THE 50th ANNIVERSARY OF
THE BEAN IMPROVEMENT COOPERATIVE

NINETEENTH BIENNIAL

Program and Abstracts

Concourse Hotel and Conference Center
Madison Wisconsin
October 29-31, 2007

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BEAN IMPROVEMENT COOPERATIVE
19TH BIENNIAL MEETING (2007)
MADISON, WISCONSIN

PROGRAM OVERVIEW

Sunday Oct. 28, 2007
BIC Registration 7:00 PM until 10:00 PM

Monday Oct 29, 2007 BIC Meeting	Wisconsin Ballroom	
BIC Registration	7:00	9:00
Breakfast Buffet	7:30	8:45
(Capital Ballroom A)		
Welcome & Introductions	8:45	9:00
Frazier-Zaumeyer Lecture	9:00	10:15
Break	10:15	10:45
PIPE Presentation	10:45	11:30
Oral Session	11:30	12:10
Lunch on your own	12:10	1:30
Oral Session	1:30	3:50
Break	3:50	4:15
Poster Session I	4:15	6:00
(University Rooms A, B, C)		
Dinner on your own		
PIPE meeting	7:00	8:30
(Conference Room 1)		
Conference Rooms 1 & 2 open for independent meetings		

Tuesday Oct, 30, 2007 BIC Meeting	Wisconsin Ballroom	
Breakfast on your own		
Oral Session	8:00	10:00
Break	10:00	10:30
Oral Session	10:30	12:10
Lunch on your own	12:10	1:30
Oral Session	1:30	3:30
Break	3:30	3:45
Poster Session II	3:45	5:30
(University Rooms A, B, C)		
Awards Banquet - Madison Ballroom		
Cocktails	6:30	7:30
Dinner	7:30	8:30
Speaker & Awards Program	8:30	9:30
Conference Rooms 1 & 2 open for independent meetings		

Wednesday Oct. 31, 2007 BIC Meeting	Wisconsin Ballroom	
Breakfast on your own		
BIC Business Meeting	9:00	10:00
Break	10:00	10:30
BIC Workshop	10:30	12:10
Lunch on your own	12:10	1:30
BIC Workshop	1:30	2:30
Phaseolus CGC	2:30	3:30
BIC Genetics Committee	3:30	4:30
Conference Rooms 1 & 2 open for independent meetings		

Thursday Nov 1, 2007 BIC W1150	Wisconsin Ballroom	
Breakfast on your own		
W1150 Meeting	8:00	10:00
Break	10:00	10:30
W1150 Meeting	10:30	12:00
Tour UW Microbial Sciences Building	10:30	1:30
Lunch on your own	12:00	1:30
Tour UW Microbial Sciences Building & Biotech Center	1:30	-
Conference Rooms 1 & 2 open for independent meetings		

BEAN IMPROVEMENT COOPERATIVE
19TH BIENNIAL MEETING (2007)
MADISON, WISCONSIN

Sunday, October 28	7:00 PM – 10:00 PM	**BIC Registration**
Monday, October 29	7:00 AM – 9:00 AM	**BIC Registration**

Monday, October 29

Capital Ballroom A

7:00 AM – 8:45 AM *Breakfast Buffet*

Wisconsin Ballroom

8:50 AM – 8:55 AM Welcome – Ken Kmiecik (Chair of the Local Organizing Committee)

FRAZIER-ZAUMEYER DISTINGUISHED LECTURESHIP

8:55-9:00 **James Kelly** – Introduction of the 2007 Frazier-Zaumeyer Awardee

9:00-10:15 **Molly Jahn** – Dean and Professor, University of Wisconsin-Madison, College of Agriculture & Life Sciences
"From Ralph Corbett's bean field to the molecular details of broad spectrum potyvirus resistance: Tales inspired by the I gene"

10:15-10:45 *Break*

PIPE Presentation

	Abstract no.	
10:45-11:30	**O-01**	**Howard Schwartz** – Western Coordinator, Pest Information Platform for Extension and Education (PIPE), Colorado State University

Oral Presentations – Wisconsin Ballroom

October, 29 Monday	**Abstract no.**	**Food, Nutrition and Abiotic Stress**	
11:30-11:50	**O-02**	Effect of *Phaseolus vulgaris* L. on the development of experimentally induced breast cancer	**Thompson, H.J.** - Colorado State University
11:50-12:10	**O-03**	Bean - Corn flour used for new extruded food products	**Delgado, E.** – Technological Institute of Durango, Mexico
12:10-1:30		*Break – Lunch on your own*	
1:30-1:50	**O-04**	Improved harvest index in drought resistant common beans and possible effects on combining ability	**Beebe, S.** - CIAT, Columbia
1:50-2:10	**O-05**	Physiology & functional genomics of chilling tolerance in *Phaseolus*	**Bett, K.E.** - University of Saskatchewan
		Breeding, Mapping, Markers, Insect Resistance, and Genomics	
2:10-2:30	**O-06**	Molecular diversity at the PvTFL1y locus, a candidate gene for the determinacy (*fin*) locus	**Kwak, M.** - University of California-Davis
2:30-2:50	**O-07**	Molecular mapping of genes involved in the phenylpropanoid pathway in bean (*Phaseolus vulgaris* L.)	**Yadegari, Z. -** University of Guelph
2:50-3:10	**O-08**	A transcript map of common bean	**McClean, P.E. -** North Dakota State University
3:10-3:30	**O-09**	Microsatellite marker diversity in common bean (*Phaseolus vulgaris* L.)	**Blair, M.W. -** CIAT, Columbia
3:30-3:50	**O-10**	APA locus proteins from tepary accession G40199 confers resistance to *Acanthoscelides obtectus* in common bean interspecific backcross lines	**Myers, J.R. -** Oregon State University
3:50-4:15		*Break*	

Poster Session I – University Rooms A, B and C

4:15 PM-6:00 PM Odd-Numbered Posters

October, 29 Monday	**Abstract no.**		
	P-01	Identification of SSR markers linked to rust resistance in Andean bean PI 260418	**Pastor-Corrales, M.A. -** USDA/ARS, Beltsville, MD
	P-03	Identification and characterization of *Phaseolus vulgaris* L. EMS mutants failing in seed development	**Silué, S.** - Faculté des Sciences Agronomiques de Gembloux, Belgique
	P-05	Beans, genes and a map	**Bett, K.E.** - University of Saskatchewan
	P-07	Lima bean breeding and genetics research at the University of Delaware	**Ernest, E.G.** - University of Delaware
	P-09	Are common bean *CO-3* and *CO-7* resistant alleles to anthracnose the same?	**dos Santos, J.B.** - Universidad Federal de Lavras, Brazil
	P-11	Legume PIPE - a new tool for disease management in legumes	**Langham, M.A.C.** - South Dakota State University
	P-13	Identification of anthracnose resistance genes in common bean cultivars from Paraná state, Brazil	**Vidigal, P.S.** - Univeridade Estadual de Maringá, Brazil
	P-15	Molecular characterization of *Colletotrichum lindemuthianum* haploids and diploids	**Gonçalves-Vidigal M.C.** - Univeridade Estadual de Maringá, Brazil

P-17	Screening of exotic dry bean drought tolerant germplasm in western Nebraska	**Urrea, C.A.** - University of Nebraska
P-19	Expression of genes for folic acid synthesis in developing bean seeds	**Pauls, K.P.** - University of Guelph
P-21	Gamete selection for improving physiological resistance to white mold in dry bean	**Terán H.** - University of Idaho
P-23	Evaluation of resistance to white mold disease in snap bean based on greenhouse and field trials	**Chung Y.S.** - University of Wisconsin-Madison
P-25	Use of multi-site nurseries to identify putative sources of *Sclerotinia sclerotiorum* resistance in common bean	**Otto-Hanson, L.K.** - University of Nebraska
P-27	Progress in the characterization and transfer of white mold resistance from runner to common bean	**Myers, J.R.** - Oregon State University
P-29	Inheritance of resistance to *beet curly top virus* in G122 common bean landrace	**Larsen, R.C.** - USDA/ARS, Prosser, WA
P-31	Progress in the identification of genetic variation for tolerance to *cucumber mosaic virus* in *Phaseolus vulgaris* L.	**Sass, M.** - University of Wisconsin-Madison
P-33	The *BCT-1* locus for resistance to *beet curly top virus* is associated with quantitative resistance to bean dwarf mosaic virus in common bean	**Miklas, P.N. -** USDA/ARS, Prosser, WA
P-35	Inheritance and allelic relationships of anthracnose resistance in common bean Mexico 222	**Gonçalves-Vidigal, M.C**. - Universidade Estadual de Maringá, Brazil
P-37	An improved *in vitro* regeneration system for common bean (*Phaseolus vulgaris* L.)	**Acosta-Gallegos J.A.** - CEBAJ-INIFAP, Mexico
P-39	Phytochemical content of black seeded bean cultivars after cooking and frying	**Acosta-Gallegos J.A. -** CEBAJ-INIFAP, Mexico

Oral Presentations – Wisconsin Ballroom

October 30 Tuesday	**Abstract no.**	**Breeding, Mapping, Markers, Insect Resistance, and Genomics (cont'd)**	
8:00-8:20	**O-11**	Breeding micronutrient dense bean varieties	**Kimani, P.M. -** University of Nairobi
8:20-8:40	**O-12**	Mutagenesis of BAT93 for tilling in common bean	**Porch, T.G. –** USDA/ARS/TARS, Puerto Rico
		Rust and Viruses	
8:40-9:00	**O-13**	Resistance to the soybean rust pathogen (*Phakopsora pachyrhizi*) in common bean cultivar CNC	**Pastor-Corrales, M.A**.- USDA/ARS, Beltsville, MD
9:00-9:20	**O-14**	Coevolution of the bean rust pathogen *Uromyces appendiculatis* with its wild, weedy and domesticated host (*Phaseolus spp.*) at a center of diversity	**Acevedo, M. -** University of Nebraska
9:20-9:40	**O-15**	Resistance to *bean golden mosaic virus* in genetically engineered common bean mediated by RNAi	**Faria, J.C. -** EAF, Brazil
9:40-10:00	**O-16**	Screening bean germplasm for cross-resistance to candidate begomoviruses and *beet mild curly top virus*	**Brown, J.K. -** University of Arizona
10:00-10:30		*Break*	
		Root Rot and Web Blight	
10:30-10:50	**O-17**	Is *Fusarium solani* f. sp. *phaseoli* or *F. lateritium* causing dry root-rot in common bean?	**Acosta-Gallegos, J.A.,** INIFAP, Mexico
10:50-11:10	**O-18**	Marker facilitated selection of root rot resistance in snap beans	**Navarro, F. -** University of Wisconsin-Madison
11:10-11:30	**O-19**	Frequency of occurrence of root rot pathogens on beans in Ecuador	**Abawi, G.S. -** Cornell University

11:30-11:50	**O-20**	Breeding beans for resistance to web blight	**Beaver, J. -** University of Puerto Rico
11:50-12:10	**O-21**	Development of a differential set of common bean lines to screen for web blight pathogen virulence	**Gonzales, N. -** University of Nebraska
12:10-1:30		*Break-Lunch on your own*	

Common Bacterial Blight and White Mold

1:30-1:50	**O-22**	Towards the identification of common bacterial blight resistance genes in *Phaseolus vulgaris*	**Perry, G. -** University of Guelph
1:50-2:10	**O-23**	Epistatic interaction between two major QTL conditioning resistance to common bacterial blight in common bean	**Miklas, P.N. –** USDA/ARS, Prosser, WA
2:10-2:30	**O-24**	Genetic diversity in *Xanthomonas campestris* pv. p*haseoli* and *X. c.* pv. p*haseoli* var. *fuscans* in the Midwestern United States and their interaction with resistant common bean	**Duncan, R.W. -** University of California-Davis
2:30-2:50	**O-25**	Evolution of screening for the physiological resistance to white mold in common bean	**Singh, S.P. -** University of Idaho
2:50-3:10	**O-26**	One cycle of recurrent selection for physiological resistance to white mold in dry beans	**Terán, H. -** University of Idaho
3:10-3:30	**O-27**	Improvement in screening for resistance to *Sclerotinia sclertiorum* in common bean through characterization of the pathogen and utilization of multi-state nurseries	**Otto-Hanson, L.K.** - University of Nebraska
3:30-3:45		*Break*	

Poster Session II – University Rooms A, B and C

3:45 PM-5:30 PM Even-Numbered Posters

October 30 Tuesday	**Abstract no.**		
	P-02	Identification and inheritance of a new source of halo blight resistance in common bean	**Duncan, R.W.** - University of California-Davis
	P-04	Genetic variability within race 65 of *Colletotrichum lindemuthianum* based on pathogenicity, anatomosis groups and RAPD markers	**dos Santos, J.B.**- Universidad Federal de Lavras, Brazil
	P-06	Improvement of the symbiotic interaction Bean – Rhizobia	**Rondino, A.P.** - MBG-CSIC, Spain
	P-08	Evaluation of navy and black bean genotypes for resistance to bacterial wilt	**Erickson, R.S.** – Agriculture and Agri-Food, Canada
	P-10	Identification of sources of bacterial wilt resistance in common beans (*Phaseolus vulgaris* L.)	**Urrea, C.A.** - University of Nebraska
	P-12	Physicochemical characteristics of common beans related to quality	**Bassinello, P.Z.** - EMBRAPA, Brazil
	P-14	Parasexual cycle and genetic variability of *Colletotrichum lindemuthianum*	**Gonçalves-Vidigal, M.C.** - Universidade Estadual de Maringá, Brazil
	P-16	Genetic variability within *Colletotrichum lindemuthianum* race 65 assessed by RAPD markers	**Gonçalves-Vidigal, M.C.** - Universidade Estadual de Maringá, Brazil

P-18	The root rot paradox	**Ronquillo, G.** - University of Wisconsin-Madison
P-20	Combining resistance to white mold from common and scarlet runner bean	**Brick, M.A.** - Colorado State University
P-22	Cooking time in slow and regular darkening pintos	**Bett, K.E.** - University of Saskatchewan
P-24	Phylogenetic relationship of lectin-like proteins expressed in tepary bean and common bean	**Myers, J.R.** - Oregon State University
P-26	Molecular characterization of *Colletotrichum lindemuthianum* haploids and diploids	**Gonçalves-Vidigal, M.C.** - Universidade Estadual de Maringá, Brazil
P-28	Evapotranspiration and water use efficiency for common bean genotypes under non-stress and drought stress conditions	**Porch, T.G.** - USDA/ARS/TARS, Puerto Rico
P-30	Molecular characterization of *Rhizoctonia solani* isolates from western Nebraska dry beans	**Venegas, J**. - University of Nebraska
P-32	A new application for SCAR marker sAE19$_{890}$	**Liebenberg, M.M. -** Agricultural Research Council-Grain Crops Institute, South Africa
P-34	Selection of markers for mapping and cloning disease resistance in common bean	**Hossain, K.G.** - Mayville State University, SD
P-36	Phytochemical equivalence of black bean cultivars to Negro 8025, an outstanding cultivar on reducing chronically degenerative diseases in rats	**Acosta-Gallegos J.A.** - CEBAJ-INIFAP, Mexico
P-38	Analysis of elements in common bean (*Phaseolus vulgaris* L.) that promote and inhibit iron assimilation	**Acosta-Gallegos J.A.** - CEBAJ-INIFAP, Mexico

Tuesday, October 29
Awards Banquet – Madison Ballroom

6:30 PM-7:30 PM	Cocktails and Social Hour
7:30 PM-8:30 PM	Dinner
8:30 PM-9:30 PM	Presentation of Graduate Student Awards Presentation of Frazier-Zaumeyer Distinguished Lectureship Award Presentation of the BIC Meritorious Service Awards Banquet Speaker - Irwin Goldman, Assoc. Dean and Professor, University of Wisconsin-Madison College of Ag. & Life Sciences “Keeping one foot in the furrow: Wisconsin plant breeding past, present and future”

Wednesday, October 30
Wisconsin Ballroom

9:00 AM-10:00 AM	BIC Business Meeting
10:00 AM-10:30 AM	*Break*
10:30 AM-12:10 PM	BIC Workshop “BIC - The Next 50 Years”
12:10 PM-1:30 PM	*Break - Lunch on your own*
1:30 PM-2:30 PM	BIC Workshop “BIC - The Next 50 Years”
2:30 PM-3:30 PM	Phaseolus CGC
3:30 PM-4:30 PM	BIC Genetics Committee

Thursday, November 1
Capital Ballroom A

8:00 AM-10:00 AM	W1150 Meeting
10:00 AM-10:30 AM	*Break*
10:30 AM-noon	W1150 Meeting
10:30 AM	Tour UW Microbial Sciences Building
Noon-1:30 PM	*Break – Lunch on you own*
1:30 PM	Tour UW Microbial Sciences Building & Biotechnology Center

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Abstracts of Oral and Poster Presentations

FRAZIER-ZAUMEYER DISTINGUISHED LECTURESHIP

FROM RALPH CORBETT'S BEAN FIELD TO THE MOLECULAR DETAILS OF BROAD SPECTRUM POTYVIRUS RESISTANCE: TALES INSPIRED BY THE I GENE.

Jahn, M.*, University of Wisconsin, Madison, WI. *Presenter (mjahn@cals.wisc.edu)

My early work in Phaseolus, initiated while a student with Michael H. Dickson, focused on the genetics of resistance to bean common mosaic virus resistance in bean conferred by the I gene, and its relationship to resistance to a large set of legume potyviruses. From this base, I moved to study other plant genes that confer resistance to multiple related potyviral species including a system of recessive resistance to Potato virus Y, pepper mottle virus and tobacco etch virus in Capsicum. These studies have defined perhaps the only plant pathosystems now known to be determined by the physical interaction of two thoroughly characterized molecules, one encoded by the virus, the other encoded by the host. I predict that the results from these studies in Capsicum may have direct relevance now in the legumes to define the identity of recessive genes for potyvirus resistance, long used to manage the necrosis related to the I gene.

Oral Presentations - Monday, October 29

O-01 PIPE - PEST INFORMATION PLATFORM for EXTENSION and EDUCATION.

Schwartz, H.F.[1*] and M.A.C. Langham.[2] [1]Dept. of Bioagr. Sci. & Pest Mgmt., Colorado State University, Fort Collins, CO – Western Coordinator; and [2]Plant Sci. Dept., South Dakota State University, Brookings, SD – Eastern Coordinator.
***Presenter (howard.schwartz@colostate.edu)**

The Legume PIPE consists of a network of 150 Sentinel plots in 30 states, provinces and districts of the U.S., Canada and Mexico. Plots are monitored for pests such as soybean rust, soybean aphid and other insects, in addition to other regionally prevalent diseases such as white mold, common bacterial blight, and viruses such as *Alfalfa mosaic, Bean pod mottle, Bean common* and *yellow mosaics, Beet curly top, Cucumber mosaic,* and *Soybean mosaic*. PIPE enhances the role of IPM specialists by providing near real-time access to legume pest observations, model output, pest management information, as well as communication tools to support pest management decision making by growers during that growing season. The public web site is available at: http://sbrusa.net.

O-02 EFFECTS OF PHASEOLUS VULGARIS L. ON THE DEVELOPMENT OF EXPERIMENTALLY INDUCED BREAST CANCER.

Thompson, H.J.[1*], M.A. Brick[2] and M.D. Thompson[1]. [1]Cancer Prevention Laboratory and [2]Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO. *Presenter (henry.thompson@colostate.edu)

Commercially processed, freeze dried and milled dry beans were incorporated into purified diets and fed to rats to investigate effects on the post initiation stage of chemically induced mammary carcinogenesis. Carcinogenesis was inhibited in a dose dependent manner. The inhibitory activity was not associated with seed coat color, antioxidant capacity or flavonoid content but differed by dry bean center of domestication. Candidate mechanisms will be discussed.

O-03 BEAN-CORN FLOUR USED FOR NEW EXTRUDED FOOD PRODUCTS.

Delgado, E.[a*], M.I. Vences-Montano[a], J. Hernandez-Rodriguez[a], N. Rocha-Guzman[a], A. Gallegos-Infante[a], S. Gorinstein[b], J. Morales-Castro[a], A. Rodriguez-Vidal[c], A. Ochoa-Martınez[a], H. Medrano-Roldan[a] and F. Ibarra[a], [a]Technological Institute of Durango, Durango, Mexico, [b]The Hebrew University of Jerusalem, Jerusalem, Israel, [c]Facultad de Ciencias Quımicas, Universidad Autonoma de Coahuila, Saltillo, Mexico. *Presenter (edelgad@itdposgrado-bioquimica.com.mx)

A combination of legumes and cereals can result in extruded products with high protein quality, even comparable to casein. Extruded bean-corn flour presented neither lectin nor any trypsin inhibitor activity. Ca and Zn complementation of bean – corn flours and extrudates, had no significant effect ($p > 0.05$) on rat weight and weight gain compared to the not complemented flours and extrudates.

O-04 IMPROVED HARVEST INDEX IN DROUGHT RESISTANT COMMON BEANS AND POSSIBLE EFFECTS ON COMBINING ABILITY.

Beebe, S.*, R. Idupulapati, J. Polonía, M. Grajales, C. Cajiao. International Center for Tropical Agriculture (CIAT), Cali, Colombia. *Presenter (s.beebe@cgiar.org)

Wild beans must compete aggressively for survival with vigorous vegetative growth, perhaps contributing to poor sink strength and low harvest index in cultivated common bean. Drought selected lines of cultivated bean display improved harvest index compared to commercial varieties, and at least one of these, SER 16, has combined well in crosses with runner bean. We suggest that selection under drought can reveal genes for better sink strength, which in turn enhance combining ability with runner bean.

O-05 PHYSIOLOGY & FUNCTIONAL GENOMICS OF CHILLING TOLERANCE IN *PHASEOLUS.*

Bett, K.*, P. Vijayan, G. Woronuk, K. McGowan and A. Vandenberg.
[1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK.
***Presenter (k.bett@usask.ca)**

We have identified accessions of *Phaseolus angustissimus* and *P. acutifolius* that have greater tolerance to chilling and sub-zero temperatures compared to the sensitive species *P. vulgaris*. Physiological and functional genomic characterizations of *P. angustissimus* and *P. vulgaris* have been carried out to identify genes associated with differences in chilling tolerance in these two species. We will report on the results of these experiments as well as efforts to introduce chilling tolerance from *P. acutifolius* into *P. vulgaris* through interspecies hybridization.

O-06 MOLECULAR DIVERSITY AT THE *PvTFL1y* LOCUS, A CANDIDATE GENE FOR THE DETERMINACY (*fin*) LOCUS.

Kwak, M.* and P. Gepts. Department of Plant Sciences, Section of Crop and Ecosystem Sciences, University of California, Davis, CA. *Presenter (mkwak@ucdavis.edu)

We will present evidence that a homologue of the Arabidopsis *TFL1* gene is a candidate gene for the *fin* locus. Sequence diversity at the *PvTFL1* locus correlates with the phenotypic variation for determinacy to a large extent, but also suggests that the trait had multiple origins in the domesticated gene pool, both in the Andean and Mesoamerican regions.

O-07 MOLECULAR MAPPING OF GENES INVOLVED IN THE PHENYLPROPANOID PATHWAY IN BEAN (*PHASEOLUS VULGARIS* L.).

Yadegari, Z.* and K.P. Pauls. Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada. *Presenter (zyadegar@uoguelph.ca)

It has been hypothesized that genes involved in the phenylpropanoid pathway correspond to some of the classical seed coat color genes in bean. The purpose of the current work is to map the positions of the phenylpropanoid genes on the common bean linkage map and determine whether their position correspond to any of the loci for classical seed coat color genes. Polymerase chain reaction (PCR) and restriction fragment length polymorphisms (RFLP) were identified for the phenylpropanoid gene sequences and their locations in the bean linkage map were determined by a JoinMap analysis.

O-08 A TRANSCRIPT MAP OF COMMON BEAN.

McConnell, M.D.[1,2] , S. Mamidi[1,2] , M. Rossi[1,3] , R.K. Lee[1,2] , P.E. McClean[1,2*]. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND; [2]Genomics and Bioinfomatics, North Dakota State University, Fargo, ND; [3]Dipartimento di Scienze degli Alimenti, Università Politecnica delle Marche, Ancona, Italy. * Presenter (phillip.mcclean@ndsu.edu)

A transcript map of common bean (*Phaseolus vulgaris* L.) was developed that consists of 273 gene-based markers. The genes include *Arabidopsis* genes in which the mutant displays an obvious phenotype; maize genes found to be under selection during domestication; genes involved in vital biochemical pathways; and homologs to random Arabidopsis genes. The LOD 2.0 is 1563 cM. Polymorphisms discovered here were screened against the parents of other commonly used mapping populations. The development process that lead to this map will be discussed.

O-09 MICROSATELLITE MARKER DIVERSITY IN COMMON BEAN.

Blair, M.W.[1], H.F. Buendia[1], L. Díaz[1], J.M. Díaz[1], M.C. Giraldo[1], E. Tovar[1], M.C. Duque[1], S.E. Beebe[1], D. Debouck[2], Bean Project and Genetic Resource Unit, CIAT - International Center for Tropical Agriculture, Cali, Colombia. *Presenter (M.BLAIR@CGIAR.ORG)

A diversity survey was used to estimate allelic diversity and heterozygosity of 129 microsatellite markers in common bean (*Phaseolus vulgaris* L.) genotypes that have been used as parents of mapping populations. Two types of microsatellites were evaluated, with gene-based microsatellites proving to be less polymorphic than genomic microsatellites in terms of both number of alleles (6.0 vs. 9.2) and PIC values (0.446 vs. 0.594). Markers that showed a high number of alleles were identified up to a maximum of 28 alleles for the marker BMd1 and the microsatellites were useful for identifying Andean and Mesoamerican genotypes, for uncovering the races within each genepool and for separating wild accessions from cultivars. Greater polymorphism and race structure was found within the Andean gene pool than within the Mesoamerican gene pool with race Peru having higher diversity compared to race Nueva Granada, and races Durango, Guatemala and Jalisco having comparable levels of diversity which were below that of race Mesoamerica.

O-10 APA LOCUS PROTEINS FROM TEPARY ACCESSION G40199 CONFERS RESISTANCE TO *ACANTHOSCELIDES OBTECTUS* IN COMMON BEAN INTERSPECIFIC BACKCROSS LINES.

Kusolwa, P.M. and J.R. Myers*. Department of Horticulture, Oregon State University Corvallis OR. *Presenter (myersja@hort.oregonstate.edu)

Some wild tepary bean accessions contain a complete arcelin - phytohaemagglutinin - α-amylase inhibitor (APA) locus. Two arcelin variants were identified in tepary accession G40199 and were transferred into common bean via interspecific hybridization to develop BC_2F_3 lines. *A. obtectus* reproduction and growth was evaluated on seeds from lines expressing or lacking the two arcelins. Significant delay for adult emergence and low number of emerged F_1 *A. obtectus* adults were observed in arcelin containing lines. Adult size was reduced and weight was halved. While not as high as the G40199 parent, levels of resistance in the introgression lines appear to be economically useful.

Oral Presentations - Tuesday, October 30

O-11 BREEDING MICRONUTRIENT DENSE BEAN VARIETIES.

**Kimani, P.M.[1*], M. Blair[2] and S. Beebe[2], [1] Dept of Plant Science and Crop Protection, University of Nairobi, Nairobi, Kenya, [2] CIAT, Cali, Colombia.
*Presenter (P.M.Kimani@cgiar.org)**

Micronutrient malnutrition is now recognized as one of the most serious health challenges facing vast sectors of Africa’s population and other regions affecting more than 2 billion people, particularly resource-poor women and children. Major deficiencies include iron, zinc, vitamin and protein. More than 66 populations segregating for mineral density and resistance to biotic and abiotic stress and marketable grain types have been generated. Selection of lines combining mineral density with superior agronomic and consumer preferred qualities are being pursued using classical and molecular techniques. Genetic analyzes indicate that grain iron and zinc concentration is quantitatively inherited with at least four QTLs involved.

O-12 MUTAGENESIS OF BAT 93 FOR TILLING IN COMMON BEAN.

Porch, T.G.[1*], M. Blair[2], P. Lariguet[3] and W. Broughton[3]
[1]USDA/ARS/TARS, Mayaguez, Puerto Rico, [2]CIAT, Palmira, Colombia. [3]University of Geneva, Geneva, Switzerland, *Presenter (timothy.porch@ars.usda.gov)

TILLING (targeted induced local lesions in genomes) of mutagenesis populations offers a unique opportunity for performing reverse genetics in common bean due to the absence of an effective transformation protocol. This study evaluated EMS concentrations of 20 to 60mM in order to confirm appropriate levels of EMS for TILLING of the genotype BAT 93. Germination, plant survival, plant height, and seed yield were evaluated, as well as optimum conditions for TILLING experiments.

O-13 RESISTANCE TO THE SOYBEAN RUST PATHOGEN (*Phakopsora pachyrhizi*) IN COMMOM BEAN CULTIVAR CNC.

Pastor-Corrales, M.A.[1]* and R.D. Frederick[2]. [1]USDA-ARS, Soybean Genomics and Improvement, Beltsville, MD and [2]USDA-ARS, Foreign Disease-Weed Science Research Unit, Ft. Detrick, MD. *Presenter (talo.pastor-corrales@ars.usda.gov)

We have identified Compuesto Negro Chimaltenango (CNC), a black-seeded Mesoamerican bean cultivar, as one of the most resistant to six isolates of the soybean rust pathogen (SBR) from Asia, Africa and Latin America. An F_2 population from the cross Mexico 309 (S) x CNC (R) was inoculated with an isolate of the SBR pathogen from Brazil. The results from evaluating 241 F_2 plants with 140 resistant and 101 susceptible plants, suggest that this resistance to SBR in CNC is controlled by two genes with complete dominance at both gene pairs but either recessive homozygote is epistatic to the effects of the other gene.

O-14 COEVOLUTION OF THE BEAN RUST PATHOGEN *UROMYCES APPENDICULATUS* WITH ITS WILD, WEEDY AND DOMESTICATED HOSTS (*PHASEOLUS SPP.*) AT A CENTER OF DIVERSITY.

Acevedo, M.[1*], J.R. Steandman[1], J.C. Rosas[2], and J. Venegas[1]. [1]Department of Plant Pathology, University of Nebraska, Lincoln, NE. [2]E.A.P Zamorano, Honduras. *Presenter (macevedo@uidaho.edu)

The virulence of the bean rust pathogen, *Uromyces appendiculatus* growing on wild, weedy and cultivated *Phaseolus* species in Honduras was examined in 28 host populations across the country. Significant differences were found among host species within populations. When comparisons among populations were made based on pathotype occurrence and frequency in each population, differences among populations were also evident.

O-15 RESISTANCE TO BEAN GOLDEN MOSAIC VIRUS IN GENETICALLY ENGINEERED COMMON BEAN MEDIATED BY RNAi.

Faria, J.C.[1*], K. Bonfim[2], E. O. P. L. Nogueira[2], E. A. Mendes[2], F. J. L. Aragão[2]. [1]Embrapa Arroz e Feijão, Santo Antônio de Goiás, Brazil; [2]Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil. *Presenter (josias@cnpaf.embrapa.br)

Bean golden mosaic is a whitefly-transmitted geminivirus. There is no immunity in *Phaseolus* germplasm to this disease. Bean transformation was achieved with a RNAi construct to silence the *rep* viral gene. Among 21 transformants, two displayed high resistance upon inoculation for the plant life cycle. Transgene-specific siRNA were detected. The transgene was inherited in a Medelian fashion in plants of the R2 generation.

O-16 SCREENING BEAN GERMPLASM FOR CROSS-RESISTANCE TO CANDIDATE BEGOMOVIRUSES AND *Beet mild curly top virus*.

Brown, J.K.[1*] and R. Larsen[2]. [1]Department of Plant Sciences, University of Arizona, Tucson, AZ; [2]USDA, Prosser, WA. *Presenter (jbrown@ag.arizona.edu)

Candidate cultivars of selected *Phaselous vulgaris* L. in a core collection (Americas) were screened for geminivirus cross-resistance by inoculating seedlings with candidate viruses from phylogenetically divergent genera *Begomovirus* and *Curtovirus* (family Geminiviridae). Field trials under natural virus pressure with *Beet mild curly top virus* (BMCTV) (previously, Worland strain) showed that Hystyle, Cardinal, G122, Othello, Zacatecano, Porrillo Sintetico, Moncayo, and Royal Red were highly resistant. Nine of 15 lines experimentally inoculated with *Bean golden yellow mosaic virus* (Puerto Rico), *Bean calico mosaic virus*, *Cotton leaf crumple virus*, and *Squash leaf curl virus* exhibited a resistance response. Of those, Cardinal, Moncayo, Othello, Royal Red, DOR, T39 and UI-114 also were resistant to BMCTV, indicating some extent of cross-resistance between virus genera and species in certain lines.

O-17 Is *Fusarium solani* f. sp. *phaseoli* OR *F. lateritium* CAUSING DRY ROOT-ROT IN COMMON BEAN?

Rodríguez-Guerra, R., J. Simpson, M.M. González-Chavira, and J.A. Acosta-Gallegos*, CEBAJ-INIFAP. Celaya, Guanajuato, MEXICO. *Presenter (acosta.jorge@inifap.gob.mx)

More than 50 isolates of *F. solani* obtained from bean roots in the highlands of Mexico were inoculated on Montcalm (reported as susceptible) and none provoked the symptoms described as caused by this species. Interestingly, isolates of *F. lateritium* caused symptoms similar to those induced by *F. solani*. Genetic analysis displayed large differences between each of above *Fusarium* species. It is likely that a misclassification exists between these two species.

O-18 MARKER FACILITATED SELECTION OF ROOT ROT RESISTANCE IN SNAP BEANS.

Navarro, F.M.*, M.E. Sass and J. Nienhuis. Department of Horticulture, University of Wisconsin, Madison, WI. *Presenter (fmnavarro@wisc.edu)

Two co-segregating repulsion phase RAPD markers, AD9.950 and S18.1500, have been previously identified in association with a major QTL for root rot resistance in snap beans. Four BC_1F_3 populations were developed using two root rot susceptible snap bean cultivars, Nicelo and Hercules, as recurrent parents and two resistant inbred lines which posses the AD9-S18 markers as donor parents. Across all populations, families homozygous for the introgressed QTL had superior plant vigor (4.0 vs. 7.0) and higher plant biomass (25.1 vs. 7.1 g) compared to heterozygotes or families or lacking the QTL when evaluated in a field with high levels of root rot inoculum.

O-19 FREQUENCY OF OCCURRENCE OF ROOT ROT PATHOGENS ON BEANS IN ECUADOR.

Falconi, E.[1], A. Murillo[1], F. Vargas[1], E. Peralta[1], and G. S. Abawi[2]*. [1]INIAP, Quito, Ecuador and [2]Dept. of Plant Path., Cornell Univ., Geneva, NY.
***Presenter (gsa1@cornell.edu)**

A diagnostic survey of root rot pathogens infecting beans in the northern and southern production areas of Ecuador was conducted during 2006 and 2007. Symptomatic and asymptomatic plants from 25 and 20 randomly selected bean fields in the northern and southern regions, respectively were examined for the incidence and severity of infections by root rot pathogens. Also, isolations were made from surface sterilized tissues on acidified potato-dextrose-agar plates to confirm the field diagnosis. The frequency of infection symptoms caused by *Fusarium solani* f. sp. *phaseoli* (Fsp), *Rhizoctonia solani* (Rs), *Sclerotium rolfsii* (Sr), *F. oxysporum* f. sp. *phaseoli* (Fop), and *Meloidogyne* spp. (root-knot nematodes, RKN) were 84, 96, 40, 16, and 24% in the northern areas, respectively; whereas their observed frequencies in the southern areas were 70, 50, 10, 40, and 20%, respectively.

O-20 BREEDING BEANS FOR RESISTANCE TO WEB BLIGHT.

Beaver, J.[1*], M. Alameda[1] and J.C. Rosas[2]. [1]Department of Agronomy and Soils, University of Puerto Rico, Mayagüez, PR, [2]Escuela Agrícola Panamericana, Tegucigalpa, Honduras.
***Presenter (jbeaver@uprm.edu)**

Web blight, caused by *Rhizoctonia solani* Kühn can reduce seed yield and quality of common bean (*Phaseolus vulgaris* L.) produced in the hot and humid zones of Central and South America, the Caribbean and Africa. The bean breeding programs at the University of Puerto Rico and Zamorano have utilized different strategies to develop lines with greater levels of resistance to this disease. Breeding lines have been developed that have greater web blight resistance than the black bean cultivar 'Talamanca' and greater seed yield quality than the check cultivar 'Morales'.

O-21 DEVELOPMENT OF A DIFFERENTIAL SET OF COMMON BEAN LINES TO SCREEN FOR WEB BLIGHT PATHOGEN VIRULENCE.

Gonzalez, N.[1*], J. Beaver[2], J.C. Rosas[3], G. Godoy-Lutz[4] and J. Steadman[1]. [1]University of Nebraska-Lincoln, Lincoln, NE, [2]University of Puerto Rico, Mayaguez, P.R., [3] Zamorano, Honduras, [4] CEDAF, Dominican Republic. *Presenter (ngonzal3@bigred.unl.edu)

Web blight is an important disease of common bean caused by *Rhizoctonia solani* in tropical areas. However, no set of lines useful for screening virulence of different *R. solani* isolates in differential bean lines/cultivars is available. Twenty-six lines that were observed to have resistance or tolerance in the field were screened with four isolates of *R. solani* from different anastomosis groups and subgroups from Dominican Republic, Puerto Rico, Honduras and Cuba using the detached leaf assay.

O-22 TOWARDS THE IDENTIFICATION OF COMMON BACTERIAL BLIGHT RESISTANCE GENES IN *PHASEOLUS VULGARIS*.

Perry, G.*, Y. Reinprecht, J. Chan, and K.P. Pauls. Department of Plant Agriculture, University of Guelph, Ontario, Canada. *Presenter (perryg@uoguelph.ca)

Common bacterial blight (CBB) is a significant disease problem in dry bean (Phaseolus vulgaris) crops throughout the world, and is caused by the pathogen *Xanthomonas axonopodis pv. phaseoli*. Although CBB-resistant lines, such as OAC-Rex and HR67, have been developed, the genes imparting this resistance have not been identified. To identify the resistance genes, BiBAC libraries for OAC-Rex and HR67 were created, and screened with previously identified CBB-resistance markers in order to assemble contigs surrounding the marker location. The contigs will be expanded using a chromosome walking technique until they cover a distance of 10cM, at which point the clones will be screened for the presence of the CBB-resistance genes by transforming susceptible plants with the BiBAC constructs and testing for disease resistance.

O-23 EPISTATIC INTERACTION BETWEEN TWO MAJOR QTL CONDITIONING RESISTANCE TO COMMON BACTERIAL BLIGHT IN COMMON BEAN.

Miklas, P.N.[1]*, D. Fourie[2], & G.J. Vandemark[1]. [1]USDA-ARS, Prosser, WA; [2]ARC-Grain Crops Institute, Potchefstroom, South Africa. *Presenter (pmiklas@pars.ars.usda.gov)

The BC420 and SU91 SCARs linked with QTL conditioning resistance to common bacterial blight and segregating in a near-isogenic background were interpreted as codominant markers by conversion to Taqman probes and assay by Real-Time PCR. Codominant markers enabled individual BC_6F_2 genotypes and the effect of allelic dosage at each QTL to be determined. The QTL expressed recessive epistasis (9:3:4 dihybrid ratio) as BC_6F_2 plants with both QTL had the highest level of resistance (9), SU91 only had intermediate resistance (3), and BC-420 only or neither QTL expressed no resistance (4).

O-24 GENETIC DIVERSITY IN *Xanthomonas campestris* pv. *phaseoli* and *X. c.* pv. *phaseoli* var. *fuscans* IN THE MIDWESTERN UNITED STATES AND THEIR INTERACTION WITH RESISTANT COMMON BEAN.

Duncan, R.W.[1*], S.P. Singh[2] and R.L. Gilbertson[1]. [1]University of California Davis, Davis, CA, [2]University of Idaho, Kimberly, ID. [*]Presenter (rwduncan@ucdavis.edu)

Strains of *Xanthomonas campestris* pv. *phaseoli* and *X. c.* pv. *phaseoli* var. *fuscans* were isolated from dark red kidney bean exhibiting typical symptoms of common bacterial blight (CBB) in 2005 and 2006 in the Midwest United States. Using repetitive-element PCR, genetic fingerprints were generated for 369 bacterial strains. Analyses of these patterns revealed two new pathogen types. These and six other representative pathogen types were inoculated onto 30 common bean accessions reported to have CBB resistance. These results will be discussed in terms of the nature of CBB resistance, host-pathogen co-evolution and resistance breeding.

O-25 EVOLUTION OF SCREENING FOR THE PHYSIOLOGICAL RESISTANCE TO WHITE MOLD IN COMMON BEAN.

Singh, S.P.* and H. Terán. Plant Soil and Entomological Sciences Department, University of Idaho-Kimberly, ID. *Presenter (singh@kimberly.uidaho.edu)

Methods of screening for the physiological resistance to white mold [WM, caused by *Sclerotinia sclerotiorum* (Lib.) de Bary] in common bean (*Phaseolus vulgaris* L.) have varied considerably over the past several decades. These will be reviewed and the effectiveness of the most recent screening technique used at the University of Idaho-Kimberly will be discussed. Also, we will discuss the implications of the new screening method for genetics and breeding for the physiological resistance to WM in the future.

O-26 ONE CYCLE OF RECURRENT SELECTION FOR PHYSIOLOGICAL RESISTANCE TO WHITE MOLD IN DRY BEAN.

Teran, H.* and S.P. Singh. Plant, Soil and Entomological Sciences Department, University of Idaho-Kimberly, ID. *Presenter (hteran@kimberly.uidaho.edu)

White mold [WM, caused by *Sclerotinia sclerotiorum* (Lib.) de Bary] is an important dry bean disease in North America. Our objective was to introgress WM resistance in dry bean, using recurrent selection (RS) involving eight parental germplasm. Results from one cycle of RS in two multiple-parent populations will be presented. Also, their implications for breeding for physiological resistance to WM will be discussed.

O-27 IMPROVEMENT IN SCREENING FOR RESISTANCE TO *SCLEROTINIA SCLERTIORUM* IN COMMON BEAN THROUGH CHARACTERIZATION OF THE PATHOGEN AND UTILIZATION OF MULTI-STATE NURSERIES.

Otto-Hanson, L.K.* and J.R. Steadman. Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE. *Presenter (lotto3@unl.edu)

Multiple sites in major production areas were used to validate putative new sources of resistance. Information on pathogen variation including compatibility tests for clonality and virulence assays were used to evaluate isolate(s) and compare field nursery populations.

Poster Presentations I - Monday, October 29

P-01 IDENTIFICATION OF SSR MARKERS LINKED TO RUST RESISTANCE IN ANDEAN BEAN PI 260418.

Pastor-Corrales, M.A.[1*], P.A. Arraes Pereira[2], K. Lewers[3], R. Vianello Brondani[2], G. Cortopassi Buso[4], M.A. Ferreira[4], W. Santos Martins[5]. [1]ARS-USDA, Soybean Genomics Lab., Beltsville, MD, [2]Embrapa Rice and Beans, Goiania, Brazil, [3]ARS-USDA, Genetic Improvement of Fruits and Vegetables Lab, Beltsville, MD, [4]Embrapa Genetic Resources and Biotechnology, Brasilia, Brazil, [5]Federal University of Goias, Informatics Department, Goiania, Brazil. *Presenter (talo.pastor-corrales@ars.usda.gov)

PI 250418 is an Andean bean with resistance to all but one of the 90 races of the bean rust pathogen (*Uromyces appendiculatus*) maintained at the USDA-ARS Bean Project in Beltsville, MD. An F_2 population (2-3773, 120 plants) from the cross Pinto 114 x PI 260418 was inoculated with four races the rust pathogen; two of these races were Andean (98 and 99) and the other two races (63 and 85) were Mesoamerican. We extracted DNA from 94 F_2 plants and identified two single sequence repeats (SSR) markers closely linked to the region that confers resistance to the rust isolates used in this study.

P-03 IDENTIFICATION AND CHARACTERIZATION OF *PHASEOLUS VULGARIS* L. EMS MUTANTS FAILING IN SEED DEVELOPMENT.

S. Silué[1]*, P. Lariguet[2], C. Pankhurst[2], J.M. Jacquemin[3], W. J. Broughton[2], and J. P. Baudoin[1]. [1]Faculté des Sciences Agronomiques de Gembloux, Unité de Phytotechnie Tropicale et d'Horticulture, Gembloux, Belgique, [2]LBMPS, Université de Genève, Suisse, and [3]CWRA, Gembloux, Belgique. *Presenter (silue.s@fsagx.ac.be)

We isolated mutants deficient in seed development from an EMS-induced mutant collection of common bean. Embryos in mutant seeds aborted within 10 to 20 days after anthesis and present abnormalities in suspensor and cotyledons. The suppressive subtractive hybridization allowed us to isolate eight cDNAs fragments differentially expressed between the wild-type and the mutants during seed development. These cDNAs were cloned and sequenced. BLAST sequence homology analyses leaded to ten groups of proteins encoded by the cDNAs isolated. We discussed five of them by studying their expression during *Phaseolus* wild-type and mutant embryo development.

P-05 BEANS, GENES AND A MAP.

Couperthwaite, A.C., P. Vijayan[2] and K.E. Bett[2]* [1]Department of Computer Science, [2]Department of Plant Sciences, University of Saskatchewan Saskatoon, SK, Canada *Presenter (k.bett@usask.ca)

We are mapping a large number of bean ESTs on the *Phaseolus vulgaris* consensus genetic map. We will describe our efforts to use bioinformatics software like cMap (developed by the GMOD Project, USA) to represent this map in an web accessible, interactive graphic form. We are also building bioinformatic tools to map bean ESTs virtually on the structural genome of the model legume *Medicago truncatula*. The integration of this software will allow the translation of genetic map information from beans to other pulse crops such as chickpea and lentil by comparison with the structural map of *M. truncatula*.

P-07 LIMA BEAN BREEDING AND GENETICS RESEARCH AT THE UNIVERSITY OF DELAWARE.

Ernest, E.G.[1]*, and W.E. Kee[1]. [1]Department of Plant and Soil Sciences, University of Delaware, Georgetown, DE. *Presenter (emmalea@udel.edu)

A lima bean breeding program has been initiated in Delaware with the goal of developing green baby lima and Fordhook lima bean varieties with increased resistance to lima bean downy mildew (*Phytophthora phaseoli*) and superior adaptation to Delaware growing conditions. In 2007 a limited number of green baby lima lines were grown in Ventura Co., California and Sussex Co., Delaware. Additionally we are developing three lima bean RIL populations for future genetic mapping: Bridgeton x Jackson Wonder, Bridgeton x Fordhook 242, and Dr. Martin x Bridgeton.

P-09 ARE COMMON BEAN *Co-3* AND *Co-7* RESISTANT ALLELES TO ANTHRACNOSE THE SAME?

Lima, I.A., J.B. dos Santos* and M.A.P. Ramalho. Universidade Federal de Lavras (UFLA), [2]Department of Biology, Lavras, MG, Brazil. *Presenter (jbsantos@ufla.br)

F_3 segregating population derived from the cross of the lines H1 (*Co-7* - derived from G2333) and Mexico 222 (*Co-3*) were all inoculated with pathotypes 8 and 65 of *C. lindemuthianum*. Both parents and the F_3 population were 100% resistant to pathotype 8 and 100% susceptible do pathotype 65 indicating that *Co-7* and *Co-3* are the same allele.

P-11 LEGUME PIPE-A NEW TOOL FOR DISEASE MANAGEMENT IN LEGUMES.

Langham, M. A. C.[1]*, S. A. Tolin[2], C. Sutula[3], H. Schwartz[4], G. Wisler[5], A. Karasev[6], D. Hershman[7], L. Giesler[8], J. Golod[9], S.T. Ratcliffe[10], and K.F. Cardwell[11]. [1]South Dakota State Univ., Brookings, SD. [2]Virginia Tech, Blacksburg, VA. [3]AgDia, Inc., Elkhart, IN. [4]Colorado State Univ., Ft. Collins, CO. [5] ARS, Horticulture and Sugar, Beltsville, MD. [6]Univ. of Idaho, Moscow, ID. [7]Univ. of Kentucky, Princeton, KY. [8]Univ. of Nebraska-Lincoln, Lincoln, NE. [9]Penn State Univ., Univ. Park, PA. [10]Univ. of Illinois, Urbana, IL. [11]USDA-CSREES, Washington, DC. *Presenter (marie.langham@sdstate.edu)

The Legume PIPE, the latest expansion of the IPM-Pest Information Platform for Education and Extension (pilot year 2007), expanded this program to dry or fresh beans, peas, or other marketable legumes. The Legume PIPE focused on important fungal, bacterial, and viral diseases, as well as insects, in 155 legume plots in 29 states with data reporting to the NPDN and PIPE database.

P-13 IDENTIFICATION OF ANTHRACNOSE RESISTANCE GENES IN COMMON BEAN CULTIVARS FROM PARANÁ STATE, BRAZIL.

Vidigal Filho, P.S.*, M.C. Gonçalves-Vidigal, A. Gonela, G. F. Lacanallo, L.L. Sousa and V.L. Sousa. Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil.
***Presenter (pedro.vidigal@pop.com.br)**

A collection of 40 accessions and 233 F_2RC_3 lines were evaluated in the combined analysis of two molecular SCARs ($SF10_{1072}$ for *Co-10* gene and SAS13 for *Co-4*^{2} allele) and in the resistance tests against the two anthracnose races, 73 and 2047 of *Colletotrichum lindemuthianum*. Twenty-three accessions presented at least one of the molecular markers $SF10_{1072}$ (linked to *Co-10* gene) and/or $SAS13_{950}$ (linked to *Co-4*^{2} allele). Out of the 233 F_2RC_3 lines analyzed by molecular marker, a number of 80 revealed the presence of $SAS13_{950}$.

P-15 MOLECULAR CHARACTERIZATION OF *Colletotrichum lindemuthianum* HAPLOIDS AND DIPLOIDS.

Gonçalves-Vidigal, M.C.[1]*, P.S. Vidigal Filho[1], A. Gonela[1], G.F. Lacanallo[1], M.A.A Castro-Prado[2], C.B. Querol[2]. [1]Dep. Agronomia, [2]Dep. Biologia, Universidade Estadual de Maringá, PR, Brazil. *Presenter (mvidigal@pop.com.br)

The analysis of auxotrophics mutants of races 2047 and 23 using RAPD molecular markers demonstrated that the recombinant Rec4 presented a band of 800bp in mutant 23.19, and another band of approximately 750bp which is present in 2047.4 mutant when analyzed with OPF5 primer. However, analyses conducted with OPC08 primer exhibited a band of 1300bp in diploid 23.14//23.15, but absent in race 23. The recombinant Rec6 has showed a band of 350bp and another of 800bp, being polymorphic in relation to 2047.4//23.19 diploid. The Rec4 recombinant had revealed to be polymorphic in relation to 23.14//23.15 diploid once it possesses a band of 1000bp.

P-17 SCREENING OF EXOTIC DRY BEAN DROUGHT TOLERANT GERMPLASM IN WESTERN NEBRASKA.

Urrea, C.A.*, C.D. Yonts, D. Lyon, R. Higgins, D. Reichardt, and D.M. Khu. University of Nebraska-Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE.
***Presenter (currea2@unl.edu)**

Identification of high-yielding, drought-tolerant dry bean lines is needed in order to reduce dependence on irrigation water, lower costs of production, and increase profit margins for dry bean growers in western Nebraska. Ten lines were tested in replicated trials near Mitchell and Scottsbluff, NE in 2006. The non-stress and stress plots were irrigated alike until flowering, and then no more irrigation was applied to the stress plots. Bill-Z used the least water usage in both non-stress and stress plots in Mitchell. In the stress plots, yield was reduced in 76.2% across both locations. The Drought Intensity Index (DII) value of 0.76 indicated severe drought conditions for the experiment. Bill Z and Beryl had a yield reduction of 70% compared to the experimental line NE16-05-77 of 91%. Beryl, Bill Z, and NE16-05-41 had the lowest Drought Susceptibility Index (S) and the largest Geometric Mean (GM) suggesting some drought tolerance.

P-19 EXPRESSION OF GENES FOR FOLIC ACID SYNTHESIS IN DEVELOPING BEAN SEEDS.

Shim, Y-S., F. Garabagi, and K. P. Pauls*. Department of Plant Agriculture, University of Guelph, Guelph, ON. *Presenter (ppauls@uoguelph.ca)

Dry beans (*Phaseolus vulgaris*) are excellent sources of dietary folic acid (Vitamin B), which plays an important role in preventing neural tube disorders in newborns and helps to prevent heart disease and cancer. However, levels of this vitamin can vary more than 3 fold among varieties. Fragments of six genes of the folic acid synthesis pathway were cloned and sequenced and their expression levels in developing seeds were assayed. This information will be used to test correlations between gene expression and folate content and may allow the development of new tools for the selection of high folate beans.

P-21 GAMETE SELECTION FOR IMPROVING PHYSIOLOGICAL RESISTANCE TO WHITE MOLD IN DRY BEAN.

Terán, H.* and S.P. Singh. Plant Soil and Entomological Sciences Dept., University of Idaho-Kimberly, ID. *Presenter (hteran@kimberly.uidaho.edu)

White mold [WM, caused by *Sclerotinia sclerotiorum* (Lib.) de Bary] is a widespread disease of dry and green bean (*Phaseolus vulgaris* L.) in the USA and other cool-humid regions of the world. Our objective was to introgress physiological resistance to WM in dry bean, using gamete selection in tow inter-gene pool populations. Selections gains obtained in the early generations will be presented and their implications for breeding for physiological resistance to WM will be discussed.

P-23 EVALUATION OF RESISTANCE TO WHITE MOLD DISEASE IN SNAP BEAN BASED ON GREENHOUSE AND FIELD TRIALS.

Chung Y.S.*, M.E. Sass and J. Nienhuis. Department of Horticulture, University of Wisconsin, Madison, WI. *Presenter (yschung3@wisc.edu)

White mold [*Sclerotinia sclerotiorum* (Lib.) de Bary] is a common pathogen in cool-wet environments. Field and greenhouse tests were performed using recombinant inbred line (GA) and independent inbred backcross (GPP) populations that share a common resistance parent, G122. All greenhouse and field evaluation methods distinguished among genotypes; however, the correlation between field and greenhouse tests was low (0.0-0.26) implying that avoidance mechanisms are more important than physiological resistance.

P-25 USE OF MULTI-SITE NURSERIES TO IDENTIFY PUTATIVE SOURCES OF *SCLEROTINIA SCLEROTIORUM* RESISTANCE IN COMMON BEAN.

Otto-Hanson, L.K.* and J.R. Steadman. Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE. *Presenter (lotto3@unl.edu)

Eight field and greenhouse locations in the US were used to screen bean lines with putative sources of white mold resistance in 2007. Twelve bean entries were tested in the field, while 17 entries were tested in greenhouse screening. Use of the multi-site screening is more reliable than individual site screening due to the fact that resistance is partial and often difficult to identify consistently.

P-27 PROGRESS IN THE CHARACTERIZATION AND TRANSFER OF WHITE MOLD RESISTANCE FROM RUNNER TO COMMON BEAN.

Myers*, J.R., B.S. Gilmore and J.E. Haggard. Department of Horticulture, Oregon State University Corvallis OR. *Presenter (myersja@hort.oregonstate.edu)

A resistant x susceptible runner bean (*Phaseolus coccineus*) F_2 population was characterized for white mold resistance and molecular markers were mapped to identify resistance quantitative trait loci (QTL). The resistant parent was also crossed to *P. vulgaris*, and a backcross – inbred population was subjected to disease evaluation and molecular marker mapping. QTL identified in the intraspecific population were different from those of importance in the interspecific cross. In the interspecific cross, some whole chromosomes and large sections of other chromosomes were not represented in the population. Some backcross inbred lines show high levels of field resistance.

P-29 INHERITANCE OF RESISTANCE TO *BEET CURLY TOP VIRUS* IN G122 COMMON BEAN LANDRACE.

Larsen, R.C.*[1], P.N. Miklas[1] and C. Kurowski[2]. [1]USDA-ARS, Prosser, WA; [2]Harris Moran Seed Company, Davis, CA. *Presenter (rlarsen@pars.ars.usda.gov)

Beet curly top virus (BCTV) is a devastating disease of common bean in the Western U.S. Genetic resistance provides effective control but can be difficult to discern in early generations. G122, an Andean landrace from India, known as Jatu Rong, appears to possess resistance independent of *Bct-1* gene as determined by allelism tests. Preliminary genetic analysis of 98 F5:7 RILs (G122/Taylor Horticulture) reveals a single QTL with major effect (34%) across multiple environments.

P-31 PROGRESS IN THE IDENTIFICATION OF GENETIC VARIATION FOR RESISTANCE TO *CUCUMBER MOSAIC VIRUS* IN *PHASEOLUS VULGARIS* L.

M.E. Sass[1]* T.L. German[2] and J. Nienhuis[1]. [1]Dept. of Horticulture and [2]Dept. of Entomology, University of WI-Madison. *Presenter (mesass@wisc.edu)

Recently, dramatic increases in aphid-transmitted viruses have adversely impacted snap bean production areas in the Great Lakes region, including Wisconsin. Although year-to-year fluctuations in aphid and virus pressure and in the number of species present have occurred, *cucumber mosaic virus* (CMV) has been detected each year. We have screened all 423 accessions from the *Phaseolus vulgaris* core collection, accessions from the reserve collection and other germplasm for resistance to CMV and have identified accession PI 619437 as having tolerance to CMV. A RIL population derived from a cross between PI 619437 (tolerant) and Hystyle (susceptible) has been developed and is currently being field evaluated to determine the inheritance of tolerance to CMV.

P-33 THE BCT-1 LOCUS FOR RESISTANCE TO *BEET CURLY TOP VIRUS* IS ASSOCIATED WITH QUANTITATIVE RESISTANCE TO BEAN DWARF MOSAIC VIRUS IN COMMON BEAN.

Miklas, P.N.[1]*, and R.L. Gilbertson[2]. [1]USDA-ARS, Prosser, WA; [2]Dept. of Plant Pathology, University of California-Davis. *Presenter (pmiklas@pars.ars.usda.gov)

Host resistance provides effective control of diseases induced by geminiviruses in common bean. We sought to examine the effect of *Bct-1* gene, which conditions resistance to *Beet curly top virus* (BCTV), against another distinct geminivirus *Bean dwarf mosaic virus* (BDMV). A population of 92 $F_{5:7}$ RILs from the cross Primo/Moncayo was challenged with BDMV. Quantitative resistance to BDMV was associated with *Bct-1* gene segregating in the same population.

P-35 INHERITANCE AND ALLELIC RELATIONSHIPS OF ANTHRACNOSE RESISTANCE IN COMMON BEAN MEXICO 222.

Gonçalves-Vidigal, M.C.*, P.S. Vidigal Filho, G. F. Lacanallo, L.L. Sousa and P.S. Perioto. Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil.
***Presenter (mvidigal@pop.com.br)**

Common bean Mexico 222 cultivar, resistant to *Colletotrichum lindemuthianum* races 7 and 23, was crossed with susceptible cultivars Michigan Dark Red Kidney (race 7) and Widusa (race 23), and with resistant cultivars PI 207262, BAT 93 and MSU 7. The segregation in the F_2 population fitted in a ratio of 3R:1S which indicates a single dominant gene in Mexico 222 conferring resistance to race 23, whereas its resistance to race 7 is conditioned by two dominant genes. The allelism tests suggest that *Co-9*, *Co-3* and *Co-7*, which were previously characterized as different genes, are in fact distinct alleles at the same locus.

P-37 AN IMPROVED IN VITRO REGENERATION SYSTEM FOR COMMON BEAN (*Phaseolus vulgaris* L.).

Quintero Jiménez, A., E. Espinosa-Huerta., J.A. Acosta-Gallegos*, H.S. Guzmán-Maldonado and M.A. Mora Avilés. CEBAJ-INIFAP. Celaya, Guanajuato, Mexico
***Presenter (acosta.jorge@inifap.gob.mx)**

Common bean regeneration using embryonic axes from mature seeds in Gamborg medium provides high shoot formation efficiency (97%) throughout organogenic regeneration in cultivars Apetito (G13637), ICA Palmar (G4523), Pinto Saltillo and Flor de Mayo Anita, in comparison to other protocols previously reported by our group. A consistent and efficient protocol for regeneration and whole plant recovery is essential for genetic transformation.

P-39 PHYTOCHEMICAL CONTENT OF BLACK SEEDED BEAN CULTIVARS AFTER COOKING AND FRYING.

Almanza-Aguilera, E., I. Guzmán-Tovar, A. Mora-Avilés, J.A. Acosta-Gallegos*, and S.H. Guzmán-Maldonado. CEBAJ-INIFAP. Celaya, Guanajuato, Mexico.
***Presenter (acosta.jorge@inifap.gob.mx)**

Phytochemical characterization is essential to study the effect of bean consumption on colon cancer and diabetes. Such information could guide us on learning, which seed component (s) are involved in the biological effect. In México, beans are consumed cooked or fried. The aim of the study was to determine the effect such processes on the phytochemical profile of several black bean cultivars. Interestingly, some phytochemicals were increased (such as phenolic compounds), meanwhile other were reduced, such as protein and anthocyanins.

Poster Presentations II- Tuesday, October 30

P-02 IDENTIFICATION AND INHERITANCE OF A NEW SOURCE OF HALO BLIGHT RESISTANTANCE IN COMMON BEAN.

Duncan, R.W.[1]*, S.P. Singh[2] and R.L. Gilbertson[1]. [1]University of California Davis, Davis, CA, [2]University of Idaho, Kimberly, ID. *Presenter (rwduncan@ucdavis.edu)

Pseudomonas syringae pv. *phaseolicola* (*Psp*) is the causal agent of halo blight, a seed-borne bacterial disease of common bean. Nine races of *Psp* have been previously described on a set of eight differential *Phaseolus* genotypes. The *Psp* Race 6 is pathogenic on all differentials, and there is no known source of resistance for this race. After screening a range of germplasm, a resistance source to *Psp* Race 6 has been identified and the nature and genetics of this resistance will be discussed.

P-04 GENETIC VARIABILITY WITHIN RACE 65 OF *COLLETOTRICHUM LINDEMUTHIANUM* BASED ON PATHOGENICITY, ANATOMOSIS GROUPS AND RAPD MARKERS.

Davide, L.M.C., F.H. Ishikawa, E.A. Souza, and J.B. dos Santos*. Universidade Federal de Lavras (UFLA), Department of Biology, Lavras, Brazil. *Presenter (jbsantos@ufla.br)

Aiming to identify the variability within race 65 from Minas Gerais State, Brazil, eleven groups were obtained based on RAPD marker and anastomosis groups analyses. Only three isolates were classified within the same anastomosis group, although these isolates showed distinct pattern by RAPD analysis. Differences in aggressivity of isolates from race 65 were detected based on inoculation in commercial cultivars. These results showed great variability within race 65, suggesting the set of differential cultivars is inefficient to detect all pathogenic variability in *C. lindemuthianum*.

P-06 IMPROVEMENT OF THE SYMBIOTIC INTERACTION BEAN - RHIZOBIA.

Rodiño, A. P., M. Santalla and A. M. De Ron*. Plant Genetic Resources Department, MBG-CSIC. Pontevedra, Spain. *Presenter (amderon@mbg.cesga.es)

Common bean (*Phaseolus vulgaris*) has a low capacity of symbiotic nitrogen fixation (SNF) with rhizobia in Europe. The N_2-dependent growth of various bean accessions belonging to the great northern, “caparron”, white kidney and canellini market classes was compared in glasshouse, under optimized symbiotic conditions with different *Rhizobium* strains collected in farmer fields in different locations in Galicia (Northwestern Spain). In the studied germplasm there was genotypic variation for nodulation and their N_2-dependent plant-growth. Thus, some breeding lines from the Iberian Peninsula could be selected for further improvement of the SNF potential in the common bean varieties currently grown in Europe.

P-08 EVALUATION OF NAVY AND BLACK BEAN GENOTYPES FOR RESISTANCE TO BACTERIAL WILT.

Erickson, R.S.[1], P.M. Balasubramanian[1*], H.H. Mündel[1,3], R.L. Conner[2] , and H.C. Huang[1,3]. Agriculture and Agri-Food Canada, [1]Lethbridge Research Centre, Lethbridge, AB. [2]Morden Research Station, Morden, MB. [3]Retired. *Presenter (parthibab@agr.gc.ca)

Genotypes from navy and black bean market classes were tested for resistance to the yellow, orange and purple strains of bacterial wilt using the hilum injury/seed inoculation method. Results of the screening tests showed significant ($P<0.05$) differences in resistance among the genotypes. The study concludes that bacterial wilt-resistant germplasm exists in the navy and black bean market classes.

P-10 IDENTIFICATION OF SOURCES OF BACTERIAL WILT RESISTANCE IN COMMON BEANS (*Phaseolus vulgaris* L.)

Urrea, C.A.*, R.M. Harveson, and K. Nielsen. University of Nebraska- Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE. *Presenter (currea2@unl.edu)

Bacterial wilt caused by *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* has been detected in more than 300 fields in Nebraska, Colorado, and Wyoming since 2003. A total of 424 accessions from the National Plant Germplasm System (NPGS) collection of common beans are being screened in the greenhouse to the most virulent Nebraska bacterial wilt isolate.

P-12 PHYSICOCHEMICAL CHARACTERISTICS OF COMMON BEANS RELATED TO QUALITY. PHYSICOCHEMICAL CHARACTERISTICS OF COMMON BEANS RELATED TO QUALITY.

Magri, N. C. N. F.[1], P. Z. Bassinello[1*] and D. P. R. Ascheri[2]. [1]Embrapa Arroz e Feijão, Santo Antônio de Goiás, Goiás, Brazil. [2] Universidade Estadual de Goiás, Anápolis, Goiás, Brazil. [*]Presenter (pzbassin@cnpaf.embrapa.br)

In this work some technological and nutritional traits of five dry bean (*Phaseolus vulgaris* L.) cultivars from carioca and black commercial groups were evaluated for soluble solid content, grain color of cooked and uncooked beans, broth rheological measurements as well as its electrical conductivity.

P-14 PARASEXUAL CYCLE AND GENETIC VARIABILITY OF *COLLETOTRICHUM LINDEMUTHIANUM*.

Castro-Prado, M.A.A.[1], C.B. Querol[1], M.C. Gonçalves-Vidigal[2*], P.S. Vidigal Filho[2], A. Gonela[2] and P.S. Perioto[2]. [1]Dep. Biologia, [2] Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil. [*]Presenter (mvidigal@pop.com.br)

The heterokaryotic and vegetative diploid phases of *Colletotrichum lindemuthianum* are described by nutritional and biochemical markers. Nitrate non-utilizing mutants derived from 2047, 89, 73, 65 and 23 races were paired in all possible combinations to obtain heterokaryons. Although pairings 2047/89, 2047/73, 65/73 and 73/23 showed complete vegetative incompatibility, prototrophic heterokaryons were obtained from pairings 2047/65, 2047/23, 65/89, 65/23, 73/89, 89/23, 2047/2047, 65/65, 89/89, 73/73 and 23/23.

P-16 GENETIC VARIABILITY WITHIN *Colletotrichum lindemuthianum* RACE 65 ASSESSED BY RAPD MARKERS.

Gonçalves-Vidigal, M.C.*, P.S. Vidigal Filho, M.V. Kvitschal, A. Gonela, and G.F. Lacanallo. Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil.
***Presenter (mvidigal@pop.com.br)**

Genetic variability among isolates *of Colletotrichum lindemuthianum* race 65 was determined using RAPD markers. Mycelial DNA from each isolate was extracted and amplified with 12 primers, producing 63 polymorphic bands. The cluster analysis using RAPD markers grouped the isolates into five groups with 0.70 relative similarity. The isolates CL 65.14 and CL 65.21 from Santa Catarina are the most similar. On the other hand, the most dissimilar isolates were CL 65.1 and CL 65.408 with 95% of dissimilarity, one originated from Paraná and the other from Minas Gerais.

P-18 THE ROOT ROT PARADOX.

Ronquillo, M.G.* and J. Nienhuis. Department of Horticulture, University of Wisconsin, Madison, WI. *Presenter (mronquillo@wisc.edu)

The distribution of root rot of beans (*Phaseolus vulgaris*) caused by a complex of pathogens including, *Fusarium solani*, *Pythium ultimum*, *Aphanomyces euteiches*, and *Rhizoctonia solani* occurs worldwide; however, pathogenicity of any given species changes according to geographic and environmental conditions. The *Aphanomyces spp. - Pythium spp*. complex is the major pathogen in Hancock, WI, a region characterized by cool, and wet springs. In contrast, more arid regions appear dominated by other pathogens, including *Fusarium spp*. We successfully isolated *Fusarium oxysporum* from plants with root rot symptoms collected near Othello, WA but not from Hancock, WI. Previous researchers have identified QTL's associated with root rot resistance to *Aphanomyces spp., Pythium spp.*, and *Fusarium spp*. The objective of this research is to determine if the QTL's are pathogen specific.

P-20 COMBINING RESISTANCE TO WHITE MOLD FROM COMMON AND SCARLET RUNNER BEAN.

Newell[1] M.A., M.A. Brick[1*], P.F. Byrne[1], H.F. Schwartz[2], J.B. Ogg, B. Gilmore[3], and J.R. Myers[3] [1]Dep. Soil and Crop Sciences and [2]Bioagricultural Sciences and Pest Management, Colorado State Univ., [3]Dep.of Horticulture, Oregon State Univ.
***Presenter (Mark.Brick@Colostate.edu)**

QTL that provide resistance to white mold previously identified in common bean line G122 and scarlet runner bean accession PI 255956 were combined into an inbred backcross line (IBL) population. Evaluation of the BC_1F_5 IBL demonstrated white mold resistance ranged from three to seven (1=resistant, 9=susceptible) using the straw test. Analyses of molecular markers linked to QTL showed segregation distortion with preferred transmission of *P. vulgaris* alleles.

P-22 COOKING TIME IN SLOW AND REGULAR DARKENING PINTOS.

K. Bett[1*], A. Vandenberg[1], K. Podhordeski[1], L. Malcolmson[2] , and A.S. Bellido[2]. [1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK. [2] Canadian International Grains Institute, Winnipeg, M. *Presenter (k.bett@usask.ca)

Slow darkening line 1533-15 has a quicker cooking time than the regular darkening line, CDC Pintium. RILs from a cross between these two parents were assessed for cooking time following harvest and 9 months after storage in the freezer or on the shelf. The relationship between seed coat darkening and cooking time will be discussed.

P-24 PHYLOGENETIC RELATIONSHIP OF LECTIN-LIKE PROTEINS EXPRESSED IN TEPARY BEAN AND COMMON BEAN.

Kusolwa, P.M. and J.R. Myers*. Department of Horticulture, Oregon State University Corvallis OR. *Presenter (myersja@hort.oregonstate.edu)

Published DNA sequences for the arcelin - phytohaemagglutinin - α-amylase inhibitor locus from common and tepary bean were compared to new sequences identified in tepary accessions G40199 and Brown Tepary. Phylogenetic analysis demonstrated that the arcelin variants from different tepary sources clustered together but was clearly separated from the arcelins of common bean. In contrast, phytohaemagglutinins from both species were closely related as were the α-amylase inhibitors. Our data supports the derivation of arcelin and α-amylase inhibitor loci from phytohaemagglutinin prior to the separation of the species.

P-26 MOLECULAR CHARACTERIZATION OF *Colletotrichum lindemuthianum* HAPLOIDS AND DIPLOIDS.

Gonçalves-Vidigal, M.C.[1*], P.S. Vidigal Filho[1], A. Gonela[1], G.F. Lacanallo[1], M.A.A Castro-Prado[2], C.B. Querol[2]. [1]Dep. Agronomia, [2]Dep. Biologia, Universidade Estadual de Maringá, PR, Brazil. [*]Presenter (mvidigal@pop.com.br)

The analysis of auxotrophics mutants of races 2047 and 23 using RAPD molecular markers demonstrated that the recombinant Rec4 presented a band of 800bp in mutant 23.19, and another band of approximately 750bp which is present in 2047.4 mutant when analyzed with OPF5 primer. However, analyses conducted with OPC08 primer exhibited a band of 1300bp in diploid 23.14//23.15, but absent in race 23. The recombinant Rec6 has showed a band of 350bp and another of 800bp, being polymorphic in relation to 2047.4//23.19 diploid. The Rec4 recombinant had revealed to be polymorphic in relation to 23.14//23.15 diploid once it possesses a band of 1000bp.

P-28 EVAPOTRANSPIRATION AND WATER USE EFFICIENCY FOR COMMON BEAN GENOTYPES UNDER NON-STRESS AND DROUGHT STRESS CONDITIONS.

Ramirez B., V.H.[1], T.G. Porch[2]* and E.W. Harmsen[1]. [1]Department of Agricultural and Biosystems Engineering, University of Puerto Rico, Mayaguez, PR, [2]USDA/ARS/TARS, Mayaguez, PR. *Presenter (timothy.porch@ars.usda.gov)

Field and greenhouse experiments were conducted to determine evapotranspiration coefficients and drought stress response at different levels of intermittent drought stress in six common bean genotypes. Evapotranspiration was estimated by the generalized Penman-Monteith model with variable aerodynamic and surface resistance, and by the use of drainage lysimeters. Drought response was evaluated in terms of yield components, water use efficiency, and the crop water stress index.

P-30 MOLECULAR CHARACTERIZATION OF *RHIZOCTONIA SOLANI* ISOLATES FROM WESTERN NEBRASKA DRY BEANS.

Venegas, J.[1*], J.R. Steadman[1] and C. Urrea[1]. [1]University of Nebraska-Lincoln, Lincoln, NE. [*]Presenter (jvenega1@bigred.unl.edu)

Rhizoctonia solani is one of the main pathogens that cause bean root and crown rot in Western Nebraska production fields. However, there have not been reports for this region on the different anastomosis groups (AGs) and subgroups involved in causing disease. Fifty-nine *R. solani* isolates collected from five Western Nebraska counties were analyzed with *R. solani* specific and polymorphic molecular markers. Isolates were able to be assigned to AG-1-ID, AG-2-2IIIB, AG-2-2IV, AG-2-2LP, and AG-4 based on use of the specific markers, and the phylogenetic analysis based on polymorphic markers confirmed the AG clusters.

P-32 A NEW APPLICATION FOR SCAR MARKER sAE19$_{890}$.

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***Presenter (LiebenbergM@arc.agric.za)**

Molecular markers are becoming increasingly important in resistance breeding. The common bean rust resistance genes *Ur-3* and *Ur-11*, linked in coupling, have been introduced into a number of breeding lines originating from the USDA-ARS-Vegetable Lab, Beltsville. Indications have been found that the SCAR marker sAE19$_{890}$, linked in repulsion to *Ur-11*, but present in some lines containing *Ur-3* such as NEP 2 and Aurora, may be useful as a coupling marker for the gene block *Ur-(3+11).*

P-34 SELECTION OF MARKERS FOR MAPPING AND CLONING DISEASE RESISTANCE IN COMMON BEAN.

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Parents of seven mapping populations were screened for polymorphism with 92 primer pairs, of which 37 were generated from eight complete coding sequences (CDs) of NBS-LRR in *Phaseolus*, 34 SSRs developed from coding and non-coding sequences of common bean, and 21 CAPs and dCAPs developed by analyzing TC (tentative consensus) sequences of common bean. Forty-nine percent (49%) of these primers were polymorphic across different parental combinations, and CPAs and dCAPS markers were found to be highly polymorphic (76%) followed by SSRs (64%), and NBS-LRR types. This project will contribute to strengthening common bean genomic resources and generating molecular markers for tagging disease resistance traits in common bean.

P-36 PHYTOCHEMICAL EQUIVALENCE OF BLACK BEAN CULTIVARS TO Negro 8025, AN OUTSTANDING CULTIVAR ON REDUCING CHRONICALLY DEGNERATIVE DIEASES IN RATS.

Guzmán-Tovar, I., E. Almanza-Aguilera, A. Mora-Avilés, J.A. Acosta-Gallegos*, and S.H. Guzmán-Maldonado. CEBAJ-INIFAP. Celaya, Guanajuato, Mexico.
***Presenter (acosta.jorge@inifap.gob.mx)**

The consumption of black seeded cultivar Negro 8025 reduces the presence of colon cancer tumors as well as levels of blood glucose and cholesterol in rats. Different phytochemicals are responsible of such effects. Given the difficulty to asses the biological effect of all black bean cultivars that are consumed, we hypothesize that if the phytochemical profile of black cultivars were similar to that of Negro 8025, then the same physiological effect may be observed. Different black seeded cultivars displayed from 10 to 150 % higher concentration of some phytochemicals as compared to Negro 8025.

P-38 ANALYSIS OF ELEMENTS IN COMMON BEAN (*Phaseolus vulgaris* L.) THAT PROMOTE AND INHIBIT IRON ASSIMILATION.

Espinosa-Huerta E., J.A. Acosta-Gallegos*, H.S. Guzmán-Maldonado, M.A. Mora-Avilés. CEBAJ-INIFAP. Celaya, Guanajuato, Mexico. *Presenter (acosta.jorge@inifap.gob.mx)

Previous trials have shown that common bean leaves are an exceptional source of iron; leaf tissue has up to 9 to 12-fold more iron than the seed. There are different elements that inhibit (tannins and phytates) and promote (organic acids, Ca and Zn) iron assimilation. Leaves have higher levels (from 5 to 12 times) of elements that promote iron assimilation than seeds, and those elements that inhibit iron assimilation are present in smaller amounts (2 to 20 less than in seeds).