PROJECT OBJECTIVES AS IN PROJECT OUTLINE:

1. Improve bean yield potential by incorporating resistance/tolerance to major biotic and abiotic stresses, broadening the genetic base, developing genomic resources, and coordinating field trial nurseries.

2. Identify and implement sustainable agricultural systems that improve bean seed yield, conserve natural resources, and protect the environment.

AS IN BLUE SHEETS, IF DIFFERENT FROM THOSE IN PROJECT OUTLINE:
The Progress Report on the above Research Project is submitted in the following pages.
Project Leader: Dr. James Beaver
Head of Department: Dr. Elvin Román Paoli
Date: 30 September 2016

FY16 ANNUAL REPORT FOR H-351

Introduction

H351-A is part of regional Hatch project W-3150 entitled "Breeding common bean (*Phaseolus vulgaris* L.) for resistance to abiotic and biotic stresses, sustainable production, and enhanced nutritional value". The objectives of the regional project are as follows: (1) Improving bean yield potential by incorporating resistance/tolerance to major biotic and abiotic stresses, broadening the genetic base, implementing/integrating genomic resources and coordinating field trial nurseries. (2) Implement sustainable and profitable agricultural systems that improve bean seed yield, conserve natural resources, and protect the environment.

Participation in this regional Hatch project provides the opportunity for cooperation with other Agricultural Experiment Stations engaged in bean research. This approach results in a more efficient use of the limited resources assigned to bean researchers in the U.S. and helps to prevent duplication of effort in particular areas of research.

The specific objectives of project H-351 are: 1) Conduct a bean breeding program by crossing promising parents and selecting lines in the F_2 to F_6 generations for adaptation, agronomic traits and disease resistance, 2) Evaluate the performance of advanced generation breeding lines on experiment stations and farms, 3) Screen breeding lines with molecular markers linked to disease resistance genes, 4) Study the inheritance of resistance to common bacterial blight, angular leaf spot and ashy stem blight, 5) Isolate and characterize pathogenic strains of bacteria and fungi. This was the first year of a five-year extension of the regional Hatch project W-3150.

RESEARCH PROGRESS FOR THE BEAN BREEDING PROGRAM

Crossing Blocks

Crossing blocks were planted in in the greenhouses of the University of Puerto Rico, Mayaguez Campus. Many of the crosses were designed to combine bean golden yellow mosaic virus (BGYMV) resistance with resistance to other diseases such as bean common mosaic necrosis virus (BCMNV), common bacterial blight (CBB), root rot, rust, angular leaf spot (ALS) and web blight (WB). Crosses were also made with sources of resistance to bruchids and leafhoppers and lines with greater tolerance to root rot and low fertility soils. 'Verano' was used as a source of resistance to common bacterial blight. PR0806-80 and PR0806-81 were used as sources of resistance to rust and BCMNV. BGYMV resistant light red kidney breeding lines were crossed with sources of resistance to BCMNV.

At present, there are several molecular markers available for bean disease resistance genes. Molecular biology laboratories at the University of Puerto Rico, Mayagüez Campus (UPRM) and the USDA/ARS/TARS were used to screen breeding lines for molecular markers. During the past year, SCAR markers were used to identify lines with disease resistance genes. The lines were also screened for the presence of QTLs (Quantitative Trait Loci) linked with resistance to

common bacterial blight (CBB) and BGYMV resistance. This information permits breeders to make crosses with a greater likelihood of combining specific resistance genes.

Bean breeding lines were screened in a UPR greenhouse for resistance to BCMNV using mechanical inoculations with the NL-3 strain of the virus. The susceptible line PR0443-151 was used to maintain the virus and 'Verano', which has the *I* gene, was planted as a susceptible check. Lines lacking virus symptoms have the *bc-3* resistance gene. DNA samples were taken from the BCMNV resistant plants and evaluated for the presence of molecular markers linked to disease resistance genes.

Early Generation Nurseries

F_2 populations were planted at the Isabela Substation in October 2015 and January 2016. Individual plants were selected from the F_2 nurseries based on agronomic traits, yield potential and seed characteristics. Several $F_{2:3}$ and $F_{3:4}$ generation nurseries were planted at the Isabela Substation in October 2015 and January 2016. Pedigree selection was used to choose adapted individual plants with good pod set, erect growth habit and absence of disease symptoms. $F_{4:5}$ lines of some populations were planted in October 2015 and January 2016 and lines of other populations will be planted at the Isabela in October 2016. Individual plants were selected for plant type, resistance to foliar diseases and seed yield potential. The most promising $F_{4:5}$ lines will be screened in the greenhouse for resistance to BCMNV and the presence of molecular markers for BGYMV and rust resistance.

Advanced Generation Nurseries

White-seeded bean lines with resistance to BGYMV, BCMNV and bruchids were selected in nurseries planted at the Isabela Substation. The bruchid screening was conducted in the laboratory at the Isabela Substation. Seed of these lines will be multiplied during the upcoming growing season to permit future evaluation in replicated field trials. We also selected white-seeded lines with BGYMV and BCMNV resistance and earlier maturity. This would provide local growers with greater flexibility in the harvest of green-shelled beans. We have developed white bean lines that may combine resistance to BGYMV, BCMV, BCMNV and common blight and are adapted to higher temperatures during the summer months.

During the past year, we conducted several performance trials including promising bean breeding lines. Pink bean F_6 lines with resistance to BGYMV, BCMNV and resistance to common bacterial blight were planted in field trials at the Isabela Substation in October and December 2015. Lines were identified that had erect plant type, common blight scores similar to the white bean cultivar 'Verano' and mean seed yields > 2,000 kg/ha from both planting dates (Table 1.)

Table 1. Performance of lines in a pink bean advanced line trial planted at the Isabela Substation in October and December 2015.

Line	Common blight[1]		Seed yield (kg/ha)	
	Oct. 2015	Dec. 2015	Oct. 2015	Dec. 2015
1519-15	4.2	3.6	2003	2711
29	3.8	3.6	2327	3143
35	4.4	3.0	2252	2690
37	4.4	3.2	2402	2929
43	4.4	3.0	2522	2795
Verano	4.2	3.0	1968	2906
Beníquez	5.2	3.4	1526	2966
Mean	4.6	3.4	2132	2924
LSD (0.05)	0.7	NS	276	397
CV (%)	12.9	15.6	10.3	10.8

[1] Rated on a scale from 1-9 where 1 = no symptoms and 9 = very severe symptoms.

White bean lines with resistance to BGYMV, BCMNV and angular leaf spot were selected in collaboration with Dr. Consuelo Estevez de Jensen (Table 2.). Seed yields in the trials planted in December 2015 were > 2,000 kg/ha and common blight scores of the breeding lines were as good as the white bean cultivar 'Verano'.

Snap bean breeding lines developed between a cross between a source of BGYMV and BCMV resistance and a snap bean with heat tolerance and rust resistance genes (*Ur-4* and *Ur-11*) were advanced to the F_5 generation in trials planted at the Isabela Substation. During the past year, we screened these lines with molecular markers for genes for resistance to BGYMV and in the greenhouse for resistance to BCMV. Lines were selected that have the *bgm* gene and the

SW12 QTL for BGYMV resistance. These lines will be screened for rust resistance in Honduras in collaboration with Zamorano. This should provide home gardeners and commercial producers in Puerto Rico with a snap bean that is well adapted to local conditions.

Table 2. Performance of UPR bean breeding white bean breeding lines with resistance to angular leaf spot planted at the Isabela Substation in December 2015.

Line	Common blight scores[1]		Seed yield (kg/ha)	Reaction to BCMNV[2]	Angular leaf spot scores[1]	
	Oct. 2015	Dec. 2015	Dec 2015	Greenhouse	2015	2016
1657-1	3	3	2369	N	333	1
1657-18	3	4	2349	N	333	1
1657-21	3	4	2718	N	111	1
1657-23	3	4	2941	N	133	1
1657-25	3	3	2520	N	111	1
1657-26	3	4	2625	N	333	1
1657-27	3	4	2902	N	333	3
1657-28	3	4	2777	N	111	1
1657-30	3	4	2593	N	333	1
PR1418-18	3	3	2685	N	333	1
PR1418-20	3	4	3283	N	111	3
PR1418-21	3	3	2974	N	333	1
Verano	3	4	2586	N		3
Beniquez	4	6	3553	H		

[1] Rated on a scale from 1-9 where 1 = no symptoms and 9 = very severe symptoms.
[1] N = necrotic reaction indicating the presence of the *I* gene.

Each year, Puerto Rico imports significant quantities of black and pinto beans. During the past year, the UPR participated in the release of the black bean cultivar XRAV-40-4. This black bean cultivar is resistant to BGYMV, BCMV and BCMNV and is well adapted to local conditions. We have developed black bean lines that have resistance to BGYMV, BCMV and BCMNV, have common blight scores similar to 'Verano' and resistance to rust at Zamorano (Table 3). The project has also developed pinto bean lines that combine BGYMV, BCMV and BCMNV that are well adapted to local conditions (Table 4). White, pinto and black beans could be produced in Puerto Rico to increase food security.

Table 3. Performance of black bean lines planted at Isabela, Puerto Rico in Oct. and Dec. 2015.

Line	Common blight[1]		Seed yield (kg/ha)	
	Oct. 2015	Dec. 2015	Oct. 2015	Dec. 2015
1564-1	3.0	3.5	1729	2020
2	3.5	3.5	1816	2478
3	3.0	3.0	1737	2438
20	4.5	4.0	1445	2701
XRAV-40-4	5.5	4.5	1516	2747
MEN 2201-64 ML	6.0	4.3	1579	2005
Mean	5.1	4.3	1205	2334
LSD (0.05)	1.8	0.9	461	NS
CV(%)	17.2	16.6	18.3	16.3

[1] Rated on a scale from 1-9 where 1 = no symptoms and 9 = very severe symptoms.

Table 4. Performance of pinto bean lines planted at Isabela, Puerto Rico in Oct. and Dec. 2015.

Identity	Common blight score[1]	Seed yield (kg/ha)	
	Dec. 2015	Oct. 2015	Dec. 2015
PR1572-10	4.8	2045	3040
26	4.4	2084	3100

37	3.2	2053	2904
38	3.4	2077	2798
Santa Fe	3.8	2103	2932
Mean	4.2	1574	2683
LSD(0.05)	1.4	544	952
CV(%)	25.8	27.5	28.3

[1] Rated on a scale from 1-9 where 1 = no symptoms and 9 = very severe symptoms.

Cultivar and Germplasm releases

PR0806-80 and PR0806-81 had the best overall performance with low common bacterial blight scores and among the highest yields in the five test environments. These white bean breeding lines have resistance to BGYMV, BCMV, BCMNV and rust. SR2 and SW12 marker results suggest the presence of *bgm* gene and the QTL for BGYMV resistance. Resistant reactions to NL3 in the greenhouse suggest the presence of the *bc3* resistance gene. These lines were also resistant to all rust races when evaluated at Beltsville, MD by Dr. Pastor Corrales. PR0806-80, 81 and 82 have both the SA14 marker for the *Ur4* gene and the SI19 marker for the *Ur5* gene for rust resistance. PR0806-83 and 84 have the SI19 marker for *Ur5* but do not have the SA14 marker for the *Ur4* gene. These white lines had less powdery mildew that most other bean lines in the DR during the 2011-2011 growing season. Common blight has not been a problem in the field but the lines were susceptible when inoculated in the greenhouse with the 3353 and 484A strains of *Xap*. All of the lines are moderately susceptible to angular leaf spot in Puerto Rico with scores ≤ 4 using the CIAT 1-9 scale. Mean seed yield of the breeding lines was similar to the checks 'Verano' and 'Morales'.

In December 2015, the project planted 4,791 bean breeding lines from Michigan State, the University of Nebraska and North Dakota State Universities in winter nurseries as a cooperative activity of Regional Hatch Project W-3150. A few lines with traits of economic value were selected from the winter nursery for use as parents in the UPR bean breeding program.

It should be noted that the bean research program has been successful leveraging funds from other donors. This support allows a level of activity that contributes to increased productivity.

Study of the resistance to angular leaf spot

An isolate from *Phaeoisariopsis griseola* was used to inoculate 63 white bean breeding lines/genotypes and susceptible check cultivars 'Verano' and 'Beníquez'. 'Ouro Negro' was included as a resistant check. The lines derived from crosses with ALS 9951-101, BMD RMR 12 and PR0443-151 and twelve standard differential lines were included to determine the ALS pathotype. The experiment was arranged in a completely randomized design with three replications and inoculated twice with isolate ALS-9029 JD2 (10^5 conidia ml^{-1}) from Juana Diaz, Puerto Rico (PR). The evaluation was carried out 21 days after the inoculations (25 days after planting) using the CIAT scale where: 1 = no visible disease symptoms and 9 = 90% of the leaf area covered with sporulating lesions. Based on the reaction of the ALS differentials, the ALS-9029-JD2 isolate was classified as pathotype 61:11. Twelve lines exhibited a susceptible reaction and 31 lines an intermediate reaction to the pathotype evaluated. Sixteen lines showed a resistant reaction to isolate ALS-9029 JD2 with no symptoms. To monitor the resistance genes in the lines identified, the SCAR marker SBA16 linked to resistance genes (Phg-ON) was tested. The primers were: forward "TTCCACGTCTATTTTGCATCA" and reverse "CACGCATCACGCAGAACT". Five genotypes amplified a 560 bp size band in an agarose gel (1%) after a PCR reaction of 35 cycles of 94 °C/30s, 58 °C/1 min and 72 °C/90s min. The genotypes were PR1418-15, BFS-139, 1488-86, Aifi Wuriti, PR 0806-81. Phenotypic evaluation of disease severity confirmed the resistance for these genotypes with the isolate inoculated. An isolate from Isabela ALS-900-ISAD was inoculated under the screenhouse conditions in Juana Diaz Substation. Genotypes G21212, SER 125, SEF-17 and SB DT1, BFS 81, BK9-2, BRT 943-20 and BFS 95 were resistant and no synemata formation was observed after 48 hours under humid chamber conditions. Additional testing as well as PCR analysis with SCAR markers will be carried out.

Study of the resistance to ashy stem blight

Charcoal rot caused by *Macrophomina phaseolina* (Tassi) Goid, is an important disease in common beans in the dry and warmer areas of Puerto Rico and in much of the tropics and subtropics worldwide. The virulence of 3 isolates from Isabela (Mph-ISA-TARS), Juana Diaz (Mph-JD) and Aguadilla (Mph-13) and the reaction to Mph-JD of different common bean genotypes were determined. The pathogen was multiplied in pasteurized rice for 15 days in the dark at room temperature. The inoculum consisted of 3 grams of rice colonized by *Macrophomina phaseolina* deposited around the seedling of six different genotypes. After 7 and 21 days of the inoculation the plants were evaluated using the CIAT

scale (1-9): 1= no visible disease symptoms and 9 = approximately 50% or more of the hypocotyl and stem tissues covered with lesions and pycnidia. In a separate experiment isolate Mph-JD was used to inoculate four common bean lines with BAT 477 used as the resistant and G-122 as a susceptible checks. Results showed that virulence varied among the three isolates and the genotypes evaluated differed in their response to the pathogen depending on the isolate. The most virulent isolate was Mph-JD isolate when compared to the isolates from Isabela and Aguadilla. In two consecutive trials 'Mecosta" (ADP-225) was the most susceptible line and G-122 (susceptible check) was not and this reaction was dependent on the isolate inoculated. TARS-MST1 was the most resistant to Mph-ISA-TARS. Consistently, 'Mecosta' and 'Zawadi' (ADP-106) were susceptible to all 3 isolates and the lesion length was significantly longer than in BAT 477 and G-122. Genotypes BAT 477, TARS-LFR1, TARS-MST1 and G-122 were similar in disease severity and lesion length at 21 days after inoculation. These results indicated that differences exist in virulence of *Macrophomina phaseolina*.

An additional trial was conducted in the BASE 120 genotypes using a *Macrophomina phaseolina* isolate from Juana Diaz. The seeds were surface sterilized and the inoculation was consisted in 1 g of the pathogen multiplied in sterilized rice following the protocol from CIAT. The experiment had two replications and four plants per pot with PROMIX. From the 93 genotypes evaluated, only six genotypes had low disease severity and BIOF 2-106, Rosetta, SB-754, SER 78, SXB-405 and TARS-MST1.

Isolation and characterization of pathogenic bacteria

Bean seeds were used to isolate and determine the presence of *Xanthomonas axonopodis* pv. *phaseoli* or *Xanthomonas fuscans.* Commercial seed from Goya® (white, black and pink colors) and released bean lines from the UPR bean project ['Badillo' (light red kidney), and 'Verano' (white)] were used. Thirty four isolates were obtained and grouped into 23 representative types. Bacteria isolated were grouped as followed: 78% in the Division Firmicutes and 22% into the Gracillicutes. Pathogenicity tests of the representative types were conducted using the strain Xap 3353 as the indicator of pathogenicity on leaves. Only one type was found pathogenic on Goya® varieties of black and pink seeded colors but not on Badillo, Verano and Goya® white seeded variety. Xap 3353 showed the same pattern of pathogenicity as described above for the representative type, although the colony and biochemical characteristics are different. Other characterization tests are in progress.

Isolation and characterization of pathogenic fungi

The virulence of *Fusarium solani* isolate ISA-Fs-008 was characterized in the BASE 120 nursery. The experiment was conducted in pasteurized sand in a screenhouse in the Substation Juana Diaz with 120 genotypes replicated twice. The common bean genotypes were inoculated twice with a suspension of 10^5 macroconida deposited at the base of the stem (1ml), 15 and 21 days after planting and evaluated 35 days after planting. The disease severity was assessed using the CIAT scale (1-9) based on the area of infection in the roots and hypocotyl. Sixteen genotypes were excluded from the evaluation because of the low germination. The severity in four plants form each genotype ranged from 1 to 7 and the genotypes with no visible symptoms of *F. solani* infection were: SEQ 342-39, SEQ 342-89, G21212, MEN 2201 and FBN 1205-31. Data of nodulation is also available.

Publications

Beaver, J.S., J.C. Rosas, T.G. Porch, M.A. Pastor-Corrales, G. Godoy-Lutz and E.H. Prophete. 2015. Registration of PR0806-80 and PR0806-81 white bean germplasm with resistance to BGYMV, BCMV, BCMNV and rust. J. Plant Reg. 9:208-211.

Cichy, K.A., T.G. Porch, J.S. Beaver, P. Cregan, D. Fourie, R. Glahn, M.A. Grusak, K. Kamfwa, D.N. Katuuramu, P. McClean, E. Mndolwa, S. Nchimbi-Msolla, M.A. Pastor-Corrales and P.N. Miklas. 2015. A *Phaseolus vulgaris* diversity panel for Andean bean improvement. Crop Sci. 55:2141-2160.

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Kusolwa P.M, J.R. Myers, T.G. Porch, Y. Trukhina, A. González-Vélez and J.S. Beaver. 2016 Registration of AO-1012-29-3-3A Red Kidney Bean Germplasm Line with Bean Weevil, BCMV, and BCMNV Resistance. Journal of Plant Registrations 10:149-153.

Valentín Torres, S., M.M. Vargas, G. Godoy-Lutz, T.G. Porch, and J.S. Beaver. 2016. Isolates of *Rhizoctonia solani* can produce both web blight and root rot symptoms in common bean (*Phaseolus vulgaris* L.). Plant Disease 110-1351-1357.

Tim Porch, USDA-ARS-TARS, Mayaguez, PR

The release of multiple disease resistant common bean germplasm was completed by the University of Puerto Rico in collaboration with multiple institutions, including the USDA-ARS. PR1146-138 is yellow bean germplasm has resistance to the bean common mosaic virus (BCMV), to the bean golden yellow mosaic virus (BGYMV), and to the leaf hopper insect. PR0806-80 and PR0806-81 are white bean germplasm with resistance to BGYMV, BCMV, BCMNV and rust. AO-1012-29-3-3A is a red kidney bean germplasm line with bean weevil, BCMV, and BCMNV resistance. This unique contribution of weevil resistance was introgressed from tepary bean into common bean by collaborators at Oregon State U. and Sokoine University.

Breeding lines developed for drought from a second cycle of recurrent selection and new bulk breeding Durango populations were selected and evaluated in the collaborative shuttle breeding project with the U. of Nebraska, and several are being considered for release. In collaboration with ARS-Prosser, over 70 Andean bulk breeding populations were evaluated and single plants selected for heat tolerance and root rot resistance. Several QTL have initially been identified for heat tolerance. A data collection cart was developed and implemented in collaboration with ARS-Arizona for high throughput evaluation of canopy height, canopy temperature, and NDVI.

Tepary bean was found to have similar cooking time and similar nutritional composition as common bean in collaboration with ARS researchers, Colorado State U. and the U. of Puerto Rico. Tepary bean showed reduced fat and ash concentration, higher sucrose concentration, and similar cooking times as compared to common bean. The variability for seed composition and cooking traits found within tepary bean can be exploited for its improvement.

Publications:

Beaver, J.S., E. Prophete, G. Démosthène, and T.G. Porch. 2016. Registration of PR1146-138 Yellow Bean Germplasm Line. Journal of Plant Registrations 10:145-148. doi:10.3198/jpr2015.09.0058crg

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Washington

David Gang, Washington State University
Theodore Kisha USDA-ARS-WRPIS
The USDA, ARS National Plant Germplasm System (NPGS) *Phaseolus* collection is maintained at the Western Regional Plant Introduction Station, Pullman, Washington. Approaching the end of FY2106, the collection totaled 17,302 accessions, 13, 092 of which have a PI number, while 4,213 are listed in the W6 category and are pending decision for PI assignment (PDF Table).

The program is on track to regenerate about 700 accessions this year. Regeneration with 17 pots, three plants per pot, in only a single row has greatly increased the number of accessions regenerated per year over the previous curator's method of 25 pots per accession with two seeds per pot in one and a half rows, with no significant difference in yield, increasing the number of regenerations by 50%.

All accessions are regenerated in the greenhouse to avoid virus contamination. No virus testing has been done this year for lack of personnel. Testing was put on hold after the loss of a knowledgeable Phaseolus Technician. A more modern ELISA system is being investigated to streamline the process, and will hopefully begin again next year. As in the past, accessions are warranted to be virus-free or the requestor is notified that the accession cannot be certified virus-free.

We received 28 new accessions, including 166 heirloom varieties, distributed 4579 accessions (4075 to 46 states, 504 to 18 countries). 4336 accessions were sent to Svalbard. Also, 8032 images and 38,679 data points from 36 descriptors from 14,170 accessions were added to GRIN.

The program received a grant for the collection of *Phaseolus polystachios* in the State and National Forests in Ohio. The collection trip proceeded in October of this fiscal year in partnership with botanist Ashley Egan of the Smithsonian Institution and found 7 populations throughout Ohio. In addition, Ashley found 2 populations in Indiana and 2 in Missouri on an unrelated trip, and 1 more in West Virginia on her return to Washington, D.C. Several of the sites had either no seed, or the seed had been weevil infested, and may not germinate. The populations are currently being increased in the greenhouse and will be available for distribution. Marker analysis shows each population to be genetically distinct, prompting the need for continued collection in intermediate states from the Midwest to Florida.

In collaboration with the Washington State University Food Science and Human Nutrition Department, about 100 accessions were sampled for protein, phenolics, antioxidant activity, raffinose, stachyose, and sucrose and descriptors for nutrients have been added to GRIN. More accessions will be tested each year, and the results will be entered in GRIN. Information contained in the GRIN web-page descriptor site has been updated and continues to be monitored and changed as additional data is obtained. Descriptors for Phaseolus can be found at: http://www.ars-grin.gov/cgi-bin/npgs/html/crop.pl?83

Availablity of photoperiod sensitive accessions continues to be at risk. Antiquated greenhouse facilities allow fewer than 200 accessions of PPS accessions per year. Given a storage life of approximately 40 years at $4°$ C, the current rate of regeneration will likely result in a loss of many accessions. Discussions are underway for the duplication of our *Phaseolus* collection at EMBRAPA Brazil. An agreement to return PPS portions of the collection over time will hopefully prevent their loss.

A targeted region amplified polymorphism (TRAP) and AFLP study has been completed on the 200 accessions of *Phaseolus acutifolius*. Additionally, an AFLP study of the populations of *Phaseolus polystachios* collected in the Midwest has also been completed. Dr. Egan from the Smithsonian Institution is planning a second trip through North Carolina and Virginia. The Plant Collection Office has indicated that money is available.

Kisha, T.J. and A. Egan. 2016 Genetic Diversity of North American Wild Kidney Bean (Phaseolus Polystachios) Collected in the Midwest. American Society of Horticultural Science. Abstracts: Aug 8-11. New Orleans, LA.

Phil Miklas, USDA-ARS, Prosser, WA.

Dry bean nurseries: Participated in four cooperative trials in 2016. The national Cooperative Dry Bean Nursery (CDBN), directed by Carlos Urrea; the Western Regional Bean Trial (WRBT), directed by Carlos Urrea; and the Cooperative Dry Bean Drought Nursery (CDBDN), also directed by Carlos Urrea. A drought intensity index of 68% indicating severe drought stress was obtained. Two pintos UI35-37 from University of Idaho and PT9-5-6 from USDA-ARS (Prosser) were the best performers in this nursery. The slow darkening breeding line SF103-8 was released as Palomino in collaboration with J. Osorno (NDSU). A new field site developed for white mold disease screening, no experimental data was collected for the Bean White Mold Nursery (BWMN), directed by Jim Steadman, in 2016.

White mold: The physical positions for 37 individual QTL were identified across 14 recombinant inbred bi-parental populations (six new, three re-genotyped, and five from the literature). A meta-QTL analysis of the 37 QTL was conducted using the genetic linkage map of Stampede x Red Hawk population as the reference. The 37 QTL condensed into 17 named loci (12 previously named and five new) of which nine were defined as meta-QTL WM1.1, WM2.2, WM3.1, WM5.4, WM6.2, WM7.1, WM7.4, WM7.5, and WM8.3. The nine meta-QTL had confidence intervals ranging from 0.42 to 5.89 Mb. Candidate genes shown to express under *S. sclerotiorum* infection in other studies including cell wall receptor kinase, *COI1*, ethylene responsive transcription factor, peroxidase, and MYB transcription factor were found within the confidence interval for five of the meta-QTL. The nine meta-QTL are recommended as potential targets for MAS for partial resistance to white mold in common bean. This work was done in collaboration with NDSU (McClean), OSU (Myers), and international partners form Spain and Brazil and leverages funding from the National Sclerotinia Initiative.

Halo blight: A new QTL for halo blight resistance was discovered on Pv04 in Rojo/CAL 143 and Canadian Wonder/PI 150414 RIL populations which conditions resistance to all nine differential races including the problematic Race 6. Another minor QTL was detected on Pv05 in both populations which conferred resistance solely to Race 6. This Pv05 QTL was also observed by GWAS in a panel of 400 ADP accessions tested against Race 6 in the field in South Africa.

3000 single plant selections were obtained from 150 F4 bulk PIC (Phaseolus Improvement Cooperative) populations. The PIC populations derive from ADP x ADP parental crosses to combine abiotic and biotic stress resistance traits into Andean lines primarily for East Africa. In this case the populations were grown in three separate stress environments in WA (low N, terminal drought, and multiple stress = terminal drought, root rot, soil compaction and low fertility). These selections will be used to improve stress tolerance in U.S. large seeded market classes. Meanwhile the subsequent selection process with these 3000 lines has been designed to enable studies of genome x environment effects.

California

University of California- Riverside, California (J.G. Waines):

Plants of genetic male-sterile lines developed by Mark Bassett in small, black-seeded common bean 5-593 were grown out for seed increase, especially MS-1, MS-8 and ian. Others will be increased in winter 2017.

Nebraska
Nebraska W3150 report for 2016
     Dry Bean Research completed by Drs. James Steadman (Department of Plant Science) and Carlos Urrea (Department of Agronomy and Horticulture): Coordinated, participated in, and distributed the national CDBN (21 entries comprising 10 pintos, 4 blacks, 1 red, 1 dark red kidney, 1 white kidney, 1 light red kidney, 1 otebo, and 2 navies) planted at CA, CO, MI, MD, MT, WA, WY, ON, NE, and PR, and the regional WRBT (13 entries comprising 4 great northern, and 9 pintos) trial planted at CO, ID, WA, and NE. Participated in the regional MRPN trial planted at ND, MI, CO, and NE. Contributed with one pinto line to the CDBN and two great northern and two Nebraska pinto bean lines to both WRBT and MRPN trials. Coordinated, participated in, and distributed the DBDN (27 entries comprising 9 lines from the Shuttle Breeding between NE and PR, 5 lines from MI, 4 lines from NE, 2 lines from WA, 3lines from CO, and 4 checks) planted at WA, CO, NE, and MI, and will be planted in PR. For the DBDN planted in NE, irrigation was stopped at flowering stage (terminal stress). The second generation of dry bean lines from the Shuttle Breeding between NE and PR was tested in 2016 under drought stress and non-stress conditions. Irrigation was stopped at flowering stage (terminal stress). Lines from the first cycle of Shuttle Breeding were used as reference checks. Plots are being harvested.

     A set of elite six great northern and six pinto lines were tested in growers' fields under the 'Mother and Baby' Trial scheme. Data from these trials, the regional trials described above, and disease screening trials are being compiled. A great northern bean 'Panhandle Pride' was released as a cultivar based on its performance in Nebraska since 2010. Breeder seed was increased in Wyoming in 2016. In 2017, foundation seed will be produced. Data from trials evaluating the yield of different market classes (great northern, pinto, reds, blacks, light red kidney, and cranberries) are being harvested. Several lines within each market class appeared to perform better than the reference checks.

     The 2016 evaluation of NE great northern and pinto lines with the rust and common bacterial blight (CBB) pathogens under field conditions was conducted at Beltsville, MD with Talo Pastor-Corrales. Of the NE lines in the pinto nursery, 24 were resistant to the prevalent races of rust and prevalent CBB. The great northern nursery had 18 entries with CBB and rust resistance. As in previous years, the spreader rows were inoculated with five races of the rust pathogen: 38, 39, 40, 41, and 43. The common bacterial blight was fairly severe due to weather conditions.

     Three bacterial wilt RILs were advanced to F3:4 through single seed descent. We will continue selfing the RILs until F4:5.

     Both field and greenhouse tests across 6 locations were conducted in 2015-16 on entries of bean breeder lines with potential white mold resistance levels. Field tests demonstrated that two pinto lines, recently released USPT-WM-12 and 039-A-5, were rated much lower in disease severity than susceptible control Beryl at some locations. Greenhouse tests across four states confirmed moderate resistance for USPT-WM-12 and the great northern 031-A-11. Also, results of multi-year and multi-site tests have identified highly aggressive, low aggressive, widely distributed in the U.S. and single location isolates (mycelial compatibility groups) that can be made available for screening bean germplasm/breeding lines. Initiated research on genotyping and fungicide sensitivity testing of 366 isolates from U.S., France, Mexico and Australia is on-going.

     Dry Bean Research completed by Drs. Vicki Schlegel and Carlos Urrea (Department of Food Science and Technology): Great northern beans (GNB) added to a diet rich in fatty foods may prevent weight gain, fatty livers and high cholesterol. Research conducted in the laboratory of Dr. Vicki Schlegel (Associate Professor, Department of Food Science and Technology), generated data that showed hamsters fed a fatty rich diet were 20% heavier than those on an analogous diet supplemented with only 5% GNB. In fact, the weights of latter group were similar to animals fed a low fat diet that did not contain GNB. Liver weights of the 5% GNB-fatty diet group were also similar to the low fat diet group, while the fatty diets resulted in liver weight gains of ~30%. As expected, both plasma and liver cholesterol markers were negatively impacted by the fatty diet, but the 5% supplemented GNB diet again resulted in comparable or even improved cholesterol markers elicited by the low fat diet. These studies included GNB characterization to

ultimately determine the components responsible for these benefits. Similar studies are now in progress using pinto beans and their hulls supplemented into fatty diets at different dosages and cooked by various processes.

Moreover, the effects of different phenols present in most dry bean market classes, i.e., kaempferol, ferulic acid, etc., were monitored for their ability to synergistically remediate the pro-inflammatory state (M1) using a macrophage cell line. The data shows that these phenols are synergists and either switch and induced pro-inflammatory macrophage to an inactive state or to an anti-inflammatory (M2) state. Also extracts from pinto beans shown similar results in that different extracts affected the state of the induced macrophage more effectively, again suggesting that not only the levels of phenols present dry beans are responsible for this health benefit, but more likely the combination present. Studies are on-going with different bean extracts and moving this research into macrophages derived from mouse bone marrow, as they elicit the effect more readily and to obtain different cultivars of the same bean and/or the same market class of bean grown in different places (i.e., Colorado vs Nebraska) to determine if locations affect the phenol composition and thus this health benefit.

Wisconsin
James Nienhuis, Dept. of Horticulture, University of Wisconsin-Madison
Understanding and improving flavor in beans : screening the USDA *Phaseolus* core collection for pod sugar and flavor compounds in snap and dry bean accessions
The objective of our W3150 research is to gain knowledge regarding variation in sugar and flavor content among a sample of dry bean and green pod-type PI accessions from the USDA Phaseolus Germplasm Core Collection, Pullman, WA. Knowledge of the variation will allow better utilization of germplasm resources in the development of new bean cultivars with more desirable sugar and flavor profiles. The results of this project could be used to market product quality and offer unique opportunities to expand market share to an increasingly health conscious population.
Dr. Kisha USDA-ARS, Pullman, WA developed a diverse sub-core of 94 Plant Introductions (PI) characterized as snap beans, Romano-types, and other beans eaten as edible immature pods, and 20 dry bean PI accessions. In addition checks included a kidney bean (Montcalm, Andean gene pool) as well as 8 cultivars (e.g. Caprice, Huntington, 04-88, OSU5402, OSU5630, Masai, Slenderpack, Tapia) representing the various market classes consumed as edible green pods currently grown commercially in the United States.
A large positive correlation (r=0.79**)was observed between the simple sugars Glucose and Fructose. In contrast a large negative correlation was observed beweeen the disaccharide sucrose with both monosaccharides, glucose (r=-0.37) and fructose (r=-0.43). Glucose concentration had a mean of 19.96 mg g-1 dry weight, and ranged from near zero to over 40mg g^{-1} dry weight. P.I accessions with high concentrations of sucrose were generally both heirloom and modern commercial snap beans cultivars, e.g. Provider, Eagle, Cascade, Hystyle and BBL47. Fructose concentration had a mean of 19.9 mg g-1 dry weight, and ranged from near zero to over 50mg g^{-1} dry weight. Sucrose had a much lower concentration of 3.7 mg g-1 dry weight, and ranged from near zero to over 14 mg g^{-1} dry weight.
Vandenlangenberg, KM, Bethke, PC and J Nienhuis. 2012. Identification of quatitative trait loci associated with fructose, glucose and sucrose concentration in snap beans. Crop Sci. 52:1593-1599
Vandenlangenberg, KM, Bethke, PC and J Nienhuis. 2012. Patterns of fructose, glucose and sucrose accumulation in snap and dry bean (Phaseolus vulgaris L.). HortScience 47: 874-878.

Michigan
W3150-REGIONAL PROJECT NO: MICL04065
Breeding Common Bean (*Phaseolus vulgaris* L.) for Resistance to Abiotic and Biotic Stresses, Sustainable Production, and Enhanced Nutritional Value

James D. Kelly and Karen A. Cichy
Plant, Soil and Microbial Sciences, USDA-ARS, Michigan State University, East Lansing MI 48824

Bean Breeding Nurseries

The MSU dry bean breeding and genetics program conducted 14 yield trials in 2016 in ten market classes and participated in the growing and evaluation of the Cooperative Dry Bean, Midwest Regional Performance, National Drought and the National Sclerotinia Nurseries in Michigan and winter nursery in Puerto Rico. The nurseries were planted in June 2016 into favorable soil moisture conditions. Weather during the early growing season was dry and hot and beans were under considerable stress during the critical flowering period. Rainfall in August resulting in plants re-greening and setting a double crop that reflected in lower yields and necessitated chemical desiccation in commercial fields. Selection for tolerance to drought stress during the extended dry period was possible in all nurseries based on performance under these conditions.

GGE biplot Analysis of Mesoamerican Bean Panel

GGE biplots were used to rank genotypes according to environments and treatments (irrigated and rainfed) within environments. A genotype-by-trait analysis was also used to identify traits relevant to yield under rainfed and irrigated environments. Significant differentiation and non-redundancy was found among the environments suggesting that resource use is efficient. Rainfed environments were better at discriminating high performing genotypes in Michigan. Genotype by trait analysis showed a significantly negative correlation between growth habit and seed yield. A common feature of the better adapted and higher yielding genotypes under Michigan conditions was the upright type II growth habit. A number of root architecture traits such as taproot diameter were independent or associated with yield in common bean under different environments. Genotypes with contrasting traits associated with yield under rainfed and irrigated conditions were identified and could be used in the development of future common bean cultivars with improved drought tolerance.

Joint Linkage QTL Mapping in a Composite Map of Three Common Bean RIL Populations

A composite linkage map was constructed using single nucleotide polymorphism (SNP) markers from the three populations and resulted in an improved version of the individual linkage maps, shown by a greater genome span covered in the composite map (909 cM). A number of QTL of different size effects were identified for seed yield (R2=15.4 to 30.7%), seed size (R2=16.4 to 20.2%), days to flowering (R2=12.4 to 36.1%), days to maturity (R2=16.2%), lodging score (R2=10.3 to 12.9%) and canopy height (R2=17%). Our study confirmed previously reported QTL on five chromosomes and identified a new QTL for canopy height on Pv10. The use of a composite map and QTL analysis under a NAM population structure increased our ability to detect small effect QTL that were segregating in at least two of the populations, but would not have been detected using individual linkage maps.

GWAS Analysis for Anthracnose Resistance in Andean Diversity Panel

GWAS was conducted on a group of 230 Andean beans for resistance to eight races (7, 39, 55, 65, 73, 109, 2047, and 3481) of anthracnose. Twenty-eight of the 230 lines tested were resistant to six out of the eight races screened, but only one cultivar Uyole98 was resistant to all included in the study. Outputs from the GWAS indicated major QTL for resistance on chromosomes, Pv01, Pv02, and Pv04 and two minor QTL on Pv10 and Pv11. An independent QTL study was conducted to confirm the physical location of the Co-1 locus identified on Pv01 in an $F_{4:6}$ RIL population. Resistance was determined to be conditioned by the single dominant gene *Co-1* that mapped between 50.16 and 50.30 Mb on Pv01, and an InDel marker (NDSU_IND_1_50.2219) tightly linked to the gene was developed.

Prediction of sensory scores for color and appearance in canned black beans using machine vision

A machine vision system was implemented and tested for automatic inspection of color (COL) and appearance (APP) in canned black beans. Various color and textural image features were extracted from drained/washed beans and brine images, and evaluated to predict the quality rates for COL and APP of a group of bean panelists using multivariate statistical models. A total of 69 commercial canned black bean samples from different brands and markets were used for analysis. In spite of the 'fair' agreement among the sensory panelists for COL and APP, as determined by multirater *Kappa* analysis, a machine vision data based on partial least squares regression analysis showed high predictive performance for both COL and APP with correlation coefficient for prediction (R_{pred}) of 0.937 and 0.871, respectively. When a classification was performed based on both COL and APP traits, a support vector machine model using simple image data was able to sort the canned bean samples into two sensory quality categories of 'acceptable' and 'unacceptable' with an accuracy of 89.7%. Using simple color and texture image data, a machine vision system showed potential for the automatic evaluation of canned black beans by COL or/and APP as a professional visual inspection.

Effects of extrusion cooking on the chemical composition and functional properties of dry bean powders

The impact of extrusion cooking on the chemical composition and functional properties of bean powders from four bean varieties was investigated. The raw bean powders were extruded under eight different conditions, and the extrudates were then dried and ground (particle size ≤ 0.5 mm). Compared with corresponding non-extruded (raw) bean powders (particle size ≤ 0.5 mm), the extrusion treatments did not substantially change the protein and starch contents of the bean powders and showed inconsistent effects on the sucrose, raffinose and stachyose contents. The extrusion cooking did cause complete starch gelatinization and protein denaturation of the bean powders and thus changed their pasting properties and solvent-retention capacities. The extrusion cooking did not alter the starch digestibility of the bean powders. The extruded bean powders displayed functional properties similar to those of two commercial bean powders.

GWAS analysis for canned bean color retention in black bean breeding lines

Black beans are distinguished from other common beans classes by high anthocyanins in the seed coat which impart the black color. The water soluble anthocyanins make the canning process for black beans challenging. Genetic variability for color retention can be exploited to select and incorporate superior genetics for this trait. The objective of this research was to assess the genotypic and phenotypic diversity for a set of 69 black bean breeding lines and cultivars from the major U.S. public bean breeding programs. Each of the lines was grown in field trials in 2013 and 2014. They were evaluated for agronomic, canning characteristics and anthocyanins profile of raw and canned seed. Color retention as determined by a trained sensory panel on a scale of 1 to 5 was highly variable and ranged from 1.4 to 4.5. Delphinidin-3-glucoside was identified as the dominant anthocyanin with the highest concentration among black bean genotypes. The anthocyanin malvidin-3-glucoside was found to be retained after canning more than the other two anthocyanins. Genome wide association analysis was conducted to determine genomic regions responsible for color retention and canning quality in black beans that were genotyped with 5398 SNP markers. A region on Pv05 at 39Mb was associated with color retention and was polymorphic candidates for MAS.

Outcomes/Impact

Black bean consumption in the U.S. has been increasing steadily since 1980 when consumption was 0.01 lbs per person per year until 2014 when consumption was 0.86 per capita (USDA-ERS; VGS-355, 2015). Currently the black bean variety Zorro from MSU breeding program is grown on 80% of the acres planted to black beans in Michigan and has provided growers with opportunity to reduce costs by direct harvesting the crop. Increase value to growers is estimated at $5m per year based on 10% yield advantage and savings in time and equipment.

Certified seed was produced of the new high-yielding, disease resistant, upright full-season black bean variety, Zenith, and the new upright navy bean variety, Alpena that has excellent canning quality and uniform maturity. Zenith possesses superior color retention following canning, a trait the processing industry needs. Alpena exhibits natural dry down at maturity which eliminates the application of desiccants prior to harvest. Foundation and certified seed of both varieties is currently under production.

Students graduated: Weijia Wang, MS; Othman Al Dossary, MS

Participants: James D. Kelly and Karen A. Cichy

Target Audience: Bean Farmers, Bean Elevator Managers in Michigan; National Food Industry and Food Processors and Consumers; Bean Researchers

Project Modifications: None

Refereed Publications:

1. Ai, Y., K A. Cichy, J. B. Harte, J. D. Kelly, and P. K.W. Ng. 2016. Effects of extrusion cooking on the chemical composition and functional properties of dry bean powders. Food Chemistry 211:538–545. doi:10.1016/j.foodchem.2016.05.095
2. Glahn, R., Tako, A. Cichy, K. and Wiesinger, J. (2016) The Cotyledon Cell Wall and Intracellular Matrix Are Factors That Limit Iron Bioavailability of the Common Bean (Phaseolus vulgaris). *Food & Function* **7**, 3193-3200
3. Goffnett, A.M., Sprague, C.L., Mendoza, F., and Cichy, K.A. (2016) Preharvest herbicide treatments affect black bean desiccation, yield, and canned bean color. Crop Sci. 56:1-8.
4. Hooper, S.; Wiesinger, J.; Echeverria, D.; Thompson, H.; Brick, M.; Nchimbi-Msolla, S.; Cichy, K. (2016) The carbohydrate profile of a dry bean (Phaseolus vulgaris L.) panel encompassing broad genetic variability for cooking time. *Cereal Chem.* (in press)
5. Hoyos-Villegas, V., E. M. Wright and J.D. Kelly. 2016. GGE biplot analysis of yield associations with root traits in a Mesoamerican bean diversity panel. Crop Sci. 56:1081-1094. doi:10.2135/cropsci2015.10.0609
6. Hoyos-Villegas, V., Q. Song, E.M. Wright, S. E. Beebe and J.D. Kelly. 2016. Joint linkage QTL mapping for yield and agronomic traits in a composite map of three common bean RIL populations. Crop Sci. 56: doi:10.2135/cropsci2016.01.0063.

7. Hoyos-Villegas, V., Q. Song, J.D. Kelly. 2016. Genomewide association analysis for drought tolerance and associated traits in common bean. The Plant Genome 9: doi:10.3835/plantgenome2015.12.0122

8. Isaacs, K.B., S.S. Snapp, J.D. Kelly and K. R. Chung. 2016. Farmer knowledge identifies competitive bean ideotype for maize-bean intercrop systems in Rwanda. Agriculture & Food Security 5:15. doi 10.1186/s40066-016-0062-8

9. Kelly, J.D., G.V. Varner, S. Hooper, K.A. Cichy, and E.M. Wright. 2016. Registration of 'Samurai' otebo bean. J. Plant Registrations 10:109-114. doi:10.3198/jpr2015.09.0051crc.

10. Mendoza, F.A, J. D. Kelly, and K. A. Cichy. 2016. Automated prediction of sensory scores for color and appearance in canned black beans (*Phaseolus vulgaris* L.) using machine vision. International Journal of Food Properties, doi:10.1080/10942912.2015.1136939.

11. Moghaddam, S.M., S. Mamidi, J. M. Osorno, R. Lee, M. Brick, J. D. Kelly, P. Miklas, C. Urrea, Q. Song, P. Cregan, J. Grimwood, J. Schmutz, and P. E. McClean. 2016. Genome-wide association study identifies candidate loci underlying seven agronomic traits in Middle American diversity panel in *Phaseolus vulgaris* The Plant Genome (in press).

12. Nakedde, T., F. J. Ibarra-Perez, C. Mukankusi, J. G. Waines, and J. D. Kelly. 2016. Mapping of QTL associated with Fusarium root rot resistance and root architecture traits in black beans. Euphytica doi: 10.1007/s10681-016-1755-6

13. Porch, T. G., Cichy, K., Wang, W., Brick, M., Beaver, J. S., Santana-Morant, D., & Grusak, M. A. (2016) Nutritional composition and cooking characteristics of tepary bean (Phaseolus acutifolius Gray) in comparison with common bean (Phaseolus vulgaris L.). *Genetic Resources and Crop Evolution*, 1-19.

14. Zuiderveen, G.H., B. A. Padder, K. Kamfwa, Q. Song and J. D. Kelly. 2016. Genome-wide association study of anthracnose resistance in Andean beans. PLoS ONE 11(6): e0156391doi:10.1371/journal.pone.0156391

Book Chapters: None

Non-refereed Publications:

1. Acosta-Gallegos, J.A., Y. Jiménez Hernández, V. Montero Tavera1, M. A. Martínez Gamiño, M. D. Herrera, J. L. Anaya López, and J.D. Kelly. 2016. Release of pinto Raramuri dry bean for the semi-arid highlands of Central Mexico. Bean Improvement Cooperative Annual Report 59:253.

2. Berry, M., Wiesinger, J, Nchimbi-Msolla, S, Miklas, P, Porch, T, Fourie, D, and Cichy, K. 2016. Breeding for a fast cooking bean: a study of genotypes across environments to determine stability of the cooking time trait in *Phaseolus vulgaris*. Bean Improvement Cooperative Annual Report 59:33-34

3. Chilvers, M.I., J.L. Jacobs, A.M. Byrne, and J.D. Kelly. 2016. Screening Andean dry bean germplasm for root rot resistance. Bean Improvement Cooperative Annual Report 59:105-106.

4. Cichy, K.A. and F. Mendoza. 2016. Color retention in canned black beans. Bean Improvement Cooperative Annual Report 59:25-26.

5. Cichy, K.A., Wiesinger, J.A., and Shaw, S. (2016) Evaluation of Yellow Bean Germplasm for Agronomic Performance and End Use Quality. 2015 Research Report Saginaw Valley Research and Extension Center. p 54-58.

6. Zuiderveen, G.H., B. Padder, K. Kamfwa and J. D. Kelly. 2016. Mapping the Co-1 locus conditioning anthracnose resistance in common bean. Bean Improvement Cooperative Annual Report 59:17-18.

Posters:

1. Cichy, K.A., Wiesinger, J., Mendoza, F., Hooper, S., Grusak, M.A., Glahn, R., and Kelly, J. (2016) A Nutritional Profile of Fast Cooking Bean Germplasm. Poster Presentation, Pan African Grain Legumes Research Conference, Livingstone, Zambia March 4.

2. Berry, M., Wiesinger, J., Nchimbi-Msolla, S., Miklas, P., Porch, T., Fourie, D., and Cichy, K.A. (2016) Breeding for a Fast Cooking Bean: Study of Genotypes across Environments to Determine Phenotypic Stability in *Phaseolus vulgaris*. Poster Presentation, Pan African Grain Legumes Research Conference, Livingstone, Zambia March 3.

3. Cichy, K.A. and Rueda, J.A. (2016). "Beans as Ingredients in "Better for You" Foods" at the Michigan Agri-Business Association Winter Conference, Michigan Bean Shippers. Dramadri, I. and J. D. Kelly. 2016. Genome wide association analysis for drought tolerance responses in Andean common beans, Poster presented NAPB conference, NCSU. Meeting Jan 12.

4. Katuuramu, D.N., Kelly, J.D., Glahn, R.P., and Cichy, K.A. (2016) Field Evaluation of Nutritionally Superior Common Bean Genotypes with Farmers in Three Agro-ecological Zones in Uganda. Oral Presentation, Pan African Grain Legumes Research Conference, Livingstone, Zambia Feb 29.

5. Wang, W, Cichy, KA, Kelly, JD, Mukankushi, CM. "QTL Analysis for Fusarium Root Rot Resistance in Common Bean (*Phaseolus vulgaris*)". Biennial Bean Improvement Cooperative Meeting, Niagara Falls, Canada. November 1-4, 2015

Thesis:
1. Wang, W. (2016) "QTL ANALYSIS AND CANDIDATE GENES IDENTIFICATION ASSOCIATED WITH FUSARIUM ROOT ROT RESISTANCE IN COMMON BEANS (*PHASEOLUS VULGARIS*)" M.S. Thesis, Michigan State University

2. Al Dossary, O. (2016) "COLOR RETENTION AND ANTHOCYANIN CONCENTRATION IN CANNED BLACK BEANS" M.S. Thesis, Michigan State University

Dissertations: None

Bulletins: None

Plant Variety Protection Certificates:
Plant Variety Protection Certificate No. 201500009 was issued for Snowdon white kidney bean variety on 2/26/2016.
Plant Variety Protection Certificate No. 201500008 was issued for Eldorado pinto bean variety on 7/6/2016
Plant Variety Protection Certificate No. 201500385 was issued for Powderhorn great northern bean variety on 6/3/2016

3150 State Report – North Dakota
Juan M. Osorno, Julie Pasche, Phil McClean
Activities:
Research activities within this project included collaborative work on: i) Midwest Regional Performance Nursery (MRPN), ii) development of pinto lines with Multiple Disease Resistance (MDR) to rust, anthracnose, and common bacterial blight (CBB), iii) Evaluation of the Andean Diversity Panel (ADP) and Mesoamerican Diversity Panel (MDP) for resistance to *Rhizoctonia solani* under greenhouse conditions, iv) evaluation of NDSU breeding lines for CBB resistance, v) development of slow darkening pinto lines, and vi) identification of genomic regions associated with plant architectural traits.
Outcomes:
A new slow darkening pinto has been jointly released between USDA-ARS and NDSU and named ND-Palomino. Certified seed will be available to growers to plant during the 2017 growing season. At least 6 pinto MDR breeding lines have been identified that offer moderate to high levels of multiple disease resistance and agronomic performance. Field/greenhouse testing of the ADP for resistance to the root rot complex and halo blight led to the identification of new potential sources of resistance with the Andean genepool, which is the most susceptible group to this problem. Several genomic regions have been identified that are associated with architectural traits such as lodging, stem diameter, stem stiffness, and plant height, among others. A region in pv07 is of special interest and it is currently under more detailed study. Routine screening of NDSU breeding lines allowed the identification of breeding lines with high levels of resistance to CBB.
Publications:
Hagerty C.H., Cuesta-Marcos A., Cregan P., Song Q., McClean P., Myers J.R. 2016. Mapping snap bean pod and color traits, in a dry bean × snap bean recombinant inbred population. Journal of the American Society for Horticultural Science, 141:131-138.
Jain, S., Chittem K., Brueggeman R., Osorno J.M., Richards J., and Nelson Jr B.D. 2016. Comparative Transcriptome Analysis of Resistant and Susceptible Common Bean Genotypes in Response to Soybean Cyst Nematode Infection. PloS one, 11(7), e0159338.

Mamidi, S., Miklas P.N., Trapp J., Felicetti E., Grimwood J., Schmutz J., Lee R., McClean P.E. 2016. Sequence-based introgression mapping identifies candidate white mold tolerance genes in common bean. The Plant Genome 9 doi: 10.3835/plantgenome2015.09.0092.
Moghaddam. S.M., Mamidi S., Osorno J.M., Lee R. Brick M., Kelly J., Miklas P., Urrea C., Song Q., Cregan P., Grimwood J., Schmutz J., McClean P. 2016. Genome-wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a

Middle American Diversity Panel of Common Bean (Phaseolus vulgaris L.). Plant Genome. doi: 10.3835/plantgenome2016.02.0012; Date posted: July 25, 2016

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Soltani A., Bello M., Mndolwa E., Schroder S., Moghaddam S.M., Osorno J.M., Miklas P., McClean P.E. 2016. Targeted Analysis of Dry Bean Growth Habit: Interrelationship Among Architectural, Phenological, and Yield Components. Crop Sci. doi: 10.2135/cropsci2016.02.0119; Date posted: June 15, 2016.

Zhang L. Gezan S., Vallejos C.E., Jones J., Boote K., Clavijo-Michelangeli J., Bhakta M., Osorno J.M., Rao I., Beebe S., Roman-Paoli E., Gonzalez A., Beaver J., Ricaurte J., Colbert R., Correll M. 2016. Development of a QTL-environment-based predictive model for node addition rate in common bean. Theor. Appl. Genet. (Submitted).

Idaho
W3150 – report for 2015-16

Strain composition of *Bean common mosaic virus* and *Bean common mosaic necrosis virus* isolates from field samples of common bean

Between 2013 and 2016, over 30 samples were submitted to the University of Idaho Plant Virology laboratory from heirloom cultivars of common bean with symptoms of mosaic, leaf distortion, and stunting. All samples came from California or Oregon, and were subjected to species-specific serotyping suggesting that samples were infected with *Bean common mosaic virus* (BCMV) or *Bean common mosaic necrosis virus* (BCMNV). These field isolates of BCMV and BCMNV were typed using a panel of bean differentials to determine their pathotype, and subjected to partial sequencing. BCMNV isolates were grouped in pathogroups (PGs) III and VI, while BCMV isolates were grouped in PG-I, III, IV, and VI. PG-VI isolates of BCMV were found to have sequences closely related to the RU-1 strain of BCMV. This data confirms a wide presence of the RU-1 related isolates of BCMV in heirloom cultivars of common bean. Several BCMV field isolates represented mixtures between different PGs, which were successfully separated using bean differentials. In at least two cases, field samples contained both BCMV and BCMNV.

W-3150 NY Station Report 2016
Breeding Common Bean (Phaseolus vulgaris L.) for Resistance to Abiotic and Biotic Stresses, Sustainable Production, and Enhanced Nutritional
P. Griffiths, SIPS-Horticulture Section, Cornell NYSAES, Geneva NY.

A major emphasis of our variety testing program has been on light red kidneys developed with resistance to white mold resistance including 'Cornell 605', 'Cornell 612', DRK-1 and LRK-1. One of the primary purposes underlying the breeding program has been to identify LRK lines with yield and canning quality comparable to or higher than 'RedKanner', but with earlier maturity similar to CELRK. New populations that were developed to transfer and select upright vine architecture in red kidney breeding lines were also planted in Geneva/Ithaca NY and promising selections were identified for population advance. Thirty selections were planted and evaluated in Freeville and Geneva NY in 2016, together with checks and snap bean selections that were advanced in the greenhouse during the Spring.

Screening and selection of common bean lines previously bred for white mold resistance was undertaken in field and greenhouse trials to improve the type of the most resistant lines, and new breeding lines were compared to varietal checks. New black kidney bean breeding lines have also been developed and stabilized. Heat tolerant germplasm has previously been selected that can reduce pod abortion or split-set during high temperatures, this was incorporated in crosses and field-tested in June 2016 at sites in Western Kenya. These genotypes were evaluated for yield under heat stress in collaboration with USDA-TARS Mayaguez, Puerto Rico and with ACL in Homabay Kenya. Snap bean breeding lines with rust resistance (Ur4 and Ur11) introgressed from USDA Beltsville, and were also increased and tested in Kenya in 2016, they were initially selected to combine the two rust genes in a heat tolerant snap bean background, together with additional crosses to pyramid the Ur5 gene, selections were made from these trials. New upright types evaluated in 2016 field trials have been identified based on field, greenhouse and seed quality selections. These include new black kidney lines with excellent canning and color retention being advanced as a potential new market class of dry beans.

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New populations will be advanced combining optimal combinations of virus resistance genes for evaluation of field resistance to CMV. These will be screened in greenhouse trials, identifying new breeding lines that can be advanced to cultivars providing yield stability. Populations of the Andean market classes snap bean and red kidney bean are also being developed with the upright vine architecture for increased yield and as options for smallholder growers. Lines developed will be tested in Mayaguez Puerto Rico in collaboration with Tim Porch, Kenya in collaboration with Charles Wasonga and multistate collaborations will be continued for white mold screening and the development od dry bean cultivars. New black kidney bean breeding lines will be advanced and field-tested with growers/seed companies including canning trials for quality.

Impact:

Abiotic and biotic stresses cause significant reductions in yield, and increased reliance on chemical management. The breeding of common beans for resistance to these stresses will enable more efficient production that is less damaging environmentally. Development of white mold resistant beans will reduce one of the largest limiting factors to bean production in the US. Heat tolerance will prevent split set or yield reduction under high temperatures, and will enable expansion of growing regions in developing countries to make agricultural practices more sustainable. The development of resistant cultivars will reduce the risk of damage from aphid-transmitted virus that has caused significant yield loss in NY and Wisconsin. Dry bean production in New York is restricted by a short growing season, and variable rainfall and growing temperatures. The objectives of this project were to screen for genotypes with relatively short plant maturity, stress tolerance (particularly at seed set) and utilization quality appropriate for processing and dry pack markets. Dry bean varieties identified from these studies will allow growers to more consistently produce a higher quality crop with higher yields while using lower levels of inputs.

Publications:

 None

W-3150 Report Update, Iowa State University, September 2016
Donna M. Winham
Food Science and Human Nutrition
College of Agriculture and Life Sciences

At Iowa State, the Winham lab has been conducting research in two main areas: 1) In vitro iron bioavailability of tepary beans, and 2) consumer knowledge of the health benefits of beans.

Iron Bioavailability
In collaboration with Timothy Porch, ARS/Puerto Rico, Karen Cichy, ARS/Michigan State University, and Mark Brick, Colorado State University, a diverse sample of pinto, black, and tepary beans were received for analysis at Iowa State. The study purpose was exploratory with the intent to determine in vitro iron bioavailability, proximate analysis, polyphenol, and phytic acid content of the samples. Since iron deficiency remains an intractable public health problem in many developing countries, increased iron bioavailability in a bean with arid climate resiliency such as tepary, can offer a sustainable solution towards improving human nutrition and health.
Whole seeds of 5 tepary white (Tep 22 – Puerto Rico; Tep 22 – Colorado; G40001 – Puerto Rico; Sonora white – Colorado; Sacaton white – Arizona), 3 tepary brown (Tep 32 – Colorado; Speckled Mitla – Colorado, Sacaton brown – Arizona), 4 black improved lines (BEL 1300 series), and 2 pinto bean varieties (Croissant, Longs Peak – Colorado) were analyzed. Polyphenol (PP) and phytic acid (PA) extractions were assessed colorimetrically. Iron and other mineral

concentrations were determined using ICP-mass spectrometry following a microwave digestion. Supernatants from the in vitro digestion were used in determining the iron bioavailability through a CaCo-2 cell culture model. For statistical analysis, results were pooled by tepary white, tepary brown, black bean, and pinto bean.

Both tepary white and tepary brown groups showed significant differences in PP content in comparison to the black and pinto ($p \leq 0.05$), whereas PA, amongst all groups, showed no significant differences ($p > 0.05$). Iron content ranged from 29.8 µg/g to 78.47 µg/g, with pinto beans having significantly lower iron concentration (mean = 33.64 µg/g). Significant differences in percent solubility were found between the pinto bean and tepary varieties ($p \leq 0.05$), but not the black. Iron bioavailability of the tepary white showed a negative correlation with PP content (high iron, low PP). The tepary white showed significantly higher iron bioavailability ($p \leq 0.02$) in comparison to both pinto and black beans. Our data suggests that the low PP and PA contributes to higher iron bioavailability in the white varieties of *Phaseolus acutifolius*. Further studies to replicate these findings are needed, followed by clinical testing of tepary white iron bioavailability in humans. The tested Sacaton white and Sacaton brown seeds were purchased from Ramona Farms, a Native American business. Since these are unknown seeds, samples were provided to Dr. Porch for future genetic typing.

Preliminary results from this study were presented at the Pan African Grain Legume conference in Livingstone, Zambia, March 2016, and at the American Society of Nutrition, San Diego, California, April 2016. Manuscript submission is in progress.

Consumer knowledge of the health benefits of beans.
We recently published our findings on the knowledge of low-income women in Arizona on the health benefits of beans (Winham et al., 2016). As part of our efforts to increase bean consumption as well as add to the body of evidence supporting the health benefits of beans in human nutrition, we are assessing the knowledge, attitudes, and consumption practices of dry beans among low-income women in Iowa. Data collection for this survey will conclude in November 2016. Results will be reported at the American Society of Nutrition conference in Chicago, April 2017.

Upcoming projects
We will be testing the glycemic response to tepary bean-and-rice meals among persons with type 2 diabetes in Spring 2017. Protocol and human subjects approval are in progress.

Reference:
Winham DM, Florian TL, Thompson SV. Low-Income US Women Under-informed of the Specific Health Benefits of Consuming Beans. PloS one. 2016 Jan 28;11(1):e0147592.

W-3150 NY Station Report 2016
Breeding Common Bean (*Phaseolus vulgaris* L.) for Resistance to Abiotic and Biotic Stresses, Sustainable Production, and Enhanced Nutritional
P. Griffiths, SIPS-Horticulture Section, Cornell NYSAES, Geneva NY

A major emphasis of our variety testing program has been on light red kidneys developed with resistance to white mold resistance including 'Cornell 605', 'Cornell 612', DRK-1 and LRK-1. One of the primary purposes underlying the breeding program has been to identify LRK lines with yield and canning quality comparable to or higher than 'RedKanner', but with earlier maturity similar to CELRK. New populations that were developed to transfer and select upright vine architecture in red kidney breeding lines were also planted in Geneva/Ithaca NY and promising selections were identified for population advance. Thirty selections were planted and evaluated in Freeville and Geneva NY in 2016, together with checks and snap bean selections that were advanced in the greenhouse during the Spring.

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Abiotic and biotic stresses cause significant reductions in yield, and increased reliance on chemical management. The breeding of common beans for resistance to these stresses will enable more efficient production that is less damaging environmentally. Development of white mold resistant beans will reduce one of the largest limiting factors to bean production in the US. Heat tolerance will prevent split set or yield reduction under high temperatures, and will enable expansion of growing regions in developing countries to make agricultural practices more sustainable. The development of resistant cultivars will reduce the risk of damage from aphid-transmitted virus that has caused significant yield loss in NY and Wisconsin. Dry bean production in New York is restricted by a short growing season, and variable rainfall and growing temperatures. The objectives of this project were to screen for genotypes with relatively short plant maturity, stress tolerance (particularly at seed set) and utilization quality appropriate for processing and dry pack markets. Dry bean varieties identified from these studies will allow growers to more consistently produce a higher quality crop with higher yields while using lower levels of inputs.

Publications:

None

James Nienhuis, Dept. of Horticulture, University of Wisconsin-Madison

Understanding and improving flavor in beans : screening the USDA *Phaseolus* core collection for pod sugar and flavor compounds in snap and dry bean accessions

The objective of our W3150 research is to gain knowledge regarding variation in sugar and flavor content among a sample of dry bean and green pod-type PI accessions from the USDA Phaseolus Germplasm Core Collection, Pullman, WA. Knowledge of the variation will allow better utilization of germplasm resources in the development of new bean cultivars with more desirable sugar and flavor profiles. The results of this project could be used to market product quality and offer unique opportunities to expand market share to an increasingly health conscious population.

Dr. Kisha USDA-ARS, Pullman, WA developed a diverse sub-core of 94 Plant Introductions (PI) characterized as snap beans, Romano-types, and other beans eaten as edible immature pods, and 20 dry bean PI accessions. In addition checks included a kidney bean (Montcalm, Andean gene pool) as well as 8 cultivars (e.g. Caprice,

Huntington, 04-88, OSU5402, OSU5630, Masai, Slenderpack, Tapia) representing the various market classes consumed as edible green pods currently grown commercially in the United States.

A large positive correlation (r-0.79**)was observed between the simple sugars Glucose and Fructose. In contrast a large negative correlation was observed beweeen the disaccharide sucrose with both monosaccharides, glucose (r=-0.37) and fructose (r=-0.43). Glucose concentration had a mean of 19.96 mg g-1 dry weight, and ranged from near zero to over 40mg g^{-1} dry weight. P.I accessions with high concentrations of sucrose were generally both heirloom and modern commercial snap beans cultivars, e.g. Provider, Eagle, Cascade, Hystyle and BBL47.   Fructose concentration had a mean of 19.9 mg g-1 dry weight, and ranged from near zero to over 50mg g^{-1} dry weight. Sucrose had a much lower concentration of 3.7 mg g-1 dry weight, and ranged from near zero to over 14 mg g^{-1} dry weight.

Vandenlangenberg, KM, Bethke, PC and J Nienhuis. 2012. Identification of quatitative trait loci associated with fructose, glucose and sucrose concentration in snap beans. Crop Sci. 52:1593-1599

Vandenlangenberg, KM, Bethke, PC and J Nienhuis. 2012. Patterns of fructose, glucose and sucrose accumulation in snap and dry bean (Phaseolus vulgaris L.). HortScience 47: 874-878.

Wyoming
W-3150 Report Update, University of Wyoming, September 2016
Jim Heitholt
    We continue to screen cultivars for tolerance to drought and to low soil N. Tests are conducted in the field at either Lingle or Powell. Greenhouse tests are conducted at Laramie.
Drought Tolerance
    In 2015, we screened 50 cultivars at two locations for tolerance to drought. At Lingle, we identified canopy temperature to be negative correlated to yield. In 2016, studies with 24 entries were conducted at Lingle and another study with 36 entries was conducted at Powell (Andi Pierson, Vivek Sharma, Camby Reynolds). We grew entries from the drought nursery supplied by Carlos Urrea at Lingle. Mike Moore conducted the CDBN at Powell and I conducted the CDBN at Lingle. Although a hail storm on 28 July 2016 at Lingle completely destroyed all plots, we collected some data prior to that time.
    At Powell in 2016, canopy temperatures were recorded mid-morning and early-afternoon on one day during bloom (18 July) for all 216 plots, half well-watered, half subjected to drought. No cultivar-by-irrigation interactions were detected. At mid-morning, canopy temperature of the drought-treated plots averaged 29.0°C compared to the well-watered plots (26.4°C). At early-afternoon, drought-treated plots averaged 35.0°C vs. 31.2°C for the well-watered. Cultivars varied significantly in canopy temperature. Averaged across the irrigation treatments, for mid-morning, the canopy of Yeti was the warmest 29.9°C vs. ND-307 which was the coolest (26.0°C). For the early-afternoon, the canopy of Powderhorn was warmest (32.2°C) vs. the canopy of CO-46348 which was the lowest (30.9°C). Within the drought plots, mid-morning and early-afternoon canopy temperatures for the 36 cultivars were correlated (r = 0.82 and r = 0.75) for the drought and well-watered plots, respectively. Plant stand was rated visually (higher value corresponding to better stand) in June. Plant stand varied across cultivars and was negatively correlated to early-afternoon canopy temperature indicating that hotter canopies could have been partly caused by poor stands (possibly due to albedo from exposed soil surface).
    At Lingle in 2016, normalized difference vegetation index (NDVI) was determined on 8 July prior to imposition of irrigation treatments. Equation was NDVI = $(R_{730} - R_{660})/(R_{730} + R_{660})$ where R is the reflectance at the two wavelengths. Rosie exhibited the highest NDVI (0.74) whereas T-9905 exhibited the lowest (0.44). Canopy temperatures were collected on 23 July for 24 cultivars after imposition of drought stress. Both late morning and mid-afternoon data were recorded. Although the late morning canopy temperature from the drought-treated plots averaged, 32.6°C compared to the well-watered canopies (29.5°C), the difference was not significant. Likewise, mid-afternoon canopy temperatures averaged 33.8°C for the drought-treated plots and 31.4°C for the well-watered plots but the difference was not significant. Cultivars varied significantly for canopy temperature. No cultivar-by-irrigation interactions were detected. The cultivar Rosie exhibited the highest late-morning canopy temperature (33.3°C) whereas Othello was the coolest (29.9°C). For the mid-afternoon, the canopy of Rosie was again the warmest (35.1°C) vs. ISB1231-1 which was the coolest (31.7°C).   For a given cultivar, canopy temperatures for the two times of day were correlated as was the case in

Powell. Within drought-treated plots, late-morning and mid-afternoon canopy temperatures were correlated (r = 0.39; n=24) but the in well-watered plots the correlation was stronger (r = 0.79).

Nitrogen Use Efficiency among Genotypes

Throughout 2015 and 2016, we (Ali Alhasan and Jim Heitholt) have launched greenhouse and field studies to identify genotypes with greater N use efficiency. Typically, we grow the cultivars in a low N soil mix. Then, we add zero fertilizer N or 60 pounds of N per acre (its equivalent in the greenhouse). So far, no conspicuous N-by-genotype interactions have been observed. Nevertheless, we have found significant and consistent differences among cultivars in leaf chlorophyll and other physiological/morphological traits associated with N. In 2016 at Lingle, the 60 pound N rate resulted in larger area per leaflet (28 cm^2 vs. 23 cm^2) and greater SPAD (42.8 vs. 40.3) chlorophyll at 50 DAP (averaged across 18 cultivars).   For cultivars, CO-46348 was consistently the highest in leaf chlorophyll through 50 DAP. The cultivars Avalanche, Eclipse, and Talon tended to have the lowest chlorophyll. For NDVI, no N effect was found. CO-46348 exhibited the highest NDVI at 0.82 vs. Avalanche (0.62) and Eclipse which exhibited 0.54.

Soil N Rate

We have also conducted tests with multiple N rates (0 to 100 pounds of N per acre). In the greenhouse (spring/summer 2016), we grew cv 'Othello' at six N rates but failed to find significant effects on seed yield, pod number, or seed size. Pod harvest index was negatively correlated to N rate dropping from 82% at the two lowest N levels (0 and 20 pounds per acre) to 79% at the two highest N levels (80 and 100 pounds per acre). Leaf chlorophyll was measured twice weekly with a SPAD unit. At 30 and 33 days after planting (DAP), leaf chlorophyll was positively and linearly related to N rate ranging from 38 to 43 SPAD units for 0 and 100 pounds of N, respectively. At 36 and 41 DAP, the same trend was observed with SPAD readings increasing from 35 to 42 at 36 DAP and from 39 to 44 at 41 DAP. At other dates, no effect of N rate was observed except for 54 DAP when the two highest N rates showed slightly reduced leaf chlorophyll. Mid-season specific leaf weight was unaffected by N rate as was average leaf area, length, and width.

In the field at Lingle in 2016, the cv. 'Poncho' but no differences in chlorophyll were found through 46 days after planting. Hail destroyed all plots in July and thus, no yield data were obtained. Overall, there continues to be some evidence to suggest that Wyoming producers could use less N fertilizer on dry bean than the current rate.

Source of Nitrogen

In one greenhouse study, we compared ammonium nitrate, urea, and potassium nitrate (and an unfertilized check) with three cultivars (Rio Rojo, CO-46348, UI -537). Rates of N were 60 pounds per acre equivalent. Rates of K were equalized across all pots. Although cultivar differences were observed, N source effects were absent.   Seed yield of UI-537 and Rio Rojo was higher than CO-46348. Rio Rojo had the heaviest root mass and CO-46348 had the lowest stalk mass.

In the second greenhouse study, five cultivars (Rio Rojo, Poncho, CO-46348, UI-537, Othello) were treated with either urea or ammonium nitrate at 60 pounds N equivalent. No zero N rate was included. As was observed in the first N source greenhouse experiment, few effects of N source were found.   A significant interaction between N source and cultivar was observed for specific leaf weight (SLW). Four cultivars exhibited a slightly higher SLW when fertilized with ammonium nitrate but UI-537 had an SLW of 4.22 with urea and 3.64 with ammonium nitrate. Chlorophyll concentration was highest in Poncho and CO-46348 and lowest in Rio Rojo.

Rhizobia Inoculant and Different Strains

We have also conducted a pair of tests with inoculants but those have proved inconclusive. We have not conducted any rhizobia strain-by-genotype tests yet but these are planned for 2017.

Other

Andrew Kniss is conducting tests that will give us a better understanding of how Wyoming might utilize direct harvest more frequently. In 2016, his lab has measured cotyledon height and unifoliate height among 18 cultivars and found significantly higher values in several pinto releases from North Dakota as compared to other entries.

Additional details can be found in the on-line publications listed below.

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