BIENNIAL MEETING OF THE

THE BEAN IMPROVEMENT COOPERATIVE

TWENTIETH BIENNIAL

Program and Abstracts

Hilton Garden Inn
Fort Collins, Colorado
October 25-28, 2009

Sponsors

Platinum

ADM Edible Bean Specialties, Inc.
Bush Brothers & Company
Harris Moran Seed Company

Gold

Seminis Vegetable Seeds, Inc.
Syngenta Seeds, Inc.

Silver

BASF Corporation
Northern Feed & Bean
Seneca Foods Corporation
Trinidad Benham Corporation

Bronze

Central Bean Company
Crites Seed, Inc
Jack's Bean Company
Kelley Bean Company
Michigan Bean Commission
Servi-Tech

BIC LOCAL ARRANGEMENTS COMMITTEE

Howard F. Schwartz, Co-Chair – Colorado State University
Mark A. Brick, Co-Chair – Colorado State University

BEAN IMPROVEMENT COOPERATIVE
20TH BIENNIAL MEETING (2009)
Fort Collins, Colorado

PROGRAM OVERVIEW

Sunday Oct. 25, 2009
BIC Registration 4:00 pm until 8:00 pm

Monday October 26

BIC Registration	7:00 am	9:00 am
Breakfast Buffet:Ballroom Hallway	7:00 am	8:00 am
Welcome & Introductions	8:15 am	8:30 am
Frazier-Zaumeyer Lectures	8:30 am	9:45 am
Break	9:45 am	10:00 am
Beans for Health Symposium	10:00 am	12:10 pm
Lunch: Ballroom Hallway	12:10 pm	1:00 pm
Oral Sessions	1:15 pm	6:00 pm
Break	3:10 pm	3:40 pm
Poster Session	8:00 am to 5:00 pm	
Dinner on your own		

Tuesday October 27

Breakfast Buffet:Ballroom Hallway	7:00 am	8:00 am
Oral Session	8:15 am	12:00 pm
Break: Hallway	10:15 am	10:30 am
Lunch :Ballrooom Hallway	12:00 pm	1:00 pm
Oral Session	1:15 pm	5:00 pm
Break	3:00 pm	3:30 pm
Poster Session	8.00 am	5:00 pm
Awards Banquet - Ballroom		
Cocktails	6:00 pm	7:00 pm
Dinner	7:00 pm	8:00 pm
Speaker & Awards Program	8:00 pm	9:15 pm

Wednesday Oct. 28, 2009

Breakfast Buffet: Banquet Hallway	7:00 am	8:00 am
BIC Business Meeting	8:30 am	9:30 am
Break	9:30 am	10:00 am
Phaseolus CGC	10:00 am	11:00 am
BIC Genetic Committee	11:00 am	12:00 pm
Lunch on your own	12:00 pm	1:30 pm
W-1150 Meeting	1:30 pm	5:30 pm

BEAN IMPROVEMENT COOPERATIVE
20 TH BIENNIAL MEETING (2009)
Fort Collins, Colorado

Monday, October 26

Main Ballroom

7:00 AM – 8:00 AM **Breakfast Buffet**

FRAZIER-ZAUMEYER DISTINGUISHED LECTURESHIP

TIME (am)	TITLE/PRESENTER
8:15-8:20	**Howard Schwartz-** Welcome Address
8:20-8-30	**James Kelly** – Introduction of the 2009 Frazier-Zaumeyer Awardees
8:30-9:00	**Maurice Bennink** – Professor, Food Science and Nutrition, Michigan State University. “**HEALTH BENEFITS ASSOCIATED WITH CONSUMPTION OF DRY BEANS**”
9:00-9:30	**Henry Thompson** – Professor, Horticulture and Landscape Architecture, Director Cancer Prevention Lab., Colorado State University. **STRATEGIC APPROACHES TO TAPPING THE HUMAN HEALTH POTENTIAL OF COMMON BEAN (*PHASEOLUS VULGARIS L.*)**
9:30-9:45	**QUESTIONS AND DISCUSSION**
9:45-10:00	**BREAK**

BEANS FOR HEALTH SYMPOSIUM

Moderator: Mark Brick, Colorado State University

TIME (AM)	**ABSTRACT NO.**	**TITLE/PRESENTER**
10:00-10:20	**O-01**	**BEAN CONSUMPTION AS A MARKER OF CULTURAL IDENTITY**. D.M. Winham. Nutrition Program, College of Nursing and Health Innovation, Arizona State University
10:20-10:40	**O-02**	**BEANS REDUCE GLYCEMIC RESPONSE AS PART OF A RICE MEAL**. A.M. Hutchins. Department of Health Sciences, University of Colorado at Colorado Springs, CO.
10:40-11:00	**O-03**	**CALCIUM NUTRITION AND BIOAVAILABILITY OF SNAP BEANS: STUDIES IN PLANT AND HUMAN NUTRITION.** M.A. Grusak. USDA-ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX.
11:00-11:20	**O-04**	**INHERITANCE OF SEED MINERAL AND PHYTATE CONCENTRATION IN COMMON BEAN** M. W. Blair. CIAT – International Center for Tropical Agriculture, A.A. 6713, Cali, Colombia.
11:20-11:40	**O-05**	**QUALITATIVE METABOLOMICS OF CANCER PREVENTION IN *Phaseolus vulgaris L.*** M.M. Mensack. Cancer Prevention Laboratory, Department of Horticulture & Landscape Architecture, Colorado State University
11:40-12:00	**O-06**	**FOOD TRENDS IMPACTING THE BEAN INDUSTRY.** S. Rose. Vice President and Director, Strategic Business Development, Bush Brothers & Company.
12:00-12:10		**QUESTIONS AND DISCUSSION**
12:10-1:00		**BUFFET LUNCH**

ORAL SESSIONS (*Student Presentations)
PRODUCTION/SEED QUALITY/GERMPLASM
Moderator: Juan M. Osorno, North Dakota State University

TIME (PM)	ABSTRACT NO.	TITLE/PRESENTER
1:15-1:30	**O-07**	**EFFECT OF SOIL COMPACTION AND IRRIGATION MANAGEMENT IN DRY BEAN PRODUCTION.** Carlos A. Urrea. University of Nebraska-Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE.
1:30-1:45	**O-08**	***FARMER CHOICES AND ENVIRONMENTAL ADAPTATION OF *PHASEOLUS* BEAN SPECIES IN OAXACA, MEXICO.** M.L. Worthington. Department of Plant Sciences, University of California, Davis, CA.
1:45-2:00	**O-09**	**PRODUCTIVITY INCREASE IN COMMON BEAN FROM SANTA CATARINA STATE.** H.T. Elias. Epagri/GPI Floranópolis, Santa Catarina, Brazil.
2:00-2:15	**O-10**	***DRY BEAN YIELD LOSS OF COMMERCIAL VARIETIES UNDER CONDITIONS OF DIRECT HARVESTING**. F.R. Eckert. Department of Plant Sciences, North Dakota State University, Fargo, ND.
2:15 -2:30	**O-11**	**DETERMINING RESISTANCE TO OXIDATION OF PINTO BEAN GENOTYPES DEVELOPED AT INIFAP-MEXICO USING A UVC LIGHT TREATMENT.** R.A. Salinas. Bean Breeding Program. INIFAP, Sinaloa, México.
2:30-2:45	**O-12**	***PHENOTYPIC CHARACTERIZATION OF CONDENSED TANNIN ACCUMULATION DURING SEED COAT DEVELOPMENT.** H. Elsadr. Department of Plant Sciences, Saskatoon, SK, S7N 5A8.
2:45-3:00	**O-13**	**PHENYLPROPANOID PATHWAY GENE EXPRESSION PATTERNS ASSOCIATED WITH NON-DARKENING IN CRANBERRY BEANS.** K. P. Pauls. Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.
3:00-3:10		**QUESTIONS AND DISCUSSION**
3:10-3:40		**BREAK (MEET THE POSTER AUTHORS)**

GENETICALLY MODIFIED BEANS

Moderator: James Beaver, University of Puerto Rico, Mayaguez, PR

3:40-4:10 **O-14** **GENETIC ENGINEERING APPLIED TO COMMON BEAN.** Francisco J. L. Aragão. Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil.

4:10-4:30 **O-15** **GENETIC ENHANCEMENT AND ITS POTENTIAL IMPACT ON GROWERS AND THE MARKETING OF GM BEAN PRODUCTS**. R. Green. Executive Director, Michigan Bean Commission, St. Johns MI 48879 (green@4wbi.net)

4:30-4:50 **O-16** **TRANSFORMATION OF COMMON BEAN: THE STATE OF THE ART.** Timothy Porch. USDA ARS SAS TARS, 2200 P.A. Campos Ave. Suite 201, Mayaguez, Puerto Rico. Presenter (Timothy.Porch@ars.usda.gov)

LEGUME IPM PIPE/BEAN CAP

4:50-5:30 **O-17** **Legume ipmPIPE — A NEW OPTION for GENERATING, SUMMARIZING and DISSEMINATING REAL-TIME PEST DATA to STAKEHOLDERS.** H.F. Schwartz, Colorado State University, Fort Collins, CO

5:30-6:00 **O-18** **THE BEAN CAP AND PHASEOLUS SEQUENCING PROJECTS.** P.E. McClean. Department of Plant Sciences, North Dakota State University, Fargo, ND.

DINNER ON YOUR OWN

Tuesday, October 27

7:00 AM – 8:00 AM **Breakfast Buffet served in Hallway**

ORAL SESSION (*Student Presentations)
GENETICS/BREEDING/PATHOLOGY
Moderator: Phillip Griffiths, Cornell University

TIME (am)	ABSTRACT NO.	TITLE/PRESENTER
8:15-8-30	**O-19**	**YIELD POTENTIAL FROM INTERSPECIFIC CROSSES OF COMMON AND RUNNER BEAN.** S. Beebe. Bean Program, CIAT, Cali, Colombia
8:30-8:45	**O-20**	**CLONING THE MAJOR CBB RESISTANCE QTL OF COMMON BEAN -CURRENT STATUS AND FUTURE PROSPECTS.** K. Yu. GPCRC, AAFC, Harrow, ON. Canada.
8:45-9:00	**O-21**	**DEVELOPMENT OF *PhaseolusGenes,* A GENOME DATABASE FOR MARKER DEVELOPMENT IN *Phaseolus vulgaris*.** P. Gepts. Department of Plant Sciences, University of California, Davis
9:00-9:15	**O-22**	***UTILIZING SYNTENY BETWEEN *Phaseolus vulgaris* AND *Glycine max* AS A MEANS OF REFINING GENOME FUNCTION AND STRUCTURE.** S. Repinski. Department of Plant Sciences, University of California - Davis, CA.
9:15-9:30	**O-23**	**EVOLUTION OF THE EUROPEAN BEAN FROM THEIR AMERICAN ANCESTORS**. M. De La Fuente. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, Spain.
9:30-9:45	**O-24***	***DEVELOPMENT AND SCREENING OF BIBAC LIBRARIES FROM TWO SOURCES OF CBB RESISTANCE IN *P. VULGARIS*.** G. Perry. University of Guelph, Guelph ON, Canada
9:45-10:00	**O-25**	**MARKER-ASSISTED PYRAMIDING OF RESISTANCE TO COMMON BACTERIAL BLIGHT AND ANTHRACNOSE IN NAVY BEAN.** A. Hou. Agriculture and Agri-Food Canada, Morden Research Station, Morden, MB.
10:00-10:15		**QUESTIONS AND DISCUSSION**

10:15-10:30		**BREAK**
		Moderator: Timothy Porch, USDA-ARS
10:30-10:45	**O-26**	**INHERITANCE AND ALLELIC RELATIONSHIPS OF ANTHRACNOSE RESISTANCE IN ANDEAN COMMON BEAN PITANGA.** M.C. Gonçalves-Vidigal. Dep. Agronomia, Universidade Estadual de Maringá, Paraná, Brazil.
10:45-11:00	**O-27**	**SUCCESSES AND CHALLENGES OF THE BEAN BREEDING PROGRAMME OF THE ARC-GRAIN CROPS INSTITUTE, SOUTH AFRICA**. D. Fourie. Agricultural Res. Council – Grain Crops Institute, Potchefstroom, South Africa.
11:00-11:15	**O-28**	***STAYGREEN* IS A CANDIDATE FOR THE PERSISTENT COLOR (PC) IN COMMON BEAN.** J.R. Myers. Department of Horticulture, Oregon State University, Corvallis, OR.
11:15-11:30	**O-29**	**POTYVIRAL VPG-INTERACTING PROTEINS AND *BEAN COMMON MOSAIC VIRUS* RESISTANCE IN *PHASEOLUS VULGARIS* L.** Masoud Naderpour. Department of Genetics and Biotechnology, University of Aarhus, Denmark.
11:30-11:45	**O-30**	**A POSSIBLE ROLE FOR *BC-U* IN *BC-U, BC-3* GENE COMBINATION IN RESISTANCE TO *BEAN COMMON MOSAIC VIRUS* IN *PHASEOLUS VULGARIS* L.** Masoud Naderpour. Department of Genetics and Biotechnology, University of Aarhus, Denmark.
11:45:12:00	**O-31**	**GENETIC DIVERSITY IN CANADIAN CONTEMPORARY COMMON BEAN: A PEDIGREE ANALYSIS.** A. Navabi. Agriculture and Agri-Food Canada, Department of Plant Agriculture, University of Guelph, Guelph, ON
12:00-12:10		**QUESTIONS AND DISCUSSION**
12:10-1:15		**BUFFET LUNCH**

Tuesday Afternoon

Moderator: Rubella S. Goswami, North Dakota State University

1:15-1:30	**O-32**	**MAPPING OF RESISTANCE TO *PEANUT MOTTLE VIRUS* IN COMMON BEAN.** R.C. Larsen. USDA-ARS, Prosser, WA.
1:30-1:45	**O-33**	**VIRUS SURVEILLANCE IN BEANS USING TISSUE BLOT IMMUNOASSAY: THREE YEARS EXPERIENCE OF THE LEGUME IPM-PIPE.** Sue A Tolin. Virginia Polytechnic Institute and State University, Blacksburg, VA
1:45-2:00	**O-34**	**CHARACTERIZATION OF RHYNCHOSIA MILD MOSAIC VIRUS (RHMMV), A NEW WHITEFLY-TRANSMITTED GEMINIVIRUS OF LEGUMES, AND RESULTS OF A 2009 SURVEY OF BEGOMOVIRUSES INFECTING ENDEMIC HOSTS IN PUERTO RICO.** J. K. Brown. School of Plant Sciences, The University of Arizona, Tucson, AZ.
2:00-2:15	**O-35**	**SELECTION FOR WHITE MOLD RESISTANCE IN COMMON BEAN.** S.P. Singh. University of Idaho, Kimberly, ID
2:15-2:30	**O-36**	**AGRONOMIC AND ECONOMIC ASSESSMENT OF INTENSIVE PEST MANAGEMENT IN DRY EDIBLE BEAN: WHITE MOLD EXPERIMENT**. G.M. Pynenburg. Department of Plant Agriculture, University of Guelph, Guelph, ON.
2:30-2:45	**O-37**	**CHARACTERIZATION OF THE RUST RESISTANCE GENE PRESENT IN THE COMMON BEAN CULTIVAR 'OURO NEGRO', THE MAIN RUST RESISTANCE SOURCE USED IN BRAZIL.** T.L.P.O. Souza. BIOAGRO, Federal University of Viçosa, Viçosa, MG, Brazil
2:45-300		**QUESTIONS AND DISCUSSION**
3:00-3:30		**BREAK (MEET THE POSTER AUTHORS)**

Moderator: Phil Miklas, USDA-ARS

3:30-3:45	**O-38**	**EVALUATION OF SNAP BEAN GENOTYPES COMBINING RUST RESISTANCE AND HEAT TOLERANCE TRAITS IN EAST AFRICA.** Charles J Wasonga. Dept. Horticultural Sciences, Cornell University NYSAES, Geneva, NY.
3:45-4:00	**O-39**	**CURRENT STATUS OF *UROMYCES APPENDICULATUS* IN BULGARIA.** Magdalena Beleva. Legume Crops Breeding, Dobrudzha Agriciltural Institute- General Toshevo, Bulgaria.
4:00-4:15	**O-40**	**REACTION OF COMMON BEAN CULTIVARS TO NEW RACES OF THE BEAN RUST PATHOGEN FROM MICHIGAN AND NORTH DAKOTA AND TO OTHER IMPORTANT RACES.** M.A. Pastor-Corrales. Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD
4:15-4-30	**O-41**	**THE CONNECTIONS BETWEEN SOIL HEALTH AND ROOT HEALTH.** George S. Abawi. Department of Plant Pathology, NYSAES, Cornell University, Geneva, NY.
4:30-4:45	**O-42**	**DRY EDIBLE BEAN PATHOGENS PREVALENT IN NORTH DAKOTA WITH SPECIAL EMPHASIS ON ROOT ROTS.** R.S. Goswami. R.S., Department of Plant Pathology, North Dakota State University, Fargo, ND.
4:45-5:00		**QUESTIONS AND DISCUSSION**

Awards Banquet –Hotel Ballroom

6:00 -7:00 pm	Cocktails and Social Hour- Hotel Lobby
7:00 -8:00 pm	Dinner-Main Ballroom
8:00 -9:15 pm	Presentation of Awards- BIC President Jim Kelly Graduate Student Presentations Frazier-Zaumeyer Distinguished Lectureship Award BIC Meritorious Service Award

Guest Speaker: Dr. Kathleen Pickering, Professor and Chair
Department of Anthropology, Colorado State University

"Beans, Corn and Squash: Native American Food Systems Past and Present"

POSTER SESSION (*Student Posters)
HOTEL BALLROOM AND FOYER
8:00 am to 5:00 pm Monday and Tuesday
AUTHORS PRESENT: Monday and Tuesday Afternoon Breaks

POSTER/ ABSTRACT NO.	Title/Authors
P-01	**EVALUATION OF LIMA BEAN LANDRACES FROM PUERTO RICO.** Luís Ruíz[1], James Beaver[1*] and Emmalea Ernest[2]. [1]Dept. of Crop & Agro-Environmental Sci., Univ. de Puerto Rico Mayagüez, PR 00681; [2]Univ. of Delaware, Research and Education Center, 16483 County Seat Highway, Georgetown, DE 19947. Presenter (James.Beaver@upr.edu)
P-02	**GENETIC DIVERSITY OF MESOAMERICAN AND ANDEAN WILD BEANS USING MICROSATELLITE MARKERS.** Galván MZ[1,2*], Hufford M[1], Worthington M[1], Balatti P[3], Menéndez Sevillano M[2], Farreyra M[2] and Gepts P[1]. [1]Department of Plant Sciences, University of California, Davis, CA; [2]EEA INTA Salta, Argentina; [3]University of La Plata, Argentina. *Presenter (martazgalvan@gmail.com)
P-03*	**SCREENING BEAN GENOTYPES FOR ENHANCED N FIXING ABILITY.** Heilig, J.A.[1*] and J.D. Kelly PhD[1]. [1]Dept of Crop and Soil Sciences, Michigan State University, East Lansing, MI. *Presenter (heiligja@msu.edu)
P-04	**SEED COAT PIGMENTATION TRAITS OF BLACK AND RED BEAN PHENOTYPES.** Marles, M.A.S. [1], Balasubramanian, P. [2] and Bett, K.E. [1*], [1]Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada; [2] Agriculture and Agri-Food Canada, Lethbridge Research Centre 5403 - 1 Ave. S., Lethbridge, Alberta T1J 4B1 *Presenter (k.bett@usask.ca)
P-05	**PLANT GENETIC RESOURCES NETWORK OF INTA-ARGENTINA**. Menéndez Sevillano, M.C[1], Clausen A.M.[2], Ferrer, M.E.[3], Rosso B.[4] and Ferreyra, M.J.[1]*. [1]EEA-Salta, [2]EEA-Balcarce, [3]Instituto de Recursos Biológicos-Castelar, [4]EEA-Pergamino. INTA. Argentina. *Presenter (mferreyra@correo.inta.gov.ar)
P-06	**THE GERMPLASM ACTIVE BANK OF EEA-INTA AT SALTA**. Menéndez Sevillano, M.C., Ferreyra, M.*, Ibarra, L. EEA-INTA, Salta. Argentina. *Presenter (mferreyra@correo.inta.gov.ar)
P-07	**THE GENE CONTROLLING SLOW- DARKENING IN PINTOS IS NOT *J*.** Bett, K.E.* and Elsadr, H. Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK, S7N 5A8. *Presenter (k.bett@usask.ca)

P-08 ***PHENOTYPIC EVALUATION OF A DRY BEAN MAPPING POPULATION FOR RESISTANCE TO POTATO LEAFHOPPER.** Brisco, E.I.[1]*, T.Porch[2], and J.D. Kelly[1]. [1]Department of Crop and Soil Sciences, Michigan State Univ East Lansing, MI. [2]Tropical Agriculture Research Station, USDA, Mayaguez, PR. *Presenter (briscoel@msu.edu)

P-09 **PROGRESS IN PYRAMIDING WHITE MOLD RESISTANCE FROM ACROSS *PHASEOLUS* SPECIES IN COMMON BEAN.** Crane, L.[1*], H. Terán, H.F. Schwartz[2], K. Otto[2] and S.P. Singh[1]. [1]University of Idaho, 3793N 3600E, Kimberly, ID 83341; [2]Colorado State University, Fort Collins, CO 80523. [*]Presenter (lcrane@kimberly.uidaho.edu)

P-10 **GENETIC GAIN FOR SEED TRAITS IN SELECTION CYCLES IN RUNNER BEAN**. De Ron, A.M.*, M. De la Fuente, E.A. Pérez, and A.P. Rodiño. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, SPAIN. *Presenter (amderon@mbg.cesga.es)

P-11 ***PHENOTYPIC AND GENOTYPIC EVALUATION OF COMMON BACTERIAL BLIGHT RESISTANCE IN A RESISTANT INTER-CROSS POPULATION OF PHASEOLUS VULGARIS.** Durham, K.M.[1*], E.A. Lee[1], K.Yu[2], K.P. Pauls[1], and A. Navabi[1,2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada. [2] Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, Harrow, ON, Canada. *Presenter (kdurham@uoguelph.ca)

P-12 **LIMA BEAN BREEDING AT THE UNIVERSITY OF DELAWARE.** Ernest, E.G.[1]* [1]Department of Plant and Soil Sciences, University of Delaware, Georgetown, DE. *Presenter (emmalea@udel.edu)

P-13 **MOLECULAR MARKERS LINKED TO ANGULAR LEAF SPOT RESISTANT GENES IN COMMON BEAN ACCESSIONS FROM BRAZIL AND AFRICA.** Vidigal Filho PS[1,2*], Gonçalves-Vidigal MC[1,2], Nchimbi-Msolla S[3], Namayanja A[4], Nsanzabera F[5], Kimani P[6], Kami J[2], & Gepts, P[2]. [1]Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil; [2]Univ. of California, Dep. of Plant Sciences, Davis, CA 95616-8780; [3]Sokoine University of Agriculture, Morogoro, Tanzania; [4]National Crops Resources Research Institute, Kampala, Uganda; [5]Institut des Sciences Agronomiques du Rwanda, Rubona, Rwanda; [6]University of Nairobi, Kabete Campus, Nairobi, Kenya [*]Presenter (pedro.vidigal@pop.com.br)

P-14 **YIELD EFFECT FOR TWO QTL CONTROLLING COMMON BACTERIAL BLIGHT RESISTANCE IN A NEAR-ISOGENIC DRY BEAN POPULATION.** Fourie, D.[1]*, and P. Miklas[2]. [1]ARC Grain Crops Institute, Potchefstroom, Republic of South Africa; [2]USDA-ARS, Vegetable and Forage Crop Research Unit, Prosser, WA. *Presenter (FourieD@arc.agric.za)

P-15 **RAPD MARKER LINKED TO ANTHRACNOSE RESISTANCE GENE *Co-13* IN ANDEAN CULTIVAR JALO LISTRAS PRETAS.** Lacanallo G.F.[1], Gonçalves-Vidigal M.G.[1*], A.K.S. Lobato[1], P.S. Vidigal Filho[1], A. Gonela[1]. [1*] Dep. Agronomia, Universidade Estadual de Maringá, Paraná, Brazil. *Presenter (mgvidigal@ucdavis.edu)

P-16 **GENETIC LINKAGE AND GENE MAPPING OF *PHG-1* AND *CO-1*^{4} RESISTANCE GENES TO ANGULAR LEAF SPOT AND ANTHRACNOSE IN THE COMMON BEAN AND 277 CULTIVAR.** Gonçalves-Vidigal[1*], M.C., A.S. Cruz[1], A. Garcia[1], P.S. Vidigal Filho[1] and M.A. Pastor-Corrales[2]. [1]Departamento de Agronomia, Universidade Estadual de Maringá, Maringá, Paraná, Brazil; [2]USDA-ARS, BARC-W, Beltsville, MD 20705. *Presenter (mgvidigal@ucdavis.edu)

P-17 ***DIFFERENTIATION OF APHID-TRANSMITTED VIRUSES IN SNAP BEANS USING REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION.** Hart, J.P.[1*] and P.D. Griffiths[1]. [1] Department of Horticultural Sciences, New York State Agricultural Experiment Station, Cornell University, Geneva, NY. *Presenter (jph248@cornell.edu)

P-18 **CONSTRUCTING A GUS-TAGGED INFECTIOUS CDNA CLONE OF *BEAN COMMON MOSAIC VIRUS*.** Masoud Naderpour[1*] and Elisabeth Johansen[1].[1]Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark. *Presenter (m.naderpour@dias.kvl.dk)

P-19 **MAPPING AND QTL ANALYSIS OF AGRONOMIC TRAITS IN COMMON BEAN : VALIDATION OF A HALO BLIGHT RESISTANCE QTL IN BEAN BREEDING PROGRAMS.** C. Robast*, P. Parmentier, P. Carreau, D. Peltier, C. Bonneau, B. Monsimier, N. Bourgeais, E. Belouard, P. Leveque, G. Tristan, M. Delisle. Vilmorin, La Ménitré, France. *Presenter (charlene.robast@vilmorin.com)

P-20 **IMP: A TOOL FOR INTRON PREDICTION COUPLED WITH PRIMER DESIGN TO AID IN MARKER DISCOVERY.** Sanderson, L., Vijayan, P., Alahakoon, I. and Bett, K.E.* Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK, S7N 5A8. *Presenter (k.bett@usask.ca)

P-21 **GENERATION MEANS ANALYSIS OF AGRONOMIC AND SEED QUALITY TRAITS IN COMMON BEAN** (*Phaseolus vulgaris* L.). Santalla, M.*, M.S. Saburido, A.P. Rodiño, M. Lores, A. Castro, M. De La Fuente. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, SPAIN. Presenter* (msantalla@mbg.cesga.es)

P-22 **COMPREHENSIVE LINKAGE MAP OF WHITE MOLD RESISTANCE QTL IN COMMON BEAN.** Soule, M.[1], P. Miklas[1]*, L. Porter[1], J. Medina[2], G. Santana[2] and M. Blair[2]. [1]USDA-ARS, Vegetable and Forage Crop Research Unit, Prosser, WA; [2]International Center for Tropical Agriculture – CIAT, Cali Colombia. (phil.miklas@ars.usda.gov)

P-23 **SINGLE NUCLEOTIDE POLYMORPHISMS (SNPs) DISCOVERY IN THE COMMON BEAN.** Souza, T.L.P.O.[1*], E.G. Barros[1], C.M. Bellato[2], E.-Y. Hwang[2], P.B. Cregan[2] and M.A. Pastor-Corrales[2]. [1]BIOAGRO, Federal University of Viçosa, Viçosa, MG 36570-000, Brazil. [2]Soybean Genomics and Improvement Laboratory, USDA/ARS, BARC-West, Beltsville, MD 20705, USA. [*]Presenter (tlposouza@gmail.com)

P-24 **PROGRESS IN BREEDING FOR WHITE MOLD RESISTANCE IN *PHASEOLUS VULGARIS* AT OREGON STATE UNIVERSITY.** Zimmerman, S.J. [1*], Myers, J.R.[1], Barrett, M.[1], Haggard, J.E.[1] and Gilmore, B.[1] [1]Department of Horticulture, Oregon State University, Corvallis, OR. Presenter (zimmerms@hort.oregonstate.edu)

P-25 **RESISTANCE TO HALO BLIGHT, COMMON BACTERIAL BLIGHT AND BACTERIAL BROWN SPOT IN SPANISH COMMON BEAN CORE COLLECTION**. Asensio, C.[1*], Asensio S-Manzanera, M.C. [1], Ibeas, A. [1] and De la Rosa, L. [2]Departamento de Hortofruticultura, ITACyL, Valladolid, Spain; [2]Centro Nacional de Recursos Fitogenéticos, Alcalá de Henares, Madrid, Spain. *Presenter (asevegma@itacyl.es)

P-26 **BACTERIAL WILT IN DRY BEAN AND INHERITANCE OF RESISTANCE TO THE DISEASE IN EARLY ROSE AND PI 136725.** Balasubramanian, P.M.[1]*, Conner, R.L.[2] and Hou, A.[2]. Agriculture and Agri-Food Canada, [1]Lethbridge Research Centre, Lethbridge, AB, [2]Morden Research Station, Morden, MB. *Presenter (parthiba.balasubramanian@agr.gc.ca)

P-27

BIOLOGICAL CONTROL OF PHYTOPATHOGENIC FUNGI IN BEAN (*Phaseolus vulgaris*, L.) WITH *Trichoderma atroviride* AND *Trichoderma virens.* Campelo[1], P., R.E. Cardoza[2], A. Lorenzana[1], M.R. Hermosa[3], E. Monte[3], S. Gutierrez[2], B. Reinoso, P.A. Casquero.[1]*. Areas of [1]Crop Production and [2]Microbiology, University of León. [3]Hispano-Portuguese Center for Agricultural Reseach, University of Salamanca. (Spain). *Presenter (pedro-casquero@unileon.es).

P-28

THE INTERACTION OF CHEMICAL CONTROLS FOR ANTHRACNOSE IN DRY BEANS. Gillard, C.L.[1*], S. Willis[1] and D. Depuydt[1]. University of Guelph, Ridgetown ON. [*]Presenter (cgillard@ridgetownc.uoguelph.ca).

P-29

GENETIC VARIABILITY OF POPULATIONS OF THE WEB BLIGHT PATHOGEN OF COMMON BEAN FROM CENTRAL AMERICA AND THE CARIBBEAN. N. Gonzalez[1], G. Godoy-Lutz[2], J. R. Steadman[1]*, S. McCoy[1] and B Higgins[1]. [1]Plant Pathology Department, University of Nebraska, Lincoln, NE and [2] Instituto Dominicano de Investigaciones Agropecuarias y Forestales . Dominican Republic. *Presenter (jsteadman1@unl.edu)

P-30

ALTERNATE HOSTS FOR THE DRY BEAN BACTERIAL WILT PATHOGEN IN WESTERN NEBRASKA? R. M. Harveson* PHREC, Scottsbluff and A. K. Vidaver, University of Nebraska, Lincoln. *Presenter (rharveso@unlnotes.unl.edu)

P-31

POTENTIAL ABILITY OF BACTERIAL BLIGHT PATHOGENS TO MOVE BETWEEN SOYBEAN AND DRY EDIBLE BEAN. Lamppa, R.S.*, Y.W. Chang, S.G. Markell, F. M. Mathew and R. S. Goswami. Department of Plant Pathology, North Dakota State University, Fargo, ND. *Presenter (robin.lamppa@ndsu.edu)

P-32

Legume ipmPIPE — A TOOL for DISEASE MANAGEMENT and EDUCATION in LEGUMES. M.A.C. Langham[1*], H.F. Schwartz[2], S.A. Tolin[3], C. Sutula[4], S. Ratcliffe[5], and K.F. Cardwell[6] [1]South Dakota State Univ., Brookings, SD; [2]Colorado State Univ., Fort Collins, CO; [3]Virginia Tech, Blacksburg, VA; [4]Agdia, Inc., Elkhart, IN; [5]Univ. of Illinois, Urbana, IL; [6]USDA-CSREES, Washington, DC [*]Presenter (marie_langham@sdstate.edu)

P-33

IMPROVEMENT IN SCREENING FOR RESISTANCE TO *SCLEROTINIA SCLEROTIORUM* IN COMMON BEAN THROUGH CHARACTERIZATION OF THE PATHOGEN. S. McCoy[1,] L. Otto-Hanson[2,] B Higgins1 and Steadman, J.R. [1*]. [1]Plant Pathology Department, Univ.of Nebraska, Lincoln, NE and 2 Plant Pathology Department, Univ. of Minnesota, St. Paul, MN. *Presenter (jsteadman1@unl.edu)

P-34

REACTION OF COMMON BEAN CULTIVARS AND LINES TO BACTERIAL BROWN SPOT IN SOUTH AFRICA. Muedi, H.T.H.[1]*, D. Fourie[1], & N.W. McLaren[2]. [1]ARC-Grain Crops Institute, Potchefstroom, South Africa; [2]University of Free State, Bloemfontein, South Africa. *Presenter (MuediH@arc.agric.za)

P-35

NEW RACES OF THE BEAN RUST PATHOGEN FROM MICHIGAN AND NORTH DAKOTA. Pastor-Corrales M.A[1*], J. D. Kelly[2], S.G. Markell[3], E.M. Wright[2], H.E. Awale[2], J.G. Jordahl[3], R.S. Lamppa[3], F.M. Mathew[3], J.M. Osorno[4], and R.S. Goswami[3]. [1*]Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD 20705, [2]Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI 20705, [3]Department of Plant Pathology and [4]Department of Plant Science, North Dakota State University, Fargo, ND 58108. *Presenter (talo.pastor-corrales@ars.usda.gov)

P-36

IDENTIFICATION OF SOURCES OF BACTERIAL WILT RESISTANCE IN COMMON BEANS (*Phaseolus vulgaris* L.). John A. Thomas*, Carlos A. Urrea, Robert M. Harveson, and Kathleen Nielsen. University of Nebraska- Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE. *Presenter (jthoma1@unlnotes.unl.edu)

P-37

ROW SPACING AND NITROGEN FERTILIZATION EFFECT ON ARCHITECTURAL TRAITS AND YIELD LOSS OF DRY BEAN VARIETIES UNDER DIRECT HARVEST. Eckert, F. R.[1*], H. J. Kandel, B. L. Johnson, G. A. Rojas-Cifuentes, A. J. VanderWal, C. Deplazes, and J. M. Osorno. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND, 58108-6050. *Presenter (fernando.eckert@ndsu.edu**)**

P-38

HYDRATION PATTERNS VARY IN DIVERSE DRY BEAN MARKET CLASSES AND CULTIVARS. Hou, A.,[1*] Conner, R.L.,[1] and Balasubramanian, P.M.[2.] Agriculture and Agri-Food Canada, [1]Morden Research Station, Morden, MB; [2]Lethbridge Research Centre, Lethbridge, AB. *Presenter (anfu.hou@agr.gc.ca)

P-39

EVALUATION OF RAISED SEEDBED ON DRY BEAN PRODUCTIVITY AND QUALITY CHARACTERISTICS FOLLOWING INTERMITTENT FLOODING. McAndrew, D.W.[1*] and R.L. Conner[1]. [1]Morden Research Station, Agriculture and Agri-Food Canada, Morden, MB. *Presenter (David.McAndrew@agr.gc.ca)

P-40 ***PERFORMANCE OF THREE MARKET CLASSES (PINTO, BLACK AND NAVY) ACROSS 24 YEARS IN MODERATE DROUGHT CONDITIONS IN THE NORTHERN PLAINS.** Angela M. Linares-Ramírez*[1], Juan M. Osorno[1], Gonzalo A. Rojas-Cifuentes[1], Steve Zwinger[2], and Blaine G. Schatz[2] [1]*Department of Plant Sciences, North Dakota State University, Fargo, ND 58108*[2]*Carrington Research and Extension Center, North Dakota State University, Carrington, ND 58421.* *Presenter (Angela.Linares@ndsu.edu)

P-41 **MOLECULAR CHARACTERIZATION OF KEY GENES FOR FOLATE SYNTHESIS IN COMMON BEAN.** W. Xie*, Y.S. Shim, F. Garabagi and K.P. Pauls. Department of Plant Agriculture, University of Guelph, Guelph, ON. *Presenter W. Xie (wxie@uoguelph.ca)

P-42 **SCREENING CULTIVARS OF *Phaseolus vulgaris* L. FOR HEALTH PROMOTING BENEFITS AND LONGEVITY EXTENSION IN *CAENORHABDITIS ELEGANS.*** Fitzgerald, V.K.*, Mensack, M.M., and Thompson, H.J. * Cancer Prevention Laboratory, Department of Horticulture & Landscape Architecture, Colorado State University, Fort Collins, CO. Presenter (vanessa.fitzgerald@colostate.edu)

P-43 **VARIATION IN REACTION TO FUSARIUM SPP. IDENTIFIED IN A COMMON BEAN (Phaseolus vulgaris L.) POPULATION DEVELOPED FOR FIELD-BASED RESISTANCE TO ROOT ROT.** M. G. Ronquillo-López, C. Grau, and J. Nienhuis*, Dep. of Horticulture, University of Wisconsin, Madison, WI. *****Presenter (nienhuis@wisc.edu)

Wednesday, October 28
Business Meetings-Main Ballroom

9:30 - 10:30 am	BIC Business Meeting-Main Ballroom
9:30 - 10:00 am	Break
10:00 - 11:00 am	Phaseolus CGAC Meeting-Main Ballroom
11:00 -12:00 pm	BIC Genetic Stocks Committee Mtg.-Board Room
12:00 – 1:30 pm	Lunch on your own
1:30 - 5:30 pm	W-1150 Meeting-Main Ballroom

Abstracts of Oral and Poster Presentations

FRAZIER-ZAUMEYER DISTINGUISHED LECTURESHIP

STRATEGIC APPROACHES TO TAPPING THE HUMAN HEALTH POTENTIAL OF COMMON BEAN (*PHASEOLUS VULGARIS L.*).

H.J. Thompson. Cancer Prevention Laboratory and Department of Soil & Crops Sciences, Colorado State University, Fort Collins, CO. *Presenter (henry.thompson@colostate.edu)

In many parts of the world, common bean is an underutilized staple food crop with remarkable yet unappreciated potential to reduce the risk for chronic diseases such as obesity, diabetes-type II, cardiovascular disease and cancer. Ongoing efforts to identify the QTL that account for human health beneficial properties of common bean will be presented including new approaches to screening of a RIL population using metabolomic profiling and a longevity extension assay in C. elegans. Assays being developed to evaluate common bean for traits related to plasma cholesterol reduction and for capacity to induce weight loss in a model of metabolic syndrome will also be discussed and candidate mechanisms for cancer inhibitory activity of common bean will be advanced.

HEALTH BENEFITS ASSOCIATED WITH CONSUMPTION OF DRY BEANS.

M.R. Bennink, Food Science and Human Nutrition, Michigan State University, East Lansing, MI. *Presenter (mbennink@msu.edu)

The nutritional importance of beans for North Americans extends far beyond simple provision of nutrients. The most significant public health problem in North America today and for at least the next 10 years is excess weight and obesity which directly increase Type II diabetes. There is strong evidence that eating diets with a low glycemic index (< 45), a low glycemic load (<100 g equivalents per day), and more than 25g per day of unavailable carbohydrate will help normalize blood glucose, blood insulin and body weight. Controlling these factors will in turn reduce the incidence of type 2 diabetes, cardiovascular diseases and cancer in certain parts of the body. Beans are the perfect food to improve glycemic control. Beans have a low glycemic index (27-42% relative to glucose) and they are rich in non-starch polysaccharides (typically 18-20%), resistant starch (5%), and oligosaccharides (4%) to give a dietary fiber value of 27 - 29%. Substituting beans for foods prepared from white flour (on an equal dry weight basis) will reduce the glycemic index of the diet by about two-thirds and glycemic load by about 80%. Inhibition of cancer and heart disease is likely related to altered gene expression. Feeding beans will reduce chemically-induced colon cancer in rodents by 50 –65%. Altered gene expression in colon mucosa suggests that colon cancer reduction is related to an improved mucosal barrier to gut microbes and antigens and a consequent reduction in inflammation in the mucosa. Eating beans will cause a small decrease in blood cholesterol, but this decrease is insufficient to explain the reduction in heart disease noted in epidemiologic studies. It is more likely that bean phytochemicals exert a direct effect on cardiac cells leading to altered cell metabolism and a decrease in the incidence of heart disease.

Oral Presentations - Monday, October 26

O-01 BEAN CONSUMPTION AS A MARKER OF CULTURAL IDENTITY. Winham, D.M. Nutrition Program, College of Nursing and Health Innovation, Arizona State University, Mesa, AZ. (dwinham@asu.edu)

Legumes are part of the traditional diet pattern in most cultures. With immigration, dietary acculturation, and increased access to prepared foods, ethnic groups may reduce their staple food consumption including their use of beans. Two ethnic or minority groups are responsible for the largest market shares of pinto beans (Hispanics) and black-eyed peas (African Americans) in the US. Survey data will be presented regarding the on consumption patterns, taste preferences, and attitudes toward beans expressed by low-income Mexican American women, and two groups of African Americans in the Southwest. Results suggest a variety of barriers for retaining beans in the diet, but high knowledge of the health benefits of beans among African Americans. Similar issues with taste preference, preparation time, and desire for already processed foods may be barriers to retention of beans in the diets of people in developing countries undergoing the nutrition transition.

O-02 BEANS REDUCE GLYCEMIC RESPONSE AS PART OF A RICE MEAL. Hutchins, A.M.[1]* and Winham, D.M[2]. [1]Department of Health Sciences, University of Colorado at Colorado Springs, Colorado Springs, CO. [2]Department of Nutrition, Arizona State University, Mesa, AZ. *Presenter (ahutchin@uccs.edu)

Legume or dry bean consumption may be beneficial in the prevention and treatment of diabetes and diabetes-related diseases, including coronary heart disease (CHD) and metabolic syndrome. The low glycemic response of beans alone has been documented, but little research has been conducted on the glycemic response to traditional food combinations such as black beans and rice, or chickpeas and rice. The results of a series of studies we conducted that examined the effects of bean consumption in combination with a high glycemic index food on glycemic response will be discussed.

O-03 CALCIUM NUTRITION AND BIOAVAILABILITY OF SNAP BEANS: STUDIES IN PLANT AND HUMAN NUTRITION. Grusak, M.A.[1*] and S.A. Abrams[1]. [1]USDA-ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX. *Presenter (mgrusak@bcm.tmc.edu)

Calcium (Ca) is an essential human nutrient that is important in bone growth and metabolism. Snap beans are a potential source of dietary Ca, but the bioavailability of Ca from this food has not been determined. To assess snap bean Ca absorption, we grew plants hydroponically and labeled them intrinsically with the stable isotope, ^{42}Ca. Thirteen teenage subjects (7 girls, 6 boys) were recruited for a two-week stay in our Metabolic Research Unit and were fed ^{42}Ca-labeled snap beans along with ^{48}Ca-enriched milk; an intravenous dose of ^{46}Ca was also administered. Blood, urine and fecal samples were collected during the two-week study. The bioavailability of Ca averaged 28% from snap beans, which was comparable to that of milk Ca. Because snap beans are a potentially good source of dietary Ca, we also have studied and will discuss the various processes that contribute to Ca accretion in developing snap bean pods. Our ultimate goal is to increase pod Ca concentrations and enhance the nutritional value of this food.

O-04 INHERITANCE OF SEED MINERAL AND PHYTATE CONCENTRATION IN COMMON BEAN M. W. Blair[1*], C. Astudillo[1], G. Caldas[1], T. Sandoval[1], S. E. Beebe[1], K. Cichy[2], M. A. Grusak[3] and R. Graham[4] [1]CIAT – International Center for Tropical Agriculture, A.A. 6713, Cali, Colombia.; [2]Department of Agronomy, USDA/Michigan State Univ., Lansing MI, USA; [3]Department of Pediatrics, Baylor College of Medicine, USDA-ARS Children's Nutrition Research Center, Houston TX, USA; [4]Department of Plant Science, University of Adelaide, Glen Osmond, SA, 5064, Australia; *Presenter (m.blair@cgiar.org)

Micronutrients are essential elements needed in small amounts for adequate human nutrition and include the elements iron and zinc while phytate is a phosphorus storage molecule that can have an anti-nutritional role by affecting micronutrient absorption. The objective of our research has been to determine the inheritance of seed iron, zinc and phytate accumulation through QTL analyses with crosses of low × high mineral genotypes. A recombinant inbred population was analyzed with two analytical methods (ICP and AAS) and variability in seed mineral concentration among the lines was larger for iron (40.0–84.6 ppm) than for zinc (17.7–42.4 ppm) with significant correlations between methods and between minerals. While QTL for phytates and minerals were distributed around the genome, one group of QTL for iron and zinc clustered on the upper half of linkage group B11, suggesting an important locus useful for marker assisted selection.

O-05 QUALITATIVE METABOLOMICS OF CANCER PREVENTION IN *Phaseolus vulgaris L.* Mensack, M.M.[1,] *, Fitzgerald, V.K.[1], McGinley, J.N.[1], Fischer, S.M.[2], and Thompson, H.J.[1]. [1]Cancer Prevention Laboratory, Department of Horticulture & Landscape Architecture, Colorado State University, Fort Collins, CO. [2] LC/MS Marketing, Agilent Technologies, Santa Clara, CA.

We have previously reported that *Phaseolus vulgaris L.* (common bean) inhibited experimentally-induced breast cancer by as much as 70% in female Sprague Dawley rats, an effect which is COD and market class dependent. The differences in cancer prevention activity are most likely due to variations in the small molecule (metabolite) profile of each market class. The work presented here begins to establish a metabolite profile of cancer prevention for common bean by comparing two market classes: white kidney bean (high cancer inhibitory activity) and navy bean (low cancer inhibitory activity). Clear differences in the metabolite profile of these common bean market classes were observed.

0-06 FOOD TRENDS IMPACTING THE BEAN INDUSTRY. Rose, Sara*. Vice President and Director, Strategic Business Development, Bush Brothers & Company. *Presenter (srose@bushbros.com)

Each year-end, food industry executives are bombarded with predictions for the upcoming year. The difficulty comes in separating fads from trends and in identifying the trends that have implications for ones' own industry. This presentation will identify the major forces impacting the food industry and implications for the bean industry.

O-07 EFFECT OF SOIL COMPACTION AND IRRIGATION MANAGEMENT IN DRY BEAN PRODCUTION.

Carlos A. Urrea*, C. Dean Yonts, and John Smith. University of Nebraska-Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE. *Presenter (currea2@unl.edu)

Limited data suggests that certain dry bean varieties or germplasm 'tolerate' soil water stress better than other varieties. In addition, soil compaction limits water use efficiency because it limits root performance and water infiltration. We evaluated these factors in combination to develop the optimal combination of variety, irrigation scheduling, and alleviation of compaction. Plots were established at Scottsbluff, NE that included combinations of variety, irrigation scheduling, and soil compaction. Four irrigation treatments were assigned to subplots, including full irrigation (100%), two limited irrigation schemes (75%, 50%), and no supplemental irrigation (0%). Nine varieties, Marquis, Matterhorn, 99-131, Emerson, Orion, Tara, Beryl-R, Roza, and UI-537 were assigned to the sub-plots. Yield was reduced significantly by 71% and 84% when soil was moderately and heavily compacted, respectively. On average yield was reduced by 35% when irrigation was reduced in 100%. In soils moderately and heavily compacted, UI-537 had the highest yield. Days to flowering and days to maturity were delayed by 2 and 3 days, and 11, and 9 when soils were moderately and heavily compacted, respectively.

O-08 FARMER CHOICES AND ENVIRONMENTAL ADAPTATION OF *PHASEOLUS* BEAN SPECIES IN OAXACA, MEXICO.

Worthington ML[1]*, Soleri D[2], and Gepts P[1].
[1]Department of Plant Sciences, University of California, Davis, CA. [2]Department of Environmental Studies, University of California, Santa Barbara, CA. *Presenter (mworthington@ucdavis.edu)

The smallholder farmers of highland Oaxaca regularly interplant a great diversity of bean landraces of three different species: common bean (*P. vulgaris*), runner bean (*P. coccineus*), and year bean [*P. dumosus* (= *P. polyanthus*)]. In this study we tested the hypothesis that the presence of these three bean species is a risk-mitigating strategy on the part of the farmers by conducting interviews and making germplasm collections from farmers' fields in the village of Santa Maria Jaltianguis in the Sierra Juárez. We then assessed the amount of genetic diversity present in those collections and investigated the role of farmers in encouraging or suppressing hybridization between the various landraces and *Phaseolus* species with cpDNA and nuclear DNA marker analysis.

O-09 PRODUCTIVITY INCREASE IN COMMON BEAN FROM SANTA CATARINA STATE.

Elias, H.T.[1*], G.A. Vogt[2], R.L. Backes[3], C.N. Nesi, S. Hemp[1]. [1*] Epagri/GPI Floranópolis, Santa Catarina, Brazil. [*]Presenter (htelias@epagri.sc.gov.br)

This work had as objective to determine the genetic progress obtained in common bean breeding programs carried out in Santa Catarina State through the periods of 1991 to 2009. A survey was made in order to monitor experiments results with different cultivars in the State. The annual average of genetic gain was superior than 1%, showing to be similar to those in common bean breeding programs in other regions of Brazil. Results demonstrated increase of bean productivity through both adoption of better adapted cultivars and improvement of production systems.

O-10 DRY BEAN YIELD LOSS OF COMMERCIAL VARIETIES UNDER CONDITIONS OF DIRECT HARVESTING.

Eckert, F. R.[1*], H. J. Kandel, B. L. Johnson, G. A. Rojas-Cifuentes, A. J. VanderWal, C. Deplazes, and J. M. Osorno. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND, 58108-6050. *Presenter (fernando.eckert@ndsu.edu)

The objective of this study was to evaluate the yield performance and market class (pinto, black, and navy) effect of dry beans varieties under conditions of conventional and direct harvest. Pinto beans had the greatest yield under conventional and direct harvest (2,101 and 1,337 kg ha^{-1}, respectively), followed by navy (1,831 and 990 kg ha^{-1}, respectively), and black beans (1,753 and 1,104 kg ha^{-1}, respectively) that yielded similarly. In general the black beans had the lowest yield loss% but they also had the lowest yield potential. The pinto variety Lariat had the greatest yield (1,738 kg ha^{-1}) and the lowest yield loss (21.68%) under direct harvest among all the varieties tested.

O-11 DETERMINING RESISTANCE TO OXIDATION OF PINTO BEAN GENOTYPES DEVELOPED AT INIFAP-MEXICO USING A UVC LIGHT TREATMENT.

Salinas, R.A., Bean Breeding Program. Campos Experimentales Valle del Fuerte, Valle del Yaqui and Costa de Hermosillo-INIFAP. Juan José Ríos, Sinaloa, México. *Presenter salinas.rafael@inifap.gob.mx.

In order to determine the oxidation rate of pinto bean lines developed in the National Bean Breeding Program at INIFAP (México), an experiment was carried out under controlled conditions, exposing one year old seeds for 72 hours to ultraviolet light at 254 nm (Model G40T10, Ushio America, Inc., Cypress, CA). Results indicate that several lines can be considered tolerant to oxidation, since these lines presented values after the light treatment between 1.67 to 3.33 (scale 1 to 9, where 1, no effect to oxidation, and 9, highly susceptible to oxidation). The check (UI 114) presented value of 7.67, which is considered susceptible to oxidation. The tolerant lines carry Andean genes on them.

O-12 PHENOTYPIC CHARACTERIZATION OF CONDENSED TANNIN ACCUMULATION DURING SEED COAT DEVELOPMENT.

Elsadr H. [1]*, Caldas G. [2], Blair M.W. [2], Marles M.A.S[1]. and Bett K.E. [1] [1]Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK, S7N 5A8. [2] CIAT, Cali, Colombia *Presenter (email: hae245@mail.usask.ca)

Condensed tannins are important groups of chemical substances found in the seed coats of many classes of dry bean. Consumption of tannin-rich foods has been associated with deficiency diseases such as anaemia in mammals (Baynes R.D. and Batchwell 1990). Manipulating the production, accumulation and form of CT in the seed coat of dry beans may, therefore, be beneficial. To assist in the understanding of CT accumulation in beans, 5 *P. vulgaris* genotypes that differ in CT at maturity were assessed for CT content throughout seed coat development.

O-13 PHENYLPROPANOID PATHWAY GENE EXPRESSION PATTERNS ASSOCIATED WITH NON-DARKENING IN CRANBERRY BEANS. Wright, L.[1], Smith, T.[1], and K. P. Pauls[1*]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada. *Presenter (ppauls@uoguelph.ca)

From crosses made between the conventional cranberry bean varieties and a nondarkening bean named Wit-rood several non-darkening cranberry-like lines as well as lines that darkened were identified in the F_3. Biochemical and gene expression analyses results indicate that the nondarkening trait is related to reduced proanthocyanidin synthesis.

O-14 GENETIC ENGINEERING APPLIED TO COMMON BEAN.
Francisco J. L. Aragão[1]& Josias C. Faria[2]. [1]Embrapa Recursos Genéticos e Biotecnologia, PqEB W5 Norte, 70770-900, Brasília, DF, Brazil. [2]Embrapa Arroz e Feijão, Rod. GO-462, km 12, 75375-000 Santo Antônio de Goiás, GO, Brazil, Presenter (aragao@cenargen.embrapa.br)

Using the biolistic process we developed a transformation system to insert exogenous DNA sequences into common bean genome. We explored the concept of using an RNA interference construct to silence the sequence region of the *AC1* viral gene from *Bean golden mosaic geminivirus* (BGMV) and generate highly resistant transgenic common bean plants. Two lines presented high resistance upon inoculation at high pressure and at a very early stage of plant development. The first field trials were carried out during the agricultural seasons of 2006, 2007 and 2008 in the state of Goiás, Brazil. Results confirmed earlier greenhouse observations. The highest average incidence of viral infection in control plots was 18% in 2007 and 83% in 2008. Non-transgenic plants revealed characteristic severe symptoms of the golden mosaic disease and no symptoms were observed in the transgenic plants. One line has been evaluated in the field in three distinct regions from Brazil. The results showed that no significant differences were observed in the seed germination, initial plant height, width of the leaves, flowering time, yield, number of seeds per pod and 100-seed weight. Biosafety evaluations are being carried out, taking into account the demands of the Brazilian Biosafety Committee and other regulatory authorities in order to obtain authorization to commercially release the first transgenic bean varieties.

O-15 GENETIC ENHANCEMENT AND ITS POTENTIAL IMPACT ON GROWERS AND THE MARKETING OF GM BEAN PRODUCTS. Green, R. Executive Director, Michigan Bean Commission, St. Johns MI 48879 (green@4wbi.net)

The positive and negative impacts of GM products in different commodities are discussed. The potential impact of no-action to develop GM bean on future bean production in the U.S. is discussed in addition to possible repercussions in marketing GM bean products.

O-16 TRANSFORMATION OF COMMON BEAN: THE STATE OF THE ART. Timothy Porch, USDA-ARS-TARS, 2200 P.A. Campos Ave. Suite 201, Mayaguez, Puerto Rico. Presenter (Timothy.Porch@ars.usda.gov**).**

Transformation in common bean is critical for both basic and applied studies, yet regeneration has continued to pose a challenge in this recalcitrant species. A number of approaches, including biolistic and Agrobacterium mediated transformation, continue to be applied in common bean resulting in considerable advances. A review of transformation of common bean will be presented, with a focus on the current state of the art techniques and methodologies.

O-17 Legume ipmPIPE — A NEW OPTION for GENERATING, SUMMARIZING and DISSEMINATING REAL-TIME PEST DATA to STAKEHOLDERS. Schwartz, H.F.[1*], M.A.C. Langham[2*], S.A. Tolin[3], J. Golod[4], J. LaForest[5], and K.F. Cardwell[6] [1]Colorado State Univ., Fort Collins, CO; [2]South Dakota State Univ., Brookings, SD; [3]Virginia Tech, Blacksburg, VA; [4]Pennsylvania State Univ., University Park, PA; [5]Bugwood Network, Univ. of Georgia, Tifton, GA; [6]USDA-CSREES, Washington, DC [*]Presenters (howard.schwartz@colostate.edu and marie_langham@sdstate.edu)

Legume ipmPIPE (Pest Information Platform for Extension and Education) enhances the role of extension specialists in IPM by providing near real-time access to observations, model output, pest management information, and diagnostic images at http://legume.ipmpipe.org. Communication tools also allow specialists to customize information for dissemination to crop consultants and growers. The diversity of pathogens, pests and hosts are uniquely suited to demonstrate the value of the ipmPIPE as a “one-stop shop” for legumes. Educators and stakeholders can easily obtain information on pathogens and pests identified in a specific area or general region. We will review progress to date and solicit input for the future.

O-18 THE BEAN CAP AND PHASEOLUS SEQUENCING PROJECTS. McClean, P.E[1]* and S.A. Jackson[2]. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND; [2]Department of Agronomy, Purdue University, West Lafayette, IN. *Presenter (phillip.mcclean@ndsu.edu)

The United States Department of Agriculture recently funded two projects that will significantly broaden the research capabilities of common bean (*Phaseolus vulgaris* L.) The BeanCAP project contains research, education, and extension activities organized around the theme of nutritional genomics, while the *Phaseolus* sequencing project will significantly impact future research by providing the first draft sequence of its genome. This presentation will describe these projects.

Oral Presentations – Tuesday, October 27

O-19 YIELD POTENTIAL FROM INTERSPECIFIC CROSSES OF COMMON AND RUNNER BEAN.

Beebe, S.*,[1] I.M. Rao[1], C. Cajiao[1], M.A. Grajales[1], and L. Butare[2]. [1]Bean Program, CIAT, Cali, Colombia; and [2]ISAR, Kigali, Rwanda. *Presenter (s.beebe@cgiar.org)

Interspecific crosses were developed from a backcross of an aluminum tolerant accession of *Phaseolus coccineus* to a drought resistant common bean line, SER 16. Pedigree selection was practiced through the F5 generation and lines were tested under drought stressed, irrigated and aluminum stressed field conditions. Lines with superior yield in certain environments were identified among the progenies.

O-20 CLONING THE MAJOR CBB RESISTANCE QTL OF COMMON BEAN -CURRENT STATUS AND FUTURE PROSPECTS.

Yu, K.[1*] Shi, C.[1] Liu, S.[1] Chaudhary, S.[1] Park, S.J.[1] Navabi, A.[1] Pauls, P.[2] McClean, P.[3] Miklas, P.N.[4] Fourie, D.[5]
[1]GPCRC, AAFC, 2585 County Rd. 20, Harrow, ON. Canada. [2] Plant Agriculture, U. of G, Guelph, ON. Canada. [3] Dept. of Plant Sci. NDSU, Fargo, ND. [4] U.S.D.A. Vegetable and Forage Crop Production Unit, Prosser, WA USA; [5]ARC Grain Crops Institute, Potchefstroom, Republic of South Africa. * Presenter: kangfu.yu@agr.gc.ca

Common bacterial blight (CBB), incited by *Xanthomonas axanopodis* pv. *Phaseoli* (Smith) Dye (*Xap*), is one of the most destructive seed-borne diseases of common bean throughout the world. Two major CBB resistance QTL, BC420 and SU91, derived from tepary bean have been mapped to Chromosome 6 and 8 respectively. This paper will discuss our efforts to clone the BC420 and SU91 QTL through map-based cloning and transcript profiling approaches.

O-21 DEVELOPMENT OF *PhaseolusGenes*, A GENOME DATABASE FOR MARKER DEVELOPMENT IN *Phaseolus vulgaris*.

Gepts P[1*], dos Santos JVG[1], Kami J[1], Schaal A[2], Fass J[2], Joshi N[2], Lu Z[2], Lin D[2],[1]Department of Plant Sciences; and [2]Bioinformatics Core, Genome Center, University of California, Davis [*]Presenter (plgepts@ucdavis.edu)

The *PhaseolusGenes* database has three goals: 1) assemble all genomic and mapping data available for *Phaseolus*, particularly *P. vulgaris*; 2) take advantage of synteny between *P. vulgaris* and other legumes, especially soybean, to maximize genetic information available for *P. vulgaris* studies; and 3) use sequence-based mapping to develop new markers tightly linked to genes controlling agronomic traits in common bean. To achieve these goals, the database is being developed with three main modules with web-based display: data entry and search, data analysis and visualization, and marker information display. Of particular interest is the data analysis and visualization, which consists of a searchable collection of markers and sequence-tagged sites supported by a relational database, a Gbrowse display of *Phaseolus* sequences mapped onto the soybean genome sequence, and a CMap display of the molecular linkage map of *P. vulgaris.* Future additions to the database will be discussed.

O-22 UTILIZING SYNTENY BETWEEN *Phaseolus vulgaris* AND *Glycine max* AS A MEANS OF REFINING GENOME FUNCTION AND STRUCTURE.

Repinski S[1*] and Gepts P[1]. [1]Department of Plant Sciences, University of California - Davis, CA. * Presenter (slrepinski@ucdavis.edu)

Previous studies, studying synteny within the legume family, have uncovered relatively high levels of synteny within botanical tribes such as the Phaseoleae (beans and soybeans). High degrees of synteny can lead to candidate gene development for agronomic traits and marker development; they may resolve issues in genome structure within the legume family. This work focuses on synteny around the determinacy gene(s) in the major crop legumes *Phaseolus vulgaris* and *Glycine max*.

O-23 EVOLUTION OF THE EUROPEAN BEAN FROM THEIR AMERICAN ANCESTORS.

De La Fuente M.*, A.M. De Ron, A.P. Rodiño, and M. Santalla. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, Spain. *Presenter: (mfuente@mbg.cesga.es)

Microsatellite markers have been enough proved to be ideal markers to distinguish the fine-scale relationships within bean gene pools and may help to reveal the history of bean introduction in the Iberian Peninsula and its widespread to other countries of the Mediterranean area. With this aim, a set of microsatellite markers were analyzed in a large and representative group of common bean populations of both American and European origins. This work increase the knowledge about the variability and population structure of the Mediterranean bean genotypes, and it is essential to understand about what part of the genome of bean varieties from America are still present in nowadays Mediterranean bean varieties.

O-24 DEVELOPMENT AND SCREENING OF BIBAC LIBRARIES FROM TWO SOURCES OF CBB RESISTANCE IN *P. VULGARIS*.

Perry G*, Singh N, Chan J, Reinprecht Y and Pauls KP. University of Guelph, Guelph ON, Canada perryg@uoguelph.ca

Common bacterial blight (CBB), caused by *Xanthomonas axonopodis*, is an aggressive foliar pathogen of common dry bean (*Phaseolus vulgaris)*, and is endemic in most regions where dry beans are cultivated. The development of commercial bean lines resistant to the pathogen represents a major step towards reducing the impact of this disease on bean production in North America and OAC-Rex represents the first CBB resistant cultivar released in North America, however the genes responsible for this resistance not yet been identified. To aid in the identification of CBB-resistance genes, binary-bacterial artificial chromosome (BiBAC) libraries were created from OAC-Rex and HR67, a second CBB-resistance *P. vulgaris* line, and the libraries were screened with CBB resistance-associated molecular markers identified by previous studies. The identified clones were-end sequenced and assembled into contigs which will be sequenced to identify potential resistance genes.

O-25 MARKER-ASSISTED PYRAMIDING OF RESISTANCE TO COMMON BACTERIAL BLIGHT AND ANTHRACNOSE IN NAVY BEAN. Hou, A.,[1*] Conner, R.L.,[1] Balasubramanian, P.M.,[2] Yu, K.,[3] and Navabi, A.[3] Agriculture and Agri-Food Canada, [1]Morden Research Station, Morden, MB; [2]Lethbridge Research Centre, Lethbridge, AB; [3]Harrow Research Centre, Harrow ON. *Presenter (anfu.hou@agr.gc.ca)

Navy bean cv. OAC Rex is moderately resistant to common bacterial blight (CBB) and the resistance is partially associated with the QTL linked to the molecular marker SU91. Morden003 is susceptible to CBB, but has resistance to anthracnose strains 73 and 105 as indicated by the presence of the molecular marker SAS13. To pyramid resistance to CBB and anthracnose, crosses were made between Morden003 and OAC Rex, and the progenies were backcrossed four times to Morden003. Evaluation with molecular markers and artificial inoculation with both pathogens are being conducted in the progenies, and the results will be discussed.

O-26 INHERITANCE AND ALLELIC RELATIONSHIPS OF ANTHRACNOSE RESISTANCE IN ANDEAN COMMON BEAN PITANGA. Meirelles, A.C.S.[1], M.C. Gonçalves-Vidigal[1*], A.S.Cruz[1], P.S. Vidigal Filho[1], L.L. Sousa[1], and G. F. Lacanallo[1]. [1*] Dep. Agronomia, Universidade Estadual de Maringá, Paraná, Brazil. *Presenter (mgvidigal@ucdavis.edu)

Andean common bean landrace Pitanga, resistant to *Colletotrichum lindemuthianum* races 2047 and 64, was crossed with susceptible cultivar AB 136 (race 2047), and also with Michigan Dark Red Kidney, Cornell 49-242, PI 207262, G 2333, SEL 1308, Michelite, Jalo Vermelho cultivars. The segregation ratio of 3R:1S was observed in F_2 population, suggesting that a single dominant gene in Pitanga is conferring resistance to race 2047. The allelism tests indicated that the gene in Pitanga is independent from *Co-1*, *Co-2*, $Co\text{-}4^3$+*Co-3/Co-9*, $Co\text{-}4^2$, *Co-11*, and *Co-12*, which were previously characterized.

O-27 SUCCESSES AND CHALLENGES OF THE BEAN BREEDING PROGRAMME OF THE ARC-GRAIN CROPS INSTITUTE, SOUTH AFRICA. Liebenberg, A.J.[1], Liebenberg, M.M.[1] and Fourie, D.[1*] [1]Agricultural Research Council – Grain Crops Institute, Potchefstroom, South Africa. *Presenter (FourieD@arc.agric.za)

The primary aim of the dry bean breeding programme at Potchefstroom, initiated in 1970, is the development of high yielding cultivars of the red speckled sugar and small white canning seed types with acceptable quality. Initially manned by a single breeder, the programme later expanded to include two pathologists, and carefully selected genes giving broad resistance to important local diseases could therefore be incorporated by means of backcrossing. Team work has been of paramount importance, and new high yielding cultivars with improved disease resistance and wide adaptation have led to yield increases of between 10 and 31%.

O-28 *STAYGREEN* IS A CANDIDATE FOR THE PERSISTENT COLOR (PC) IN COMMON BEAN. Davis, J.[1], J.R. Myers[1]*, P. McClean[2] and R. Lee[2]. [1]Department of Horticulture, Oregon State University, Corvallis, OR 97331. [2]Department of Plant Sciences, Genomics and Bioinformatics Program, North Dakota State University, Fargo, ND USA.
*Presenter (myersja@hort.oregonstate.edu)

The *persistent color* (*pc*) trait is valued by snap bean processors for a dark, uniform green pod color. We hypothesized that the gene controlling *pc* was a member of the *STAYGREEN* (*SGR*) family described in rice, garden pea, and Arabidopsis. Using pea *SGR* sequence, we identified putative common bean orthologs, and constructed primers that produced a polymorphic band that co segregated with the phenotype. A SNP was discovered in the parents of the BAT96 x Jalo EEP558 mapping population and used to map the locus on Pv2.

O-29 POTYVIRAL VPG-INTERACTING PROTEINS AND *BEAN COMMON MOSAIC VIRUS* RESISTANCE IN *Phaseolus vulgaris* L. Masoud Naderpour[1*], Ole Søgaard Lund[1], Gloria Santana[2], Matthew Blair[2], M., and Elisabeth Johansen[1].[1]Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark.[2]International Center for Tropical Agriculture (CIAT), Cali, AA6713, Colombia, *Presenter (m.naderpour@dias.kvl.dk)

A study was made to find candidates for the *bc*-genes conferring resistance to systemic movement of potyviruses *Bean common mosaic virus* (BCMV) and *Bean common mosaic necrosis virus* (BCMNV) in *Phaseolus vulgaris*. Homologues of *Arabidopsis thaliana PVIP1* and *PVIP2* (potyviral VPg-interacting proteins) genes important in systemic movement of a wide range of potyviruses were cloned from different genotypes of *P. vulgaris*. Two alleles of *PVIP2* gene, annotated as *PvPVIP2*^{1} and *PvPVIP2*^{2}, differentiated the majority of *BC-1*^{1} from *bc-1*^{1} cultivars according to their deduced amino acid levels. A CAPS marker was developed for *PvPVIP2* alleles but no positive correlation was found between the mutated *PvPVIP2*^{2} allele and *bc-1*^{1} resistance, and instead plants homozygous for *PvPVIP2*^{2} appeared to support high level of viral multiplication.

O-30 A POSSIBLE ROLE FOR *BC-U* IN *BC-U, BC-3* GENE COMBINATION IN RESISTANCE TO *BEAN COMMON MOSAIC VIRUS* IN *PHASEOLUS VULGARIS* L. Masoud Naderpour[1*], Ole Søgaard Lund[1], and Elisabeth Johansen[1]. [1]Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark.
*Presenter (m.naderpour@dias.kvl.dk)

Recessive resistance against *Bean common mosaic virus* (BCMV) and *Bean common mosaic necrosis virus* (BCMNV) in *P. vulgaris* is mediated by three loci, *bc-1*, *bc-2* and *bc-3*, and a fourth locus, *bc-u*, has been suggested as a complementary strain-unspecific gene for resistance conferred by the *bc*-numbered genes. To elucidate a possible function to the *bc-u*, we present genetic evidences on the basis of *Bc-u, bc-3* and *bc-u, bc-3* gene combinations that suggest fundamental role for the *bc-u* in preventing the *bc-3* gene from being overcome by BCMV.

O-31 GENETIC DIVERSITY IN CANADIAN CONTEMPORARY COMMON BEAN: A PEDIGREE ANALYSIS.

Navabi, A.*[1], P. Balasubramanian[2], and K.P. Pauls[3]. [1] Agriculture and Agri-Food Canada, Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada, [2] Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB Canada, [3] Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada *Presenter (Alireza.Navabi@agr.gc.ca)

A pedigree database was developed for bean varieties of different market classes released in Canada since 1930. The coefficient of parentage was estimated for all possible pair-wise combinations of varieties, parental and (or) ancestral genotypes. The application of this dataset in a study of genetic diversity in Canadian common bean will be presented and novel applications of pedigree information in plant breeding research will be discussed

O-32 MAPPING OF RESISTANCE TO *PEANUT MOTTLE VIRUS* IN COMMON BEAN.

Larsen R.C.* and P.N. Miklas. USDA-ARS, Prosser, WA. *Presenter (richard.larsen@ars.usda.gov)

Snap beans grown in Texas showing symptoms of severe pod necrosis and large necrotic ringspots were observed in 2008 and 2009 in the vicinity of peanut fields. The virus unexpectedly did not react with the universal potyvirus monoclonal antibody in ELISA tests but was positively identified as *Peanut mottle virus* (PeMoV) using RT-PCR, results of which indicate that this is a new strain of PeMoV infecting snap beans. Reaction to this virus strain was evaluated across a RIL population derived from a cross between Belneb-RR-1 (R) and A55 (S). Resistance to PeMoV derived from BelNeb-RR-1 is tentatively assigned to linkage group 3 on the *Phaseolus* core map in the vicinity of the $bc\text{-}1^2$ gene conferring resistance to *Bean common mosaic virus*.

O-33 VIRUS SURVEILLANCE IN BEANS USING TISSUE BLOT IMMUNOASSAY: THREE YEARS EXPERIENCE OF THE LEGUME IPM-PIPE.

Tolin, Sue A.[1]* and Marie A. C. Langham[2]. [1]Virginia Polytechnic Institute and State University, Blacksburg, VA and [2]South Dakota State University, Brookings, SD. *Presenter (stolin@vt.edu).

One of the initial objectives of the Legume ipmPIPE (Pest Information Platform for Extension and Education) was to monitor viruses, as increased prevalence of viruses had been reported with the introduction of the soybean aphid. The tissue blot immunoassay (TBIA) was selected as a practical, high-throughput method for virus detection to support the inclusion of viruses in survey and plant pest surveillance programs. An experimental kit with necessary reagents was designed and provided through Agdia, Inc. for NPDN laboratories and researchers in Legume ipmPIPE participating states. Fifty-plant samples from each plot or field were collected by transect design, at two dates, in 2007 and 2008. In 2009, up to half of the samples were of symptomatic plants, and the scope of legume species sampled was broadened. Viruses included in the tests each of the three years were: *Alfalfa mosaic alfamovirus* (AMV), *Bean common mosaic potyvirus* (BCMV), *Bean yellow mosaic potyvirus* (BYMV), and *Cucumber mosaic cucumovirus* (CMV). In 2007, two soybean rust sentinel plots were sampled in each state and tested for *Bean pod mottle comovirus* (BPMV) and *Soybean mosaic potyvirus* (SMV). The yearly and cumulative results of virus prevalence and incidence in various legume species will be presented and discussed.

O-34 CHARACTERIZATION OF RHYNCHOSIA MILD MOSAIC VIRUS (RHMMV), A NEW WHITEFLY-TRANSMITTED GEMINIVIRUS OF LEGUMES, AND RESULTS OF A 2009 SURVEY OF BEGOMOVIRUSES INFECTING ENDEMIC HOSTS IN PUERTO RICO. Brown, J.K.* and A.M. Idris. School of Plant Sciences, The University of Arizona, Tucson, AZ. *Presenter (jbrown@ag.arizona.edu)

We recently identified a previously undescribed begomovirus (*Begomovirus; Geminiviridae*), *Rhynchosia mild mosaic virus* (RhMMV), from endemic *Rhynchosia minima* plants in Puerto Rico and showed that it causes severe symptoms in bean *Phaselous vulgaris* (L.). Here we demonstrate Koch's Postulates (causality) for RHMMV in bean and in several other eudicot species using the cloned bipartite genome and biolistic inoculation, and report the experimental host range and molecular and phylogenetic characterization of RHMMV. In addition, results are reported for a survey in Puerto Rico of endemic plant species undertaken to document the present status of begomovirus prevalence during 1998-2009 in selected island locations, including the vicinity of the Isabela Station (Aguadilla) where bean and soybean germplasm are screened and/or increased for the U.S. and international bean-breeding programs

O-35 SELECTION FOR WHITE MOLD RESISTANCE IN COMMON BEAN. Singh, S.P.[1*], H. Terán, L. Crane, H.F. Schwartz and K. Otto. [1]University of Idaho, 3793N 3600E, Kimberly, ID 83341; [2]Colorado State University, Fort Collins, CO 80523. [*]Presenter (singh@kimberly.uidaho.edu)

Partial white mold resistance is found in Andean and Middle American gene pools and interspecific breeding lines derived from *Phaseolus coccineus* and other secondary gene pool species of the common bean. Breeding strategies for pyramiding resistance from diverse sources of germplasm and transferring high levels of resistance into pinto bean will be described. We also will discuss progress made thus far in pyramiding and introgression of white mold resistance.

O-36 AGRONOMIC AND ECONOMIC ASSESSMENT OF INTENSIVE PEST MANAGEMENT IN DRY EDIBLE BEAN: WHITE MOLD EXPERIMENT. Pynenburg, G.M.[1*] and C.Gillard[2], P. Sikkema[2], D. Robinson[2], G. Boland[1] and R.Vyn[2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON. [2]Ridgetown Campus, Ridgetown,ON. [*]Presenter (gpynenbu@uoguelph.ca)

Interactions between weeds and white mold (*Sclerotinia sclerotiorum*) in edible dry beans were examined, with various herbicides, seed treatments and fungicides. The economic herbicide program, combined with thiamethoxam treated seed and fluazinam foliar fungicide delivered the highest return on investment to the grower. However, the economic herbicide program can result in increased weed pressure, therefore influencing microclimatic conditions which can generate a more conducive environment for white mold development.

O-37 CHARACTERIZATION OF THE RUST RESISTANCE GENE PRESENT IN THE COMMON BEAN CULTIVAR 'OURO NEGRO', THE MAIN RUST RESISTANCE SOURCE USED IN BRAZIL. Souza, T.L.P.O.[1*], S.N. Dessaune[1], D.A. Sanglard[1], M.A. Moreira[1] and E.G. Barros[1]. [1]BIOAGRO, Federal University of Viçosa, Viçosa, MG 36570-000, Brazil. [*]Presenter (tlposouza@gmail.com)

The main goal of the present work was to characterize the rust resistance (RR) gene present in the common bean cultivar 'Ouro Negro' (*Ur-ON*), the main RR source used in Brazil. We compared the 'Ouro Negro' RR spectrum with those of other bean lines harboring known RR genes when inoculated with nine selected races of *Uromyces appendiculatus*. In addition, all bean lines were screened with molecular markers linked to *Ur-ON* aiming to identify additional evidence for the presence of alleles for this locus in the screened RR sources. Finally, we tested the allelic relationships of *Ur-ON* with RR genes already characterized from lines resistant to at least one race of the pathogen. The results showed that *Ur-ON* is distinct from those genes with which it was compared. We propose this gene is unique and be designated *Ur-14*.

O-38 EVALUATION OF SNAP BEAN GENOTYPES COMBINING RUST RESISTANCE AND HEAT TOLERANCE TRAITS IN EAST AFRICA. Charles J Wasonga[1*], Pastor-Corrales M.A.[3], Tim Porch[3] and Phillip D Griffiths[4] **[1,4]** *Dept. Horticultural Sciences, Cornell University NYSAES, Geneva, NY 14456;* **[2]** *USDA-ARS, Beltsville, MD;* **[3]** *USDA-ARS Tropical Agriculture Research Station, Mayagüez, PR*
[*] Presenter (*cjw56@cornell.edu*)

Common bean rust (*Uromyces appendiculatus*) and high temperatures (heat stress) limit snap bean (*Phaseolus vulgaris* L.) production in many areas in the tropics. Snap bean breeding lines were developed with rust resistance and heat tolerance traits combined in the same genetic background from crosses between BelJersey-RR-15 and BelFla-RR-1 (each containing the *Ur-4* and *Ur-11* rust resistance genes) and heat tolerant snap bean breeding lines HT601 and HT611. Lines were field tested at six sites in Kenya and Tanzania and exhibited tolerance to higher growth temperatures and also resistance to the local rust races indicating potential utility for improving snap bean cultivars for East Africa and other tropical regions.

O-39 CURRENT STATUS OF *UROMYCES APPENDICULATUS* IN BULGARIA.
Magdalena Beleva[1*],Ivan Kiryakov[1] and Dimitar Genchev[1]. [1]Legume Crops Breeding Department, Dobrudzha Agriciltural Institute - General Toshevo, Bulgaria. Presenter
[*]magdalena.beleva@yahoo.com

One hundred and ten single-uredinium cultures of *Uromyces appendiculatus* were isolated from leave samples collected from mountain and plain regions in Bulgaria. Ninety pathotypes were identified, which had to be referred to nine physiological races. Forty eight accessions were immune to the pathogen, and 22 had partial resistance under field conditions. Variety 'Beslet' was resistant to all pathotypes identified. The resistance of the variety is determined by a single dominant gene which does not correspond to genes *Ur-4, Ur-13* and *Ur-CNC* and is not identical to genes *Ur-3, Ur-6, Ur-7, Ur-9, Ur-260* and the resistance gene in cultivar Montcalm.

O-40 REACTION OF COMMON BEAN CULTIVARS TO NEW RACES OF THE BEAN RUST PATHOGEN FROM MICHIGAN AND NORTH DAKOTA AND TO OTHER IMPORTANT RACES. Pastor-Corrales M.A[1*], J. Rayapati[2], J.M. Osorno[3], J. D. Kelly[4], E.M. Wright[4], Mark A. Brick[5], S.G. Markell[6], and R.S. Goswami[6]. [1*]Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD 20705, [2]JRRRC, ADM, Decatur, IL, 62521, [3]Department of Plant Science and [6]Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, [4]Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI 20705, and [5]Department of Crop and Soil Sciences, Colorado State University, Fort Collins CO 80524. *Presenter (talo.pastor-corrales@ars.usda.gov)

Approximately 40 U.S. common bean cultivars were inoculated with the two new races of the bean rust pathogen (*Uromyces appendiculatus*) from Michigan and North Dakota. Cultivars with resistance to at least one these races were subsequently inoculated with some or all races 41, 44, 47, 53, 67, 73 and 108, used in the identification of rust resistance genes *Ur-3*, *Ur-4*, *Ur-6* and *Ur-11*. Various check cultivars with single genes and combinations of two or more rust resistance genes were used as checks. The results revealed new cultivars with broad rust resistance. The implications of these results are discussed.

O-41 THE CONNECTIONS BETWEEN SOIL HEALTH AND ROOT HEALTH. George S. Abawi[1*], John W. Ludwig[1], and Beth K. Gugino[2]. [1]Department of Plant Pathology, NYSAES, Cornell University, Geneva, NY 14456; [2] Dept. of Plant Pathology, The Pennsylvania State University, University Park, PA. * Presenter (gsa1@cornell.edu)

The emerging concept of soil health deals with integrating and optimizing the soil physical, chemical and biological properties for improving soil functions and crop productivity in a sustainable and environmentally compatible manner. Soil health management practices consist of numerous modifications and combinations of reduced tillage systems, crop rotations, cover crops and/or soil amendments. All these practices directly or indirectly impact populations of root pathogens, severity of root diseases, and often the quality and quantity of marketable yield. In addition, root pathogens are most damaging to beans and other agronomic crops in poor quality soils. Thus, root health assessment is a good indicator of overall soil health status. Specific examples will be discussed during the presentation to illustrate the influence of soil health status and management options on selected root pathogens and their root diseases on beans and other crops.

O-42 DRY EDIBLE BEAN PATHOGENS PREVALENT IN NORTH DAKOTA WITH SPECIAL EMPHASIS ON ROOT ROTS. Goswami, R.S.*, A. Gambhir, Y.W. Chang, and R.S. Lamppa. Department of Plant Pathology, North Dakota State University, Fargo, ND. *Presenter (Rubella.Goswami@ndsu.edu)

North Dakota accounts for nearly half of the dry bean production in the US (USDA-NASS), and diseases are one of the main limiting factors in the state. Economically important foliar and stem diseases reported in the upper great-plains include; white mold, rust, anthracnose and common bacterial blight. Root rots are common to the region and a recent survey of dry beans in Minnesota found a very high incidence of root rots. However, Minnesota production consists largely of kidney beans and under irrigation, while production in North Dakota is largely pintos under dry-land conditions and no data is available regarding the prevalence of root diseases in North Dakota. The objective of this study was to assess the prevalence of foliar and root pathogens on dry beans in the 2007, 2008 and 2009 growing seasons. The findings showed the sustained prevalence of the white mold and bacterial blight but absence of anthracnose. A new race of rust was detected. Root rots were found to be widespread and a change in the pathogens commonly associated with this disease was noted.

Poster Abstracts

P-01 EVALUATION OF LIMA BEAN LANDRACES FROM PUERTO RICO. Luís Ruíz[1], James Beaver[1*] and Emmalea Ernest[2]. [1]Dept. of Crop & Agro-Environmental Sci., Univ. de Puerto Rico Mayagüez, PR 00681; [2]Univ. of Delaware, Research and Education Center, 16483 County Seat Highway, Georgetown, DE 19947. *Presenter (james.beaver@upr,edu).

The Lima bean (*Phaseolus lunatus* L.) is a heat and drought tolerant grain legume that is produced and consumed throughout the Caribbean. The USDA and CIAT bean germplasm collections contain very few accessions from the region. These collections currently have 2 accessions from Haiti, ≤ 3 accessions from Puerto Rico and no accessions from the Dominican Republic. Fifteen landrace varieties of Lima beans, collected from different locations in Puerto Rico, were evaluated in Puerto Rico and Delaware for morphological and agronomic traits, photoperiod response and for HCN concentration in the leaves and seed. Seed of the landraces will be submitted to the USDA bean germplasm collection. One or two of the most promising landrace varieties will continue to be evaluated and possibly considered for release in Puerto Rico.

P-02 GENETIC DIVERSITY OF MESOAMERICAN AND ANDEAN WILD BEANS USING MICROSATELLITE MARKERS. Galván MZ[1,2*], Hufford M[1], Worthington M[1], Balatti P[3], Menéndez Sevillano M[2], Farreyra M[2] and Gepts P[1]. [1]Department of Plant Sciences, University of California, Davis, CA; [2]EEA INTA Salta, Argentina; [3]University of La Plata, Argentina. *Presenter (martazgalvan@gmail.com)

Knowledge of the center of bean domestication is important to identify a potential area of origin for agriculture several millennia ago and to better understand the genetic, physiological, and ecological characteristics of the domesticate bean gene pool. The putative Mesoamerican domestication center of *Phaseolus vulgaris* is located in the Lerma-Santiago Basin of Mexico. Our objective in this study is to analyze the genetic structure of wild Mexican and Andean bean populations and to study their relation with landraces of the same regions. As a first step, we are characterizing genetic diversity among these accessions with a set of microsatellite markers distributed throughout the genome followed by an analysis with the software STRUCTURE

P-03 SCREENING BEAN GENOTYPES FOR ENHANCED N FIXING ABILITY. Heilig, J.A.[1*] and J.D. Kelly PhD[1]. [1]Dept of Crop and Soil Sciences, Michigan State University, East Lansing, MI. *Presenter (heiligja@msu.edu)

Thirty four diverse bean genotypes, including a non nodulating genotype, were screened for nitrogen fixation. Genotypes were grown in greenhouse conditions, planted in sterilized media and inoculated with Rhizobium etli strain UMR 1597 and fertilized with a nutrient solution lacking N; plant biomass and total N content were used to evaluate the N fixing ability of the genotypes. Plant architecture may predict N fixation potential.

P-04 SEED COAT PIGMENTATION TRAITS OF BLACK AND RED BEAN PHENOTYPES. Marles, M.A.S. [1], Balasubramanian, P. [2] and Bett, K.E. [1*], [1]Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada; [2] Agriculture and Agri-Food Canada, Lethbridge Research Centre 5403 - 1 Ave. S., Lethbridge, Alberta T1J 4B1 *presenter (k.bett@usask.ca)

Black bean (*Phaseolus vulgaris* L.) loses most of its attractive colour during the soaking, blanching and canning process. Red bean appears to behave differently. Seed coat extracts were examined by HPLC separation and UV-spectral analysis to establish components in these tissues that affect seed coat colour. Compounds other than anthocyanin glycosides may contribute to pigments that are more resistant to leaching during soaking and canning. Beans with such traits would yield a more attractive cooked product.

P-05 PLANT GENETIC RESOURCES NETWORK OF INTA- ARGENTINA. Menéndez Sevillano, M.C[1], Clausen A.M.[2], Ferrer, M.E.[3], Rosso B.[4] and Ferreyra, M.J.[1]*. [1]EEA-Salta, [2]EEA-Balcarce, [3]Instituto de Recursos Biológicos-Castelar, [4]EEA-Pergamino. INTA. Argentina. *Presenter (mferreyra@correo.inta.gov.ar)

The germplasm network of INTA is composed by nine gene banks and 11 active collections of plant genetic resources, that conserves in short-medium term species of current and potential interest, together with a base bank which conserves backup duplicates of the accessions in long-term. The objectives of the network are to conserve agrobiodiversity and valorize plant genetic resources through morphological, genetic, biochemical and molecular characterization and evaluation, as well as documentation. The network participates at national, regional and international level in exchange and protection of plant genetic resources, including development of legal regulations and the implementation of conventions and treaties.

P-06 THE GERMPLASM ACTIVE BANK OF EEA-INTA AT SALTA. Menéndez Sevillano, M.C., Ferreyra, M.*, Ibarra, L. EEA-INTA, Salta. Argentina. *Presenter (mferreyra@correo.inta.gov.ar)

The EEA-INTA germplasm active bank at Salta is a part of the Plant Genetic Resources Conservation Network of INTA. It is located in Cerrillos, in the Lerma Valley, province of Salta (latitude 24º 53' S; longitude 65º 28' W; 1240 masl). It preserves seeds of beans, tobacco, native aromatics, tree tomato and amaranth. Bean is the most important collection that is composed of landraces of cultivated beans (*Phaseolus vulgaris* L) and wild populations (*Phaseolus vulgaris* var *aborigineus*. (Burk.) Baudet). Collections have been done through Northwestern Argentina totaling 561 accessions, of which 400 have been characterized. Seeds are preserved to medium term in climatic chambers (temperature 5-7 ºC and seed moisture 6 to 7%). The activities undertaken include collection, introduction and exchange, regeneration and multiplication, characterization, evaluation and conservation, as well as periodic monitoring of seed viability.

P-07 THE GENE CONTROLLING SLOW- DARKENING IN PINTOS IS NOT *J*. Bett, K.E.* and Elsadr, H. Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK, S7N 5A8. *Presenter (k.bett@usask.ca)

There are at least three post harvest darkening phenotypes: non darkening (ND), slow darkening (SD) and regular darkening (RD). The gene *J* has been associated with after-darkening in beans and *jj* beans tend not to darken. Through crosses with lines homozygous for *j*, we have found that the SD phenotype is not controlled at this locus but rather at another locus on a different chromosome and ND is epistatic to SD.

P-08 PHENOTYPIC EVALUATION OF A DRY BEAN MAPPING POPULATION FOR RESISTANCE TO POTATO LEAFHOPPER. Brisco, E.I.[1]*, T.Porch[2], and J.D. Kelly[1].
[1]Department of Crop and Soil Sciences, Michigan State Univ East Lansing, MI.
[2]Tropical Agriculture Research Station, USDA, Mayaguez, PR. *Presenter (briscoel@msu.edu)

A genetic study examining resistance to the temperate potato leafhopper *Empoasca fabae* was conducted in Michigan using a dry bean mapping population of Matterhorn, a susceptible Michigan commercial variety, by EMP507, a line developed by CIAT for resistance to the tropical leafhopper *E. kraemeri.* Preliminary field data reveal strong segregation for damage symptoms associated with potato leafhopper feeding and potato leafhopper nymph counts, both of which are indicators of insect resistance mechanisms.

P-09 PROGRESS IN PYRAMIDING WHITE MOLD RESISTANCE FROM ACROSS *PHASEOLUS* SPECIES IN COMMON BEAN. Crane, L.[1*], H. Terán, H.F. Schwartz[2], K. Otto[2] and S.P. Singh[1]. [1]University of Idaho, 3793N 3600E, Kimberly, ID 83341; [2]Colorado State University, Fort Collins, CO 80523. [*]Presenter (lcrane@kimberly.uidaho.edu)

White mold (WM) is a severe disease of dry bean (*Phaseolus vulgaris*). Partial resistance is found in Andean and Middle American gene pools and *P. coccineus* and other secondary gene pool species. The objectives were to (1) pyramid resistance from diverse sources of germplasm, and (2) transfer high levels of resistance into pinto bean. Three WM resistant interspecific breeding lines and genotypes from Andean and Middle American gene pools were crossed and gamete selection is being used for pyramiding and transfering high levels of WM resistance into pinto bean. Progress achieved thus far and future prospects will be discussed.

P-10 GENETIC GAIN FOR SEED TRAITS IN SELECTION CYCLES IN RUNNER BEAN. De Ron, A.M.*, M. De la Fuente, E.A. Pérez, and A.P. Rodiño. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, SPAIN. *Presenter (amderon@mbg.cesga.es)

The objective of this research was to display the genetic gain after a recurrent selection program within runner bean (*Phaseolus coccineus* L.) valuable landraces being selection criteria high yield and large seed size. The selection coefficient and the genetic gain were calculated for each generation in each family. The results indicate an average genetic gain of 41 % in four generations of selection with regard to dry seed weight, the most important commercial trait of the runner bean seeds.

P-11 PHENOTYPIC AND GENOTYPIC EVALUATION OF COMMON BACTERIAL BLIGHT RESISTANCE IN A RESISTANT INTER-CROSS POPULATION OF PHASEOLUS VULGARIS. Durham, K.M.[1*], E.A. Lee[1], K.Yu[2], K.P. Pauls[1], and A. Navabi[1,2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada. [2] Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, Harrow, ON, Canada. *Presenter (kdurham@uoguelph.ca)

Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *phaseoli* (*Xap*), is a damaging widespread disease of common bean (*Phaseolus vulgaris L.*). Genetic resistance to CBB in common bean is limited, but has been introgressed through inter-specific crosses with tepary bean (*P. acutifolius*). A recombinant inbred line population of a cross between the resistant genotypes OAC Rex and HR45, known to carry different resistance QTL, was evaluated for resistance to CBB and genotyped with molecular markers associated with the two CBB QTL. Segregation of CBB response in the population, the effect of each QTL and the interaction effect of the two QTL will be discussed.

P-12 LIMA BEAN BREEDING AT THE UNIVERSITY OF DELAWARE. Ernest, E.G.[1]* [1]Department of Plant and Soil Sciences, University of Delaware, Georgetown, DE. *Presenter (emmalea@udel.edu)

A lima bean (*Phaseolus lunatus*) breeding program was initiated at University of Delaware in 2004. The breeding program now includes three different commercial classes: baby limas, Fordhook limas and large-seeded pole limas. Twelve baby lima lines developed by the program were evaluated in a replicated yield trial in 2008 and eleven such lines were similarly evaluated in 2009. Six Fordhook lima lines were also evaluated for yield in 2009. Ten Fordhook varieties were screened for resistance to lima bean downy mildew (caused by *Phytophthora phaseoli*) races E and F in summer 2009. One variety with resistance to race E and two varieties with resistance to race F were identified. None of the varieties had resistance to both races. Nine F_1 hybrid, large-seeded pole lima beans were evaluated in a replicated yield trial. Fourteen additional pole lima varieties and landraces were also evaluated.

P-13 MOLECULAR MARKERS LINKED TO ANGULAR LEAF SPOT RESISTANT GENES IN COMMON BEAN ACCESSIONS FROM BRAZIL AND AFRICA. Vidigal Filho PS[1,2*], Gonçalves-Vidigal MC[1,2], Nchimbi-Msolla S[3], Namayanja A[4], Nsanzabera F[5], Kimani P[6], Kami J[2], & Gepts, P[2]. [1]Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil; [2]Univ. of California, Dep. of Plant Sciences, Davis, CA 95616-8780; [3]Sokoine University of Agriculture, Morogoro, Tanzania; [4]National Crops Resources Research Institute, Kampala, Uganda; [5]Institut des Sciences Agronomiques du Rwanda, Rubona, Rwanda; [6]University of Nairobi, Kabete Campus, Nairobi, Kenya *Presenter (pedro.vidigal@pop.com.br)

Thirty-one common bean accessions from Brazil and ninety-one from eastern Africa were analyzed to verify the presence of three SCAR markers linked to angular leaf spot resistance genes. The SH13 marker (linked to the *Phg-1* gene) was present in 27 % of accessions from Africa, but was absent among the accessions from Brazil. The SNO2 marker (*Phg-2* gene) was present in Brazilian (32%) and African (53 %) accessions. Lastly, the SMO2 marker (*Phg-ON* gene) was present in all accessions evaluated. The microsatellite Pvag-004 (Phg^{G5686A} allele) was present only in 12% and 11% of accessions from Brazil and Africa, respectively.

P-14 YIELD EFFECT FOR TWO QTL CONTROLLING COMMON BACTERIAL BLIGHT RESISTANCE IN A NEAR-ISOGENIC DRY BEAN POPULATION.

Fourie, D.[1]*, and P. Miklas[2]. [1]ARC Grain Crops Institute, Potchefstroom, Republic of South Africa; [2]USDA-ARS, Vegetable and Forage Crop Research Unit, Prosser, WA. FourieD@arc.agric.za

The effect common bacterial blight (CBB) resistance has on yield is not well characterized. This yield study tested near-isogenic lines (NILs) homozygous for presence/absence of two QTL (SU91 and BC420) backcrossed six times into 'Teebus' small white bean. Absent disease, across six location-years, all NILs had similar yield, but for diseased plots NILs with SU91 QTL were significantly higher yielding. The lack of yield drag effects from deployment of these QTL is a promising result for breeders.

P-15 RAPD MARKER LINKED TO ANTHRACNOSE RESISTANCE GENE *Co-13* IN ANDEAN CULTIVAR JALO LISTRAS PRETAS.

Lacanallo G.F.[4], Gonçalves-Vidigal M.G.[1*], A.K.S. Lobato[1], P.S. Vidigal Filho[1], A. Gonela[1]. [1*] Dep. Agronomia, Universidade Estadual de Maringá, Paraná, Brazil. [*]Presenter (mgvidigal@ucdavis.edu)

The utilization of molecular markers associated with Andean genes resistant to anthracnose, consists on a powerful tool for breeding programs in order to obtain cultivars with ample and durable resistance spectrum. The present work had the objective of identifying RAPD molecular markers associated with *Co-13* gene, present in the Andean cultivar Jalo Listras Pretas (JLP), through F$_2$ population derived from cross between JLP (resistant to race 73) and Cornell 49-242 (susceptible to race 73). Molecular analyses provided the identification of OPV20$_{700}$ marker, associated with gene *Co-13* in coupling phase, at a distance of 1.8 centimorgan (cM) in the Linkage Group B3.

P-16 GENETIC LINKAGE AND GENE MAPPING OF *PHG-1* AND *CO-1*^{4} RESISTANCE GENES TO ANGULAR LEAF SPOT AND ANTHRACNOSE IN THE COMMON BEAN AND 277 CULTIVAR.

Gonçalves-Vidigal[1*], M.C., A.S. Cruz[1], A. Garcia[1], P.S. Vidigal Filho[1] and M.A. Pastor-Corrales[2]. [1]Departamento de Agronomia, Universidade Estadual de Maringá, Maringá, Paraná, Brazil; [2]USDA-ARS, BARC-W, Beltsville, MD 20705. *Presenter (mgvidigal@ucdavis.edu)

The common bean cultivar AND 277 has the *Phg-1* gene, which confers resistance to *Pseudocercospora griseola*, and the *Co-1*^{4} allele, which confers resistance to *Colletotrichum lindemuthianum*. This study was conducted to elucidate the inheritance of the resistance of AND 277 to angular leaf spot and anthracnose using an F$_2$ population derived from the AND 277 x Rudá cross and F$_{2:3}$ families from the AND 277 x Ouro Negro crosses. Co-segregation analysis revealed that a single dominant gene in AND 277 confers resistance to races 73 and 2047 of *C. lindemuthianum* and race 63-23 of *P. griseola*. The *Co-1*^{4} and *Phg-1* genes are tightly linked (0.0 cM) to each other; both are linked to the SH13 marker in coupling phase.

P-17 DIFFERENTIATION OF APHID-TRANSMITTED VIRUSES IN SNAP BEANS USING REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION.

Hart, J.P.[1*] and P.D. Griffiths[1]. [1] Department of Horticultural Sciences, New York State Agricultural Experiment Station, Cornell University, Geneva, NY. [*]Presenter (jph248@cornell.edu)

A complex of aphid-transmitted viruses has been causing considerable yield losses in snap bean production throughout the Great Lakes region of the United States since 2000.The sampling of infected fields has revealed the presence of a number of distinct aphid-transmitted viruses that include *Cucumber mosaic virus* (CMV), *Alfalfa mosaic virus* (AMV), *Clover yellow vein virus* (ClYVV), *Bean yellow mosaic virus* (BYMV), *Bean common mosaic virus* (BCMV), *Soybean mosaic virus* (SMV), *Watermelon mosaic virus* (WMV-2), and *Peanut stunt virus* (PSV). The primers reported in the literature for these viruses were evaluated using positive control samples to determine their effectiveness in detecting and differentiating the viruses associated with the aphid-transmitted virus complex of snap bean in the Great Lakes region of the United States.

P-18 CONSTRUCTING A GUS-TAGGED INFECTIOUS CDNA CLONE OF *BEAN COMMON MOSAIC VIRUS.*

Masoud Naderpour[1*] and Elisabeth Johansen[1]. [1]Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark. *Presenter (m.naderpour@dias.kvl.dk)

An infectious cDNA clone of *Bean common mosaic virus* strain RU1 was constructed, between the 35S promoter and NOS terminator, using overlapped fragments of the virus that were amplified with the primer pairs designed on the basis of previously posted sequence of RU1 (AY863025). To circumvent the toxicity of viral genome to *Escherichia coli* an intron was integrated into the viral genome and the whole cassette was introduced into *Agrobacterium tumefaciens*. Finally viral cDNA was tagged with the GUS gene for feasible study of BCMV-host interaction.

P-19 MAPPING AND QTL ANALYSIS OF AGRONOMIC TRAITS IN COMMON BEAN : VALIDATION OF A HALO BLIGHT RESISTANCE QTL IN BEAN BREEDING PROGRAMS.

C. Robast*, P. Parmentier, P. Carreau, D. Peltier, C. Bonneau, B. Monsimier, N. Bourgeais, E. Belouard, P. Leveque, G. Tristan, M. Delisle.
Vilmorin, La Ménitré, France. *Presenter (charlene.robast@vilmorin.com)

A population of 188 recombinant inbred lines, highly relevant to the gene pool used by bean breeders, was used to develop a genetic linkage map consisting of 99 simple sequence repeats (SSR) and four sequence characterized amplified region (SCAR) markers. 26 phenotypic traits of agronomic interest (physiological, morphological, disease resistance) were evaluated. The map has a total length of 289cM distributed across 10 linkage groups. The quantitative trait loci (QTL) analysis revealed 12 QTLs identified for 10 agronomic traits. A major QTL involved in resistance to halo blight was detected and is currently being used to select for resistance in bean breeding programs through marker assisted selection (MAS).

P-20 IMP: A TOOL FOR INTRON PREDICTION COUPLED WITH PRIMER DESIGN TO AID IN MARKER DISCOVERY. Sanderson, L., Vijayan, P., Alahakoon, I. and Bett, K.E.* Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK, S7N 5A8. *Presenter (k.bett@usask.ca)

We have developed IMP, an automated pipeline that will take ESTs or other partial sequence data from one species and use genomic sequence data from another species, usually a model plant, to identify putative introns and design primers that will amplify the intronic region in the species of interest. We have validated a set of primers designed from bean ESTs using this strategy and mapped them using SSCP. The pipeline is available at Sourceforge.

P-21 GENERATION MEANS ANALYSIS OF AGRONOMIC AND SEED QUALITY TRAITS IN COMMON BEAN (*Phaseolus vulgaris* L.). Santalla, M.*, M.S. Saburido, A.P. Rodiño, M. Lores, A. Castro, M. De La Fuente. Plant Genetic Resources Department, Misión Biológica de Galicia, CSIC, Pontevedra, SPAIN. Presenter* (msantalla@mbg.cesga.es)

When common bean was introduced in the Iberian Peninsula in century XVI, from both Mesoamerican and Andean pools, it was adapted to new atmospheres and germplasm of both heaps began to be cultivated in proximity. This gave rise to the recombination of both heaps, appearing intermediate forms between them. It is important to know to what extent the intermediate forms allow to improve germplasm of one or another origin to be able to develop varieties of great grain thus, with commercial quality and good yield. In order to reach this objective four populations derived from simple crossovers between lines PHA-0419 and PHA-0399 evaluate themselves, both recombinant natural ones of Mesoamerican origin and cultivars of Mesoamerican origin, in the case of Matterhorn and Andean origin in the case of Beluga. The obtained lines and their ancestors were evaluated in the experimental property of the MBG-CSIC.

P-22 COMPREHENSIVE LINKAGE MAP OF WHITE MOLD RESISTANCE QTL IN COMMON BEAN. Soule, M.[1], P. Miklas[1]*, L. Porter[1], J. Medina[2], G. Santana[2] and M. Blair[2]. [1]USDA-ARS, Vegetable and Forage Crop Research Unit, Prosser, WA; [2]International Center for Tropical Agriculture – CIAT, Cali Colombia. (phil.miklas@ars.usda.gov)

Partial resistance to white mold in common bean is complexly inherited. Numerous QTL conferring partial resistance have been identified but relationships among them are not fully understood. To gain a better understanding, all 37 QTL identified to date were integrated into a common linkage map. This comprehensive linkage map provides a blueprint of resistance genes available to breeders, will facilitate marker-assisted breeding, and provide a framework for integrating and interpreting future QTL studies. New QTL nomenclature guidelines were used.

P-23 SINGLE NUCLEOTIDE POLYMORPHISMS (SNPs) DISCOVERY IN THE COMMON BEAN.

Souza, T.L.P.O.[1*], E.G. Barros[1], C.M. Bellato[2], E.-Y. Hwang[2], P.B. Cregan[2] and M.A. Pastor-Corrales[2]. [1]BIOAGRO, Federal University of Viçosa, Viçosa, MG 36570-000, Brazil. [2]Soybean Genomics and Improvement Laboratory, USDA/ARS, BARC-West, Beltsville, MD 20705, USA. [*]Presenter (tlposouza@gmail.com)

SNPs were discovered in common bean (*Phaseolus vulgaris* L.) via resequencing of sequence-tagged sites (STSs) developed by PCR primers designed to soybean shotgun and BAC-end sequences, to common bean genes and microsatellite flanking regions. From an initial set of 1,880 PCR primer pairs tested, 265 robust STSs were obtained, amplified and sequenced in six contrasting *P. vulgaris* genotypes of the Andean and Mesoamerican gene pools. In the resulting 131,120 bp of aligned sequence, a total of 677 SNPs were identified, including 555 single-base changes (295 transitions and 260 transversions) and 122 small nucleotide insertions/deletions (indels). The frequency of SNPs was 5.16 SNPs/Kb and the mean nucleotide diversity expressed as Halushka's theta was 0.00226.

P-24 PROGRESS IN BREEDING FOR WHITE MOLD RESISTANCE IN *PHASEOLUS VULGARIS* AT OREGON STATE UNIVERSITY.

Zimmerman, S.J. [1*], Myers, J.R.[1], Barrett, M.[1], Haggard, J.E.[1] and Gilmore, B.[1] [1]Department of Horticulture, Oregon State University, Corvallis, OR. *Presenter(zimmerms@hort.oregonstate.edu)

White mold disease, caused by *Sclerotinia sclerotiorum*, is a serious disease in common bean, where losses can reach up to 100%. We have been improving resistance to white mold disease in common bean using 1) highly resistant *Phaseolus coccineus* accessions, and 2) pyramiding G122 and NY6020 sources of resistance from the *P. vulgaris* gene pool:. The pyramiding scheme produced moderately resistant lines, and germplasm from the interspecific 91G x PI255956 backcross inbred population has been entered in the national white mold nursery.

P-25 RESISTANCE TO HALO BLIGHT, COMMON BACTERIAL BLIGHT AND BACTERIAL BROWN SPOT IN SPANISH COMMON BEAN CORE COLLECTION.

Asensio, C.[1*], Asensio S-Manzanera, M.C. [1], Ibeas, A. [1] and De la Rosa, L. [2]Departamento de Hortofruticultura, ITACyL, Valladolid, Spain; [2]Centro Nacional de Recursos Fitogenéticos, Alcalá de Henares, Madrid, Spain. *Presenter (asevegma@itacyl.es)

Halo blight caused by *Pseudomonas syringae* pv. *phaseolicola*, common bacterial blight caused by *Xanthomonas campestris* pv. *phaseoli* and bacterial brown spot caused by *Pseudomonas syringae* pv. *syringae*, are among the major constraints of common bean (*Phaseolus vulgaris* L.) production in the North Central part of Spain. Depending on environmental conditions of each year, these bacterioses can be found together or separately in this area. The Spanish Plant Genetic Resources Centre hold the active bean collection which includes 2661 accessions collected in Spain. A core collection, based on seed morphology and passport data, which includes 211 accessions, has been stabilised. The objective of this study was to evaluate the Spanish Core Collection against the three major bacterial pathogens in order to use it for breeding purposes.

P-26 BACTERIAL WILT IN DRY BEAN AND INHERITANCE OF RESISTANCE TO THE DISEASE IN EARLY ROSE AND PI 136725. Balasubramanian, P.M.[1]*, Conner, R.L.[2] and Hou, A.[2]. Agriculture and Agri-Food Canada, [1]Lethbridge Research Centre, Lethbridge, AB, [2]Morden Research Station, Morden, MB. *Presenter (parthiba.balasubramanian@agr.gc.ca)

Bacterial wilt, a seed-borne disease of dry bean, is caused by yellow, orange, purple or pink variants of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (Cff). Since 1995, a resurgence of bacterial wilt disease has been observed in Canada and the USA. Development of cultivars with resistance to Cff is the most economical and environmentally sustainable means of control for this disease. Bean genotypes with resistance to Cff were identified. Preliminary results from inheritance studies indicate the pink bean cv. Early Rose and germplasm line PI 136725 each carry a dominant resistance gene. Results also indicate the resistance genes are different. Molecular markers linked to these genes, when developed may enable rapid detection of bacterial wilt resistant lines.

P-27 BIOLOGICAL CONTROL OF PHYTOPATHOGENIC FUNGI IN BEAN (*Phaseolus vulgaris*, L.) WITH *Trichoderma atroviride* AND *Trichoderma virens.* Campelo[1], P., R.E. Cardoza[2], A. Lorenzana[1], M.R. Hermosa[3], E. Monte[3], S. Gutierrez[2], B. Reinoso, P.A. Casquero.[1]*. Areas of [1]Crop Production and [2]Microbiology, University of León. [3]Hispano-Portuguese Center for Agricultural Reseach, University of Salamanca. (Spain). (pedro-casquero@unileon.es).

Pathogen fungi are one of the major problems affecting bean establishment and growth in the northwest plateau of Iberian Peninsula. The biocontrol agents *Trichoderma atroviride* and *Trichoderma virens* have been tested to control fungi in bean, which had been isolated from bean fields in the province of León (Spain). Both biocontrol agents have shown good control of pathogenic fungi using *in vitro* conditions, but in general *T. virens* applied individually showed better control than *T. atroviride* with all tested isolates.

P-28 THE INTERACTION OF CHEMICAL CONTROLS FOR ANTHRACNOSE IN DRY BEANS. Gillard, C.L.[1*], S. Willis[1] and D. Depuydt[1]. University of Guelph, Ridgetown Campus. Ridgetown ON. [*]Presenter (cgillard@ridgetownc.uoguelph.ca).

Pyraclostrobin and azoxystrobin fungicides were evaluated alone and in combination with two seed treatments (metalaxyl/fludioxonil/azoxystrobin and diazinon/captan/thiophanate methyl) for anthracnose control in dry beans. Treatment differences for crop emergence and vigour, leaf vein and pod disease severity, crop yield, pick, dockage and economic returns to the grower will be discussed.

P-29 GENETIC VARIABILITY OF POPULATIONS OF THE WEB BLIGHT PATHOGEN OF COMMON BEAN FROM CENTRAL AMERICA AND THE CARIBBEAN.

N. Gonzalez[1], G. Godoy-Lutz[2], J. R. Steadman[1]*, S. McCoy[1] and B Higgins[1]. [1]Plant Pathology Department, University of Nebraska, Lincoln, NE and [2] Instituto Dominicano de Investigaciones Agropecuarias y Forestales (IDIAF). Dominican Republic. *Presenter (jsteadman1@unl.edu)

The genetic variability of populations of *Rhizoctonia solani* subgroups, AG-1-1IE and AG-1-IF were determined by Universal Rice Primers (UPR) and Inter Simple Sequence Repeat (ISSR). AMOVA analysis showed more variation within populations of both subgroups than between populations from Honduras, Puerto Rico and Dominican Republic indicating ongoing sexual reproduction. PHIst values between populations ranged from 0.1-0.3 suggesting limited gene flow between them. Mycelial compatibility tests indicated that most isolates were incompatible and not clonal.

P-30 ALTERNATE HOSTS FOR THE DRY BEAN BACTERIAL WILT PATHOGEN IN WESTERN NEBRASKA?

R. M. Harveson* PHREC, Scottsbluff and A. K. Vidaver, University of Nebraska, Lincoln. *Presenter (rharveso@unlnotes.unl.edu)

Bacterial wilt of dry beans, caused by *Curtobacterium flaccumfaciens* pv *flaccumfaciens* (*Cff*), was an economically important problem in western Nebraska decades ago, but has now re-emerged and been documented from more than 400 dry bean fields since 2004. Recently, bacterial isolates identified as *Cff* from soybeans, wheat, and corn have caused wilt-like disease symptoms on dry beans after artificial inoculations. Based on these findings, a survey of production fields in western Nebraska was conducted in 2008-2009 to document the incidence of bacterial wilt isolates found in association with other crops grown in rotation with dry beans. Approximately 10% of isolates obtained from 400 scouted production fields to date are suspected to be potential candidates based on several criteria and will be further tested for pathogenicity on dry beans.

P-31 POTENTIAL ABILITY OF BACTERIAL BLIGHT PATHOGENS TO MOVE BETWEEN SOYBEAN AND DRY EDIBLE BEAN.

Lamppa, R.S.*, Y.W. Chang, S.G. Markell, F. M. Mathew and R. S. Goswami. Department of Plant Pathology, North Dakota State University, Fargo, ND. *Presenter (robin.lamppa@ndsu.edu)

Pseudomonas syringae pv phaseoli (PSP) and *Pseudomonas syringae pv syringae* (PSS) cause bacterial brown spot and halo blight on dry beans and a similar pathogen *Pseudomonas syringae pv glycinea* (PSG) causes bacterial blight of soybean. These pathogens are known to be able to infect both crops which have traditionally been grown in different regions until recently. Soybeans and dry beans are now being seen in neighboring fields and are often grown in rotation in North Dakota which greatly increases the disease risk. Our study evaluated the pathogenicity and aggressiveness of PSG isolates from soybeans on dry beans and PSP and PSS isolates from dry beans on soybeans. Preliminary results indicate that certain PSG isolates may be more pathogenic on dry beans than soybean.

P-32 Legume ipmPIPE — A TOOL for DISEASE MANAGEMENT and EDUCATION in LEGUMES. M.A.C. Langham[1*], H.F. Schwartz[2], S.A. Tolin[3], C. Sutula[4], S. Ratcliffe[5], and K.F. Cardwell[6] [1]South Dakota State Univ., Brookings, SD; [2]Colorado State Univ., Fort Collins, CO; [3]Virginia Tech, Blacksburg, VA; [4]Agdia, Inc., Elkhart, IN; [5]Univ. of Illinois, Urbana, IL; [6]USDA-CSREES, Washington, DC [*]Presenter (marie_langham@sdstate.edu)

Legume ipmPIPE (Pest Information Platform for Extension and Education) enhances the role of extension specialists in IPM by providing near real-time access to observations, model output, pest management information, and diagnostic images at http://legume.ipmpipe.org. Communication tools also allow specialists to customize information for dissemination to crop consultants and growers. The diversity of pathogens, pests and hosts are uniquely suited to demonstrate the value of the ipmPIPE as a "one-stop shop" for legumes. Educators and stakeholders can easily obtain information on pathogens and pests identified in a specific area or general region. We will review progress to date and solicit input for the future.

P-33 IMPROVEMENT IN SCREENING FOR RESISTANCE TO *SCLEROTINIA SCLEROTIORUM* IN COMMON BEAN THROUGH CHARACTERIZATION OF THE PATHOGEN. S. McCoy[1,] L. Otto-Hanson[2,] B Higgins1 and Steadman, J.R. [1*].
[1]Plant Pathology Department, University of Nebraska, Lincoln, NE and 2 Plant Pathology Department, University of Minnesota, St. Paul, MN. *Presenter (jsteadman1@unl.edu)

Four microsatellite markers reported in the literature have been used to characterize 253 *Sclerotinia sclerotiorum* isolates collected from bean white mold screening nurseries and producers fields across the United States over five years. These isolates formed 86 mycelial compatibility groups (MCG) which are being compared to microsatellite data. Aggressiveness tests indicate isolates belonging to an MCG do not differ within an MCG, but significant differences in isolate aggressiveness have been found between MCG's.

P-34 REACTION OF COMMON BEAN CULTIVARS AND LINES TO BACTERIAL BROWN SPOT IN SOUTH AFRICA. Muedi, H.T.H.[1]*, D. Fourie[1], & N.W. McLaren[2]. [1]ARC-Grain Crops Institute, Potchefstroom, South Africa; [2]University of Free State, Bloemfontein, South Africa. *Presenter (MuediH@arc.agric.za)

Bacterial brown spot (BBS), caused by *Pseudomonas syringae* pv. *syringae* (Pss), is an important disease of common bean (*Phaseolus vulgaris*) in South Africa on account of its widespread occurrence and reported yield losses of 55%. All locally grown commercial cultivars are susceptible to BBS and it is therefore important that sources of resistance, that can be used in backcross breeding, be identified to improve resistance of these cultivars. Twenty seven dry bean genotypes were screened for BBS resistance in artificially infected field trials during the 2007/08 and 2008/09 growing seasons. Significant differences ($P<0.05$) in resistance were observed among genotypes and results correlated over seasons. Ratings ranging from 1.1-2.1 (on a 1-9 scale) indicated the availability of sources of resistance. Greenhouse screenings will be conducted to confirm field results.

P-35 NEW RACES OF THE BEAN RUST PATHOGEN FROM MICHIGAN AND NORTH DAKOTA. Pastor-Corrales M.A[1*], J. D. Kelly[2], S.G. Markell[3], E.M. Wright[2], H.E. Awale[2], J.G. Jordahl[3], R.S. Lamppa[3], F.M. Mathew[3], J.M. Osorno[4], and R.S. Goswami[3]. [1*]Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD 20705, [2]Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI 20705, [3]Department of Plant Pathology and [4]Department of Plant Science, North Dakota State University, Fargo, ND 58108. *Presenter (talo.pastor-corrales@ars.usda.gov)

Isolates of the bean rust pathogen (*Uromyces appendiculatus*) were found in 2007 and 2008 in Michigan and North Dakota respectively, infecting dry bean varieties with the *Ur-3* rust resistance gene that was previously resistant to rust. All isolates were characterized by inoculating them on a set of six Andean and six Middle American differential cultivars. An isolate from Michigan was characterized as race 22-2 and three isolates from North Dakota as race 20-3; both races infected cultivars Montcalm (Unknown rust resistance gene), Golden Gate Wax (*Ur-6*) and Aurora (*Ur-3*). Only the 22-3 Michigan Race infected Redlands Pioneer (*Ur-13*) and only the 20-3 North Dakota race infected Great Northern 1140 (*Ur-7*).

P-36 IDENTIFICATION OF SOURCES OF BACTERIAL WILT RESISTANCE IN COMMON BEANS (*Phaseolus vulgaris* L.). John A. Thomas*, Carlos A. Urrea, Robert M. Harveson, and Kathleen Nielsen. University of Nebraska- Lincoln, Panhandle Res. & Ext. Center, Scottsbluff, NE. *Presenter (jthoma1@unlnotes.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 1600 accessions from the International Center for Tropical Agriculture (CIAT) collection of common beans are being screened in the greenhouse to the most virulent Nebraska bacterial wilt isolate. Two seeds are planted for each accession. At the V2 stage of development, one plant is punctured between the first and second node with a needle after dipping into a 48-hour old bacterial culture, and the other plant is used as a negative control. Orion and Emerson are used as susceptible and resistant controls in an augmented block design. The plants are evaluated 7, 14, 21, and 28 days after inoculation for detection of bacterial wilt. A 1-9 scale, where 1= immune and 9= very susceptible is used. The experiment is replicated three times.

P-37 ROW SPACING AND NITROGEN FERTILIZATION EFFECT ON ARCHITECTURAL TRAITS AND YIELD LOSS OF DRY BEAN VARIETIES UNDER DIRECT HARVEST. Eckert, F. R.[1*], H. J. Kandel, B. L. Johnson, G. A. Rojas-Cifuentes, A. J. VanderWal, C. Deplazes, and J. M. Osorno. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND, 58108-6050. *Presenter **(**fernando.eckert@ndsu.edu)

The objective of this study was to evaluate the effect of Nitrogen (N) fertilization (56 kg ha^{-1}, and 112 kg ha^{-1}) and row spacing (30 cm, 46 cm, and 76 cm) on yield performance and yield loss due to direct harvesting of the pinto varieties Lariat, Stampede and Maverick. Preliminary conclusions show that Lariat was the highest yielding variety when direct harvested and also had the lowest seed loss. The increase in the N fertilization did not affect significantly the yield and yield loss of the varieties.

P-38 HYDRATION PATTERNS VARY IN DIVERSE DRY BEAN MARKET CLASSES AND CULTIVARS.

Hou, A.,[1*] Conner, R.L.,[1] and Balasubramanian, P.M.[2]
Agriculture and Agri-Food Canada, [1]Morden Research Station, Morden, MB; [2]Lethbridge Research Centre, Lethbridge, AB. *Presenter (anfu.hou@agr.gc.ca)

Understanding the dynamic patterns of the dry bean hydration process is critical for rapid screening of bean lines for improved hydration capacity and seed hardness. Ten genotypes of navy, pinto, black, great northern, and small red bean market classes were soaked for a period of 24 hours at room temperature, and 4 hours in boiling water. Dynamic changes in water absorption and percent stone seed will be discussed.

P-39 EVALUATION OF RAISED SEEDBED ON DRY BEAN PRODUCTIVITY AND QUALITY CHARACTERISTICS FOLLOWING INTERMITTENT FLOODING.

McAndrew, D.W.[1*] and R.L. Conner[1]. [1]Morden Research Station, Agriculture and Agri-Food Canada, Morden, MB. *Presenter (David.McAndrew@agr.gc.ca)

Dry bean often suffers yield losses of up to 100% due to flooding in the production areas in southern Manitoba. This study evaluates the effects of very slightly raised beds created with a potato planter on the survival, diseases, yield and quality of 4 market classes of dry beans. Irrigation was used in two of the three years to create conditions of waterlogged soils for at least 2 days prior to flower initiation. The raised beds have resulted in an average 10% yield increase and a significant reduction in common bacterial blight in several of the cultivars.

P-40 PERFORMANCE OF THREE MARKET CLASSES (PINTO, BLACK AND NAVY) ACROSS 24 YEARS IN MODERATE DROUGHT CONDITIONS IN THE NORTHERN PLAINS.

Angela M. Linares-Ramírez*[1], Juan M. Osorno[1], Gonzalo A. Rojas-Cifuentes[1], Steve Zwinger[2], and Blaine G. Schatz[2] [1]*Department of Plant Sciences, North Dakota State University, Fargo, ND 58108*[2]*Carrington Research and Extension Center, North Dakota State University, Carrington, ND 58421.* *Presenter (Angela.Linares@ndsu.edu)

Over the past two decades, dry bean variety trials had been conducted under dryland and irrigated conditions simultaneously at the Carrington Research Station, ND. The data provided gives us the opportunity to obtain a preliminary assessment of the performance of the market classes and varieties of dry beans under drought conditions. In general, black beans were the most affected by drought stress with a yield reduction of 36.3% (1130.6 kg ha-1), followed by navy and pinto beans with reductions of 35.5 and 32.4%. Data shows that among the three market classes, pinto beans resulted to be the less affected by drought stress.

P-41 MOLECULAR CHARACTERIZATION OF KEY GENES FOR FOLATE SYNTHESIS IN COMMON BEAN.

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

Previous results have shown that high levels of folate content in bean (*Phaseolus vulgaris*) varieties are correlated with high levels of expression of aminodeoxychorismate synthase (ADCS) and dihydroneopterin aldolase (DHNA) in the folate synthesis pathway. Positive clones of DHNA were identified from two BAC libraries (OAC-Rex and G19833), and sequencing of those clones is underway to characterize the gene. The gene ADCS was mapped on chromosome 4 by a SNP marker. The information should be useful for developing new tools to select beans with enhanced levels of folate content

P-42 SCREENING CULTIVARS OF *Phaseolus vulgaris* L. FOR HEALTH PROMOTING BENEFITS AND LONGEVITY EXTENSION IN *CAENORHABDITIS ELEGANS.*

Fitzgerald, V.K.*, Mensack, M.M., and Thompson, H.J. * Cancer Prevention Laboratory, Department of Horticulture & Landscape Architecture, Colorado State University, Fort Collins, CO. Presenter (vanessa.fitzgerald@colostate.edu)

Agricultural sciences rely almost entirely on chemical assays to screen the thousands of crop cultivars generated in a crop improvement program for potential human health benefits. Here we introduce a new, relatively high-throughput method incorporating the microscopic *Caenorhabditis elegans* nematode which is suitable for screening chemical extracts for bioactivity without the need for robotics. This system was chosen because longevity extension in *C. elegans* has been previously associated with human health benefits. Extracts from two market classes of dry bean, white kidney and navy, showed differential effects on longevity in *C. elegans* suggesting differential health benefits when consumed by higher animals.

P-43 VARIATION IN REACTION TO FUSARIUM SPP. IDENTIFIED IN A COMMON BEAN (Phaseolus vulgaris L.) POPULATION DEVELOPED FOR FIELD-BASED RESISTANCE TO ROOT ROT.

M.G. Ronquillo-López, C. Grau, and J. Nienhuis*, Dep. of Horticulture, University of Wisconsin, Madison, WI. *****Presenter (nienhuis@wisc.edu)

Root rot is a generic term used in beans (Phaseolus vulgaris L.) to describe redish-brown lesions on the hypocotyl and tap roots, vascular discoloration, foliar chlorosis, and seedling death all of which can result in yield reduction. Two Fusarium species, Fusarium oxysporum Schlecht. f.sp. phaseoli (FOP) Kendrick and Synder and Fusarium solani (Mart.) Sacc. f.sp. phaseoli (FSP) (Burkholder) W. C. Synder & H. N. Hans. are often associated with wilt and root rot symptoms in beans. Eagle is a white seeded Andean snap bean that is susceptible, and Puebla 152 is a black seeded Mexican landrace that is resistant to root rot in the Central Sand Region of Wisconsin. The objectives of this study were to determine if variation for reaction to FOP and FSP could be observed in the Eagle × Puebla 152 RIL population in which high levels of resistance to A. euteiches f.sp phaseoli had been previously identified. An additional objective was to determine if QTLs previously identified associ ated with resistance to A. euteiches f.sp phaseoli were consistent with those associated with resistance to FOP and FSP. The narrow sense heritabilities for foliar and root response to FOP observed in this experiment were 0.25±0.07 and 0.29±0.07, respectively. Similarly to FOP, the narrow sense heritability for FSP was 0.23±0.12. Two QTLs, W13.350 on linkage group B6, and AG13.600 on linkage group B8 were identified associated with FOP root and foliar reaction; and additional QTL, U12.500 on linkage group B2 was also identified associated with the FOP foliar response. The consistency of QTLs suggests that indirect selection for QTLs associated with FOP should result in improved resistance to both foliar and root symptoms. Two QTLs, AM2.400 and U20.1150 on linkage groups B3 and B8, respectively, were identified associated with resistance to FSP. The QTLs associated with FOP, FSP and A. eutiches, are independent, indicating that it may be possible to use RAPD markers to pyramid resistance to all three soil borne pathogens.

NOTES