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SUMMARY OF EDIBLE LEGUMES RESEARCH ACCOMPLISHMENTS 2007-2011

by
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2011

Development and Release of Fusarium Wilt and Root Rot Resistant Green Pea Breeding Lines. ***(Dr. Lyndon Porter, 509-786-9237)***
Fusarium root diseases are currently a major concern of the green and dry pea industries worldwide and resistant germplasm lines to these diseases with agronomically acceptable characteristics are seriously lacking. Six advanced breeding lines containing both high levels of field resistance to Fusarium root rot and Fusarium wilt races 1 and 2 were developed and released. These breeding lines reduced mean root rot severity in field trials by 38 to 50% compared to the susceptible commercial standard, Bolero. In an artificial inoculation study in a greenhouse, these lines were also resistant to Fusarium wilt race 5. In addition to Fusarium disease resistance, these lines have desirable agronomic traits such as double or triple pods per node and four of the six lines have the afila leaf-type which is in high demand by breeders in the pea industry since it promotes the development of uniform seed coat color and improves anti-lodging characteristics which facilitates harvest. These lines are currently being used by private breeders as a resource for developing root-rot-resistant cultivars serving the canning, freezer, and dry pea industries.

White Mold Resistance Markers for Dry Beans ***(Dr. Phil Miklas, 509-786-9258)***
White mold is a major disease problem of dry bean in the United States. Breeding for resistance to white mold disease is complex because it is quantitatively inherited. Markers linked with resistance to white mold are needed to facilitate marker-assisted breeding efforts. We generated markers linked with white mold resistance traits (QTL, quantitative trait loci) in two common bean populations. In addition, a comprehensive genetic linkage map of 35 QTL conditioning resistance to white mold was constructed. The comparative map revealed 21 distinct QTL for white mold resistance. Six QTL most suitable for

marker-assisted breeding were highlighted. The new resistance-linked markers generated will be used by breeders to develop beans with improved resistance to white mold. The comparative linkage map represents a useful resource for interpreting past, present, and future QTL and fine-mapping studies concerning partial resistance to white mold in common bean

2010

Seven organic or potentially organic pea seed treatments improved plant health by significantly improving several plant health parameters *(Dr. Lyndon Porter, 509-786-9237)*
Seed and root rotting pathogens severely reduce the stand counts of non-treated seed in organic pea production. Most organic pea growers do not use seed treatments on their pea seed or feel that currently available seed treatments are not effective. Organic pea growers often plant twice the amount of seed that is commonly used in conventional production to compensate for poor stand development. Seven organic or potentially organic pea seed treatments improved plant health by significantly improving one of the following plant health parameters: seed germination, plant height, root health, or yield compared to seed receiving no seed treatment in at least one of three field experiments in 2007 to 2008. These treatments included Bacillus subtillus, cuprous oxide, calcium, corn flour, boron, fermented stinging nettle and natural plant extracts from seaweed. Seed treated with a combination of cuprous oxide and pre-gelitenized corn flour improved pea yields above that of non-treated seed by 13.2 and 12.2% in separate field trials.

identification and characterization of a new source of quantitative resistance effective against BDMV *(Dr. Phil Miklas, 509-786-9258)*
Bean dwarf mosaic is a white-fly vectored viral disease (BDMV) that is problematic for dry bean production in the tropics. Genetic resistance can be used to control this disease but sources are lacking. A Research Geneticist, USDA-ARS, at Prosser, WA, led a team of scientists from UC-Davis, in the identification and characterization of a new source of quantitative resistance effective against BDMV. The quantitative resistance is associated with the *Bct* gene which confers qualitative resistance against a completely different virus disease, Beet curly top (BCTV), which is vectored by a leaf hopper. This work provides breeders with a new source of resistance to combat BDMV. Knowledge generated enables breeding for resistance to two disparate viral diseases simultaneously.

Eight PI accessions identified for germplasm with high resistance to *Pea enation mosaic virus* (PEMV) *(Dr. Richard Larsen, 509-786-9259)*
Chickpea can be seriously affected by *Pea enation mosaic virus* (PEMV) in the Pacific Northwest region of the USA and other areas of the world. Use of pesticides to manage PEMV vector transmission is ineffective and PEMV-resistant chickpeas have not been identified. Eight PI accessions were identified that consisted of germplasm with high resistance to the virus. The sources are all of the small-seeded Desi type. One accession of the large-seeded Kabuli type also was identified with a tolerance response to PEMV. These germplasm lines will provide for the first time, the opportunity for breeders to introgress

resistance genes into advanced breeding lines and commercial cultivars to produce new varieties with resistance to PEMV.

2009

Characterization and Molecular tagging and mapping of two genes conferring resistance to potato blight *(Dr. Phil Miklas, 509-786-9258)*
Halo blight is a seed-borne bacterial disease of common bean that is prevalent in cooler humid regions of the upper Midwest (MI, MN, ND, NE) and in similar climates worldwide. Genetic resistance can be used to control this disease but inheritance is not well understood. A Research Geneticist, USDA-ARS, at Prosser, WA, led a team of scientists from South Africa and the International Center for Tropical Agriculture in Colombia, South America, in the characterization, and molecular tagging and mapping of two genes conferring resistance to halo blight. The genes Pse-1 and Pse-2 confer resistance to four and seven isolates of the pathogen, respectively, and both are located on the same chromosome but are loosely linked. The molecular markers linked with these genes, via marker-assisted selection, will facilitate development and deployment of resistant bean cultivars for better control of this disease in the U.S.A. and worldwide.

Demonstration of Resistance to Clover Yellow Vein Virus (ClYVV) in various lines of snap bean *(Dr. Phil Miklas, 509-786-9258*; *Dr. Richard Larsen, 509-786-9259)*
Clover yellow vein virus (ClYVV) continues to plague snap bean crops in the upper Midwest States where the soybean aphid is the common vector of the virus. There are currently very limited sources of resistance to the virus in dry bean and no resistance has been identified in snap bean. In collaboration with Dr. Phil Miklas ARS geneticist, we demonstrated that dry bean lines USLK-1, USLK-2, USLK-3, USDK-4 USDK-5, USWK-6, USCR-7, USCR-8, USCR-9 show good resistance to ClYVV. This evidence indicates that the *bc-3* gene contained in these lines that confers resistance to *Bean common mosaic virus* also may be linked to resistance to ClYVV. We also demonstrated using a molecular marker that the *PveILF4E*^{R} allele of the eukaryotic initiation factor eIF4E is closely associated with the *bc-3* gene and resistance to ClYVV. In addition, a selection from a recombinant inbred line population was identified with resistance to ClYVV but does not possess the *bc-3* gene. The genetic background of the recombinant line is being explored to identify an additional potential source resistance or tolerance. Because insecticides are not effective against ClYVV in bean, identification of resistance and development of resistant breeding lines will be significant in reducing future losses in snap bean.

2008

Seed transmission of Pea enation mosaic virus (PEMV) ***(Dr. Richard Larsen, 509-786-9259)***

PEMV has never been definitively demonstrated to be seed transmitted and as such, has been a point of issue in movement of pea seed from the U.S. to other countries such as Australia and New Zealand. We sought to determine whether the virus actually is seed-borne and seed transmitted. A highly sensitive assay called real-time PCR (qRT-PCR) was used to detect PEMV on seeds collected from infected plants and to assess the relative concentrations of viral RNA responsible for the disease. Results from qRT-PCR showed that PEMV was present in very small amounts on seed coats but was not able to infect plants emerging from the seed. The lack of evidence for seed transmission is provided in support of relaxing restrictions on international movement of pulse seed which will be a major benefit to the U.S seed industry with sales to New Zeland and Australia.

Evaluate bean germplasm for resistance to Clover yellow vein virus (ClYVV) ***(Dr. Phil Miklas, 509-786-9258)***

ClYVV continues to plague snap bean crops in the upper Midwest States where the soybean aphid is the common vector of the virus that causes severe pod necrosis resulting in beans that are unmarketable. Nine dry bean lines were identified with good resistance to ClYVV. Over 60 commercial snap bean cultivars were screened for resistance to ClYVV and only one was shown to have a high level of tolerance to the virus. Because insecticides are not effective against ClYVV in bean, identification of resistance genes and development of resistant breeding lines will be significant in reducing future losses in snap bean

Sources of resistance to Fusarium root rot of pea ***(Dr. Lyndon Porter, 509-786-9237)***

F. solani f. sp. pisi is a serious root rot pathogen affecting peas in all pea growing areas of the USA and is damaging in both dryland and irrigated pea fields. Yield reductions of 30% have been reported for eastern Washington and no current commercial cultivars are resistant to F. solani. In collaborative research with the Plant Germplasm Introduction and Testing Research Unit, Pullman, WA, three pea lines, W6 26740, W6 26743 and W6 26745 were identified and released demonstrating favourable horticultural characteristics in addition to Fusarium root rot resistance. Pea lines developed by Dr. Clarice Coyne were screened in a disease nursery specifically developed for identifying Fusarium root rot resistant pea germplasm. The resistant lines formally released from this research are currently being used as parental lines by breeders of dry pea companies such as ProGene to increase the root rot resistance in their spring and winter dry pea cultivars for commercial dry pea production.

Characterizing, tagging, and mapping halo blight resistance genes in dry bean ***(Dr. Phil Miklas, 509-786-9258)***

Halo blight is a seed-borne bacterial disease of common bean that is prevalent in cooler humid regions of the upper Midwest (MI, MN, ND, NE) and in similar climates worldwide. Genetic resistance can be used to control this disease but inheritance is not well understood. Characterization and molecular tagging and mapping of two genes conferring resistance to halo blight have been completed. The genes Pse-1 and Pse-2 confer resistance to four and seven isolates of the pathogen, respectively, and both are located on the same chromosome but are loosely linked. The molecular markers linked with these genes, via marker-assisted selection, will facilitate development and deployment of resistant bean cultivars for better control of this disease in the U.S.A. and worldwide.

2007

Markers linked to resistance genes to common bacterial blight of common beans. ***(Dr. George Vandemark, 509-786-9218)***

Common bacterial blight (CBB) of common bean (Phaseolus vulgaris L.), which is caused by Xanthomonas campestris cv. phaseoli, is a disease of global importance to bean production. Susceptible cultivars can suffer losses from CBB that exceed 40% of yield potential. The most effective method for controlling CBB is to grow resistant bean cultivars. However, it is difficult for plant breeding programs to effectively screen for CBB resistance because resistance is complexly inherited and environmental factors such as temperature and humidity influence the expression of disease. A promising alternative to disease screening for identifying genotypes with resistance to CBB has been to screen beans for molecular markers that are closely linked to disease resistance genes. Two markers of particular interest to breeding programs focused on enhancing resistance to CBB are the markers BC420 and SU91. Unfortunately, both BC420 and SU91 are dominant markers. Dominant markers cannot easily be used to distinguish plants with one copy of a gene (heterozygous) from plants with two copies of a gene (homozygous). The erroneous selection of a heterozygous plant will result in the introduction of deleterious alleles conditioning disease susceptibility into a breeding program. To identify plants with the desired homozygous genotypes it is necessary to self pollinate all plants that amplify the marker and perform a progeny test for disease resistance. This both increases costs and delays progress of breeding programs, as the process of self pollination and progeny testing requires up to four months for completion. Real-time PCR assays were developed for both BC420 and SU91 and were used to determine the role of dosage effects of these two QTLs on the expression of resistance to CBB. It was found that there is a duplicate recesssive epistatic interaction between the two genes, in which a plant that has two copies of the recessive allele for SU 91 will be highly susceptible to CBB even if it has two copies of the dominant allele for BC 420. A single copy of the dominant allele for SU 91 is required for the plant to even have partial resistance to CBB. The most resistant plants have at least a single copy of both BC 420 and SU 91. The most desired genotypes have been determined for conferring resistance to CBB through the interactions of BC 420 and SU 91. Plants can be selected at the seedling stage for the most desirable genotype, which consists of two copies of both genes (BC420 BC420 SU 91 SU 91). This will save breeders considerable time and also reduce costs associated with breeding for CBB resistance. This accomplishment should also improve strategies for breeding beans with CBB resistance, as breeders are now aware that resistance cannot be conferred by BC420 alone in genetic backgrounds that do not also contain SU 91. This accomplishment resulted from collaborations between Dr. Vandemark and Dr. Phillip Miklas.

Real-time PCR test to confirm lack of seed transmission of pea enation mosaic virus. ***(Dr. Richard Larsen, 509-786-9259)***
Pea enation mosaic virus (PEMV) is considered as one of the most important virus diseases of pea in the world. Currently, phytosanitary certification is required in many countries including the U.S, of seed to be imported or exported because of dated reports of seed transmission of the virus in pea seed. This research examined the extent to which PEMV is seed-borne and its potential, if any, to be seed-transmitted. Results from real-time RT-PCR showed that PEMV was seed-borne, but at very low levels in embryo tissues, the tissues that must be infected for a virus to be seed transmitted. Virus accumulation was demonstrated to be at least 1000 times lower in embryo tissue than in the seed coat. Therefore, transmission may not occur because of the very low levels of the PEMV viral genomes in embryo tissues from infected plants. In evidence supporting this hypothesis, seed transmission was not observed by growing out over 50,000 seeds from infected plants nor was the virus detected by ELISA examination of 286 plants grown out from seeds collected from infected plants. Seed testing for certification is a tedious and expensive process for seed companies, as the seed must be tested by certified laboratories. Currently, any seed lots from the U.S. that PEMV has been shown to be only seed-borne and not seed-transmitted, are subject to rejection by other countries, and also are not permitted to be grown in the U.S. The loss of this seed due to required destruction can result in millions of dollars in potential losses to seed companies. The results of our research are being used to relieve phytosanitary restrictions on PEMV for movement of pea germplasm and commercial seed on an international basis beginning with the Washington State Department of Agriculture and the Ministry of Forestry-Biosecurity New Zealand.

Development of a comprehensive genetic linkage map of biotic and abiotic stress resistance traits in beans. ***(Dr. Phil Miklas, 509-786-9258)***
A genetic linkage map is a useful tool for interpreting inheritance studies and coordinating genomic research, serves as a repository for accumulation of genes and markers, and provides a framework to plant breeders from which to generate trait-linked markers for marker-assisted selection and combine specific traits. For the map to be more useful periodic integration of genetic data is needed to update the common bean linkage map. Dr. Phil Miklas, Research Geneticist, USDA-ARS, at Prosser, WA, led a team of scientists from Michigan State University and the International Center for Tropical Agriculture (CIAT, Cali, Colombia, SA) in the development of a comprehensive genetic linkage map of biotic and abiotic stress resistance traits. The map contains more that 100 genes and QTL conditioning resistance to diseases, insects, and abiotic stresses. The cumulative mapping of disease resistance traits revealed new resistance gene clusters while adding to others, and reinforces the co-location of QTL conditioning resistance with specific resistance genes and defense related genes. Biotic and abiotic stresses severely limit yield and quality of dry bean resulting in significant lost revenue to bean growers on a yearly basis. The

comprehensive genetic linkage map of resistance traits will expand marker-assisted selection in dry bean and facilitate development of germplasm lines and cultivars with improved resistance to multiple stresses. Stress resistant beans will improve profitability, increase water use efficiency, and reduce fertilizer and pesticide use.

Selection of white mold resistant pea germplasm lines and progress towards developing gene markers for marker assisted selection. ***(Dr. Lyndon Porter, 509-786-9237)***

White mold, caused by Sclerotinia sclerotiorum, is a common foliar pathogen of many legumes including peas. White mold often causes serious disease in irrigated and dryland peas throughout the United States, and as stated in, "The Status of Pea Crop Vulnerability", submitted by the Pisum Crop Germplasm Committee to the USDA National Project Staff, white mold is considered to be a serious potential threat to the expanding pea production in the United States. Additionally, in the Columbia Basin of Washington, pea acreage grown under center-pivot irrigation is increasing which favors the environments promoting the development of this pathogen. Due to poor economic returns to pea growers, expensive foliar fungicides used to manage white mold are cost prohibiting. Identifying novel sources of resistance to white mold in the Pisum core collection would be highly beneficial to provide breeders with resistant plant accessions to develop future fresh and dry pea cultivars resistant to the white mold pathogen. The entire Pisum (Pea) Core Collection (498 pea lines) and four woody-stem selections from John Kraft's (ARS, Prosser, WA, Retired Plant Pathologist) Germplasm Collection were screened for resistance to the white mold pathogen. Fifty-one lines from 18 different countries were identified as demonstrating some level of tolerance to the white mold pathogen based on stem lesion expansion and nodal resistance data collected. Information on the white-mold-resistant lines in the Pisum Core Collection is available to pea breeders. The pea lines are available to them through the Western Regional Plant Introduction Station in Pullman, WA. Dr. Kevin McPhee, a pea breeder with the USDA-ARS in Pullman, WA has used the above mentioned screening results and selected four white-mold-tolerant pea lines and is currently developing gene mapping population to identify the genes associated with this resistance. These mapping populations will lead to gene markers that will be used in marker-assisted selection to quickly screen future pea cultivars for resistance to this pathogen.