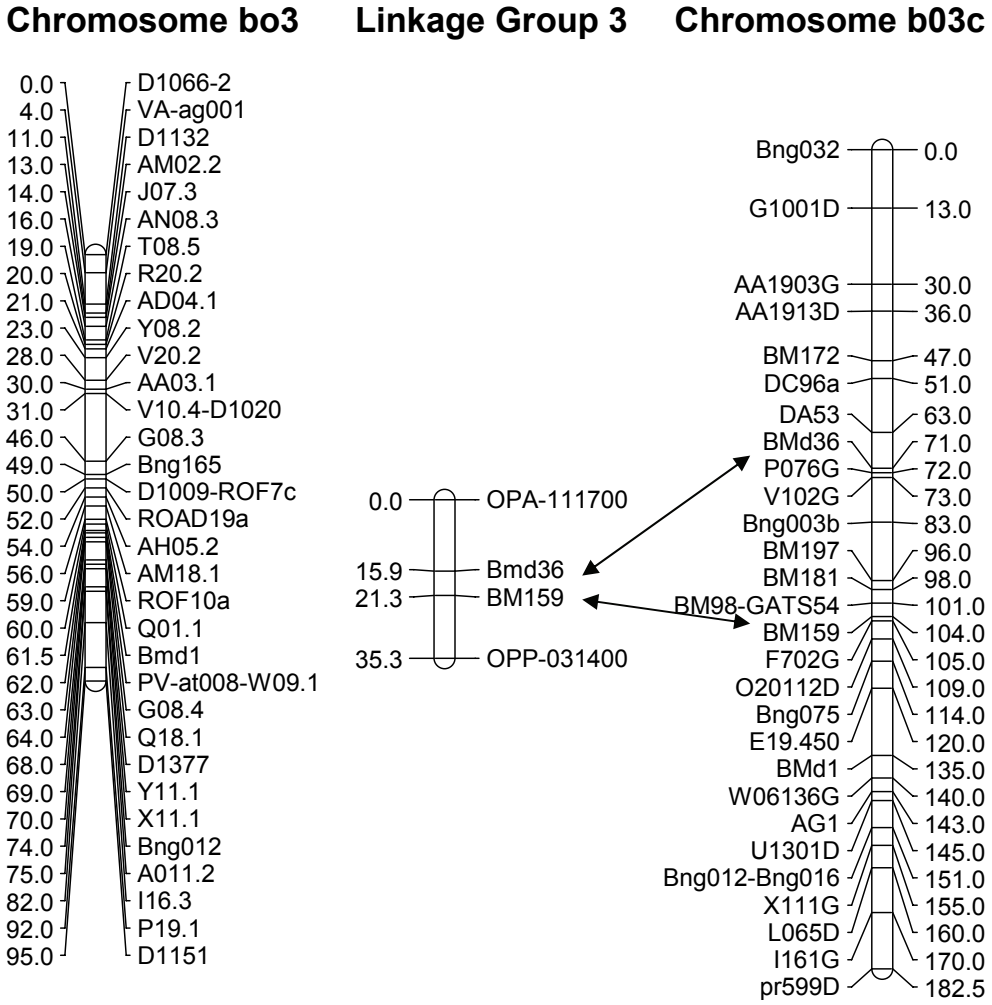


Figure 3.4 (Continued)

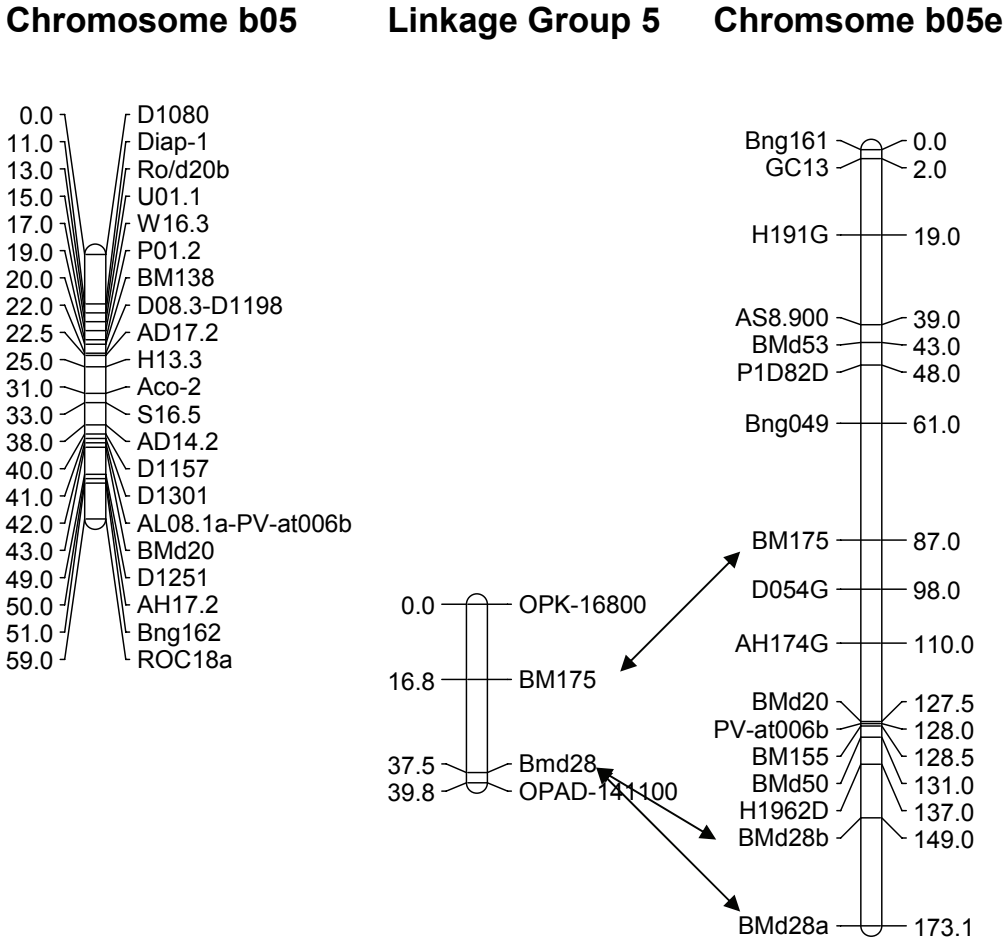
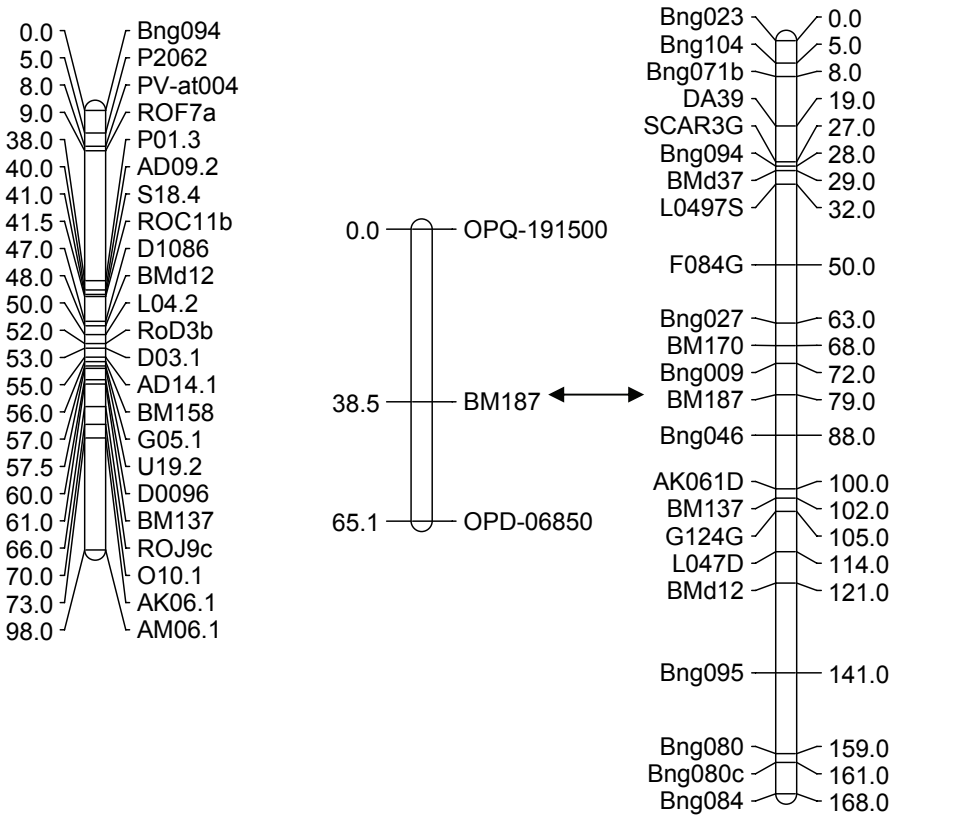


Figure 3.4 (Continued)



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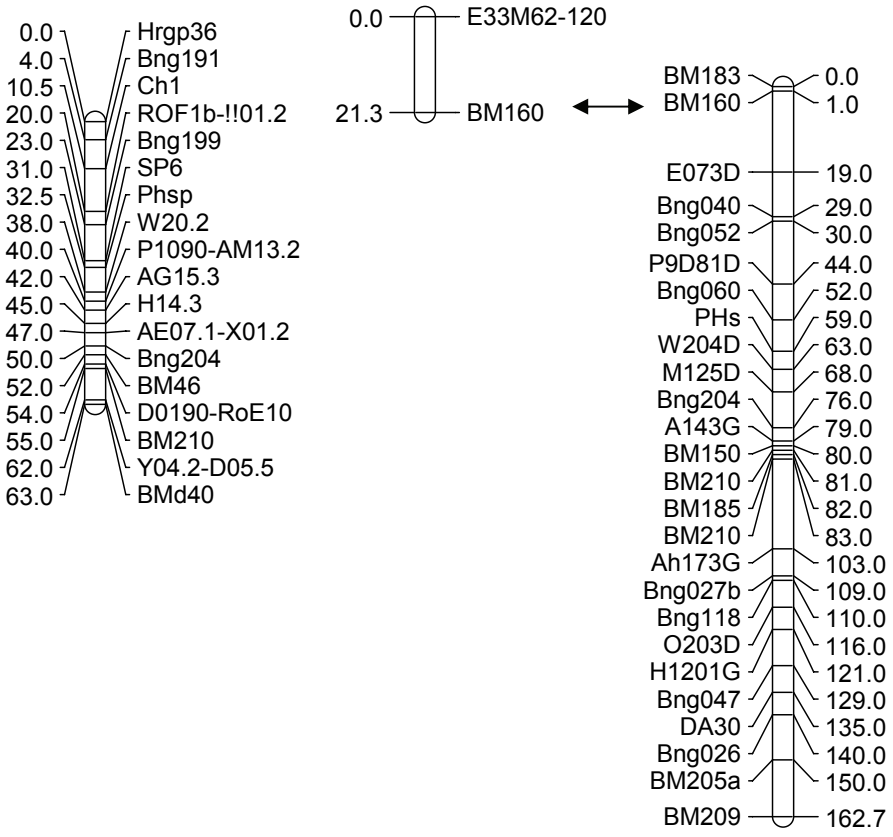

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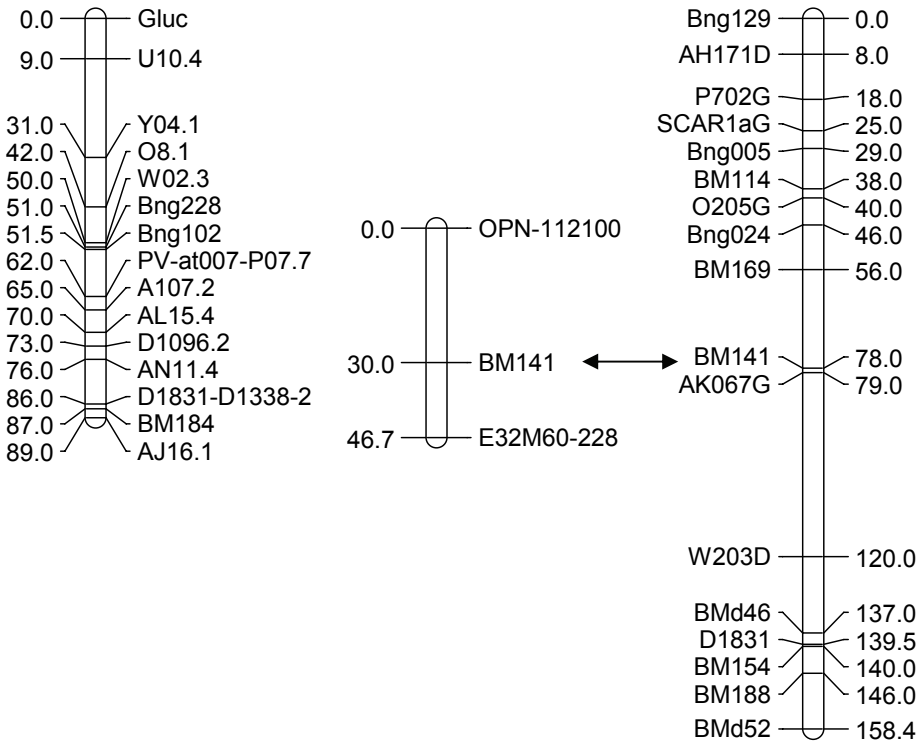


Figure 3.4 (Continued)

Resistance QTL associated with eight day straw test

Single marker analysis suggested the possibility that QTL were located on linkage groups LG 1a, LG 1c, LG D, LG Db and LG 5, Table 3.8. Only the LG 1c and LG D QTL were highly significant. No QTL were located by interval mapping, but composite interval mapping identified two QTL, the first located on LG 1c and the second on LG 5. Based on a significance level of 0.001 and 1000 permutations, the percent variance explained (R^2) for these two QTL were 7.2% and 6.6% respectively.

These two QTL are shown on our linkage map (Figure 3.1). Multiple interval mapping analysis located three QTL, but all had LOD scores under 1.5 and could not be placed on the linkage groups. Bayesian interval mapping located five QTL on five linkage groups, but these were not consistent with QTL identified by other methods. Also only 11,452 times out of the 100,000 iterations that BIM calculated were the five QTL found was closest to this QTL and contributed up to 21.3% of phenotypic variation for resistance. The LOD score for this QTL was a relatively low 2.8. Both QTL were also identified by Bayesian Interval Mapping using 99,000 iterations.

Table 3.8 Summary of WinQTLCartographer white mold resistance at eight days QTL mapping results in a Wolven Pole/PI 255956 F_2 population.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD[y]	R^2 (%)	Additive effect	Domin-ance effect	No. of iterations
SMA	LG 1a	E33M62-102	14.3	.030*						
	LG 1a	OPN-08-1700	88.36	.020*						
	LG 1c	E33M62-106	73.15	.003**						
	LG 1c	E33M62-73	89.66	.003**						
	LG D	OPN-14-1700	5.85	.020*						
	LG D	OPM-04-700	6.81	.027*						
	LG D	OPJ-11-400	7.24	.030*						
	LG D	OPAE-16-1900	8.73	.036*						
	LG D	E32M59-412	10.13	.032*						
	LG D	E33M62-227	10.57	.025*						
	LG D	OPF-20-1000	12.08	.010*						
	LG D	OPAA-18-900	13.28	.015*						
	LG D	Bmd37	13.64	.014*						
	LG D	OPAE-05-1000	15.41	.017*						
	LG D	E33M62-194	16.47	.013*						
	LG D	OPV-15-500	17.96	.007**						
	LG D	OPF-20-1700	20.59	.043*						
	LG D	OPT-20-1400	22.42	.030*						
	LG D	OPW-07-950	28.63	.022*						
	LG Db	OPN-11-500	0	.015*						
	LG Db	OPP-09-350	0	.015*						
	LG 5	OPK-16-800	0	.027*						

Table 3.8 Continued.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD [y]	R^2 (%)	Additive effect	Domin-ance effect	No. of iterations
	LG 5	OPE-08-900	7.09	.012*						
	No QTL									
Im	Found									
CIM	LG 1a	E32M47-167	98.5		0.001	2.67	7.2	0.02	0.37	
	LG 5	OPK-16-1300	12.7		0.001	2.63	6.6	-0.15	0.27	
MIM	LG 1a	OPA-07-700	99.5		0.001	1.2		-0.1948	-0.4816	
	LG 1c	E33M62-73	82.2		0.001	1.34		-0.3569	0.0838	
	LG 2	E32M60-385	17.7		0.001	0.4		0.0135	0.1498	
BIM	LG 1c	E33M62-73	87.4			2.86		-0.1187	-0.2054	99900
	LG 5	BMd28	36.73			2.86		-0.0935	0.0626	99900
	LG 2	OPAB-08-1400	73.84			2.86		-0.0528	-0.0055	99900
	LG 9	E32M60-228	44.62			2.86		-0.0268	-0.0545	99900
	LG A	OPQ-111700	8.37			2.86		0.0035	0.117	99900

[z]SMA = Single Marker Analysis, Im = Interval Mapping, CIM = Composite Interval Mapping, MIM = Multiple Interval Mapping, BIM = Bayesian Interval mapping. [y]LOD (base 10 algorithm of the likelihood ratio) threshold of 2.5 used for QTL detection, LOD thresholds based on 1000 permutations as suggested by Churchill and Doerge (Churchill and Doerge 1994).

Table 3.9 Summary of WinQTLCartographer white mold resistance over five weeks QTL mapping results in a Wolven Pole/PI 255956 F_2 population.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD[y]	R^2 (%)	Additive Effect[t]	Dominance effect[u]	No. of iterations
SMA	LG 1a	E33M62-350	0	.035*						
	LG 1a	OPU-03_{950}	56.79	.044*						
	LG 1a	E32M47-331	57.62	.036*						
	LG 1a	OPI-15_{1000}	51.35	.029*						
	LG 1a	E32M60-123	85.71	.035*						
	LG 1c	E33M62-73	89.66	.044*						
	LG C	OPQ-11_{1700}	8.41	.029*						
	LG C	E32M59-418	20.32	.008**						
	LG 6	OPY-04_{700}	17.22	.021*						
Im	LG 1e	E32M47-232	0.1201		0.001	3.2	9.5	0.247	-0.545	
	LG C	OPQ-11_{1700}	0.1241		0.001	10.3	71.6	0.531	3.223	
CIM	LG 1c	E32M60-122	0.0601		0.001	2.8	21.6	-0.032	1.489	
	LG C	OPQ-11_{1700}	0.0601		0.001	7.4	60.2	-3.569	0.260	
	LG C	OPQ-11_{1700}	0.1241		0.001	9.9	68.0	0.595	3.174	
MIM	LG C	OPQ-11_{1700}	13.4		0.001	5.4	71.7	-0.501	3.044	
BIM	LG 1c	E32M60-122	11.7			45.8		-0.006	1.890	99900
	LG C	OPQ-11_{1700}	14.7			45.8		-0.217	2.616	99900

[z]SMA = Single Marker Analysis, Im = Interval Mapping, CIM = Composite Interval Mapping, MIM = Multiple Interval Mapping, and BIM = Bayesian Interval mapping. [y]LOD (base 10 algorithm of the likelihood ratio) threshold of 2.5 used for QTL detection, LOD thresholds based on 1000 permutations (Churchill and Doerge 1994).

Resistance QTL associated with five week straw test

Using Windows QTL Cartographer© and Single Marker Analysis to search for QTL relating to physiological resistance to white mold (five week straw test), we observed QTL on LG1a, LG1c, LG C and LG D, but only the QTL on LG C was highly significant (Table 3.9). Interval mapping with significance level set at 0.001 and 1000 permutations, revealed QTL on LG C and LG1e. The percent phenotypic variation explained by these QTL was 71.6% and 9.5%, respectively. The LOD score was relatively low for LG 1e at 3.2, but very informative for LG C at 10.3. SMA and Interval Mapping results do not completely agree with CIM and BIM. Using CIM, the same two QTL identified by IM were found on LG1c and LG C. LG 1c, was independently mapped to LG 1 by JoinMap®, but could not be combined in a single analysis. Of the three markers associated with the QTL on LG C, two were RAPD markers (OPQ-11_{1700} and OPQ-11_{1750}) and one was an AFLP marker (E32M59-418). OPQ-11_{1700} was closest to this QTL (LOD 9.9) and contributed up to 68.6% of the phenotypic variation for partial physiological resistance to *S. sclerotiorum* with the five week straw test. LG C did not match to any chromosomes on any consensus map. However, OPQ-11_{1700} maps to LG 11 on the OSU 5630/Minuette map (Myers et al. 2004). Because a major criticism of the use of RAPD markers is that bands of similar molecular weight may not be identical in sequence, we cannot conclude that LG C is part of consensus LG 11, but it suggests where additional mapping could be focused. E32M60-122 and E33M62-235 AFLP markers were associated with the QTL on LG 1c. E32M60-122 was closest to this QTL and contributed up to 21.3% of phenotypic

variation for resistance. The LOD score for this QTL was a relatively low 2.8.

Both QTL were also identified by Bayesian Interval Mapping using 99,000 iterations.

a) Linkage Group 1c QTL.

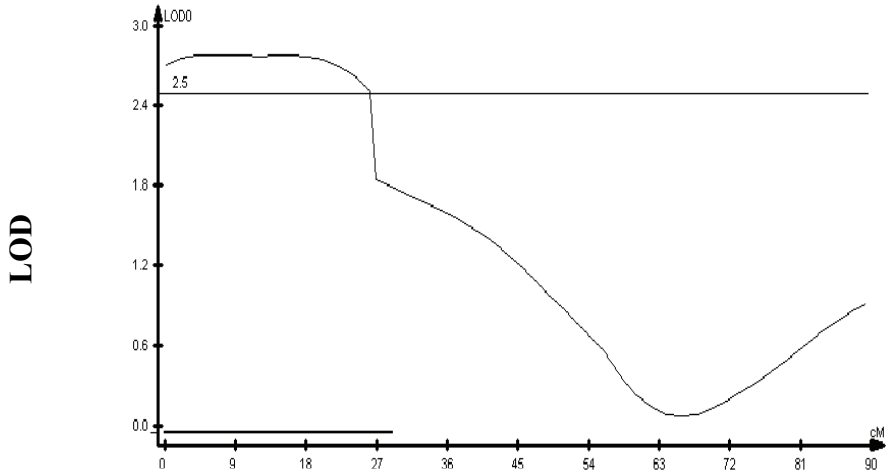
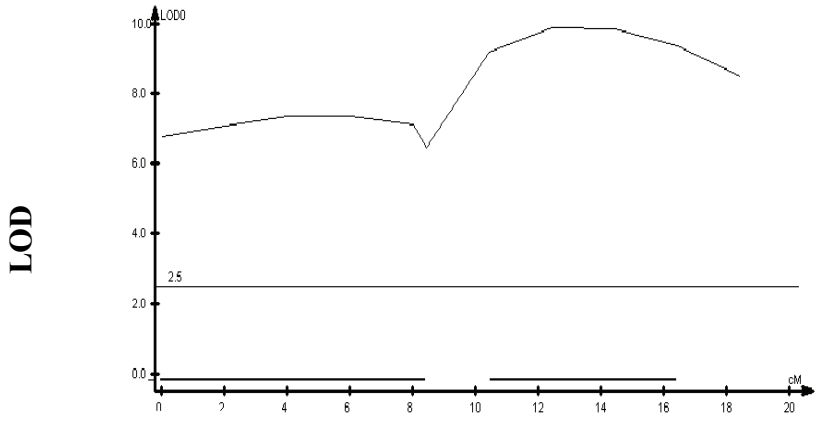


Figure 3. 5 Graphical representation of QTLs for white mold resistance in the five week straw test for a Wolven Pole/PI 255956 F_2 population. LOD scores are from composite interval mapping and scores above the threshold level of 2.5 indicate an experiment-wise error rate of 0.001 determined by 1000 permutations. The x-axis corresponds to cM distance on Figure 3.1.

b) Linkage Group C QTL



Discussion

Our *P. coccineus* map spans 797 cM, and consists of thirteen LGs. Because *P. coccineus* has only eleven chromosomes (n = 11) two of the 13 LGs could be associated with others with enough marker saturation of the map. In our study, seven LGs were anchored by SSR markers, leaving four LGs unknown with six candidate fragments. The length of our map is comparable to other maps published in *P. vulgaris*. The longest *P. vulgaris* maps were created by Blair et al. (2003) at 1,720cM, and the consensus map at 1,226 cM (Freyre et al. 1998). Other published maps have ranged from Paris map at 567.5 cM (Adam-Blondon et al. 1994), the Davis map of 827 cM (Nodari et al. 1993) and the Florida map, which was 960 cM in length (Vallejos et al. 1992). If the consensus map figure of 1,226 cM is used as a reference, the *P. coccineus* map developed here covers approximately 65% of the genome.

Common bean consists of two major gene pools, Andean and Mesoamerican and within these gene pools only low levels of polymorphism can be found. To obtain the highest levels of polymorphism mapping projects include parents from both pools to dramatically increase polymorphism among genotypes (Singh 1999). About 14% of our RAPD primers were polymorphic within our population, well below the 60% rate seen in the intra-gene pool polymorphism and 80% for between gene pools (Singh 1999). We also found a much lower rate of polymorphism, 14%, in our SSRs than Blair et al. (2003). They found polymorphism rates depending on the population and the type of microsatellites of 42.2 to 65.4%, but they were using a Mesoamerican X Andean population (Blair et al. 2003)

In our experience with evaluating *P. coccineus* accessions, we have never found one as susceptible to white mold as most *P. vulgaris* lines. In general, the worst *P. coccineus* is about as resistant as the best *P. vulgaris* lines. Thus, in creating this population by crossing a moderately susceptible accession with a highly resistant one, we hypothesized that the standard eight day straw test would not be sufficient to distinguish between incremental differences in resistance. The data revealed that fewer QTL related to straw test reading at eight days were found than when a more extended rating period was used. PI 255956 had a straw test score of three at eight days and by four weeks had moved to a four. Wolven Pole at eight days had a straw test score of five with the lesion slowly but continually progressing until removed.

LG 1 and LG 5 have had QTL associated with white mold resistance located on *P. vulgaris* maps. Miklas et al. (2001) located four QTL on two linkage groups using a G122/A55 population, with two agronomic traits on LG b01 related to canopy porosity and plant height. Plant architecture almost certainly influenced field resistance in the Miklas et al. study because G122 is determinant and A55 is indeterminate (upright short vine). The most informative QTL in the G122/A55 population was found on LG b07, explaining 38 and 26% of the phenotypic variance for the straw test and field results, respectively (Miklas et al. 2001). Ender and Kelly (2003, 2005) developed two *P. vulgaris* populations that had Bunsi as the white mold resistant parent. From these populations they discovered two QTL on LG b02, one QTL on LG b05, one QTL on LG b08 and two on LG b07 all relating to white mold resistance (Ender et al. 2003; Ender and Kelly 2005).

Measuring resistance to white mold using the five week straw test allowed better discrimination of level of resistance among progeny, and revealed other QTL with stronger effect. It is interesting to note that the QTL observed in the eight day straw test were found on different LGs from those found in the five week straw test. While both ratings placed QTL on LG 1, they were placed in different locations, and in fact, different methods placed QTL at different locations for LG 1 for the five week straw test data (Table 3.9). The QTL found on LG C appears particularly strong, explaining 60 – 72% of phenotypic variation. What is unusual about this QTL is that it appears to actually be two tightly linked major QTL, each being contributed by Wolven Pole. Since LG C consists of only three markers we are considering the QTL as one instead of two QTL. It seems very reasonable that as more markers were added to the map, it would become one. Unfortunately, we have been unable to anchor this LG C to the consensus map. Based on the map location of OPQ-11_{1700} on the OSU 5630/Minuette map, we suspect that it may reside on LG 11. In any case, it appears that the QTL for partial white mold resistance identified in this study are unlikely to match any found by other researchers when mapping *P. vulgaris*. Markers for our QTL that explains 68% of the phenotypic variance need to be converted to SCARs and placed on the consensus map.

In 2004 we published a preliminary molecular marker map paper in the Annual Report of the Bean Improvement Cooperative (Gilmore and Myers 2004). We used interval mapping to place five QTL for white mold resistance on five separate linkage groups. The only QTL that matched to the newest map is that placed on LG C. The

other four QTL were linked to groups that have no QTL in the present map. The five QTL in the previous map when combined explained more than 100% of the phenotypic variance. The present map explains 72 – 90% depending on the method used. Our explanation for difference is that the previous version of the map was based on ninety-four RAPD markers and eleven SSR markers in a population that was represented by only ninety-four F_2 progeny. In the current map version, the eleven SSR markers were placed in the complete population, as were the one hundred AFLPs. We feel that the explanation for the excessive phenotypic variation explained in our preliminary map was that the population was too small for QTL with minor effect to be identified.

As mentioned previously, all accessions of *P. coccineus* that we tested have an innate resistance that is lacking in most *P. vulgaris* accessions. One implication of this is that an interspecies cross population should generate more QTL than identified here, assuming that the innate difference between the species is heritable. It is possible that the innate difference is related to a fundamental difference in metabolism or morphology of the two species, and may not be successfully transferred from *P. coccineus* to *P. vulgaris*. Others have encountered difficulty transferring various traits to *P. vulgaris* (Lamprecht 1957; Wall and York 1957; Manshardht and Bassett 1984), but it is apparent that some portion of white mold resistance is transferable as shown by M0162 and other of the "M0" lines generated by Lamprecht from *P. coccineus* x *P. vulgaris* crosses (Haggard and Myers 2007).

While some researchers have reported quantitative inheritance (Adams et al. 1973), others have reported a single dominant gene in *P. coccineus* being responsible for white mold resistance (Abawi et al. 1978; Schwartz et al. 2004; Schwartz et al. 2006). One difficulty with developing a qualitative model for resistance to white mold is that disease reaction in a continuous variable, and one does not know where to draw the line between resistance and susceptibility. Finding a QTL that explains 68% of phenotypic variation could indicate that resistance to white mold is fairly simply controlled. In studies where the environmental variation can be carefully controlled, it may be possible to distinguish qualitative inheritance with a QTL of such large magnitude. Overall, we expect that additional QTL in *P. coccineus* will be found because so many different defense pathways are thought to be involved.

To our knowledge, this map represents the first linkage map for *P. coccineus*. The two QTL for partial white mold resistance are valuable resources in the effort to develop white mold resistant snap and dry beans. As the value of *P. coccineus* becomes more appreciated as a donor parent for resistance to white mold, this map will acquire added importance. We have seen several different mechanisms of resistance in *P. coccineus*, with perhaps the most significant being its tolerance to oxalic acid. Some work has been conducted in this area (Chipps et al., 2005), but more work is needed to explore why some *P. coccineus* accessions are able to tolerate much higher levels of oxalic acid solutions than do other *Phaseolus* species. There are also hints that other plant defense pathways may be involved with *P. coccineus* resistance to white mold. For example we sometimes observed the appearance of

putative phytoalexins at the edge of the lesion caused by the pathogen. *P. coccineus* also managed to slow and in some cases, stop the spread of a white mold lesion down the stem. The mechanism by which it accomplishes the attenuation of infection needs study. Although white mold possesses many weapons to facilitate its attack on the host, but *P. coccineus* seems to have many defenses to these weapons, and deserves further study.

CHAPTER 4. GENERAL CONCLUSION

Introduction

The common bean (*Phaseolus vulgaris*) is a cheap and nutritious food available to many people in areas of the world that do not have easy access to animal proteins in their diet (Gepts 1988; Young and Pellett 1994). Common bean is the most widely grown of the grain legumes, both for dry seed consumption as well as vegetable uses.

White mold caused by *Sclerotinia sclerotiorum* (Lib,) de Bary, causes widespread loss of yield and quality in both snap and dry beans. In some extreme instances, there can be a one hundred percent yield loss under irrigated situations (Hall 1994). In green beans when the pod infection incidence exceeds 5%, the processor will reject the field (Stivers 2000). Foliar applications of fungicides applied prophylactically can control white mold. Timing is critical, and two applications may be needed. Fungicides currently available are expensive and may eliminate any net profit realized by the grower when their crop is sold to the processor. No fungicide currently exists that effectively controls white mold after the disease is widespread in the field (Hall 1994; du Toit et al. 2006). The environmental and human health impacts are concerns as well. In 2005, Ronalin, the most effective fungicide registered for white mold control was removed from the market by EPA because of health and environment concerns (Pscheidt 2006).

Significance of the present research

Our initial work was focused on examining many different sources of common bean to find physiological resistance to white mold. The cultivars and lines tested were all decimated by the disease, with little genetic variation for resistance. We then examined other species, beginning with *P. coccineus*. Our first cultivars from a Thompson & Morgan seed catalog had more resistance then we had previously seen in any *Phaseolus* species, including other *P. coccineus* varieties. The number of *P. coccineus* accessions available commercially is small, and we needed to acquire more material to evaluate.

Our preliminary effort was to examine the collection of *P. coccineus* from the U.S. Department of Agriculture National Plant Germplasm System. We found an amazing array of genetic variation contained in the collection, and a relatively high degree of resistance within the collection compared to *P. vulgaris*. The *P. coccineus* collection had not had previous extensive testing for any character apart from bean golden mosaic virus resistance. At the time of this study, the species identity of *P. dumosus* was clarified. We identified this species and *P. vulgaris* in the collection, sometimes as mislabeled accessions, sometimes as mixtures with *P. coccineus*.

When examining the accessions for resistance to white mold, the adjusted means by species ranked *P. coccineus* having the lowest mean score, followed by *P. vulgaris* and last by *P. dumosus*. Based on comparison to the checks, *P. vulgaris* and *P. dumosus* do not differ significantly, but *P. coccineus* is significantly most resistant.

This confirmed our hypothesis that there is greater resistance in *P. coccineus* then in the accessions that we sampled of the other two species.

In the past, selected *P. coccineus* accessions were screened for white mold resistance (Adams et al. 1973; Abawi et al. 1978; Lyons et al. 1985), but the results we presented here represent the first time that the entire available *P. coccineus* plant introduction collection was tested with the pathogen *S. sclerotiorum*.

Using the most resistant plants of the accessions we tested we developed F_2 populations for testing. We discovered that some F_2 populations had very skewed resistance/susceptibility ratios from the expected ratio of 3:1 or 1:2:1. With that in mind we focused our efforts on a cross that had excellent resistance in the F_2 population and a normal resistance/susceptibility ratio for the second phase of our work.

From our chosen F_2 population (Wolven Pole/PI 255956), we developed a linkage map for *P. coccineus/P. coccineus.* Our *P. coccineus* map spans 797 cM, and consists of thirteen LGs. Because *P. coccineus* has only eleven LGs (n=11) two of the 13 LGs are probably associated with others and could be oriented with sufficient marker saturation. In our study, seven LGs were anchored by SSR markers, leaving four LGs unknown with six candidate fragments. The length of our map is comparable to other maps published in *P. vulgaris*. The longest *P. vulgaris* map is 1,720 cM (Blair et al. 2003), and the consensus map is 1,226 cM (Freyre et al. 1998). Other published maps ranged from 567.5 cM for the Paris map (Adam-Blondon et al. 1994), the Davis map of 827 cM (Nodari et al. 1993) and the Florida map, which was 960 cM (Vallejos et al.

1992). If the consensus map figure of 1,226 cM is used as a reference, the *P. coccineus* map developed here covers approximately 65% of the genome.

In 2004 we published a preliminary molecular marker map paper in the Annual Report of the Bean Improvement Cooperative (Gilmore and Myers 2004). We used interval mapping to place five QTL for white mold resistance on five separate linkage groups. The only QTL that matched to the newest map is that placed on LG C. The other four QTL were linked to groups that have no QTL in the present map. The five QTL in the previous map when combined explained more than 100% of the phenotypic variance. The present map explains 72 – 90% depending on the method used. Our explanation for difference is that the previous version of the map was based on ninety-four RAPD markers and eleven SSR markers our population that were represented by only ninety-four F_2 progeny. In the current map version, the eleven SSR markers were placed in the complete population, as were the one hundred AFLPs. We feel that the explanation for the excessive phenotypic variation explained in our preliminary map was that the population of 94 individuals was too small for QTL with minor effect to be identified. In the present map, the major QTL on LG C is associated with the susceptible parent, Wolven Pole. We would very much have liked to find the QTL linked to the donor parent PI255956. In our interspecific crossing program, we have used PI 255956 but not Wolven Pole as the source parent for transfer of white mold resistance into common bean. In the one interspecific population mapped so far, the AFLP marker segregates in the population, but is unlinked (unpublished data). The present study suggests that we should create SCAR

markers from the Wolven Pole RAPD markers on LG C, that would potentially be useful for marker assisted selection.

To our knowledge, this map represents the first linkage map for *P. coccineus*. The two QTL for partial white mold resistance are valuable resources in the effort to develop white mold resistant snap and dry beans. As the value of *P. coccineus* becomes more appreciated as a donor parent for resistance to white mold, this map will acquire added importance. We have seen several different mechanisms of resistance in *P. coccineus*, with perhaps the most significant being its tolerance to oxalic acid. Some work has been conducted in this area (Chipps et al., 2005), but more work is needed to explore why some *P. coccineus* accessions are able to tolerate much higher levels of oxalic acid solutions than do other *Phaseolus* species. There are also hints that other plant defense pathways may be involved with *P. coccineus* resistance to white mold. For example we sometimes observed the appearance of putative phytoalexins at the edge of the lesion caused by the pathogen. *P. coccineus* also managed to slow and in some cases, stop the spread of a white mold lesion down the stem.

As mentioned previously, all accessions of *P. coccineus* that we tested have an innate resistance that is lacking in most *P. vulgaris* accessions. There are many of these accessions of *P. coccineus* that should to be further examined to determine if the same genes are responsible for white mold resistance throughout the genus. If so, their mechanisms of resistance should be determined, and then used in breeding programs.

The questions arises, why not just transform the common bean with mechanisms to prevent white mold infection? The answer is that the genus *Phaseolus* until very recently was unable to be transformed. It remains a recalcitrant species with only low efficiency transformation. This mandated that the genes for resistance to any disease had to be a constituent of the gene pool. In our work we identified those individuals that possessed the necessary traits that could be used to donate the needed DNA. Even if beans are routinely genetically modified in the future, the *P. coccineus* collection has the necessary genes for resistance to white mold and other diseases.

The main objective of this program was to find resistance to white mold and we succeeded. We were able to identify, quantify and incorporate partial physiological resistance in *P. coccineus* and move part of that resistance into *P. vulgaris*. As more of the lines that have resistant *P. coccineus* accessions as their recurrent parent become advance enough to be evaluated, the severity of this disease may be reduced.

BIBLIOGRAPHY

Abawi, G. S. and R. G. Grogan (1979). "Epidemiology of diseases caused by *Sclerotinia* species." Phytopathology **69**: 899-904.

Abawi, G. S. and J. E. Hunter (1979). "White mold of beans in New York." New York (State). Agricultural Experiment Station, Geneva. New York's food and life sciences bulletin(77).

Abawi, G. S., R. Provvidenti, D. C. Crosier and J. E. Hunter (1978). "Inheritance of resistance to white mold disease in *Phaseolus coccineus* (Scarlet runner beans)." Journal of heredity **69**: 200-202.

Adam-Blondon, A. F., M. Sevignac, M. Dron and H. Bannerot (1994). "A genetic map of common bean to localize specific resistance genes against anthracnose." Genome **37**(6): 915-924.

Adams, P. B. and W. A. Ayers (1979). "*Sclerotinia sclerotiorum*: ecology of *Sclerotinia* species." Phytopathology **69**: 896-899.

Adams, P. B., C. J. Tate, R. D. Lumden and J. P. Meiners (1973). "Resistance of *phaseolus* species to *Sclerotinia sclerotiorum*." Bean Improvement Cooperative. Annual report **16**: 8-9.

Agrios, G. N. (1997). Plant Pathology. San Diego, Academic Press.

Arcade, A., F. Anselin, P. Faivre Rampant, L. Lesage, E. Paques and D. Prat (2000). "Application of AFLP, RAPD and ISSR markers to genetic mapping of European and Japanese larch " TAG Theoretical and Applied Genetics **100**(2): 299-307.

Baggett, J. R. (1956). "The inheritance of resistance to strains of bean yellow mosaic virus in the interspecific cross *Phaseolus vulgaris X P. coccineus*." Plant Disease Reporter **40**: 702-707.

Bassett, M. J., Ed. (1986). Breeding Vegetable crops. Westport, Connecticut, Avi Publishing company, Inc.

Bassett, M. J. (1993). "A new gene for flower color pattern, white banner *(wb),* in progeny of an interspecific hybrid between common bean and scarlet runner beans." Journal of the American Society for Horticultural Science **118**: 878-880.

Bassett, M. J. (2003). "Inheritance of scarlet color and vein pattern in flowers and oxblook red seedcoat color derived from the interspecific cross of common bean with scarlet runner bean (*Phaseolus coccineus* L.)." Journal of the American Society for Horticultural Science **128**: 559-563.

Bateman, D. F. and S. V. Beer (1965). "Simultaneous Production and Synergistic Action of Oxalic Acid and Polygalacturonase during Pathogenesis by *Sclerotium rolfsii*." Phytopathology **55**: 204-211.

Beckman, C. H., W. C. Mueller and M. E. Mace (1974). "The Stabilization of Artificial and Natural Cell Wall Membranes by Phenolic Infusion and its Relation to Wilt Disease Resistance." Phytopathology **64**: 1214-1220.

Blair, M. W., G. Iriarte and S. E. Beebe (2006). "QTL analysis of yield traits in an advanced backcross population derived from a cultivated Andean x wild common bean (*Phaseolus vulgaris* L.) cross." TAG Theoretical and Applied Genetics **112**: 1149-1163.

Blair, M. W., F. Pedraza, H. F. Buendia, E. Gaitan-Solis, S. E. Beebe, P. Gepts and J. Tohme (2003). "Development of a genome-wide anchored microsatellite map for common bean (Phaseolus vulgaris L.) " Theoretical and Applied Genetics **107**(8): 1362-1374.

Boland, G. J. and R. Hall (1987). "Epidemiology of white mold of white bean in Ontario." Canadian Journal of Plant Pathology **9**: 218-224.

Boland, G. J. and R. Hall (1994). "Index of Plant Hosts of *Sclerotinia sclerotiorum*." Canadian Journal of Plant Pathology **16**: 93-108.

Caesar, A. J. and R. C. Pearson (1983). "Environmental Factors Affecting Survival of Ascospores of *Sclerotinia sclerotiorum*." Phytopathology **73**(7): 1024-1030.

Callahan, F. E. and D. E. Rowe (1991). "Use of a Host-Pathogen Interaction System to Test Whether Oxalic Acid is the sole Pathogenic Determinant in the Exudate of *Sclerotinia trifoliorum*." Phytopathology **81**(12): 1546-1550.

Carlderon, E., L. Velasquez and R. Bressani (1992). "Comparative study of the chemical composition and nutritive value of runner bean (*Phaseolus coccineus*) and of common bean (*Phaseolus vulgaris*)." Archivos Latinoamericanos de Nutrición **42**(1): 64-71.

Cessna, S. G., V. E. Sears, M. B. Dickman and P. S. Low (2000). "Oxalic acid, a pathogenicity factor for *Sclerotinia sclerotiorum*, suppresses the oxidative burst of the host plant." Plant Cell **12**(11): 2191-2199.

Chipps, T. J., B. Gilmore, J. R. Myers and H. U. Stotz (2005). "Relationship between oxalate, oxalate oxidase activity oxalate sensitivity, and white mold susceptibility in Phaseolus coccineus." Phytopathology **95**: 292-299.

Churchill, G. A. and R. W. Doerge (1994). "Empirical threshold values for quantitative trait mapping." Genetics **138**: 963-971.

Coffman, C. J., R. W. Doerge, M. L. Wayne and L. M. McIntyre (2003). Intersection tests for single marker QTL analysis can be more powerful than two marker QTL analysis. BMC Genetics. **4**.

Cotton, P., Z. Kasza, C. Bruel, C. Rascle and M. Fevre (2003). "Ambient pH controls the expression of endopolygalacturonase genes in the necrotrophic fungus *Sclerotinia sclerotiorum*." FEMS Microbiology Letters **227**: 163-169.

Davidson, R. M. and R. S. Byther (1982). Sclerotinia Disease (White Mold) of Bean, Washington State University cooperative Extension**:** 1-3.

de Bary, A. (1886). "Ueber einige Sclerotinien and Sclerotienkrankheiten." Botanische Zeitung **44**: 377-474.

Do Vale, F. X. R., J. E. Parlevliet and L. Zambolim (2001). "Concepts in Plant Disease Resistance." Fitopatologia Brasileira **26**(3): 577-589.

du Toit, L., K. Eastwell, D. H. Gent, R. E. Ingham, C. M. Ocamb, N. K. Osterbauer and J. W. Pscheidt (2006). Plant Disease Control, Oregon State University Extension.

Dutton, M. V. and C. S. Evans (1996). "Oxalate production by fungi: its role in pathogenicity and ecology in the soil environment." Canadian Journal of Microbiology **42**: 881-895.

Ender, M. and J. D. Kelly (2005). "Identification of QTL associated with white mold resistance in common bean." Crop science **45**: 2482-2490.

Ender, M., J. D. Kelly and J. M. Kolkman (2003). "Use of inbred backcross method to introduce resistance to white mold from exotic germplasm into common bean." Bean Improvement Cooperative. Annual report **46**: 13-14.

Favaron, F., P. Alghisi, P. Marciano and P. Magro (1988). "Polygalacturonase isoenzymes and oxalic acid produced by *Sclerotinia sclerotiorum* in soybean hypocotyls as elicitors of glyceollin." Physiological and Molecular Plant Pathology **33**: 385-395.

Federer, W. T., M. Reynolds and J. Crossa (2001). "Combining results from aumented designs over sites." Agronomy Journal **93**: 389-395.

Ferrar, P. H. and J. R. L. Walker (1993). "*o*-Diphenol oxidase inhibition--an additional role for oxalic acid in the phytopathogenic arsenal of *Sclerotinia sclerotiorum* and *Sclerotium rolfsii*." Physiological and Molecular Plant Pathology **43**: 415-422.

Ferwerda, F. H. and M. J. Bassett (2000). "Barriers to Interspecific Hybridization in Crosses between *Phaseolus coccineus* L. (G35172) and *Phaseolus vulgaris* L." Bean Improvement Cooperative. Annual report **43**: 21-22.

Freyre, R., P. W. Skroch, V. Geffroy, A. F. Adam-Blondon, A. Shirmohamadali, W. C. Johnson, V. Llaca, R. O. Nodari, P. A. Pereira, S.-M. Tsai, J. Tohme, M. Dron, J. Nienhuis, C. E. Vallejos and P. Gepts (1998). "Towards an integrated linkage map of common bean. 4. Development of a core linkage map and alignment of RFLP maps." TAG Theoretical and Applied Genetics **97**: 847-856.

Freytag, G. F. and D. g. Debouck (2002). Taxonomy, distribuution, and Ecology of the Genus *Phaseolus* (Leguminosae-Papilionoideae). Tort Worth, Texas, Brit Press.

Fuller, P. A., D. P. Coyne and J. R. Steadman (1984). "Inheritance of resistance to white mold disease in a diallel cross of dry beans." Crop science **24**(5): 929-933.

Gaitan-Solis, E., M. C. Duque, K. J. Edwards and J. Tohme (2002). "Microsatellite Repeats in Common Bean (*Phaseolus vulgaris*); Isolation, Characterization, and Cross-Species Amplification in *Phaseolus* ssp." Crop Science **42**: 2128-2136.

Gepts, P., Ed. (1988). Genetic Resources of *Phaseolus* Beans: their maintenance, domestication, evolution, and utilization. Dordrecht, Kluwer Academic Publishers.

Gilmore, B. and J. R. Myers (2000). "Examining the *Phaseolus coccineus* collection for white mold resistance." HortScience **35**: 367.

Gilmore, B. and J. R. Myers (2004). "A preliminary molecular marker map for Phaseolus coccineus." Bean Improvement Cooperative. Annual report **47**: 87-88.

Gilmore, B., J. R. Myers and D. Kean (2002). "Completion of testing of *Phaseolus coccineus* plant introductions (PIs) for white mold, *Sclerotinia sclerotiorum,* resistance." Bean Improvement Cooperative. Annual Report **45**: 64-65.

Girard, V., M. Fevre and C. Bruel (2004). "Involvement of cyclic AMP in the production of the acid protease Acp1 by *Sclerotinia sclerotiorum*." FEMS Microbiology Letters **237**: 227-233.

Godoy, G., J. R. Steadman, M. B. Dickman and R. Dam (1990). "Use of mutants to demonstrate the role of oxalic acid in pathogenicity of *Sclerotinia sclerotiorum* on *Phaseolus*." Physiological and Molecular Plant Pathology **37**(179-191).

Grafton, K. F. (1998). Resistance to White Mold in Dry Bean. Proceedinings of the *Sclerotinia* Workshop, Minnesota/North Dakota In-Sercice Extension Workshop, Fargo, North Dakota, North Dakota State University.

Griffiths, A. J., J. H. Miller, D. T. Suzuki, R. C. Lewontin and W. M. Gelbart (1996). An Introduction To Genetic Analysis. New York, W.H. Freeman and Company.

Guimaraes, R. L. and H. U. Stotz (2004). "Oxalate production by Sclerotinia sclerotiorum deregulates guard cells during infection." Plant Physiol **136**(3): 3703-11.

Guo, M., D. W. S. Mok and M. C. Mok (1989). "Isozyme Banding Patterns and Embryo Development in Interspecific Crosses of *Phaseolus*." Journal of Heredity **80**: 29-32.

Guo, S. and H. U. Stotz (2007). Partitioning of oxalate from induced and systemic resistance to *Sclerotinia sclerotiorum*. Unplublished

Haggard, J. E. and J. R. Myers (2007). "Interspecific Hybrid Derived-Lines Developed by Herbert Lamprecht: A Source of Disease Resistance for Common Bean." Bean Improvement Cooperative. Annual Report **in press**.

Hall, R. (1994). Compendium of Bean Diseases. St. Paul, The American Phytopathological Society.

Hambleton, S., C. Walker and L. M. Kohn (2002). "Clonal lineages of *Sclerotinia sclerotiorum* previously known from other crops predominate in 1999-2000 samples from Ontario and Quebec soybean." Canadian Journal of Plant Pathology **24**: 309-315.

Hassan, A. A., D. H. Wallace and R. E. Wilkinson (1971). "Genetics and heritability of resistance to *Fusarium solani* f. *phaseoli* in beans." Journal of American Society of Horticulture Science **96**: 623-627.

Hayashi, E., H.-C. Chi, S. K. Boyer and D. W. Still (2005). "Amplified Fragment Length Polymorphism Protocol for Plant Science on CEQ Series Genetic Analysis System." Beckman Coulter, Inc.: 1-11.

Hongtrakul, V., M. B. Slabaugh and S. J. Knapp (1998). "DFLP, SSCP, and SSR markers for 9-stearoly-acyl carrier protein desaturases strongly expressed in developing seeds of sunflower: intron lengths are polymorphic among elite inbred lines." Molecular Breeding **4**: 195-203.

Huang, H. C. and J. Dueck (1980). "Wilt of sunflower from infection by mycelial-germinating sclerotia of *Sclerotinia sclerotiorum*." Canadian Journal of Plant Pathology **2**(47-52).

Irzykowska, L. and B. Wolko (2004). "Interval mapping of QTLs controlling yield-related traits and seed protein content in Pisum sativum." J Appl Genet **45**(3): 297-306.

Iyer, V., D. K. Salunkhe, S. K. Sathe and L. B. Rockland (1980). "Quick-cooking beans (*Phaseolus vulgaris* L.): I. Investigations on quality." Plant Foods for Human Nutrition (Dordrecht) **30**(1): 27-43.

Jones, C. J., K. J. Edwards, S. Castaglione, M. O. Winfield, F. Sala, C. van de Wiel, G. Bredemeijer, B. Vosman, M. Matthes, A. Daly, R. Brettschneider, P. Bettini, M. Buiatti, E. Maestri, A. Malcevschi, N. Marmiroli, R. Aert, G. Volchaert, J. Rueda, R. Linaceri, A. Vazquez and A. Karp (1997). "Reproducibility testing of RAPD, AFLP and SSR markers in plants by a network of European laboratories." Molecular breeding: new strategies in plant improvement **3**(5): 381-390.

Kang, M. S., Ed. (2002). Quantitative Genetics, Genomics and Plant Breeding. New York, NY, CABI Publishing.

Kelly, J. D., J. M. Kolkman and K. Schneider (1998). "Breeding for yield in dry bean (*Phaseolus vulgaris* L.)." Euphytica : international journal of plant breeding **102**(3): 343-356.

Kelly, J. D., B. Long, N. Blakely and K. A. Terpstra (2004) "2004 Dry Bean Yield Trials." Dry Bean Report, Michigan State University **Volume**, 1-11 DOI:

Kobayashi, M., J.-Z. Lin, J. Davis, L. Francis and M. T. Clegg (2000). "Quantitative analysis of avocado outcrossing and yield in California using RAPD markers " Scientia Horticulturae (Amsterdam) **86**(2): 135-149.

Kolkman, J. M. and J. D. Kelly (2003). "QTL conferring resistance and avoidance to white mold in common bean." Crop science **43**(2): 539-548.

Kurian, P. and D. A. Stelzig (1979). "The Synergistic Role of Oxalic Acid and Endopolygalacturonase in Bean Leaves Infected by *Cristulariella pyramidalis*." Phytopathology **69**(12): 1301-1304.

Lamprecht, H. (1945). "Intra- and interspecific genes." Agri Hortique Genetica **3**: 45-60.

Lamprecht, H. (1948). "On the effect and linkage of genes transmitted from *Phaseolus coccineus* to *Ph. vulgaris*." Agri Hortique Genetica **6**: 64-81.

Lamprecht, H. (1957). "Artifizielle Unwandlung einer Spezies in eine andere." Agri Hortique Genetica **15**: 194-206.

Li, J. Z., X. Q. Huang, F. Heinrichs, M. W. Ganal and M. S. Roder (2005). "Analysis of QTLs for yield, yield components, and malting quality in a BC3-DH population of spring barley." Theor Appl Genet **110**(2): 356-63.

Li, R., R. Rimmer, L. Buchwaldt, A. G. Sharpe, G. Seguin-Swartz and D. D. Hegedus (2004). "Interaction of *Sclerotinia sclerotiorum* with *Brassica napus*: cloning and characterization of endo- and exo-polygalacturonases expressed during saprophytic and parasitic modes." Fungal Genetics and Biology **41**: 754-765.

Lindig-Cisneros, R., B. Benrey and F. J. Espinosa-Garcia (1997). "Phytoalexins, Resistance Traits, and Domestication Status in *Phaseolus coccineus* and *Phaseolus lunatus*." Journal of Chemical Ecology **23**(8): 1997-2011.

Lioi, L., R. Bollini, F. Sparvoli, C. Lanave, I. Galasso and M. Santantonio (2006). "Lectin gene sequences and species relationships among cultivated legumes." Genetic Resources and Crop Evolution **53**: 1615-1623.

Lorz, H. and G. Wenzel, Eds. (2005). Molecular Marker Systems in Plant Breeding and Crop Improvement. Biotechnology in Agriculture and Forestry. Verlag, Springer.

Lumsden, R. D. (1976). "Pectolytic enzymes of *Sclerotinia sclerotiorum* and their localization in infected bean." Canadian Journal of Botany **54**: 2630-2641.

Lyons, M. E., M. H. Dickson and J. E. Hunter (1987). "recurrent Selection for Resistance to White Mold in *Phaseolus* Species." Journal of the American Society for Horticultural Science **112**(1): 149-152.

Lyons, M. E., J. E. Hunter and M. H. Dickson (1985). "The use of recurrent selection in breeding for white mold resistance in beans." Bean Improvement Cooperative. Annual Report **28**: 99-100.

Mahunku, G. S., C. Jara, C. Cajiao and S. E. Beebe (2003). "Sources of resistance to angular leaf spot (*Phaeoisariopsis griseola)* in common bean core collection, wild *Phaseolus vulgaris* and secondary gene pool." Euphytica : international journal of plant breeding **130**: 303-313.

Manshardht, R. m. and M. J. Bassett (1984). "Inheritance of stigma position of *Phaseolus vulgaris* x *P. coccineus* hybrid populations." Journal of Heredity **75**: 45-50.

Marciano, P., P. Di Lenna and P. Magro (1983). "Oxalic acid, cell wall-degrading enzymes and pH in pathogenesis and their significance in the virulence of two *Sclerotinia sclerotiorum* isolates on sunflower." Physiological Plant Pathology **22**: 339-345.

Marciano, P., P. Magro and F. Favaron (1989). "*Sclerotinia sclerotiorum* growth and oxalic acid production on selected culture media." FEMS Microbiology Letters **61**: 57-60.

Martel, M. B., C. Herve du Penhoat, R. Letoublon and M. Fevre (2002). "Purification and characterization of a glucoamylase secreted by the plant pathogen *Sclerotinia sclerotiorum*." Can J Microbiol **48**(3): 212-8.

Maxwell, J., X. Shan, J. B. Ogg, R. Henson, M. Brick, P. Byrne and H. Schwartz (2006). "Quantitative trait loci for resistance to white mold in common bean." Bean Improvement Cooperative. Annual Report **49**: 63-64.

Miklas, P. N. (2006). "Potential marker-assisted selection for resistance to Sclerotinia white mold in pinto and great northern bean." Bean Improvement Cooperative. Annual report: 67-68.

Miklas, P. N. and R. Delorme (2003). "Identification of QTL Conditioning Resistance to White Mold in Snap Bean." Journal of American Society of Horticulture Science **128**(4): 564-570.

Miklas, P. N., R. Delorme, R. Hannan and M. H. Dickson (1999). "Using a Subsample of the Core Collection to Identify New Sources of Resistance to White Mold in Common Bean." Crop Science **39**: 569-573.

Miklas, P. N., K. F. Grafton, G. A. Secor and P. E. McClean (1992). "Use of Pathogen Filtrate to Differentiate Physiological Resistance of Dry Bean to White Mold Disease." Crop Science **32**: 310-312.

Miklas, P. N., W. C. Johnson, R. Delorme and P. Gepts (2001). "QTL Conditioning Physiological Resistance and Avoidance to White Mild in Dry Bean." Crop Science **41**: 309-315.

Miklas, P. N., J. D. Kelly, S. E. Beebe and M. W. Blair (2006). "Common bean breeding for resistance against biotic and abiotic stresses: From classical to MAS breeding." Euphytica : international journal of plant breeding **147**: 105-131.

Miklas, P. N., K. M. Larsen, K. A. Terpstra, D. C. Hauf, K. F. Grafton and J. D. Kelly (2007). "QTL Analysis of ICA Bunsi-Derived Resistance to White Mold in a Pinto X Navy Bean Cross." Crop Science **47**: 174-179.

Myers, J. R., J. W. Davis, D. Kean and B. Yorgey (2004). "Genetic analysis of processing traits in greenbean *(Phaseolus vulgaris* L.*)*." Acta Horticulturae **637**: 369-375.

Nakamura, Y., M. Leppert, P. O'Connell, R. Wolff, T. Holm, M. Culver, C. Martin, E. Fujimoto, M. Hoff, E. Kumlin and R. White (1987). "Variable Number of Tandem Repeat (VNTR) Markers for Human Gene Mapping." Science **235**: 1616-1622.

Nelson, B. (1998). Biology of *Sclerotinia*. Proceedings of the *Sclerotinia* Workshop, Minnesota/North Dakota In-Service Extension Workshop. Fargo, North Dakota, North Dakota State University.

Nodari, R. O., S.-M. Tsai, R. Gilbertson and P. Gepts (1993). "Towards an integrated linkage map of common bean. II. Development of an RFLP -based linkage map." TAG Theoretical and Applied Genetics **85**(5): 513-520.

Osorno, J. M., J. S. Beaver, F. H. Ferwerda and P. N. Miklas (2003). "Two genes from *Phaseolus coccineus* L. confer resistance to bean golden yellow mosaic virus." Bean Improvement Cooperative. Annual Report **46**: 147-148.

Park, S. O., D. P. Coyne, J. R. Steadman and P. W. Skroch (2001). "Mapping of QTL for resistance to white mold disease in common bean." Crop science **41**(4): 1253-1262.

Petzoldt, R. and M. H. Dickson (1996). "Straw test for resistance to white mold in beans." Bean Improvement Cooperative. Annual report: 142-143.

Poussereau, N., S. Creton, G. Billon-Grand, C. Rascle and M. Fevre (2001). "Regulation of *acp1,* encoding a non-aspartly acid protease expressed during pathogenesis of *Sclerotinia sclerotiorum*." Microbiology (Reading) **147**: 717-726.

Powell, A. L. T., J. van Kan, A. ten Have, J. Visser, L. C. Greve and A. B. Bennett (2000). "Transgenic Expression of Pear PGIP in Tomato Limits Fungal Colonization." Molecular Plant-Microbe Interactions **13**(9): 942-950.

Pscheidt, J. W. (2006). PNW Plant Disease Control. Corvallis, OR, Oregon State University Extension.

Purdy, L. H. (1979). "*Sclerotinia sclerotiorum*: History, Diseases and Symptomatology, Host Range, Geographic Distribution, and Impact." Phytopathology **69**(8): 875-880.

Riou, C., G. Freyssinet and M. Fevre (1991). "Production of Cell Wall-Degrading Enzymes by the Phytopathogenic Fungus *Sclerotinia sclerotiorum*." Applied and Environmental Microbiology **57**(5): 1478-1484.

Roberds, J. H., T. L. Kubisiak, P. C. Spaine, S. F. Covert and R. L. Doudrick (1997). Selection of RAPD Markers for investigation of Genetic Populations Structure in Fusiform Rust Fungus Infecting Loblolly Pine. 24th Biennial southern Forest Tree Improvement Conference. Orlando, FL, Southern Research Station**:** 293-298.

Santalla, M., A. B. Monteagudo, A. M. Gonzalez and A. M. d. Ron (2004). "Agronomical and quality traits of runner bean germplasm and implications for breeding." Euphytica : international journal of plant breeding **135**: 205-215.

Sato, M. (1980a). "Inhibition by Oxalates of Spinach Chloroplast Phenolase in Unfrozen and Frozen States." Phytochemistry (Oxford) **19**: 1613-1617.

Sato, M. (1980b). "Reactivation By Copper Of Phenolase Pre-Inactivated By Oxalate." Phytochemistry (Oxford) **19**: 1931-1933.

Schwartz, H. F., D. H. Casciano, J. A. Asenga and D. R. Wood (1987). "Field measurement of white mold effects upon dry beans with genetic resistance or upright plant architecture." Crop science **27**(4): 699-702.

Schwartz, H. F., K. Otto, H. Teran, M. Lema and S. P. Singh (2006). "Inheritance of White Mold Resistance in *Phaseolus vulgaris* x *P. coccineus* Crosses." Plant Disease **90**(9): 1167-1170.

Schwartz, H. F., S. P. Singh, H. Teran and K. Otto (2004). "Inheritance of white mold resistance in the interspecific crosses of pinto cultivars Othello and UI 320 and Phaseolus coccineus L. accessions PI 433246 and PI 439534." Bean Improvement Cooperative. Annual report **47**: 279-280.

Schwartz, H. F. and J. R. Steadman (1977). "*Sclerotinia Sclerotiorum* Inoculum Production in Western Nebraska." Bean Improvement Cooperative. Annual report **20**: 69-70.

Schwartz, H. F., J. R. Steadman and D. P. Coyne (1978). "Influuence of *Phaseolus vulgaris* Blossoming Characteristics and Canopy Structure upon Reaction to *Sclerotinia sclerotiorum*." Phytopathology **68**: 465-470.

Shii, C. T., A. Rabakoarihanta, M. C. Mok and D. W. S. Mok (1982). "Embryo Development in Reciprocal Crosses of *Phaseolus vulgaris* L. and *P. coccineus* Lam." Theoretical and Applied Genetics **62**: 59-64.

Singh, S. P., Ed. (1999). Common Bean Improvement in the Twenty-First Century. Develpments in Plant Breeding. Dordrecht, Kluwer Academic Publishers.

Smartt, J. (1970). "Interspecific Hybridization Between Cultivated American species of the Genus *Phaseolus*." Euphytica : international journal of plant breeding **19**: 480-489.

Smartt, J. and N. W. Simmonds, Eds. (1995). Evolution of Crop Plants. Essex, England, Longman Scientific & Technical.

Soledade, M., C. Pedras, P. W. K. Ahiahonu and M. Hossain (2004). "Detoxification of the cruciferous phytoalexin brassinin in *Sclerotinia sclerotiorum* requires an inducible glucosyltransferase." Phytochemistry (Oxford) **65**: 2685-2694.

Steadman, J. R. (1983). "White Mold-A-Serious Yield-Limiting disease of Bean." Plant Disease **67**(4): 346-350.

Steadman, J. R., J. M. Kolkman and K. M. Eskridge (2002). "Screening for and Identifying Sources of Resistance to *Sclerotinia sclerotiorum* in Common Bean." Bean Improvement Cooperative. Annual Report **45**: 48-49.

Stivers, L. (2000). "Crop Profile: Snap Beans in New York." Pesticide Management Education Program (PMEP).

Sutton, D. C. and B. J. Deverall (1984). "Phytoalexin accumulation during infection of bean and soybean by ascospores and mycelium of *Aclerotinia sclerotiorum*." Plant Pathology (Oxford) **33**: 377-383.

Tanksley, S. D. (1993). "Mapping Polygenes." Annual Review of Genetics **27**: 205-233.

Terpstra, K. A. and J. D. Kelly (2006). "Preliminary QTL analysis for white mold resistance in a black bean x wild Mexican bean inbred backcross mapping population." Bean Improvement Cooperative. Annual report **49**: 103-104.

Tu, J. C. (1985). "Tolerance of white bean *(Phaseolus vulgaris)* to white mold *(Sclerotinia Sclerotiorum)* associated with tolerance to oxalic acid." Physiological Plant Pathology **26**: 111-117.

Tu, J. C. (1989). "Oxalic acid induced cytological alterations differ in beans tolerant or susceptible to white mould." New Phytologist **112**(4): 519-525.

Vallejos, C. E., N. S. Sakiyama and C. D. Chase (1992). "A Molecular Marker-Based Linkage Map of *Phaseolus vulgaris* L." Genetics **131**: 733-740.

Van Ooijen, J. W. (2006). JoinMap 4.0, Software for the calculation of genetic linkage maps in experimental populations. Wageningen, Netherlanews, Kyazma B.V.

Venette, J. R. (1998). *Sclerotinia* spore formation, transpor, and infection. Proceedings of the *Sclerotinia* Workshop, Minnesota/North Dakota In-Service Extension Workshop, Fargo, North Dakota, North Dakota State University.

Voorrips, R. E. (2002). "MapChart: Software for the graphical presentation of linkage maps and QTLs." Journal of Heredity **93**(1).

Vos, P., R. Hogers, M. Bleeker, M. Reijans, T. van de Lee, M. Hornes, A. Frijters, J. Pot, J. Peleman, M. Kuiper and M. Zabeau (1995). "AFLP: a new technique for DNA fingerprinting." Nucleic Acids Research **23**(21): 4407-4414.

Wakefield, E. M. (1924). "On the names *Sclerotinia sclerotiorum* (Lib.*)* Massee*,* and *S. libertiana* Fuckel." Phytopathology **14**(126-127).

Wall, J. R. and T. L. York (1957). "Inheritance of Seedling Cotyledon Position in *Phaseolus* Species." Journal of Heredity **48**: 71-74.

Wang, S., C. J. Basten and Z. B. Zeng (2006). Windows QTL Cartographer version 2.5. Raleigh, NC, Department of Statistics North Carolina State University.

Young, V. R. and P. L. Pellett (1994). "Plant proteins in relation to human protein and amino acid nutrition." The American Journal of Clinical Nutrition **59**(5): 1203S-1212S.

Table 3.8 Summary of WinQTLCartographer white mold resistance at eight days QTL mapping results in a Wolven Pole/PI 255956 F_2 population.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD[y]	R^2 (%)	Additive effect	Domin-ance effect	No. of iterations
SMA	LG 1a	E33M62-102	14.3	.030*						
	LG 1a	OPN-08-1700	88.36	.020*						
	LG 1c	E33M62-106	73.15	.003**						
	LG 1c	E33M62-73	89.66	.003**						
	LG D	OPN-14-1700	5.85	.020*						
	LG D	OPM-04-700	6.81	.027*						
	LG D	OPJ-11-400	7.24	.030*						
	LG D	OPAE-16-1900	8.73	.036*						
	LG D	E32M59-412	10.13	.032*						
	LG D	E33M62-227	10.57	.025*						
	LG D	OPF-20-1000	12.08	.010*						
	LG D	OPAA-18-900	13.28	.015*						
	LG D	Bmd37	13.64	.014*						
	LG D	OPAE-05-1000	15.41	.017*						
	LG D	E33M62-194	16.47	.013*						
	LG D	OPV-15-500	17.96	.007**						
	LG D	OPF-20-1700	20.59	.043*						
	LG D	OPT-20-1400	22.42	.030*						
	LG D	OPW-07-950	28.63	.022*						
	LG Db	OPN-11-500	0	.015*						
	LG Db	OPP-09-350	0	.015*						
	LG 5	OPK-16-800	0	.027*						

Table 3.8 Continued.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD [y]	R^2 (%)	Additive effect	Domin-ance effect	No. of iterations
	LG 5	OPE-08-900	7.09	.012*						
	No QTL									
Im	Found									
CIM	LG 1a	E32M47-167	98.5		0.001	2.67	7.2	0.02	0.37	
	LG 5	OPK-16-1300	12.7		0.001	2.63	6.6	-0.15	0.27	
MIM	LG 1a	OPA-07-700	99.5		0.001	1.2		-0.1948	-0.4816	
	LG 1c	E33M62-73	82.2		0.001	1.34		-0.3569	0.0838	
	LG 2	E32M60-385	17.7		0.001	0.4		0.0135	0.1498	
BIM	LG 1c	E33M62-73	87.4			2.86		-0.1187	-0.2054	99900
	LG 5	BMd28	36.73			2.86		-0.0935	0.0626	99900
	LG 2	OPAB-08-1400	73.84			2.86		-0.0528	-0.0055	99900
	LG 9	E32M60-228	44.62			2.86		-0.0268	-0.0545	99900
	LG A	OPQ-111700	8.37			2.86		0.0035	0.117	99900

[z]SMA = Single Marker Analysis, Im = Interval Mapping, CIM = Composite Interval Mapping, MIM = Multiple Interval Mapping, BIM = Bayesian Interval mapping. [y]LOD (base 10 algorithm of the likelihood ratio) threshold of 2.5 used for QTL detection, LOD thresholds based on 1000 permutations as suggested by Churchill and Doerge (Churchill and Doerge 1994).

Table 3.9 Summary of WinQTLCartographer white mold resistance over five weeks QTL mapping results in a Wolven Pole/PI 255956 F_2 population.

Method[z]	Linkage Group	Marker	Map Position (cM)	Prob. > (F)	Signif. level	LOD[y]	R^2 (%)	Additive Effect[t]	Dominance effect[u]	No. of iterations
SMA	LG 1a	E33M62-350	0	.035*						
	LG 1a	OPU-03_{950}	56.79	.044*						
	LG 1a	E32M47-331	57.62	.036*						
	LG 1a	OPI-15_{1000}	51.35	.029*						
	LG 1a	E32M60-123	85.71	.035*						
	LG 1c	E33M62-73	89.66	.044*						
	LG C	OPQ-11_{1700}	8.41	.029*						
	LG C	E32M59-418	20.32	.008**						
	LG 6	OPY-04_{700}	17.22	.021*						
Im	LG 1e	E32M47-232	0.1201		0.001	3.2	9.5	0.247	-0.545	
	LG C	OPQ-11_{1700}	0.1241		0.001	10.3	71.6	0.531	3.223	
CIM	LG 1c	E32M60-122	0.0601		0.001	2.8	21.6	-0.032	1.489	
	LG C	OPQ-11_{1700}	0.0601		0.001	7.4	60.2	-3.569	0.260	
	LG C	OPQ-11_{1700}	0.1241		0.001	9.9	68.0	0.595	3.174	
MIM	LG C	OPQ-11_{1700}	13.4		0.001	5.4	71.7	-0.501	3.044	
BIM	LG 1c	E32M60-122	11.7			45.8		-0.006	1.890	99900
	LG C	OPQ-11_{1700}	14.7			45.8		-0.217	2.616	99900

[z]SMA = Single Marker Analysis, Im = Interval Mapping, CIM = Composite Interval Mapping, MIM = Multiple Interval Mapping, and BIM = Bayesian Interval mapping. [y]LOD (base 10 algorithm of the likelihood ratio) threshold of 2.5 used for QTL detection, LOD thresholds based on 1000 permutations (Churchill and Doerge 1994).

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	150932		P. cocc.	G35021	Acoyote			Queretaro, Mexico	5/1/1945	San Juan del Rio	01-May-1945. From: Federal District, Mexico.	CM
P. cocc.	Yes	NA	165421		P. cocc.	G35022		NI-629	No. 1052	Oaxaca, Mexico		Markets in City of Oaxaca.	Jun-1948. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	165436		P. cocc.	G35023	Frijolan	NI-663	No. 1067	Ecuitalapa, Oaxaca	5/6/1948	Grown at Ecuitalapa, Oaxaca.	18-Jun-1948. From: Maryland, United States	LR
P. cocc.	NA	NA	171806		P. cocc.	G35024	Eysek		HARLAN 7157	Turkey		Kisanta, Bayburt, Gumusane	Dec-1948. From: Maryland, United States.	CM
P. cocc.	Yes	NA	175829		P. cocc.	G35025			Harlan 5164	Turkey		Ankara. Elevation: 1033 meters	Mar-1949. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	175855		P. cocc.	G35026	Cicek		HARLAN 9048	Turkey	9/20/1948	Vegetable market in Yozgat	Mar-1949. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	175858		P. cocc.	G35027			HARLAN 9065	Turkey	9/20/1948	Vegetable market in Yozgat	Mar-1949. From: Maryland, United States	CM
P. cocc.	Yes	NA	175860		P. cocc.	G36010			HARLAN 9085	Turkey	9/20/1948	Purchased from only seed dealer in Kirsehir	Mar-1949. From: Maryland, United States.	CM
P. cocc.	Yes	NA	176672		P. cocc.	G35028			HARLAN 8888	Turkey	9/17/1948	Collected by one dealer in Erzincan from other dealers	Mar-1949. From: Maryland, United States.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	176675		P. cocc.	G35029	Sohret		HARLAN 8895	Turkey	9/17/1948	Collected by one dealer in Erzincan from other dealers	Mar-1949. From: Maryland, United States.	CM
P. cocc.	Yes	NA	176695		P. cocc.	G35030	Cicek		HARLAN 9369	Turkey	9/24/1948	Purchased at market-place in Aksehir, Konya	Mar-1949. From: Maryland, United States.	CM
P. cocc.	NA	NA	181596		P. cocc.				No. 8	Guatemala			10-May-1949. From: Guatemala.	LR
P. cocc.	NA	NA	181597		P. cocc.				No. 9	Guatemala			10-May-1949. From: Guatemala.	LR
P. cocc.	NA	NA	181598		P. cocc.				No. 10	Guatemala			10-May-1949. From: Guatemala.	LR
P. cocc.	Yes	NA	181790		P. cocc.		Baladi		No. 9938	Lebanon	11/2/1948	Chtura	10-May-1949. From: Maryland, United States.	CM
P. cocc.	NA	NA	182008		P. cocc.				No. 13	Guatemala			26-May-1949. From: United States.	LR
P. cocc.	Yes	Avail.	183412		P. cocc.	G25244			KOELZ 11549	Madhya Pradesh, India	3/20/1949	From Barmakot, Bastar.	27-Jun-1949. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	183464		P. cocc.	G25245			KOELZ 11547	Madhya Pradesh, India	5/2/1905	Barmakot, Bastar.	30-Jun-1949. From: Maryland, United States.	CM

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P. cocc.	Yes	Avail.	189023		P. cocc.	G35568	Pa Xai			Huehuetenango, Guatemala		Jacaltenango	28-Apr-1950. From: United States.	LR
P. cocc.	Yes	Avail.	193045		P. cocc.	G36051				Huehuetenango, Guatemala		Market, San Pedro, Soloma	31-Oct-1950. From: United States.	LR
P. cocc.	Yes	Avail.	195338		P. cocc.	G35879			NORVELL 2730	Totonicapan, Guatemala	3/14/1951	Market in Totonicapan. Elevation: 2438 meters	16-Apr-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	195372		P. cocc.	G35571			NORVELL 2673	Quezaltenango, Guatemala	3/12/1951	Market in Quezaltenango, Quezaltenango. Elevation: 1829 meters	16-Apr-1951. From: Maryland, United States	LR
P. cocc.	NA	NA	196412		P. cocc.		Chamborote			Guatemala	PRE 1951.	San Mateo Ixatan	17-May-1951. From: United States	LR
P. cocc.	Yes	Avail.	196413		P. cocc.					Guatemala	5/4/1905	San Juan Ixcoy	17-May-1951. From: United States	LR
P. cocc.	NA	NA	201293		P. cocc.				No. 3154	Puebla, Mexico	5/5/1905	State of Puebla	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201295		P. cocc.	G35043			NORVELL 3156	Puebla, Mexico	5/5/1905		08-May-1952. From: California, United States	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	201297		P. cocc.	G35044			NORVELL 3158	Puebla, Mexico	1952		08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201299		P. cocc.	G35045			NORVELL 3160	Puebla, Mexico	1952		08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201300		P. cocc.	G35046			NORVELL 3161	Puebla, Mexico	1952		08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201301		P. cocc.	G35047			NORVELL 3162	Puebla, Mexico	1952		08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201304		P. cocc.	G35048		NI-520	NORVELL 3165	Puebla, Mexico	1952		08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201305		P. cocc.	G35049			NORVELL 3167	Tlaxcala, Mexico	1952	Apizaco	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201306		P. cocc.				No. 3168	Tlaxcala, Mexico	5/5/1905	Market in Apizaco	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201309		P. cocc.	G35050			NORVELL 3171	Tlaxcala, Mexico	1952	Market in Apizaco	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201310		P. cocc.	G35051			NORVELL 3172	Tlaxcala, Mexico	1952	Market in Apizaco	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201312		P. cocc.	G35052			NORVELL 3174	Tlaxcala, Mexico	5/5/1905	Market in Apizaco	08-May-1952. From: California, United States	LR

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P. cocc.	Yes	Avail.	201320		P. cocc.	G35053			NORVELL 3183	Tlaxcala, Mexico			08-May-1952. From: California, United States	LR
P. cocc.	Yes	NA	201328		P. cocc.	G35055			NORVELL 3192	Hidalgo, Mexico			08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201336		P. cocc.	G35057			NORVELL 3201	Hidalgo, Mexico		Tulancingo	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201352		P. cocc.	G35064.			NORVELL 3219	Hidalgo, Mexico		Pachuca	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201356		P. cocc.				No. 3225	Mexico, Mexico		Toluca. Elevation: 2675 meters	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201366		P. cocc.	G35065			NORVELL 3565	Chiapas, Mexico		Tuxtla Gutierrez	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201389		P. cocc.	G35066			NORVELL 3596	Oaxaca, Mexico		Oaxaca	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201477		P. cocc.	G 23861			No. 7095	Chiapas, Mexico	8/14/1951		May-1952. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	202129		P. cocc.	G35067			FOX 5823	Veracruz, Mexico	15-Jul-1652	Market in Jalapa	25-Jul-1952. From: Maryland, United States	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	203931		P. cocc.	G35068			GENTRY 12299	Hidalgo, Mexico	10/18/1952	Market in Pachuca de Soto. Elevation: 1000 meters	10-Dec-1952. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	205360		P. cocc.	G35572			GENTRY 12465	Alta Verapaz, Guatemala	1/25/1953	Coban. Elevation: 1219 meters	12-Feb-1953. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	209663		P. cocc.				No. 1	Hidalgo, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	Avail.	209664		P. cocc.	G35069.			WOOD NO.2	Puebla, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	Avail.	209665		P. cocc.				No. 4	Hidalgo, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	NA	209666		P. cocc.	G35070.			WOOD NO.5	Hidalgo, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	Avail.	209667		P. cocc.	G35071.			WOOD NO.6	Puebla, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	Avail.	209669		P. cocc.	G35072			WOOD NO.9	Puebla, Mexico			07-Jul-1953. From: Colorado, United States.	LR
P. cocc.	Yes	NA	223803		P. cocc.	G35073	Lobia		SMITH 1144	Badakhshan, Afghanistan	9/1/1954	Jurm. Elevation: 1463 meters	15-Feb-1955. From: Maryland, United States	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	224711		P. cocc.	G35574	Botil		CORRELL NO.6	Chiapas, Mexico	3/4/1955	Market in San Cristobal de las Casas. Elevation: 2150 meters	12-Apr-1955. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	224784		P. cocc.	G35575			CORRELL NO. 41	Chiapas, Mexico		Market in Comitan	20-Apr-1955. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	226594		P. cocc.		Scarlet Runner Bean						21-Jun-1955. From: Costa Rica.	CM
P. cocc.	Yes	NA	229618		P. cocc.	G35074			GENTRY 15405	Iran	8/1/1955	Market in Maragheh, Azerbaijan. Elevation: 1920 meters	25-Oct-1955. From: Maryland, United States.	CM
P. cocc.	Yes	NA	247303		P. cocc.	G35075				Ethiopia			29-Apr-1958. From: Ethiopia.	CM
P. cocc.	Yes	NA	255573		P. cocc.	G35076	Beli Turski Fizol		L-90	Yugoslavia			16-Feb-1959. From: Slovenia.	CM
P. cocc.	Yes	NA	255956		P. cocc.		Mayan White Runner		G 6753	Guatemala			18-Mar-1959. From: New York, United States.	CV
P. cocc.	Yes	NA	255957		P. cocc.	G55380	Carters Prize Winner		GENEVA 6754	England, United Kingdom			18-Mar-1959. From: New York, United States.	CV

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P. cocc.	Yes	Avail.	257221		P. cocc.				Col. No. 113	Colombia			27-Apr-1959. From: California, United States	LR
P. cocc.	Yes	Avail.	257222		P. cocc.				Col. No. 114	Colombia			27-Apr-1959. From: California, United States.	LR
P. cocc.	Yes	NA	273448		P. cocc.	G35078	Mexican Black Bean	NI-607	GENEVA G9582	Mexico			27-Mar-1961. From: New York, United States.	CM
P. cocc.	Yes	NA	273449		P. cocc.	G35259.	Hall Lima		GENEVA G10534	New York, United States		From Hall, New York	27-Mar-1961. From: New York, United States.	CM
P. cocc.	Yes	Avail.	273666		P. cocc.	G35079.			HARLAN 1994	Kefa, Ethiopia		Village 13 miles west of Jimma	04-Apr-1961. From: Maryland, United States.	CM
P. cocc.	Yes	NA	273667		P. cocc.				HARLAN 2031	Kefa, Ethiopia		Farm in the Nadda region	04-Apr-1961. From: Maryland, United States.	CM
P. cocc.	Yes	NA	277802		P. cocc.	G35080				Turkey		Selected from the predominantly white seeded PI 176672	03-Jan-1962. From: Washington, United States.	CM
P. cocc.	Yes	NA	282119		P. cocc.		Pallares Corrientea						19-Jul-1962. From: Chile.	CV
P. cocc.	Yes	Avail.	304749		P. cocc.		Di Spagna Bianco						16-Mar-1965. From: Italy.	CV

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P. cocc.	Yes	Avail.	307663		P. cocc.				20659	San Jose, Costa Rica		Santa Maria de Dota	07-Sep-1965. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	307664		P. cocc.				20660	San Jose, Costa Rica		Santa Maria de Dota	07-Sep-1965. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	307665		P. cocc.		Piloy		20663	San Jose, Costa Rica		Santa Maria de Dota	07-Sep-1965. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	307778		P. cocc.				S-198-R	Morazan, El Salvador		Cacaopera	28-Sep-1965. From: El Salvador.	LR
P. cocc.	Yes	NA	309694		P. cocc.		Frijol Aluvia		21119	Mexico		Market in Zamora	09-Dec-1965. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	309888		P. cocc.				20661	San Jose, Costa Rica		Santa Maria de Dota	09-Dec-1965. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	309889		P. cocc.				20662	San Jose, Costa Rica		Santa Maria de Dota.	09-Dec-1965. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	311176		P. cocc.	G35087	Piloya		Gentry 20809	Guatemala		Market in Totonicapan. Elevation: 2660 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311180		P. cocc.	G35583.	Piloya		Gentry 20803	Quiche, Guatemala		Market in Chichicasten ango. Elevation: 2330 meters	19-Jan-1966. From: Maryland, United States.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	311185		P. cocc.	G35583			Gentry 20848	Quezaltenango, Guatemala		Market in Quezaltenango. Elevation: 2000 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311202		P. cocc.	G35092	Curuna		Gentry 20930	Jalapa, Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311204		P. cocc.	G35589	Piloya		Gentry 20985	Baja Verapaz, Guatemala		Market in San Jeronimo	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311210		P. cocc.	G35177			Gentry 21003	Alta Verapaz, Guatemala		Market in Carcha. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311211		P. cocc.	G35594	Piloya		Gentry 21008	Alta Verapaz, Guatemala		Market in Carcha. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311214		P. cocc.	G35596			Gentry 21015	Alta Verapaz, Guatemala		Market in Totonicapan. Elevation: 1500 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311218		P. cocc.	G35096	Piloya		Gentry 210402	Guatemala		Market in Totonicapan. Elevation: 2660 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311819		P. cocc.	G35597	Piloy		Gentry 21727	Guatemala	Pre 1965	Tactic. Elevation: 1400 meters	23-Feb-1966. From: Maryland, United States.	LR

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P. cocc.	Yes	Avail.	311826		P. cocc.	G35098	Piloy		Gentry 21738	Guatemala	Pre 1965	Coban. Elevation: 1330 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311827		P. cocc.	G35598	Piloy		Gentry 21736	Guatemala	Pre 1965	Coban. Elevation: 1330 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311879		P. cocc.		Piloy		21799	Guatemala, Guatemala	Pre 1965	Market in Amatitlan. Elevation: 1000 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311880		P. cocc.	G35601	Piloy		Gentry 21799	Guatemala, Guatemala	Pre 1965	Market in Amatitlan. Elevation: 1000 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311882		P. cocc.	G35601	Piloy		Gentry 21808	Huehuetenango, Guatemala	Pre 1965	Along road to Huehuetenango, 21 miles north of San Cristobal road fork. Elevation: 2830 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311920		P. cocc.	G35102	Ayocote		Gentry 21242	Puebla, Mexico	Pre 1965	Market in Tehuacan. Elevation: 1660 meters	24-Feb-1966. From: Maryland, United States	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	311939		P. cocc.	G35602	Ayocote		Gentry 212	Mexico	Pre 1965	Market in Mendoza. Elevation: 1000 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311950		P. cocc.	G35103	Ayocote		Gentry 21270	Mexico	1965	Market in Orizaba. Elevation: 1330 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311953		P. cocc.	G35104	Ayacote		Gentry 21273	Mexico	1965	Market in Cordoba. Elevation: 1000 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	NA	311977		P. cocc.	G35105	Ayocote		Gentry 21318	Mexico	1965	Market in Oaxaca. 1660 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311981		P. cocc.	G35106	Botin		Gentry 21822	Mexico	1965	Market in Comitan. Elevation: 2000 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311985		P. cocc.	G35603	Botil		Gentry 21830	Mexico	1965	Market in Comitan. Elevation: 2000 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	312009		P. cocc.	G35604	Botin		Gentry 21854	Mexico	1965	Market in San Cristobal las Casas. Elevation: 2330 meters	24-Feb-1966. From: Maryland, United States	LR

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P. cocc.	Yes	Avail.	312013		P. cocc.	G35605			Gentry 21863	Mexico	5/18/1905	Market in San Cristobal las Casas. Elevation: 2330 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	312035		P. cocc.	G35605	Botiles		Gentry 21883	Mexico	5/18/1905	San Cristobal las Casas. Collected at market in Tuxtla Gutierrez. Elevation: 2330 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	NA	312076		P. cocc.	G35097	Ayocote		Gentry 21939	Mexico	5/18/1905	Market in Mexico City. Elevation: 2600 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	312080		P. cocc.	G35170	Frijol Aluvia Gordo		Gentry 21943	Mexico	5/18/1905	Market in Mexico City. Elevation: 2530 meters	24-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	313221		P. cocc.	G35646	Pato blanco		C. Exp. Pab 27(27-1)	Mexico	5/1/1905	Elevation: 1960 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	313268		P. cocc.	G35607	Votil		X-9009	Mexico		San Cristobal de Las Casas. Elevation: 1330 meters	19-Apr-1966. From: Federal District, Mexico.	LR

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P. cocc.	Yes	NA	313455		P. cocc.	G35608	Ayocote		ZACATECAS 185	Mexico		Miranda. Tlaltenango. Elevation: 3330 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	313496		P. cocc.	G35107	Ayocote Negro		PUEBLA 56-C	Mexico	4/30/1905	Zacapoaxtla market. Elevation: 1960 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	NA	313497		P. cocc.	G35108	Ayocote		PUEBLA 84	Mexico		San Lucas El Grande. Elevation: 2560 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	NA	313500		P. cocc.	G35109	Ayocote Negro		Puebla 124	Mexico	5/1/1905	Palmar de Bravos. Elevation: 2430 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	313503		P. cocc.	G35609			Puebla 141-B	Mexico		Matamoros. Elevation: 1760 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	313506		P. cocc.		Ayocote Negro Brill		X-9196	Mexico		Hueyapa, Tlatlauqui. Elevation: 1660 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	317572		P. cocc.	G35110	Piloy negro de Chichicastenango		Plot No. 1507	Chimaltenango, Guatemala			22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317580		P. cocc.	G35615	Mezcla de piloy		Plot No. 1613	Alta Verapaz, Guatemala		Coban	22-Nov-1966. From: Chimaltenango, Guatemala	LR

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P. cocc.	Yes	Avail.	317596		P. cocc.		Piloy de Totonicapan		Plot No. 1486	Chimaltenango, Guatemala			22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	319449		P. cocc.	G35112	Patola		Col. No. 22140	Aguascalientes, Mexico	5/19/1905	Market in Aguascalientes. Elevation: 2000 meters	04-Apr-1967. From: Maryland, United States.	LR
P. cocc.	Yes	NA	321088		P. cocc.	G35618	Noe		Col. No. 4642	Kenya		Market in Thompson's Falls	10-Jul-1967. From: Maryland, United States.	LR
P. cocc.	Yes	NA	325584		P. cocc.		Acahuacate		Gentry 22443	Mexico		Near Teteles, Puebla. Habitat: Moist mountain slope in milpa. Elevation: 1960 meters	14-Feb-1968. From: Maryland, United States	WM
P. cocc.	Yes	Avail.	325588		P. cocc.	G35619	Ayocote		Gentry 22352	Oaxaca, Mexico		Near Ayutla, Tamazulapan District. Elevation: 2167 meters	14-Feb-1968. From: Maryland, United States	LR

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P. cocc.	Yes	Avail.	325589		P. cocc.	G35113			Gentry 22362	Oaxaca, Mexico		Nacaltepec, 20 mile north of Telixtlahuaca. Elevation: 2133 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	325590		P. cocc.	G35114	Aycote		Gentry 22414	Mexico		Market in Tehuacan.	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	325591		P. cocc.	G35115	Shaushana		Gentry 22436	Veracruz, Mexico		Altotonga. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	325592		P. cocc.	G35116	Ayocote		Gentry 22440	Mexico		Market in Altotongo. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	325593		P. cocc.	G35117	Ayocote		Gentry 22448	Mexico		Market in Zacapoaxtla. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	325594		P. cocc.	G35118	Ayocote		Gentry 22459	Mexico		Market in Tlatlauqui. Cool moist, cloudy climate. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR

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P. cocc.	Yes	Avail.	325595		P. cocc.	G35119	Ayocote		Gentry 22460	Mexico		Market in Tlatlauqui. Cool moist, cloudy climate. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	325596		P. cocc.	G35620	Ayocote		Gentry 22463	Chiapas, Mexico		Market in Tezuitlan. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	NA	325597		P. cocc.	G35120	Shanshana		Gentry 22464	Chiapas, Mexico		Market in Tezuitlan. Cool, moist, cloudy climate. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	325598		P. cocc.	G35179			Gentry 22490	Morelos, Mexico		64km along toll road north of Cuernavaca. Elevation: 2167 meters	14-Feb-1968. From: Maryland, United States	WM
P. cocc.	Yes	Avail.	325599		P. cocc.	G35121	Frijol Chuparosa		Gentry 22514	Mexico		Ixtlan de Juarez. Elevation: 2500 meters	14-Feb-1968. From: Maryland, United States	LR

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P. cocc.	Yes	Avail.	325600		P. cocc.	G35621	Frijol Chuparosa		Gentry 22515	Mexico		Ixtlan de Juarez. Elevation: 2500 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	325601		P. cocc.	G35122			Gentry 22522	Mexico		Ayutla, 33 miles east of Mitla.	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	325603		P. cocc.	G35124			Gentry 22527	Mexico		Nacaltepec, 20 miles north of Telixtlahuaca. Elevation: 2133 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	NA	325606		P. cocc.	G35127	Acalete		Gentry 22458	Mexico		Market in Tlatlaqui. Moist, foggy, cool climate. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	NA	325607		P. cocc.	G35128	Acalete		Gentry 22462	Chiapas, Mexico		Market in Tezuitlan. Moist, cloudy, cool climate. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR

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P. cocc.	Yes	NA	346950		P. cocc.					Federal District, Mexico		Santa Marta. Near penitentiary of Mexico City. Elevation: 2250 meters	16-Dec-1969. From: Maryland, United States.	WM
P. cocc.	Yes	Avail.	346951		P. cocc.	G35370				Mexico			16-Dec-1969. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	355423		P. cocc.				SAM 2675	Ecuador		Mercado del Sur, Guayaquil. Elevation: 660 meters	06-Oct-1970. From: California, United States.	CM
P. cocc.	Yes	Avail.	358088		P. cocc.		Edar Bel		462	Yugoslavia		Opila . Elevation: 600 meters	2-15-1970. From: Macedonia.	CM
P. cocc.	Yes	NA	358089		P. cocc.		Bivoleski		692	Yugoslavia		Zelznica . Elevation: 630 meters	2-15-1970. From: Macedonia.	CM
P. cocc.	Yes	Avail.	358090		P. cocc.	G36052	Belpritkas		782	Yugoslavia		Rataec . Elevation: 400 meters	2-15-1970. From: Macedonia.	CM
P. cocc.	Yes	Avail.	358091		P. cocc.		Probistipski		805	Yugoslavia		Buciste . Elevation: 390 meters	2-15-1970. From: Macedonia.	CM
P. cocc.	Yes	NA	358092		P. cocc.		Probistipski		812	Yugoslavia		Buciste . Elevation: 390 meters	2-15-1970. From: Macedonia.	CM

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P. cocc.	Yes	NA	358093		P. cocc.	G35623	Saren		818	Yugoslavia		Rataec . Elevation: 400 meters	2-15-1970. From: Macedonia.	CM
P. cocc.	Yes	NA	361302		P. cocc.				PLB 181	Jammu and Kashmir, India		Parakharpore	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361310		P. cocc.	G35276			PLB 190	Jammu and Kashmir, India		Chandanwari	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361327		P. cocc.	G35277			PLB 217	Himachal Pradesh, India		Kalpa	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361328		P. cocc.	G35278			PLB 218	Himachal Pradesh, India		Kalpa	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361351		P. cocc.	G35279			PLB 254	Uttar Pradesh, India		Benakuli	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361354		P. cocc.				PLB 257	Bhutan		Lachar, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361355		P. cocc.	G35280			PLB 258	Bhutan		Lachar, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361356		P. cocc.	G35281			PLB 259	Bhutan		Becho, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361357		P. cocc.	G35282.			PLB 260	Bhutan		Becho, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361358		P. cocc.	G35283			PLB 261	Bhutan		Lalchung, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361359		P. cocc.	G35284.			PLB 263	Bhutan		Lalchung, Sikkim	17-Feb-1971. From: India	CM

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P. cocc.	Yes	Avail.	361360		P. cocc.	G35285			PLB 265-1	Bhutan		Mugar, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361361		P. cocc.	G35286			PLB 266	Bhutan		Sanchi, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361370		P. cocc.	G35287			PLB 283	Bhutan		Lackhen, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361371		P. cocc.				PLB 284-1.	Bhutan		Beechor, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361372		P. cocc.	G35288			PLB 284-2	Bhutan		Beechor, Sikkim	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361451		P. cocc.	G35289			PLB 388	India		Ootacamund. Elevation: 1000 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361480		P. cocc.	G35290			PLB 423	Tamil Nadu, India		Shambagnur	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361509		P. cocc.	G35291			IC 7797	India		Sarhan. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361510		P. cocc.	G35292			IC 7798	India		Sarhan. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361511		P. cocc.	G35293			IC 7798-1	India		Sarhan. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361512		P. cocc.	G35293			IC 7798-2	India		Sarhan. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361514		P. cocc.	G35295			IC 7801	India		Sarhan. Elevation: 1660 meters	17-Feb-1971. From: India	CM

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P. cocc.	Yes	NA	361519		P. cocc.	G35296			IC 7805	India		Sarhan, Gopalpur. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361520		P. cocc.	G35297			IC 7805-2	India		Sarhan, Gopalpur. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	361538		P. cocc.	G35298.			IC 8261-A	India		Simla. Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361539		P. cocc.	G35299			IC 8261-B	India		Elevation: 1660 meters	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361551		P. cocc.	G35300			IC 9571	Sikkim, India		Zeema	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361553		P. cocc.	G35301			IC 9574	Sikkim, India		Zachung	17-Feb-1971. From: India	CM
P. cocc.	Yes	Avail.	361578		P. cocc.	G35302			IC 9668	Sikkim, India		Sirbadam	17-Feb-1971. From: India	CM
P. cocc.	Yes	NA	367903		P. cocc.					United States	10/29/1971			CM
P. cocc.	Yes	NA	368709		P. cocc.	G36011	Bel Grav		1327	Yugoslavia		Dukatino . Elevation: 380 meters	01-Jun-1971. From: Macedonia	CM
P. cocc.	Yes	NA	368710		P. cocc.	G36053	Bakla		1547	Yugoslavia		Topolovic . Elevation: 510 meters	01-Jun-1971. From: Macedonia	CM
P. cocc.	Yes	NA	368711		P. cocc.	G36054	Bakla		1570	Yugoslavia		Duracka Reka . Elevation: 720 meters	01-Jun-1971. From: Macedonia	CM

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P. cocc.	Yes	NA	368714		P. cocc.	G35303.	Rasteski V		1161	Yugoslavia		Rastes . Elevation: 820 meters	01-Jun-1971. From: Macedonia	CM
P. cocc.	Yes	NA	370507		P. cocc.	G36012	Bel Cvet		1865	Yugoslavia	5/24/1905	Markova Susica. Elevation: 400 meters	26-Jan-1972. From: Macedonia.	CM
P. cocc.	Yes	NA	370508		P. cocc.		Visok		1914	Yugoslavia	5/24/1905	Matejce. Elevation: 490 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	NA	370509		P. cocc.	G36031	Pritkas		1932	Yugoslavia	5/24/1905	Dumanovce. Elevation: 590 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	NA	370510		P. cocc.	G35884	Kumanovski		1940	Yugoslavia	5/24/1905	Lipkovo. Elevation: 410 meters	26-Jan-1972. From: Macedonia.	CM
P. cocc.	Yes	NA	370511		P. cocc.	G35884	Kumanovski		1970	Yugoslavia	5/24/1905	Lipkovo. Elevation: 410 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	NA	370512		P. cocc.		Grcki		2029	Yugoslavia	5/24/1905	Ljubojno. Elevation: 900 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	Avail.	370534		P. cocc.	G35304	Krupen		1906	Yugoslavia	5/24/1905	Barovo. Elevation: 700 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	NA	370550		P. cocc.	G35305	Edar Pritkas		1958	Yugoslavia	5/24/1905	Lukovica. Elevation: 660 meters	26-Jan-1972. From: Macedonia	CM
P. cocc.	Yes	Avail.	379426		P. cocc.		Pritkar		2263	Yugoslavia		Ivankovci . Elevation: 500 meters	29-12-1972. From: Macedonia.	CM

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P. cocc.	Yes	NA	379427		P. cocc.		Bel		2347	Yugoslavia		Gostirazni . Elevation: 710 meters	29-12-1972. From: Macedonia.	CM
P. cocc.	Yes	Avail.	390414		P. cocc.				W-C 956	Colombia		Market at Puerto Tejada	03-Sep-1974. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	406785		P. cocc.				W-C 1473	Costa Rica		Claude Hope Farm, Cartago	03-Feb-1976. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	406936		P. cocc.				W-C 1682	Honduras		Public market, Tegucigalpa, Central District	27-Feb-1976. From: Maryland, United States.	CM
P. cocc.	Yes	Avail.	406938		P. cocc.				W-C 1584	Honduras		Public market, Tegucigalpa, Central District	27-Feb-1976. From: Maryland, United States.	CM
P. cocc.	Yes	NA	407387		P. cocc.					China			04-Nov-1975. From: California, United States.	UIS.
P. cocc.	Yes	Avail.	417585		P. cocc.				M7054-1	Mexico		Ixtlan	10-Jun-1977. From: California, United States	CM
P. cocc.	Yes	Avail.	417586		P. cocc.		Frijolillo		M7271-B	Chihuahua, Mexico		Rancho Los Caracoles	10-Jun-1977. From: California, United States.	LR
P. cocc.	Yes	Avail.	417587		P. cocc.		Ayocote		M-7285-A	Veracruz, Mexico		Perote	10-Jun-1977. From: California, United States.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	417588		P. cocc.		Ayocote		M7285-B	Veracruz, Mexico		Perote.	10-Jun-1977. From: California, United States	LR
P. cocc.	NA	NA	417589		P. cocc.				M7399-D	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian).	10-Jun-1977. From: California, United States	CM
P. cocc.	NA	NA	417590		P. cocc.				M7399-U	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian)	10-Jun-1977. From: California, United States	UIS
P. cocc.	Yes	NA	417592		P. cocc.				M7399-W	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian)	10-Jun-1977. From: California, United States	UIS
P. cocc.	Yes	NA	417593		P. cocc.				M7400-D	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian)	10-Jun-1977. From: California, United States	UIS

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	417594		P. cocc.				M7402-C	Chihuahua, Mexico		Below Rancho Los Caracoles	10-Jun-1977. From: California, United States	UIS
P. cocc.	NA	NA	417596		P. cocc.				M7402-N	Chihuahua, Mexico		Below Rancho Los Caracoles	10-Jun-1977. From: California, United States	UIS
P. cocc.	Yes	NA	417602		P. cocc.				M7417-A	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM
P. cocc.	Yes	Avail.	417603		P. cocc.				M7417-B	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	417604		P. cocc.				M7417-C	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM
P. cocc.	Yes	Avail.	417605		P. cocc.				M7417-D	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM
P. cocc.	Yes	Avail.	417607		P. cocc.				M7417-F	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	417608		P. cocc.				M7417-G	Jalisco, Mexico		Rio Buche near Santa Maria del Valle (near bridge on highway going to San Miguel El Alto).	10-Jun-1977. From: California, United States.	WM
P. cocc.	NA	NA	417609		P. cocc.				M7421-A	Jalisco, Mexico		Along Rio Buche, 2km from highway near Santa Maria del Valle.	10-Jun-1977. From: California, United States.	WM
P. cocc.	Yes	NA	417610		P. cocc.				M7421-B	Jalisco, Mexico		Along Rio Buche, 2km from highway near Santa Maria del Valle.	10-Jun-1977. From: California, United States.	WM
P. cocc.	Yes	NA	417611		P. cocc.				M7423-A	Jalisco, Mexico		Cerro Aguila, Barranca del Muerto, Santa Maria del Valle	10-Jun-1977. From: California, United States.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	417755		P. cocc.		Cachara		M7361	Veracruz, Mexico		Tlapacoyan.	10-Jun-1977. From: California, United States.	LR
P. cocc.	Yes	NA	420322		P. cocc.				22	Italy	5/29/1905	Mestre market	14-Dec-1977. From: Indiana, United States	CM
P. cocc.	Yes	Avail.	430174		P. cocc.				M8027	Puebla, Mexico		Azumbilla	11-Oct-1974. From: California, United States.	UIS.
P. cocc.	NA	NA	430175		P. cocc.				M7271C	Chihuahua, Mexico		Rancho Los Caracoles	11-Oct-1978. From: California, United States.	CV
P. cocc.	NA	NA	430177		P. cocc.				M7399B	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian).	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430178		P. cocc.				M7399K	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian).	11-Oct-1978. From: California, United States.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	430179		P. cocc.				M7399L	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian).	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430180		P. cocc.				M7399X	Durango, Mexico		Cerro de Espinosa del Diablo (between San Miguel El Alto and San Julian).	11-Oct-1978. From: California, United States.	WM
P. cocc.	NA	NA	430181		P. cocc.				M7402B	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430182		P. cocc.				M7402G	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430183		P. cocc.				M7402H	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430185		P. cocc.				M7402K	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	NA	430187		P. cocc.				M7402P	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	430188		P. cocc.				M7402R	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430189		P. cocc.				M7402S	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430190		P. cocc.				M7402T	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430191		P. cocc.				M7402U	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	Avail.	430192		P. cocc.				M7402V	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	NA	Avail.	430194		P. cocc.				M7402X	Chihuahua, Mexico		Below Rancho Los Caracoles	11-Oct-1978. From: California, United States.	WM
P. cocc.	Yes	NA	432581		P. cocc.		Witte Pronker			Netherlands		Barneveld	01-Mar-1979. From: Netherlands	LR
P. cocc.	Yes	NA	432583		P. cocc.		Pronkboon			Netherlands		Aalsmeer	01-Mar-1979. From: Netherlands.	LR
P. cocc.	Yes	NA	433235		P. cocc.		Peligua			Chimaltenango, Guatemala		Chimaltenango.	01-Dec-1978. From: Tennessee, United States.	CV

APPENDIX 1.1 *Phaseolus coccineus* passport data.

Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	433236		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	Avail.	433237		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	Avail.	433238		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	Avail.	433239		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	NA	433242		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	Avail.	433243		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV
P. cocc.	Yes	NA	433244		P. cocc.		Piloy			Solola, Guatemala		Solola. Elevation: 2113 meters	01-Dec-1978. From: Tennessee, United States	CV

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	433245		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	NA	433246		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433247		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	NA	433248		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433249		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433250		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433251		P. cocc.		Piloy			Chimaltenango, Guatemala		Chimaltenango. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	433252		P. cocc.		Piloy			Chimaltenango, Guatemala		Itzapa. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433253		P. cocc.		Piloy			Chimaltenango, Guatemala		Itzapa. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	Yes	Avail.	433254		P. cocc.		Piloy			Chimaltenango, Guatemala		Itzapa. Elevation: 1800 meters	01-Dec-1978. From: Tennessee, United States.	CV
P. cocc.	NA	NA	433626		P. cocc.					Minnesota, United States			01-Apr-1979. From: Minnesota, United States	CV
P. cocc.	Yes	NA	433627		P. cocc.					Minnesota, United States			01-Apr-1979. From: Minnesota, United States	CV
P. cocc.	Yes	Avail.	433927		P. cocc.					Hawaii, United States		Maui, Hawaii	01-Apr-1979. From: California, United States	CV
P. cocc.	Yes	Avail.	438597		P. cocc.					Guatemala	2/27/1979	Public market, Coban, Alta Verapaz Dept	01-Dec-1979. From: Maryland, United States	CV

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	438598		P. cocc.					Guatemala	2/28/1979	Public market, Chichicastenango, Quiche Dept.	01-Dec-1979. From: Maryland, United States	CV
P. cocc.	Yes	Avail.	438910		P. cocc.		Frijol botel			Guatemala	2/16/1979	Public market, San Cristobal de las Casas, Chiapas.	01-Dec-1979. From: Maryland, United States	CV
P. cocc.	Yes	NA	439534		P. cocc.		Pronker			Netherlands		Woubrugge	01-Feb-1980. From: Netherlands	LR
P. cocc.	Yes	NA	439535		P. cocc.		Pronker			Netherlands		Wageningen	Date: 01-Feb-1980. From: Netherlands.	LR
P. cocc.	Yes	NA	439536		P. cocc.		Grote Zwarte			Netherlands		Woubrugge	01-Feb-1980. From: Netherlands	LR
P. cocc.	Yes	NA	442540		P. cocc.					Belgium		Antwerp	Apr-1979. From: Belgium	WM
P. cocc.	Yes	Avail.	449381		P. cocc.					Veracruz, Mexico		Market, Poza Rica	01-Mar-1980. From: California, United States	CM
P. cocc.	Yes	Avail.	451862		P. cocc.					Guatemala		Bus Terminal Market, Guatemala City	01-Jul-1980. From: Guatemala.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	451863		P. cocc.					Guatemala		Bus Terminal Market, Guatemala City	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	NA	451866		P. cocc.					Guatemala		Bus Terminal Market, Guatemala City	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	NA	451867		P. cocc.					Solola, Guatemala		Market, Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	Avail.	451868		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	Avail.	451869		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	Avail.	451870		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	NA	451871		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	Avail.	451872		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	Avail.	451873		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	451874		P. cocc.					Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	NA	451883		P. cocc.		Piloy			Solola, Guatemala		Solola	01-Jul-1980. From: Guatemala.	CM
P. cocc.	Yes	NA	458561		P. cocc.		Soepboon			Netherlands		Venray	01-Mar-1981. From: Netherlands	CM
P. cocc.	Yes	NA	458562		P. cocc.		Pronker (Steense Boon)			Netherlands		Oude Wetering	01-Mar-1981. From: Netherlands	CM
P. cocc.	Yes	NA	475745		P. cocc.		Emergo			Netherlands			01-Nov-1982. From: Netherlands	CV
P. cocc.	Yes	Avail.	476704		P. cocc.					Guatemala	10/9/1978	San Juan Ixcoy, Km 321.5 Hwy 9N. Elevation: 2222 meters	01-Sep-1980. From: Puerto Rico	WM
P. cocc.	Yes	NA	477015		P. cocc.		Spek Snijboon			Netherlands		Ubachtsberg	01-Mar-1983. From: Netherlands.	CV
P. cocc.	Yes	Avail.	494068		P. cocc.					Chile			Dec-1984. From: Maryland, United States	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	510637		P. cocc.				23794	Durango, Mexico	11/3/1984	Market in Ciudad de Durango. Elevation: 1829 meters	14-Feb-1985. From: California, United States.	CM
P. cocc.	NA	NA	549448	W6 7409	P. cocc.		Scarlet Runner			Missouri, United States			1961. From: Missouri, United States.	CV
P. cocc.	Yes	NA	549449	W6 7410	P. cocc.		Thayer Pole			New York, United States			1985. From: New York, United States.	CV
P. cocc.	NA	NA	549450	W6 7411	P. cocc.		Desiree			Colorado, United States			1985. From: Colorado, United States.	CV
P. cocc.	NA	NA	549451	W6 7412	P. cocc.		Goliath			Colorado, United States	6/7/1905		1985. From: Colorado, United States.	CV
P. cocc.	NA	Avail.	549452	W6 7413	P. cocc.		White Czar Runner Pole			Colorado, United States	6/7/1905		1985. From: Colorado, United States.	CV
P. cocc.	NA	NA	549489	W6 7450	P. cocc.		Oregon Lima			Oregon, United States	1964		1964. From: Oregon, United States.	CV
P. cocc.	NA	NA	550296	W6 8014	P. cocc.		Aztec 215			Colorado, United States	6/9/1905		1978. From: Maine, United States.	CV
P. cocc.	NA	NA	550439	W6 8111	P. cocc.		Painted Lady			Colorado, United States	1/1/1991		1987. From: Colorado, United States.	CV

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	583553	W6 6281	P. cocc.				PV4-2	Hokkaido, Japan	10/21/1990	Farmer's garden, 10km northwest of Highway 242, by En'garu (city), Abashiri District, Hokkaido Prefecture.	30-Nov-1990. From: Washington, United States	CM
P. cocc.	Yes	NA	583554	W6 6289	P. cocc.				PV6-5	Hokkaido, Japan	10/22/1990	Farmer's garden, 7km northeast of Highway 903, near Lake Kussharo, Abashiri District, Hokkaido Prefecture	30-Nov-1990. From: Washington, United States.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	583555	W6 6290	P. cocc.				PV6-6	Hokkaido, Japan	10/22/1990	Farmer's garden, 7km northeast of Highway 903, near Lake Kussharo, Abashiri District, Hokkaido Prefecture	30-Nov-1990. From: Washington, United States.	CM
P. cocc.	NA	NA	583556	W6 6301	P. cocc.				PV8-2	Hokkaido, Japan	10/24/1990	Farmer's garden, 10km from Highway 38, Kushiro District, Hokkaido Prefecture.	30-Nov-1990. From: Washington, United States	CM
P. cocc.	NA	Avail.	640977	W6 20519	P. cocc.				3077	Guatemala	1/1/1995	Almolonga, 3 km southeast of Almolonga. Elevation: 2070 meters	15-Jan-1998. From: Guatemala	WM
P. cocc.	Yes	Avail.	W6 10126		P. cocc.				DE-CH92-08	Los Lagos, Chile	2/5/1992	Public market, Temuco. Elevation: 500 meters	03-Mar-1992. From: Washington, United States	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 10443		P. cocc.					Kazakhstan		Government store, Alma Ata Market.	30-Apr-1992. From: Missouri, United States	CM
P. cocc.	NA	NA	W6 10514		P. cocc.				PDF 92003	Nepal	1992	Sermathang Village, Sinou Palchok District. Elevation: 2614 meters	8-Jul-92	CM
P. cocc.	NA	NA	W6 11573		P. cocc.					Colorado, United States	1987	Said to be found in a crock in part of the Mesa Verde National Park Indian cave-dwellings which were opened in 1987	30-Apr-1993. From: Colorado, United States.	WM
P. cocc.	NA	NA	W6 14859		P. cocc.		Granny Tiller White Runner			United States			27-Dec-1993. From: Maine, United States.	CV
P. cocc.	NA	NA	W6 14860		P. cocc.		Meccarello's Striped Romanian runnerbean			United States			27-Dec-1993. From: Maine, United States.	CV
P. cocc.	NA	NA	W6 14861		P. cocc.		Lillibridge Runnerbean						27-Dec-1993. From: Maine, United States.	CV

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 14862		P. cocc.		Slovak #4			Slovakia			27-Dec-1993. From: Maine, United States.	CV
P. cocc.	NA	NA	W6 14870		P. cocc.				870606-01	Spain	6/6/1987	Purchased in Supermercado Alfaro in Madrid	01-Jul-1987. From: Washington, United States.	CM
P. cocc.	NA	NA	W6 15594		P. cocc.		Habas Asturianas		BKK& WJK-2	Spain	3/31/1994	Purchased in Central Market (Mercado de Abastos) in Santiago de Compostela, Galacia Province	16-May-1994. From: Washington, United States	CV
P. cocc.	NA	NA	W6 19052		P. cocc.					Albania	11/23/1944	Street market in town of Lushnje	28-Nov-1994	UIS
P. cocc.	NA	NA	W6 20123		P. cocc.				GN 828		PRE 1985		1985	CM
P. cocc.	NA	NA	W6 20165		P. cocc.				851111-02	Baja Sur, Mexico	PRE 1985	Near town of Santa Rosalia.	25-Mar-1985	CM
P. cocc.	NA	NA	W6 20166		P. cocc.		Patolmorado		851111-01	Baja Sur, Mexico	PRE 1985	Near town of Santa Rosalia	25-Mar-1985	CM
P. cocc.	NA	NA	W6 20505		P. cocc.	G35172	Violet 5		NI-016	Rwanda	PRE 1998	19KM from Astrida	06-Feb-1998. From: Colombia	CM

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P. cocc.	NA	NA	W6 20506		P. cocc.	G35171	Blanc 5		NI-015	Rwanda	PRE 1998	19KM from Astrida	06-Feb-1998. From: Colombia.	CM
P. cocc.	NA	NA	W6 20510		P. cocc.				3062	Guatemala	1/1/1995	San Miguel Duenas, 1 km west of Concepcion Calderas.	15-Jan-1998. From: Guatemala	WM
P. cocc.	NA	Avail.	W6 20524		P. cocc.				3084	Guatemala	1/1/1995	Zunil, 1.5 km northeast of Estancia de la Cruz, Aguas Amargas. Elevation: 500 meters	15-Jan-1998. From: Guatemala	WM
P. cocc.	NA	NA	W6 20526		P. cocc.				3087	Guatemala	1/1/1995	Zunil, 2.0 km northeast of Estancia de la Cruz, Aguas Amargas. Elevation: 1800 meters	15-Jan-1998. From: Guatemala	WM
P. cocc.	NA	NA	W6 20527		P. cocc.				3088	Guatemala	1/1/1995	Cantel, 1.0 km north northeast of Cantel, Aldea Pachaj. Elevation: 2180 meters	15-Jan-1998. From: Guatemala	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 21022		P. cocc.					Collville, Washington			15-Oct-1998. From: Washington, United States	CM
P. cocc.	NA	NA	W6 21081		P. cocc.				TARS 030	Morelos, Mexico		Cueravaca. Elevation: 2400 meters	04-Apr-1999. From: Puerto Rico.	WM
P. cocc.	NA	NA	W6 21083		P. cocc.				TARS 036	Puerto Rico			04-Apr-1999. From: Puerto Rico.	UIS.
P. cocc.	NA	NA	W6 21099		P. cocc.				TARS 225	Guatemala	PRE Apr-1999		04-Apr-1999. From: Puerto Rico	UIS.
P. cocc.	NA	NA	W6 21107		P. cocc.				TARS 311				04-Apr-1999. From: Puerto Rico.	UIS.
P. cocc.	NA	NA	W6 21629		P. cocc.					New Mexico, United States		from Native American sources	09-Jul-1999. From: United States.	CM
P. cocc.	NA	NA	W6 21647		P. cocc.				TARS 214	Solola, Guatemala		Sta. Lucia Utatl n- Sta. C. Laguna. Elevation: 2330 meters	04-Apr-1999. From: Puerto Rico.	WM
P. cocc.	NA	NA	W6 21667		P. cocc.				G019	Macedonia, Greece	8/1/1999	Arsinioi Papageorgiou in Papingo. Elevation: 0 meters	Sep-1999..	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 21704		P. cocc.				GN 751103.	New Mexico, United States	5/27/1905	Near Albuquerque		CM
P. cocc.	NA	NA	W6 22173		P. cocc.				P 061	Poland	7/1/1999	Stary Kornin 42. Elevation: 0 meters	27-Jan-2000. From: Wisconsin, United States	CM
P. cocc.	NA	NA	W6 22463		P. cocc.				PC-00-01	Yunnan, China		Collected in Yunnan Province, China in either the town of Lijiang or Dali. Elevation: 1515 meters	10-May-2000. From: Maine, United States	CM
P. cocc.	NA	NA	W6 22464		P. cocc.				PC-00-02	Yunnan, China		town' Dali (or 'town' Lijiang). Elevation: 1515 meters	10-May-2000. From: Maine, United States	CM
P. cocc.	NA	NA	W6 3079		P. cocc.					Hebei, China			05-Feb-1990. From: Washington, United States	UIS
P. cocc.	NA	NA	W6 3677		P. cocc.				1-61	Nepal			14-Mar-1990. From: Italy.	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 4499		P. cocc.				WJK-PRC-41	Sichuan, China	5/28/1990	Market vendor, Chengdu, Sichuan Province	12-Jul-1990. From: Washington, United States.	CM
P. cocc.	NA	NA	W6 4500		P. cocc.				WJK-PRC-42	Sichuan, China	5/28/1990	Market vendor, Chengdu, Sichuan Province	12-Jul-1990. From: Washington, United States.	CM
P. cocc.	NA	NA	W6 4536		P. cocc.				WJK-PRC-78	Yunnan, China	6/4/1990	Market, Xi Zhou village, Dali Prefecture, Yunnan Province. Elevation: 2000 meters	12-Jul-1990. From: Washington, United States.	CM
P. cocc.	NA	NA	W6 6279		P. cocc.				PV3-1	Hokkaido, Japan	10/21/1990	Farmer's garden, 8km northeast of Highway 242, by En'garu (city), Abashiri District, Hokkaido Prefecture	30-Nov-1990. From: Washington, United States	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 6284		P. cocc.				PV5-3	Hokkaido, Japan	10/22/1990	Farmer's garden, 5km northeast of Highway 903, near Lake Kussharo, Abashiri District, Hokkaido Prefecture	30-Nov-1990. From: Washington, United States	CM
P. cocc.	NA	NA	W6 6294		P. cocc.				PV7-3	Hokkaido, Japan	10/23/1990	Farmer's garden, on Highway 243, south of Lake Kussharo,, Kushiro District, Hokkaido Prefecture	30-Nov-1990. From: Washington, United States.	CM
P. cocc.	NA	NA	W6 6298		P. cocc.				PV7-7	Hokkaido, Japan	10/23/1990	Farmer's garden, on Highway 243, south of Lake Kussharo, Kushiro District, Hokkaido Prefecture.	30-Nov-1990. From: Washington, United States.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	NA	NA	W6 6302		P. cocc.				PV8-3	Hokkaido, Japan	10/24/1990	Farmer's garden, 10km from Highway 38, Kushiro District, Hokkaido Prefecture.	30-Nov-1990. From: Washington, United States	CM
P. cocc.	NA	NA	W6 6544		P. cocc.				WJK-PRC-41.2	China	5/28/1990	Open-air market Chengdu, Sichuan Province	12-Jul-1990. From: Washington, United States	WM
P. cocc.	NA	NA	W6 8183		P. cocc.					Loja, Ecuador		Loja market. Grown locally in Loja area	03-Sep-1991. From: Loja, Ecuador	CM
P. cocc.	NA	NA	W6 9681		P. cocc.		Konstantin		523	Bulgaria	1/21/1992			CV
P. cocc.	NA	Not in th	200905		P. cocc.					Alta Verapaz, Guatemala	4/1/1952			
P. cocc.	NA	Not in th	201291		P. cocc.					Mexico	5/5/1905			
P. cocc.	NA	Not in th	201367		P. cocc.					Mexico	5/5/1905			
P. cocc.	NA	Not in th	W6 20518		P. cocc.				3076	Guatemala				

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P. cocc. subsp. form.	NA	NA	325609		P. cocc. var. cocc.				Gentry 22388	Oaxaca, Mexico		10 miles southeast of Miahuatlan. Habitat: Arid, limestone rocky slope with cutover oaks..	14-Feb-1968. From: Maryland, United States	WM
P. cocc. subsp. cocc.	NA	NA	535275		P. cocc. var. cocc.				TARS 032	Veracruz, Mexico	6/3/1905	Zongolica. Elevation: 1800 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	Yes	Avail.	535276		P. cocc. var. cocc.				TARS 034	Jalisco, Mexico	6/3/1905	Chiquilistlan. Elevation: 1630 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	535277		P. cocc. var. cocc.				TARS 039D	Mexico, Mexico	6/3/1905	Texcoco. Elevation: 2760 meters	21-Feb-1989. From: Puerto Rico	CM
P. cocc. subsp. cocc.	Yes	NA	535278		P. cocc. var. cocc.				TARS 046A	Veracruz, Mexico	6/3/1905	Zongolica. Elevation: 1800 meters	21-Feb-1989. From: Puerto Rico	CM
P. cocc. subsp. cocc.	Yes	NA	535279		P. cocc. var. cocc.				TARS 188	Guatemala		Castillo, Pat-Patz	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	Yes	NA	535280		P. cocc. var. cocc.				TARS 212	Sacatepequez, Guatemala		Crossroads Yepo-Duenos. Elevation: 1980 meters	21-Feb-1989. From: Puerto Rico	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. cocc.	Yes	NA	535281		P. cocc. var. cocc.				TARS 213	Guatemala		Top of hill, Parra-Yepo. Elevation: 2025 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	535282		P. cocc. var. cocc.				TARS 215	Solola, Guatemala		Km 159 S.C.Laguna. Elevation: 1910 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	Yes	Avail.	535283		P. cocc. var. cocc.				TARS 216	Solola, Guatemala		Hill to Godinez. Elevation: 2310 meters	21-Feb-1989. From: Puerto Rico	CM
P. cocc. subsp. cocc.	Yes	Avail.	535284		P. cocc. var. cocc.				TARS 217	Solola, Guatemala		Hill to Godinez. Elevation: 2310 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	535285		P. cocc. var. cocc.				TARS 219	Jalapa, Guatemala		Jalapa-Miramundo. Elevation: 2100 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	Yes	NA	535286		P. cocc. var. cocc.				TARS 221	Jalapa, Guatemala		Mataquesquintla. Elevation: 1950 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	Yes	NA	535287		P. cocc. var. cocc.				TARS 222	Sacatepequez, Guatemala		Road Volcan de Aqua. Elevation: 1940 meters	21-Feb-1989. From: Puerto Rico.	CM

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P. cocc. subsp. cocc.	NA	NA	535288		P. cocc. var. cocc.				TARS 224	Totonicapan, Guatemala		Totonicapan. Elevation: 2490 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	535289		P. cocc. var. cocc.				TARS 285	Morelos, Mexico		Cuer. km 67. Elevation: 1800 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	535290		P. cocc. var. cocc.				TARS 286A	Morelos, Mexico		Progreso. Elevation: 1430 meters	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. cocc.	NA	NA	W6 21103		P. cocc. var. cocc.				TARS 286D	Morelos, Mexico		Progreso. Elevation: 1430 meters	04-Apr-1999. From: Puerto Rico	UIS.
P. cocc. subsp. cocc.	NA	NA	W6 21104		P. cocc. var. cocc.				TARS 287	Morelos, Mexico		Progreso. Elevation: 1430 meters	04-Apr-1999. From: Puerto Rico	UIS.
P. cocc. subsp. cocc.	NA	NA	W6 21105		P. cocc. var. cocc.				TARS 288	Morelos, Mexico		Progreso. Elevation: 1430 meters	04-Apr-1999. From: Puerto Rico	UIS.
P. cocc. subsp. cocc.	NA	NA	W6 21106		P. cocc. var. cocc.				TARS 290	Morelos, Mexico		Progreso. Elevation: 1430 meters	04-Apr-1999. From: Puerto Rico	UIS.
P. cocc. subsp. cocc.	NA	NA	W6 21114		P. cocc. var. cocc.			NI-1122		Morelos, Mexico		Amatlan, Morelos, Mexico. Elevation: 1700 meters	04-Apr-1999. From: Puerto Rico	UIS.
P. cocc. subsp. cocc.	NA	NA	W6 21643		P. cocc. var. cocc.				TARS 031	Veracruz, Mexico	PRE Apr-1999		04-Apr-1999. From: Puerto Rico.	WM

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P. cocc. subsp. form.	NA	NA	W6 2333		P. cocc. var. cocc.				M178				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2334		P. cocc. var. cocc.				M201				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2335		P. cocc. var. cocc.				3138				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2336		P. cocc. var. cocc.				3139				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. form.	NA	NA	W6 2337		P. cocc. var. cocc.				3141				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. form.	NA	NA	W6 2338		P. cocc. var. cocc.				3142				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2339		P. cocc. var. cocc.				3143				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2340		P. cocc. var. cocc.				3144				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2341		P. cocc. var. cocc.				3145				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2342		P. cocc. var. cocc.				3323				31-Oct-1989. From: California, United States.	WM

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P. cocc. subsp. form.	NA	NA	W6 2343		P. cocc. var. cocc.				3324				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. form.	NA	NA	W6 2344		P. cocc. var. cocc.				3325				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. form.	NA	NA	W6 2345		P. cocc. var. cocc.				3326				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. form.	NA	NA	W6 2346		P. cocc. var. cocc.				3327				31-Oct-1989. From: California, United States.	WM
P. cocc. subsp. form.	NA	NA	W6 2347		P. cocc. var. cocc.				3328				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. obval.	NA	NA	W6 2354		P. cocc. var. cocc.				M673				31-Oct-1989. From: California, United States	WM
P. cocc. subsp. obval.	NA	NA	W6 2355		P. cocc. var. cocc.				M674				31-Oct-1989. From: California, United States	WM
P. cocc.	NA	NA	182012		P. dumo.				No. 17	Guatemala			26-May-1949. From: United States.	LR
P. cocc.	Yes	Avail.	190074		P. dumo.	G35569	Nimex Jat			Huehuetenango, Guatemala		Jacaltenango.	03-Jul-1950. From: United States.	LR
P. cocc. subsp. darw.	NA	NA	190080		P. dumo.	G35624	Ubal			Huehuetenango, Guatemala		Chajzunil	03-Jul-1950. From: United States.	LR

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P. cocc.	Yes	Avail.	194575		P. dumo.	G35032			NORVELL 2522	Chimaltenango, Guatemala	3/3/1951	Market in Chimaltenango.	23-Mar-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	194585		P. dumo.	G35570			NORVELL 2556	Solola, Guatemala	3/5/1951	Market in Solola. Elevation: 2113 meters	23-Mar-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	194586		P. dumo.	G35033			NORVELL 2557	Solola, Guatemala	3/5/1951	Market in Solola. Elevation: 2113 meters	23-Mar-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	195336		P. dumo.	G25911			NORVELL 2751	Retalhuleu, Guatemala	3/15/1951	Near Retalhuleu, Retahuleu. Elevation: 240 meters	16-Apr-1951. From: Maryland, United States.	WM
P. cocc.	Yes	Avail.	195337		P. dumo.	G25223			NORVELL 2754	Retalhuleu, Guatemala	3/15/1951	Near Retalhuleu, Retalhule, Depto. de Retalhuleu, toward Haunde Santa Fe. Elevation: 240 meters	16-Apr-1951. From: Maryland, United States	WM
P. cocc.	Yes	Avail.	195352		P. dumo.	G35034			NORVELL 2669	Quezaltenango, Guatemala	3/12/1951	Quezaltenango. Elevation: 2333 meters	16-Apr-1951. From: Maryland, United States	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	195353		P. dumo.	G35035			NORVELL 2672	Quezaltenango, Guatemala	3/12/1951	Quezaltenango. Elevation: 2333 meters	16-Apr-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	195359		P. dumo.	G35036			NORVELL 2591	Zacapa, Guatemala	3/8/1951	Antigua, Zacatepequez. Elevation: 1530 meters	16-Apr-1951. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	195363		P. dumo.	G35037.			NORVELL 2741	Suchitepequez, Guatemala	3/14/1951	Market in Mazatenango, Suchitepequez. Elevation: 460 meters	16-Apr-1951. From: Maryland, United States.	LR
P. cocc.	Yes	NA	195381		P. dumo.	G35038			NORVELL 2670	Quezaltenango, Guatemala	3/12/1951	Market in Quezaltenango. Elevation: 371 meters	16-Apr-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	195388		P. dumo.	G35039			NORVELL 2729	Totonicapan, Guatemala	3/14/1951	Market in Totonicapan. Elevation: 2495 meters	16-Apr-1951. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	195389		P. dumo.	G35040			NORVELL 2731	Totonicapan, Guatemala	3/14/1951	Market in Totonicapan. Elevation: 2495 meters	16-Apr-1951. From: Maryland, United States.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	195395		P. dumo.	G35041			NORVELL 2749	Retalhuleu, Guatemala	3/15/1951	Market in Retalhuleu. Elevation: 230 meters	16-Apr-1951. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	195399		P. dumo.	G35042			NORVELL 2769	Zacapa, Guatemala	3/16/1951	Market in Antigua, Zacatepequez. Elevation: 1530 meters	16-Apr-1951. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	201290		P. dumo.	G8892			NORVELL 3150	Puebla, Mexico			08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201323		P. dumo.	G35054			M 3186	Hidalgo, Mexico		Tulancingo	08-May-1952. From: California, United States	LR
P. cocc.	Yes	Avail.	201335		P. dumo.	G35056			NORVELL 3200	Hidalgo, Mexico		Tulancingo	08-May-1952. From: California, United States	LR
P. cocc.	Yes	NA	201337		P. dumo.	G35058			M 3202	Hidalgo, Mexico		Tulancingo	08-May-1952. From: California, United States	LR
P. cocc.	Yes	NA	201338		P. dumo.	G35059			M 3203	Puebla, Mexico		Huauchinango	08-May-1952. From: California, United States	LR
P. cocc. subsp. darw.	Yes	Avail.	201340		P. dumo.	G35060		NI-520	No. 3205	Puebla, Mexico		Huauchinango	08-May-1952. From: California, United States	LR
P. cocc. subsp. darw.	NA	NA	201342		P. dumo.	G35061		NI-519	No. 3208	Puebla, Mexico		Huauchinango	08-May-1952. From: California, United States	LR

APPENDIX 1.1 *Phaseolus coccineus* passport data.

Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. darw.	NA	NA	201344		P. dumo.	G35062			No. 3210	Puebla, Mexico		Huauchinango	08-May-1952. From: California, United States	LR
P. cocc. subsp. darw.	Yes	Avail.	201347		P. dumo.	G35063			No. 3213	Puebla, Mexico		Huauchinango	08-May-1952. From: California, United States	LR
P. cocc. subsp. darw.	Yes	NA	209502		P. dumo.	G35573			No. 3837	Cartago, Costa Rica		Market in Cartago	19-Jun-1953. From: California, United States	LR
P. cocc. subsp. darw.	Yes	Avail.	311165		P. dumo.	G35082	Piloya		Col. No. 20796	Solola, Guatemala	PRE Jan-1966	Store in Nahuala. Lat/lon accurate to Nahuala. Elevation: 2500 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311168		P. dumo.	G35083	Piloya		Gentry 20801	Guatemala		Market in Totonicapan	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311171		P. dumo.	G35084	Piloya		Col. No. 20805	Totonicapan, Guatemala	PRE Jan-1966	Market in Totonicapan. Elevation: 2500 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311174		P. dumo.	G35084	Piloya		Col. No. 20808	Totonicapan, Guatemala	PRE Jan-1966	Market in Totonicapan. Lat/lon accurate to Totonicapan. Elevation: 2660 meters	19-Jan-1966. From: Maryland, United States	LR

APPENDIX 1.1 *Phaseolus coccineus* passport data.

Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. darw.	Yes	NA	311178		P. dumo.				Col. No. 20816	Quiche, Guatemala	PRE Jan-1966	Market in Chichicastenango. Elevation: 2330 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311179		P. dumo.	G35088	Piloya		Col. No. 20819	Quiche, Guatemala	PRE Jan-1966	Market in Chichicastenango. Elevation: 2330 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311182		P. dumo.	G35582	Piloya		Col. No. 20832-A	Quiche, Guatemala	PRE Jan-1966	Market in Chichicastenango. Elevation: 2330 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311183		P. dumo.	G35089	Piloya		Col. No. 20834	Quiche, Guatemala	PRE Jan-1966	Market in Chichicastenango. Elevation: 2330 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311184		P. dumo.	G35090	Piloya		Col. No. 20843	Quezaltenango, Guatemala	PRE Jan-1966	Market in Quezaltenango. Elevation: 2000 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311186		P. dumo.	G35091	Piloya		Gentry 20850	Quezaltenango, Guatemala		Market in Quezaltenango. Elevation: 2000 meters	19-Jan-1966. From: Maryland, United States.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	311188		P. dumo.	G35175	Piloya		Gentry 20860	Chimaltenango, Guatemala		Store in Tecpan. Elevation: 2160 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311194		P. dumo.	G35584	Juruna		Gentry 20914	Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311196		P. dumo.	G35585	Juruna		Gentry 200918	Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311198		P. dumo.	G35586	Curuna		Gentry 20923	Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311199		P. dumo.	G35587	Curuna Piloya		Gentry 20925	Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc. subsp. darw.	Yes	NA	311201		P. dumo.	G50728	Piloya		Col. No. 20928	Guatemala		Market in Jalapa. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311203		P. dumo.	G35588	Piloya		Gentry 20984	Baja Verapaz, Guatemala		Market in San Jeronimo	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311205		P. dumo.	G35589	Piloya		Col. No. 20985	Alta Verapaz, Guatemala	PRE 1966	Market in Coban. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States	LR

APPENDIX 1.1 *Phaseolus coccineus* passport data.

Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. darw.	Yes	Avail.	311206		P. dumo.	G35591	Piloya		Col. No. 20990	Alta Verapaz, Guatemala	PRE 1966	Market in Coban. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311207		P. dumo.	G35176	Nung		Gentry 20991	Alta Verapaz, Guatemala		Market in Coban. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311208		P. dumo.	G35592	Nung		Col. No. 20994	Alta Verapaz, Guatemala	PRE 1966	Market in Coban. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311209		P. dumo.	G35593	Piloya		Gentry 20997	Alta Verapaz, Guatemala		Market in Coban. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311212		P. dumo.	G35595			Gentry 21009	Alta Verapaz, Guatemala		Market in Carcha. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc. subsp. darw.	Yes	Avail.	311213		P. dumo.		Piloya		Col. No. 21010	Alta Verapaz, Guatemala	PRE 1966	Market in Carcha. Elevation: 1430 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc. subsp. darw.	Yes	Avail.	311215		P. dumo.	G25216	Piloya		Col. No. 21018	Alta Verapaz, Guatemala	PRE 1966	Market in San Cristobal. Elevation: 1500 meters	19-Jan-1966. From: Maryland, United States.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. darw.	Yes	Avail.	311216		P. dumo.	G35093	Pilillo		Col. No. 21378	Sacatepequez, Guatemala	PRE 1966	Market in Antigua. Elevation: 1667 meters	19-Jan-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311217		P. dumo.	G35096	Piloya		Gentry 21400	Guatemala		Elevation: 2667 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311219		P. dumo.	G35096	Piloya		Gentry 21407	Guatemala		Market in Totonicapan. Elevation: 2667 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311220		P. dumo.		Piloya		Gentry 21410	Guatemala		Market in Quezaltenang o. Elevation: 2417 meters	19-Jan-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311833		P. dumo.	G35099	Pilieu		Gentry 21744	Guatemala	1965	San Cristobal. Elevation: 1330 meters	23-Feb-1966. From: Maryland, United States	LR
P. cocc. subsp. darw.	Yes	Avail.	311847		P. dumo.	G35100	Poleu		Col. No. 21766	Quiche, Guatemala	PRE 1965	Market in Chichicasten ango. Elevation: 2167 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	311850		P. dumo.	G35178	Pileua		Gentry 21769	Guatemala	Pre 1965	Market in Chichicasten ang. Elevation: 2160 meters	23-Feb-1966. From: Maryland, United States.	LR

APPENDIX 1.1 *Phaseolus coccineus* passport data.														
Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	311855		P. dumo.	G35645			Gentry 2177A	Guatemala	1965	Market in Chichicastenango. Elevation: 2160 meters	23-Feb-1966. From: Maryland, United States	LR
P. cocc.	Yes	Avail.	311859		P. dumo.	G35101	Piloy Negro		Gentry 21778	Guatemala	1965	Market in Chichicastenango. Elevation: 2160 meters	23-Feb-1966. From: Maryland, United States.	LR
P. cocc.	Yes	Avail.	313310		P. dumo.	G8909			DURANGO 28	Mexico	1952	Guadalupe Victoria. Elevation: 2160 meters	19-Apr-1966. From: Federal District, Mexico	LR
P. cocc. subsp. darw.	Yes	Avail.	313417		P. dumo.	G35639	Morado pardo		10	Mexico, Mexico		Toluca market. Elevation: 2675 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	317550		P. dumo.		Piligue Rojo Antigua		Plot No. 1216				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	NA	317551		P. dumo.		Piloy De Antigua		Plot No. 1217				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317552		P. dumo.		Enredo rojo Antigua		Plot No. 1219				22-Nov-1966. From: Chimaltenango, Guatemala	LR

APPENDIX 1.1 *Phaseolus coccineus* passport data.

Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	317554		P. dumo.		Piloy rojo		Plot No. 1235	Guatemala		Tecpan	22-Nov-1966. From: Chimaltenango, Guatemala.	LR
P. cocc.	Yes	Avail.	317562		P. dumo.	G35610	Piloy rojo de Comanchaj		Plot No. 1389				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317563		P. dumo.	G35611	Piligue Chuy		Plot No. 1400				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317571		P. dumo.	G35612	Piloy de Chichicasten ango		Plot No. 1493				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317573		P. dumo.	G35613	Mexcla de piloy de Chichicasten ango		Plot No. 1509				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317574		P. dumo.	G35111	Piloy de Quetzaltenan go		Plot No. 1514				22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317575		P. dumo.	G35882	Piloy de Tecpan		Plot No. 1528				22-Nov-1966. From: Chimaltenango, Guatemala.	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	317576		P. dumo.		Mezcla de piloy		Plot No. 1591	Jalapa, Guatemala			22-Nov-1966. From: Chimaltenango, Guatemala.	LR
P. cocc.	Yes	Avail.	317577		P. dumo.	G35614	Mezcla de piloy		Plot No. 1597	Jalapa, Guatemala			22-Nov-1966. From: Chimaltenango, Guatemala.	LR
P. cocc.	Yes	Avail.	317582		P. dumo.	G35616	Mezcla de piloy		Plot No. 1623	Baja Verapaz, Guatemala		Rabinal	22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317583		P. dumo.	G35617	Mezcla de piloy		Plot No. 1636	Alta Verapaz, Guatemala		Carcha	22-Nov-1966. From: Chimaltenango, Guatemala	LR
P. cocc.	Yes	Avail.	317584		P. dumo.	G35883	Mezcla de piloy		Plot No. 1651				22-Nov-1966. From: Chimaltenango, Guatemala.	LR
P. cocc.	Yes	Avail.	317585		P. dumo.		Mezcla de piloy		Plot No. 1654				22-Nov-1966. From: Chimaltenango, Guatemala.	LR
P. cocc.	Yes	Avail.	325602		P. dumo.	G35123			Gentry 22523.	Oaxaca, Mexico		Ayutla, 33 miles east of Mitla. Elevation: 2300 meters	14-Feb-1968. From: Maryland, United States	LR

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	NA	325604		P. dumo.	G35125	Acalete		Gentry 22444	Mexico		Market in Zacapoaxtla. Moist mountain. Elevation: 1900 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc.	Yes	NA	325605		P. dumo.	G35126	Acalete		Gentry 22454	Mexico		Market in Altotongo. Elevation: 2000 meters	14-Feb-1968. From: Maryland, United States.	LR
P. cocc.	Yes	NA	325608		P. dumo.	G35129	Acalete		Col. No. 22479	Veracruz, Mexico		From market in Coscomatepe c. Elevation: 1554 meters	14-Feb-1968. From: Maryland, United States	LR
P. cocc. subsp. darw.	NA	NA	535291		P. dumo.	G35941		NI-1112	TARS 309	Guatemala		Semetabaj-Panaj	21-Feb-1989. From: Puerto Rico.	CM
P. cocc. subsp. darw.	NA	Avail.	W6 20514		P. dumo.				3067	Guatemala	1/1/1995	San Lucas Toliman, 3 km northeast junction to San Lucas highway 11 to Godinez. Elevation: 1630 meters	15-Jan-1998. From: Guatemala	WM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc. subsp. darw.	NA	Avail.	W6 20520		P. dumo.				3078	Guatemala	1/1/1995	Almolonga, 4 km southeast of Almolonga. Elevation: 2050 meters	15-Jan-1998. From: Guatemala	WM
P. cocc. subsp. darw.	NA	NA	W6 20529		P. dumo.				3093	Guatemala	1/1/1995	Santa Maria de Jesus, 0.5 km east of Santa Maria de Jesus, El Dique Dam. Elevation: 1460 meters	15-Jan-1998. From: Guatemala.	WM
P. cocc.	NA	Not in the NPGS Collect-ion	202080		P. vulgaris		Frijol Ayocote			Mexico	7/10/1952			
P. cocc.	Yes	Avail.	313313		P. vulgaris	G8911	Bayo rata		103 31	Durango, Mexico	5/5/1905	Elevation: 1898 meters	19-Apr-1966. From: Federal District, Mexico.	LR
P. cocc.	Yes	Avail.	313573		P. vulgaris				Antioquia 18	Antioquia, Colombia			15-Apr-1966. From: Maryland, United States	CM
P. cocc.	Yes	Avail.	358087		P. vulgaris	G8934	Poluvisok		256	Yugoslavia		Ohrid. Elevation: 760 meters	15-Feb-1970. From: Macedonia.	CM

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Previous Species Cat.[s]	Avail. in 2001[t]	Avail. 2007 from NPGS[u]	NPGS PI #	NPGS extra #	CIAT ID[v]	CGIAR Int. Center Identifier	local names	Insti-tute #[w]	Collector id.[x]	Country Collected From	When Collected	Locality[y]	Donated	Dom. Stat[z]
P. cocc.	Yes	Avail.	358094		P. vulgaris	G8935	Kukurecanski		1117	Yugoslavia		Kukurecani. Elevation: 600 meters	15-Feb-1970. From: Macedonia.	CM

Previous Species Cat.[s] Species labled at time of testing.

Avail. in 2001[t] Accessions available for testing in 2001.

Avail. 2007 from NPGS[u] Accessions available in 2007

CIAT ID[v] Identifying number from CIAT

COLLECT id.[x] Number given to sample by collector

Locality[y] Location where sample was found

Dom. Stat[z] Domestication status, cv=cultivar, cm=cultivated material, wm=wild material, LR= landrace, UIS unimprovement status