BIENNIAL MEETING OF THE

BEAN IMPROVEMENT COOPERATIVE

2013 MEETING

PROGRAM AND ABSTRACTS

DoubleTree Hotel
Portland, Oregon, USA
October 27 – 30, 2013

Bean Improvement Cooperative
Portland, Oregon, USA

2013 BIC Program at a Glance

Sunday, 27 October		**Location**
5:00-9:00 PM	Registration	Main Lobby
Monday, 28 October		
7:00-8:15 AM	Registration & breakfast	PNW Foyer
7:00-8:15 AM	BIC Steering Committee	Portland
8:15-8:25 AM	Welcome and Introductions	PNW Ballroom
8:25-9:15 AM	***Frazier-Zaumeyer Distinguished Lectureship***	PNW Ballroom
9:15-10:15 AM	***Special session – New Landscapes in International Bean Research***	PNW Ballroom
10:15-10:30 AM	Coffee Break	PNW Foyer
10:30 AM-12:00 PM	***Special session – New Landscapes in International Bean Research***	PNW Ballroom
12:00-1:15 PM	Lunch on your own	
1:15-3:00 PM	***Session II Genomics***	PNW Ballroom
3:00-3:15 PM	Coffee Break	PNW Foyer
3:15-4:45 PM	***Session III Utilization***	PNW Ballroom
5:00-6:30 PM	Posters (authors present – even numbers)/ Reception hosted by America Pulse Association	Exhibit Hall
6:30 PM	Dinner on your own	
Tuesday, 29 October		
7:00-8:00 AM	Registration & Breakfast	PNW Foyer
8:00-9:45 AM	***Session IV Intellectual Property, Plant Breeding and Abiotic Stress***	PNW Ballroom
9:45-10:00 AM	Coffee Break	PNW Foyer
10:00 AM -12:00 PM	***Session V Plant Nutrition, Snap Bean Traits, and Biotic Stress***	PNW Ballroom
12:00-1:15 PM	Lunch on your own	
1:15-3:00 PM	***Session VI Plant Disease Resistance I***	PNW Ballroom
3:00-3:15 PM	Coffee Break	PNW Foyer
3:15-4:45 PM	***Session VII Plant Disease Resistance II***	PNW Ballroom
4:45-5:00 PM	Business meeting	PNW Ballroom
5:00-6:30 PM	Posters (authors present – odd numbers)	Exhibit Hall
6:30-7:00 PM	Cash bar	Willamette Ballroom
7:00-8:30 PM	Banquet	Willamette Ballroom
Wednesday, 30 October		
8:00-11:30 AM	W-2150; Phaseolus CGC	Adams Jefferson
11:30 AM- 1:00 PM	Lunch on your own	
1:00-6:30 PM	Regional Farm Tour	
7:00-9:00 PM	BIC Genetics Committee	Oregon

Abstracts –Oral Presentations

Frazier-Zaumeyer Distinguished Lectureship **Monday 28 October**	Moderator: Ken Grafton
8:25-9:15 AM	**The Changing Face of Bean Breeding; Past and Future.** Kelly, J.D. Department of Plant, Soil and Microbial Sciences, Michigan State University, MI 48824. (kellyj@msu.edu) Major changes have taken place in bean breeding programs to confront greater competition from major commodities, to gain better access to new technologies and funding opportunities, respond to the expanding scientific information and collaborations and meet the increased demand for different seed types suited to different management systems. Despite these changes, and the important international role that beans play in food security, productivity gains have been modest and have failed to keep pace with cereals. Do bean breeders have the knowhow and resources to address the real challenges confronting bean producers in the future?
Special session – New Landscapes in International Bean Research	Moderator: Jim Beaver
9:15-9:45 AM	**Enhancing Global Food Security through International Legumes Research.** Long, J. Bureau for Food Security, U.S. Agency for International Development, Washington, DC. (jlong@usaid.gov) Legumes research is an integral component of the Feed the Future Initiative's efforts to improve child nutrition and increase incomes of poor farmers, especially women, in developing countries. Feed the Future's legumes research portfolio has a significant emphasis on common bean both geographically and scientifically. Efforts range from the Central American highlands to East and Southern Africa and research activities span genetics and genomics, on-farm productivity, as well as social science research on farmers' adoption of new technologies and access to market opportunities. Emerging efforts on technology scaling will facilitate availability of and access to bean and other legume technologies for smallholder farmers to help improve their livelihoods.
9:45-10:15 AM	**Legume Innovation Lab Program Extension- Strategic Objectives and Research Portfolio.** Widders I.E.* and C. Donovan. Legume Innovation Lab Management Office, Michigan State University, MI. *Presenter (widders@anr.msu.edu) USAID's Bureau of Food Security extended the Feed the Future Innovation Lab for Collaborative Research on Grain Legumes (know previously as the Pulse CRSP) through September 2017. Strategic research objectives give priority to enhancing grain legume productivity, transforming grain legume systems and of enhancing dietary quality and nutrition of young children through increased grain legume consumption. An overview of collaborative research and capacity building projects supported in 14 countries and of coordination with the CG's Grain Legume program will be presented.

10:30-11:00 AM	**American Pulse Association: International Year of Pulses and Potential Impact on Global Research and Funding.** Rueda J.M. American Pulse Association, Moscow, ID (rueda@americanpulsecrops.org) In collaboration with Pulse Canada, Grains & Legumes Nutrition Council Australia and CICILS/IPTIC, the American Pulse Association is working towards the designation of 2016 as the International Year of Pulses (IYP). With the final step in the approval process scheduled for December 2013, efforts are underway to organize events and activities of the IYP. Strategic planning details of the Health, Nutrition & Food Security and Sustainability & Production working groups will be presented, and the potential impact of the IYP on global pulse research will be discussed.
11:00-11:30 AM	**The Grain Legumes CGIAR Research Program: Its Content and Value to the American Bean Community.** Beebe, S. Bean Program, CIAT, A.A. 67-13, Cali, COLOMBIA. (s.beebe@cgiar.org) The international agricultural research centers of the CGIAR have been reorganized around cross-center thematic programs known as CRPs or CGIAR Research Programs. One of these coordinates and integrates research on grain legumes, and involves CIAT, ICARDA, ICRISAT and IITA. The common bean is one of eight legume crops that currently forms part of the research agenda. Eight product lines have been formulated within the CRP, and bean participates in three of these with a heavy component of genetic improvement: tolerance to drought and low soil phosphorus; heat tolerance; and enhanced nitrogen fixation. Other research objectives of biotic stress resistance, crop management, market development, and demand analysis are folded into these product lines. While these products are targeted to low input systems in East and southern Africa and in Central America, drought and heat tolerance and nitrogen fixation are of wider interest, and the traits implicit in low P tolerance could be useful to improve the efficiency of inputs in more technified systems. Cross-legume learning will be beneficial to all research programs on legumes, and will be an additional positive output of the CRP.
11:30-12:00 AM	**Inheritance and Performance of Bruchid Resistance into Farmers' Preferred Common Bean (*P. Vulgaris*) Varieties In Tanzania.** Kusolwa P.M. [1]*, Mwatawala M.W. [1], Mwaitulo S. [1], Msolla S.N. [1], Mgembe E.R. [1], Muhamba T. [1] and Myers J.R.[2]. [1]Department of Crop Science and Production Sokoine University of Agriculture, Tanzania. [2]Department of Horticulture, Oregon State University, Corvallis, OR 97331. *Presenter (kusolwap@gmail.com) Bean bruchids (*Acanthoscelides obtectus*) are the major bean storage pest causing up to 100% loss of bean quality in household storage. Three major bean market classes and farmers' preferred varieties of dry common beans were introgressed with arcelins, alpha amylase inhibitor-like and phytohaemagglutinins seed storage proteins (SSPs) from tepary bean (*P. acutifolius*) through backcrossing. Confirmation of inheritance the SSPs by DNA and proteins markers were confirmed among progeny lines and their performance demonstrating levels of bruchid resistance are presented.

Session II Genomics	Moderator: Paul Gepts
1:15-1:30 PM	**Behind the Scenes of the Common Bean Genome.** McClean, P.E.[1*], Cregan, P.B.[2], Jackson, S.A.[3], Lee, R.[1], Mafi Moghaddam, S.[1], Mamidi, S.[1], Rokshar, D.S.[4],Schmutz, J.[4,5] and Song, Q.[2]. [1]Department of Plant Sciences, North Dakota State University, Fargo, ND; [2]Soybean Genomics and Improvement Laboratory, Agricultural Research Service, Beltsville, MD; [3]Center for Applied Genetic Technologies, University of Georgia, Athens, GA; [4]US Department of Energy Joint Genome Institute, Walnut Creek, CA; [5]HudsonAlpha Institute for Biotechnology, Huntsville, AL. *Presenter (phillip.mcclean@ndsu.edu) The recent release of version 1.0 of the common bean (*Phaseolus vulgaris* L.) genome sequence provides an unprecedented opportunity for the bean community to better understand the form and function of this essential societal crop and to use the sequence as a tool for crop improvement. Several examples will be presented that highlight aspects of the sequencing project and features of the genome itself that should be considered when using the sequence for detailed mapping and candidate gene identification. Principal among the features are the abundance and distribution of transposable elements and the location of the high- and low-recombination regions of the genome.
1:30-1:45 PM	**Federated Genomic Tools for Facilitating Crop Improvements Across Legume Species.** Cannon, S.B.[1*], Farmer A.D.[2]. [1]USDA-ARS, Ames, IA; [2]NCGR, Santa Fe, NM. *Presenter (steven.cannon@ars.usda.gov) More than a dozen "warm-season legumes" have been domesticated as crops for human consumption. Identifying corresponding trait loci between species is not straightforward, but is facilitated by widespread use of: common vocabularies to describe traits and growth characteristics; standard data formats; stable, accessible data repositories; and widely-used genomic and computational tools. We will describe some tools, methods, and formats for helping transfer information across legume crops, including a network of genomic web resources and tools; some common data formats and data collection templates; some protocols for sharing data between groups; and integrative data such as completed genome sequences and mappings between species. We will describe some ways that such resources can be used together, and will propose some next steps to build a stronger federation for sharing genomic information about legume crops.
1:45-2:00 PM	**Development and Application of Epigenomic Methods Towards a Better Understanding of the Common Bean Genome.** Kalavacharla, V.K*. and V. Ayyappan, College of Agriculture & Related Sciences, Delaware State University, Dover, DE 19901; *Presenter (vkalavacharla@desu.edu) One area that is lacking in common bean research is the understanding of the role of the epigenome in abiotic and biotic stress, and necessary tools and techniques to understand the interplay between the genome, transcriptome, and epigenome. To this effect, we have developed a method for chromatin immunoprecipitation sequencing (ChIP-seq) of common bean in order to develop a genome-wide survey

	of the location of two epigenetic marks in several genotypes of common bean. These initial studies serve as a first step towards development of a broader, more comprehensive understanding of the epigenomic landscape of common bean.
2:00-2:15 PM	**Association of Genes Coding for Phenypropanoid Pathway Enzymes and Regulatory Elements with Flower and Seed Coat Colour in *Phaseolus vulgaris.*** Yadegari Z.[1], Reinprecht Y.[1]., Perry G.E.[1], Siddiqua M.[1], Wright L.C.[1], McClean P.E.[2] and Pauls K.P.[1*] [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada. [2] North Dakota State University, Department of Plant Sciences, Fargo 58105, ND, USA *Presenter (ppauls@uoguelph.ca) Seed coat colour is a defining characteristic of market classes and genes involved in the phenylpropanoid pathway are thought to correspond to some of the classical seed coat colour genes. The locations of 18 phenylpropanoid pathway genes were mapped with the BAT93 × Jalo EEP 558 RIL population and 5 were mapped with an OAC Rex × SVM Taylor RIL population. Five of these genes mapped within 2-17 cM of colour gene loci and DFR1 mapped 14 cM from a flower colour locus. Further studies are needed to confirm the roles of the phenylpropanoid genes as potential colour genes.
2:15-2:30 PM	**Molecular Genetic Analysis of the *Phaseolus vulgaris P* Locus.** Mafi Moghaddam, S.[1*], Stonehouse, R.[2], Lee, R.[1], Mamidi, S.[1], Bello, M.[3], Miklas, P.[3], McClean, P.E.[1], Bett, K.E.[2] [1]Department of Plant Sciences, North Dakota State University, Fargo, ND; [2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK; [3]USDA-ARS, Prosser, WA *Presenter (samira.mafi@ndsu.edu) The ground factor, *P*, is a classical genetic locus in the field of genetics. It is a master switch controlling the production of colour compounds in common bean plant tissues. A combination of molecular markers, association mapping and diversity analysis has been used to identify a candidate gene which has a surprisingly obvious regulatory function.
2:30-2:45 PM	**High-Resolution Mapping of the *I* Gene Conferring Resistance to BCMV Using Bulked-Segregant Analysis and Whole-Genome Resequencing.** Bello, M.H[*] and Miklas, P.N. USDA-ARS, Vegetable and Forage Crop Production Unit, Prosser, WA. *Presenter (marco.bello@ars.usda.gov) *Bean common mosaic virus* (BCMV) and its related necrotic strain BCMNV, are the most prevalent potyviruses in common bean (*Phaseolus vulgaris*). Although molecular markers (e.g., SW13, SBD5, ROC11) for BCMV resistance are commonly employed in breeding programs, their usefulness may be hampered by gene pool specificity and recombination. Here, we combine bulked segregant analysis and next-generation whole-genome resequencing on a RIL population (G122/Montcalm) to discover causal polymorphisms in candidate disease resistance NBS-LRR genes at the *I* locus for development of gene-based markers for MAS.

2:45-3:00 PM	**What's So Different About Tepary Beans?** Bett, KE [1*], B. Tesfaye[1,3], L. Ramsay[1,2], A.G. Sharpe[2]. [1] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, [2] National Research Council, Saskatoon, SK, [3] Hawassa University, Ethiopia. *Presenter (k.bett@usask.ca) Targeted 3'-cDNA transcript profiling using 454 sequencing technology was carried out on 6 common bean (*Phaseolus vulgaris*) and 2 tepary bean (*Phaseolus acutifolius*) genotypes and SNPs were identified. The level of sequence diversity between the two species was too great to develop SNP assays that would work in both species so a 768-SNP Illumina GoldenGate array was developed for genotyping in each separately. An F_2 population from the cross W6 15578 (*P. acutifolius* spp. *acutifolius*) x PI 430219 (*P. acutifolius* spp. *tenuifolius*) was genotyped with the tepary array for genetic map development and comparison with common bean.
Session III Utilization	Moderator: Carlos Urrea
3:15-3:30 PM	**Nutrition Education and School Gardens to Promote the Consumption of Dry Beans.** Miles, C.[1*], K. Atterberry[1], L.A. Riddle[2], and D. Betz[2]. Washington State University; [1]Mount Vernon, Northwestern Washington Research and Extension Center, and [2]WSU Extension Whatcom County; *Presenter (milesc@wsu.edu) To increase consumption of dry beans among K-12 students, we created a STEM-based curriculum that combines exposure to dry beans in a school garden setting with classroom nutrition education. The garden project includes growing 'Rockwell', a local heirloom dry bean variety that has been grown on Whidbey Island since the 1880s. Other studies have shown that children who observe and participate in growing and tasting food are more likely to regularly consume the targeted food. In collaboration with the school food service staff, we will also be conducting a pre- and post-education evaluation of students' preferences for eating prepared dry beans in school meals using plate waste studies.
3:30-3:45 PM	**Overcoming Dry Bean Production Constraints in Western Washington.** Brook Brouwer[1*] Carol Miles[2], Kelly Atterberry[2], and Stephen Jones[1]. Washington State University - Mount Vernon Northwestern Washington Research and Extension Center; [1]Dept. Crop and Soil Sciences, and [2] Dept. Horticulture. *Presenter (brook.brouwer@wsu.edu) To identify constraints to dry bean production in northwest Washington, we developed and distributed an on-line survey to growers throughout the 12 county region. Of the 119 survey respondents, 108 are growing or would like to grow dry beans. Personal use was ranked as the primary reason for growing dry beans, followed by crop diversity (N=74). Being unable to dry beans in the field was ranked as the main challenge limiting production, followed by high labor demand and lack of access to suitable machinery (N=63). In conjunction with this survey, we collected seed of 20 heirloom dry bean varieties that have been grown in the region for more than 20 years, with some dating back to 1880s. We are conducting field trials to compare regional heirloom varieties with commercial standards for stand establishment, days to maturity, yield, and bean size.

3:45-4:00 PM	**Diversity for Cooking Time in Andean Dry Beans.** Cichy K. A.*[1] Wiesinger J.[1] Porch, T.[2] and Miklas, P.[3] [1]USDA-ARS Sugarbeet and Bean Research Unit, East Lansing, MI, USA. [2]USDA-ARS TARS, Puerto Rico. [3]USDA-ARS Prosser, WA. * Presenter (karen.cichy@ars.usda.gov) A diversity panel of 250 dry bean lines from the Andean gene pool was evaluated for cooking time. Cooking time ranged from 15 to 103 min with an average of 36 min. In depth characterization of two genotypes with contrasting cooking time but similar seed type and size was conducted.
4:00-4:15 PM	**Dietary Fiber and Oligosaccharide Content of Dry Bean Varieties.** Brick, M.A.[1*], D. Echeverria[1], A. Kleintop[1], H.J. Thompson[1], and J. Osorno[2]. [1]Colorado State University and [2]North Dakota State University. *Presenter (mark.brick@colostate.edu) Dietary fiber (DF) has been shown to be an important component in the human diet and intake is related to reduced incidence of heart disease, cancer, obesity, and type 2 diabetes. Seed from dry bean varieties (*Phaseolus vulgaris L.*) grown in Colorado and North Dakota as part of the Common Bean Coordinated Agricultural Project (Bean CAP) were analyzed for DF using the AOAC 2011.25 method. Total DF and oligosaccharide content ranged from 22.8 to 30.2 % and 3.70 to 5.45%, repectively.
4:15-4:30 PM	**Mineral Allocation to Pod Walls and Seeds in Common Bean.** Grusak M.A.[1]*, Coghlan C.J.[2] and Miklas P.N.[3]. [1]USDA-ARS Children's Nutrition Research Center, Dept. of Pediatrics, Baylor College of Medicine, Houston, TX; [2]St. Edward's University, Austin, TX; [3]USDA-ARS Vegetable and Forage Crop Research Unit, Prosser, WA. *Presenter (mike.grusak@ars.usda.gov) Common bean is an important source of dietary nutrients, energy, and fiber. Because we are interested in improving the mineral nutritional quality of bean seeds, we have investigated various temporal and spatial aspects of whole-plant mineral transport in an attempt to identify rate-limiting steps. For this study we focused on the role of pod walls in the trafficking of minerals to seeds. We analyzed final mineral content in seeds and pod walls of greenhouse-grown and field-grown Andean bean lines. Seed allocation of minerals ranged from >94% of total pod mineral for copper, iron, phosphorus, sulfur and zinc, to 42% of total pod mineral for calcium. We also measured the dynamics of mineral flow in developing pod walls and seeds. The profiles we have identified will be used to discuss strategies for manipulating pod and seed nutrient allocation in bean, in order to enhance seed nutritional quality.

4:30-4:45 PM	**Genomic Analysis of Mutations Conferring Storage Protein Deficiency in Common Bean.** Pandurangan S.[1,2], Crosby W.[3], Pauls K.P.[4] and F. Marsolais[1,2*]. [1]Department of Biology, University of Western Ontario, London, ON. Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, London, ON. [3]Department of Biological Sciences, University of Windsor, Windsor, ON. [4]Department of Plant Agriculture, University of Guelph, Guelph, ON. *Presenter (Frederic.Marsolais@agr.gc.ca) A series of genetically related lines of common bean (*Phaseolus vulgaris*) integrate a progressive deficiency in major storage proteins, the 7S globulin phaseolin and lectins. To understand the genomic basis for variations in protein profiles previously determined by proteomics, the four genotypes were submitted to short-fragment genome sequencing using an Illumina HiSeq 2000 platform. Reads were aligned to reference sequences from G19833, BAT-93 and OAC-Rex, and a genomic clone of the lectin locus from an arcelin-5 genotype. The results of the analyses identified mutations responsible for the lack of specific storage proteins, as well as polymorphisms associated with large differences in storage protein expression.
Session IV Intellectual Property, *Plant Breeding and Abiotic Stress,* **Tuesday, 29 October** Moderator: Juan Osorno	
8:00-8:15 AM	**What Ever Happened to General Public License?** Michaels, T. E.[1*] and J. R. Kloppenburg[2]. [1]Department of Horticultural Science, University of Minnesota Twin Cities, St. Paul, MN. [2]Department of Community and Environmental Sociology, University of Wisconsin – Madison, Madison, WI. *Presenter (michaels@umn.edu) At the 1999 BIC meeting in Calgary, AB, Michaels proposed a germplasm exchange agreement called General Public License for Plant Germplasm (GPLPG) to protect the unencumbered and free exchange of breeding material. Since then, public and private institutions alike have intensified the intellectual property protection of their plant germplasm releases, resulting in conditions and restrictions on use of this germplasm by other breeders. In 2011 a broad-based group of plant breeders, agricultural policy activists, farmer advocates and students responded by reviving the GPLPG proposal and forming the Open Source Seed Initiative (OSSI). OSSI recently drafted licenses that protect germplasm sharing and seeks comments from the plant science community on the utility of these licenses and broader discussion of appropriate intellectual property protection for plant germplasm.
8:15-8:30 AM	**Toward A Better Bean: Improving Genetic, Genomic, Breeding, and Crop Management Resources for Lima Bean (*Phaseolus lunatus*).** Johnson G.C.*[1], N. Donofrio[2], E.G. Ernest[1], T.A. Evans[2], N.F. Gregory[2], R.J. Wisser[2], K.L. Everts[3], B.C. [1]Department of Plant and Soil Sciences, Univ. of Delaware, Georgetown, DE, [2]Department of Plant & Soil Sciences, Univ. of DE, Newark, DE, [3] Department of Plant Science and Landscape Architecture, Univ. of Maryland, Salisbury, MD *Presenter (gcjohn@udel.edu) Lima bean is a cornerstone crop of the Mid-Atlantic vegetable processing industry, centered in Delaware, and extending into Maryland, New Jersey, and Virginia. There are multiple challenges to production in the region including diseases and

	lack of adapted cultivars. A sponsored Specialty Crop Research Initiative in lima bean is generating genomic tools to support the lima breeding program, developing improved identification, assessment and predictive tools and developing crop management practices to reduce the need for pesticides for four important diseases of lima bean: downy mildew (*Phytophthora phaseoli*), root knot nematode (*Meloidogyne incognita*), *Phytophthora capsici,* and white mold (*Sclerotinia sclerotiorum*).
8:30-8:45 AM	**Dry Bean Breeding and Genetics Research in South-Western Ontario.** T. H. Smith[1], T. Rupert[1], B. Zhang[1], A. J. Burt[1], W. Xie[1], R. Khanal[1], K. P. Pauls[1], and A. Navabi[1]*. Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program. *Presenter (Alireza.Navabi@agr.gc.ca). Since 2008, a collaborative dry bean (*Phaseolus vulgaris* L.) breeding program, formed through a merger of the University of Guelph and the federal government bean breeding programs has been responsible for public dry bean breeding efforts in south-western Ontario. The program targets developing high yielding, high quality dry beans of several market classes for sustainable production, with a focus on breeding for resistance to major biotic and abiotic stress factors. This presentation will report and discuss recent advances in developing dry bean germplasm and varieties in Ontario.
8:45-9:00 AM	**Ureide Accumulation in Bean Leaves During Conditions of Abiotic Stress.** Souter J.R.[1]*, K. Bett[2], and C. Todd[1]. [1]Department of Biology, University of Saskatchewan, Saskatoon, SK. [2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK. *Presenter (jodi.souter@usask.ca). Ureides, nitrogen transport molecules in tropical legumes, have been previously quantified as a tool to assess the capacity of nitrogen fixation. It has also been shown that ureides accumulate during purine remobilization and may serve as scavengers of reactive oxygen species during abiotic stress. Ureide accumulation during water limitation, chilling and induced oxidative stress will be discussed as well as the possibility of using ureide quantification as a tool to measure abiotic stress resistance in beans.
9:00-9:15 AM	**Drought Tolerance QTL Identified In The Buster X Ser 22 RIL Population.** Linares, A.M.[1*], C.A. Urrea[2†], T.G. Porch[3†], S. Mamidi[1], P.E. McClean[1], and J.M. Osorno[1]. [1]Dept. of Plant Sci., North Dakota State Univ., Fargo, [2]Univ. of Nebraska - Lincoln, Scottsbluff Res. & Ext. Center, NE, [3]USDA-ARS Tropical Agriculture Res. Sta., Mayagüez, PR. *Presenter (Angela.Linares@ndsu.edu) [†]The authors contributed equally to this work. Identification of loci associated with drought tolerance could be an important strategy for future Marker Assisted Selection. A population of 335 recombinant inbred lines was derived from the cross between 'Buster', a drought susceptible pinto cultivar, and SER 22, a drought tolerant small red germplasm line developed at CIAT. Evaluation in replicated irrigated and non-irrigated trials was performed at two locations (Mitchell, NE and Juana Díaz, PR) over three years (2011-2013), for a

	total of total of twelve environments. Three quantitative trait loci (QTL) for yield were found on two linkage groups using composite interval mapping, others QTL were identified for agronomic and physiological traits.
9:15-9:30 AM	**Evaluation of the Andean BeanCAP Lines to Terminal Drought in Western Nebraska.** Carlos A. Urrea, University of Nebraska, Panhandle Res. & Ext. Center, Scottsbluff, NE (currea2@unlnotes.unl.edu) Although dry beans are 100% irrigated in the Great Plains, drought is the most limiting abiotic stress affecting yield production. In recent years, ground water decline due to overuse has resulted in pumping restrictions in many areas of Nebraska. Identification of high-yielding, drought-resistant dry bean lines is needed in order to reduce dependence on irrigation water, lower costs of production, and increase profit margins for dry bean growers in western Nebraska. In 2013, 49 Andean BeanCAP lines were evaluated in replicated trials under drought and non-drought stress at Mitchell, NE, in irrigated and non-irrigated plots adjacent to each other. Moderate to high level of terminal drought stress were created under non-irrigated conditions. Daily rainfall during the growing season is being recorded. In addition to seed yield (kg ha^{-1}), data is being recorded for 100-seed weight (g), number of days to flowering and maturity, and leaf temperature. In order to quantify drought severity, drought intensity index, drought susceptibility index, and geometric mean will be estimated. The same set of lines was evaluated in North Platte, NE for common bacterial blight.
9:30-9:45 AM	**Identifying Heat Tolerant Lima Bean (*Phaseolus lunatus*) Germplasm and Development of Heat Tolerance Field Screening Techniques.** Ernest E.G.[1]*, R.J. Wisser[2] and G.C. Johnson[1]. [1]Department of Plant and Soil Sciences, University of Delaware, Georgetown, DE, [2]Department of Plant and Soil Sciences, University of Delaware, Newark, DE. *Presenter (emmalea@udel.edu) Heat stress reduces yields of May and early June planted lima beans (*Phaseolus lunatus*) on the Delmarva Peninsula. High temperatures during flowering and pod set reduce or delay set and can result in later harvest, lower yield and split sets. Breeding heat tolerant baby and Fordhook type lima beans is one goal of the University of Delaware lima bean breeding program. To this end, several approaches to field heat tolerance screening were tested on successive plantings with flowering during periods of low and high levels of heat stress: pod set ratings, use of a chlorophyll fluorometer to measure photosynthetic yield, counts of pollen shed onto stigma and style, and yield component measurements. A total of 18 genotypes were evaluated, including both known heat susceptible and reported heat tolerant varieties.

Session V Plant Nutrition, Snap Bean Traits, and Biotic Stress	Moderator: Phillip Griffiths
10:00-10:15 AM	**Genetic Variability for Nitrogen Fixation in the Andean Diversity Panel.** Kamfwa K*, Cichy K. and J, Kelly. Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI. *Presenter (kamfwake@msu.edu) Characterizing the genetic variability for biological nitrogen fixation (BNF) is the basis for its genetic improvement. The objectives of this study were (i) Characterize genetic variability for BNF and its associated traits in the Andean genepools (ii) Identify superior Andean genotypes for BNF. A diversity panel comprised of 270 Andean genotypes was evaluated in 2012 in the field and greenhouse in Michigan for BNF using Nitrogen difference and N^{15} Natural abundance methods. Significant differences among genotypes were identified for nodulation, chlorophyll content, biomass and total nitrogen indicating existence of genetic variability for BNF and traits associated with it. Some genotypes such as Mecosta and TZ-37 from Michigan (US) and Tanzania (Africa) respectively, showed consistent superior performance for BNF in both field and greenhouse experiments
10:15-10:30 AM	**Snap Bean Breeding for Enhanced Nitrogen Use Efficiency (NUE).** B.W. Hughey* and J. Nienhuis. Department of Horticulture, University of Wisconsin, Madison, WI. *Presenter (bhughey@wisc.edu) Two inbred backcross populations were developed using a high nitrogen fixing Mesoamerican dry bean landrace as the donor parent ('Puebla 152') and two snap bean cultivars ('Eagle' and 'Hystyle') as recurrent parents to combine a superior root with quality snap beans. Results from field evaluations designed to measure the Nitrogen Stability Index, an indicator of NUE, in a randomized split plot incomplete block design of these two populations show significant genotypic variation in regard to NUE indicating strong breeding potential for this trait. Incorporating NUE, a quantitative trait, in modern snap bean cultivars will lower input costs for farmers, increase production in organic systems, and combat water pollution issues associated with excessive N fertilizer use.
10:30-10:45 AM	**Estimation of Heritability for Pod Characteristics of Andean Snap Bean x Mesoamerican Dry Bean Population.** Raja Mohd Anuar R.F.* and James Nienhuis. Department of Horticulture, University of Wisconsin, Madison, WI. *Presenter (rajamohdanua@wisc.edu) Pod characteristics such as pod length, spur length, and pod shape are important in snap bean quality compared to the dry bean, where dry bean focus is more on the seed quality. The heritability of traits associated with snap bean domestication were estimated using a recombinant inbred line (RIL) population derived from a cross between an Andean snap bean cultivar (Eagle) and Mesoamerican dry bean landrace (Puebla 152). Seventy five RILs from the Eagle x Puebla 152 were evaluated in three consecutive years (2008-2010) at West Madison Agricultural Research Station, WI using a random complete block design (RCBD). Significant genotype x year (GxY) effects were observed for pod length, spur length, and pod shape. Nevertheless, the mean squares for the GxY were at least three times

	smaller than those associated with variation among genotypes. Heritability estimates were high for pod length and spur length, 0.93 and 0.92 respectively, while the heritability estimate was moderate for pod shape, 0.63. The high heritability of these traits suggests phenotypic based selection would result in producing superior quality in the common bean.
10:45-11:15 AM	**Uncovering the Genetic Basis of Sugar Accumulation in Snap Bean Pods.** Natalie Mello[1*], James Nienhuis[1], and Paul Bethke[2]. [1]Department of Horticulture, University of Wisconsin, Madison, WI. [2]USDA-ARS, Univ. of Wisconsin, Madison, WI. *Presenter (nmello@wisc.edu) Flavor is an essential component to the marketability of fresh and processed snap bean varieties, and sugar content is one major flavor determinant in the pods. The snap bean's nutritional benefits are also desirable. When these traits are bred in combination, snap beans become more marketable, especially in an increasingly health conscious population. This study explores the genetic basis behind variation in sugar content among green pod-type beans including commercially grown cultivars and inbred backcross (IBC) lines. Among pods in the selected IBC lines, sucrose, glucose, and fructose levels range from 0.038-33.09, 0.78-62.60, and 6.10-85.00 mg/g dry wt. respectively, and selected commercial cultivars range from 0.01-16.27, 0.04-60.34, and 3.29-72.22 mg/g dry wt. respectively. A key objective of this sugar profile analysis is to confirm putative QTLs associated with sugar accumulation in snap bean pods using SNP markers. A deeper understanding of genetic variation in pod sugar among these lines will facilitate development of new snap bean cultivars with more desirable sugar content and flavor.
11:15-11:30 AM	**Western Bean Cutworm, *Striacosta albicosta* (Smith) Lepidoptera: Noctuidae, Oviposition Preference, Larval Survival, and Insecticide Efficacy in Dry Bean.** Goudis, L.A.[1]*, R.H. Hallett[1], and C.L. Gillard[2] [1] School of Environmental Sciences, University of Guelph, Ontario, CA. [2]Department of Plant Agriculture, University of Guelph, Ontario, CA. *Presenter (lgoudis@uoguelph.ca) The western bean cutworm is a relatively new pest to Ontario, and its impact to the dry bean industry is not well understood. A series of greenhouse and laboratory studies were conducted to examine oviposition preferences and larval survival. Insecticide efficacy and timing trials were also performed in the field to determine their impact on western bean cutworm feeding on dry bean plants. Moths looking for oviposition sites do not seem to be influenced by dry bean market class when given access to eight market classes simultaneously. When examining larval feeding in a no-choice study, market class as well as tissue type appear to be important factors in determining larval survival. Low damage levels were seen in insecticide field trials with minor differences in efficacy between the differing active ingredients tested.

11:30-11:45 AM	**Occurrence of Endornaviruses In Wild, Landraces, and Cultivars of *Phaseolus vulgaris* from the Mesoamerican and Andean Regions.** Khankhum J. and Rodrigo Valverde*. Dept. of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA. *Presenter (ravalve@lsu.edu) Genotypes of wild, landraces, and cultivars of *Phaseolus vulgaris* from various countries of the two centers of domestication, Mesoamerica and the Andes, were tested for endornaviruses. Endornaviruses were found to be more prevalent in cultivars and landraces than in wild genotypes.
11:45-12:00 AM	**Heating Things Up for Controlling Seed-Borne Diseases in Dry Bean.** Friesen, A.P.[1]* W.R. Barton[2], D.E. Robinson[1], R.L. Conner[3] and C.L. Gillard[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON. [2]BASF Canada, Mississauga, ON. [3]Agriculture and Agri-Food Canada, Morden, MB. *Presenter (afriesen@uoguelph.ca) The use of microwave radiation to control seed-borne diseases of dry bean was evaluated in lab and field studies in 2012 and 2013 using seed infected with *Colletotrichum lindemuthianum, Xanthomonas axonopodis* pv. *phaseoli,* or *Pseudomonas syringae* pv. *phaseolicola* A maximum exposure time between 40-60 s was determined for a large and small seeded market class for each disease. The maximum exposure and a half rate were applied and were evaluated alone and in combination with two chemical seed treatments, a BASF experimental and an industry standard. When microwave radiation was applied no adverse effects were seen on emergence and vigour. In the lab, disease control was increased with the application of microwave treatment, but in field studies was similar to the infected control. The combination of microwave and chemical seed treatment provided the same level of control as the chemical seed treatments on their own.
Session VI Plant Disease Resistance I	Moderator: Alex Karasev
1:15-1:30 PM	**Characterized Isolates of *Sclerotinia sclerotiorum* can Facilitate Identification and Verification of Resistance to White Mold in Dry and Snap Beans.** R. Jhala, R. Higgins and J.R. Steadman*, University of Nebraska, Lincoln, NE. *Presenter (Jsteadman1@unl.edu) Phenotypic and genotypic variation of over 300 isolates of *Sclerotinia sclerotiorum* from the major bean production areas of the USA were described. Mycelial compatibility of groupings and microsatellite loci defined genetic relationships between the isolates while disease severity on inoculated bean stems separated isolate aggressiveness. Isolates with high or low aggressiveness and similar or distant relatedness will be available for screening for white mold resistance.
1:30-1:45 PM	**Changes in Primary and Secondary Metabolism Associated with Tolerance to *Sclerotinia sclerotiorum i*n Common Bean.** Heuberger AL[1*], Robison FM[1], Prenni JE[1], Schwartz HF[2], and Brick MA[3]. [1]Proteomics & Metabolomics Facility, [2]Bioagricultural Sciences & Pest Management [4]Soil & Crop Sciences; Colorado State University, Fort Collins, CO; *Presenter (adam.heuberger@colostate.edu)

	Common bean (*Phaseolus vulgaris* L.) metabolites associated with tolerance to white mold (*Sclerotinia sclerotiorum*) infection may provide novel molecular targets to breed for enhanced resistance. The metabolic changes that occur during *Sclerotinia* infection of a detached leaf were characterized using a non-targeted metabolomics workflow spanning primary and secondary metabolism of a tolerant and susceptible cultivar. Many metabolites were found to vary only in the tolerant cultivar and include compounds involved in plant defense cell signaling, cell homeostasis, phytoalexins and other processes. Overall, the diversity in metabolic changes observed in the tolerant cultivar point towards a multi-faceted mechanism for tolerance to *Sclerotinia*.
1:45-2:00 PM	**Comprehension of Genetic Variability and Virulence of *Colletotrichum lindemuthianum* in Common Bean.** Nunes, M.P.*, M.C. Gonçalves-Vidigal, G.F. Lacanallo, and G.K. Coimbra. Departamento de Agronomia, Universidade Estadual de Maringá, Paraná, Brazil. *Presenter (nunesmpb@yahoo.com.br). The present study aimed to gather data from diversified countries regarding the incidence of common bean *Colletotrichum lindemuthianum* physiological races based on described literature and binary nomenclature system from the period of 1991 to 2013. The data investigation revealed incidence of 247 distinct races in 28 different countries, demonstrating the wide variability of this pathogen. Disease control is a worldwide concern and it depends on constant monitoring of the pathogen, due to wide variability and emergence of new races.
2:00-2:15 PM	**The Transmission and Control of Anthracnose (*Colletotrichum lindemuthianum*) in Dry Bean (*Phaseolus vulgaris L.).*** E. LeClair[1]*, R. Connor[2], D. Robinson[1], and C. Gillard[1], [1]Department of Plant Agriculture, University of Guelph Ridgetown Campus, Ridgetown, ON, N0P 2C0, [2]Agriculture and Agri-food Canada, Morden, MB. *Presenter (eleclair@uoguelph.ca) Disease transmission by common materials, chemical controls and the interaction of these factors was examined for anthracnose (*Colletotrichum lindemuthianum)* in dry beans (*Phaseolus vulgaris* L.) during 2012 and 2013 field seasons*. C. lindemuthianum* was transmitted via denim, leather, rubber and metal in a dry and wet bean canopy using two artificial anthracnose inoculums as well as naturally infected plants. Differences in anthracnose control were found when evaluating the efficacy of foliar fungicide standards and potential new products. Disease transmission of *C. lindemuthianum* on rubber occurred despite a foliar fungicide application immediately after inoculating plants in both a dry and wet bean canopy.
2:15-2:30 PM	**Development of Molecular Techniques for Detection of Pathogenic Isolates of *R. solani* in Beans.** Mosquera G.M., Cotes C., and Jara C.* Cento Internacional de Agricultura Tropical, Cali,Colombia. *Presenter (c.jara@cgiar.org) In order to establish a method of diagnosis for rapid and specific identification of pathogenic strains of Rhizoctonia solani, pathogenicity of 19 isolates from beans, 1 from rice and 2 from Brachiaria were tested, in a set of bean varieties in

	greenhouse conditions at CIAT. The mycelia of the strains, was used in DNA extraction. The sequences obtained were purified and analyzed for conserved fragments that were implemented in the design of primers able to recognize those isolates found to be pathogenic for beans. After examining the sequences, we were able to design two primers, the first one (RhP), in combination with the first ITS1, is able to discriminate all isolates pathogenic on bean, Rice Brachiaria and non-pathogenic. The second primer obtained (rhfp), also of 20bp (5'-GACCTCCAATACCAAAGCAG-3 '), was designed in conjunction with the first ITS1, was able to specifically detect pathogenic isolates *R. solani* in beans.
2:30-2:45 PM	**Host QTL by Strain Interaction and Discovery of New QTL for Common Bacterial Blight Resistance in the VAX Dry Bean Breeding Lines.** Viteri, D.M.[1*], J. Trapp[2], P. Cregan[3], P. N. Miklas[2], and S.P. Singh[1]. [1]Plant, Soil and Entomological Sciences Department, University of Idaho, Kimberly Research & Extension Center, 3793 North 3600 East, Kimberly, ID 83341-5076; [2]USDA-ARS, Vegetable and Forage Crop Research Unit, 24106 N. Bunn Rd., Prosser, WA 99350. [3]USDA-ARS, Soybean Genomics and Improvement Laboratory, BARC-West, Beltsville, MD 20705. *Presenter (dviteri@uidaho.edu) Common bacterial blight is a severe disease of common bean worldwide. Low levels of resistance occur in common and scarlet runner beans and the highest levels in the tepary bean. The BC420 resistance QTL from the tepary bean is linked with undesirable seed coat color and the SU91 QTL is associated with low yield, thus justifying search for new resistance QTL. Identification of a new major tepary bean derived QTL in VAX 1 and VAX 3 breeding lines and its interaction with previously known resistance QTL will be discussed.
2:45-3:00 PM	**Identifying CBB-Resistance Gene Candidates through Comparative Genomics between OAC-Rex and G19833.** Perry G.E.[1*], Dinatale C.[2], Xie W.[3], Navabi A.[3], Reinprecht Y.[1], Crosby W.[2], Yu, K.[3], Shi C.[3] and Pauls K.P[1]. [1]University of Guelph, Department of Plant Agriculture, Guelph, ON. [2]Department of Biology, University of Windsor, Windsor ON. [3]Agriculture and Agri-Food Canada, Guelph, ON. [4]Agriculture and Agri-Food Canada, Harrow, ON. *Presenter (perryg@uoguelph.ca) Genetic resistance to common bacterial blight, *caused by Xanthomonas axonopodis* pv. phaseoli, in *Phaseolus vulgaris* has been shown to involve multiple QTL across many chromosomes, with the SU91 marker on chromosome 8 as the most significant contributor in varieties derived from interspecific crosses with *P. acutifolius*. As part of efforts to fully sequence the genome of OAC-Rex, a CBB-resistant, white bean variety of Mesoamerican origin, comparative genomics were used to compare the gene content surrounding the Pv-CTT001, SU91 and SAP6 markers on chromosome 4, 8, and 10, respectively, between G19833 and OAC-Rex. Fifty nine genes unique to OAC Rex were identified, with resistance gene homologues making up the largest category (10 genes identified). Two unique genes in OAC-Rex located within the SU91 resistance QTL have homology to Niemann Pick cholesterol transporters as well as *P. acutifolius* ESTs, and may be potential sources of CBB resistance.

Session VII Plant Disease Resistance II	Moderator: Jim Steadman
3:15-3:30 PM	**Breeding Common Bean for Quantitatively Inherited Disease Resistance.** Singh, Shree P. University of Idaho, 3793N 3600E, Kimberly, ID 83341. (singh@kimberly.uidaho.edu) Several bacterial, fungal, and viral diseases adversely affect common bean production worldwide. Quantitatively inherited partial resistance to some major diseases may be found in different common bean races and gene pools, which complicate the breeding process. Breeding strategies for introgressing, pyramiding, and transferring high levels of resistance into cultivars will be described.
3:30-3:45 PM	**Screening the Andean Diversity Panel for Reaction to Rust Under Field Condions In Cedara, Kwazulu-Natal, South Africa.** Pastor-Corrales M.A.[1*], D. Fourie[2], and H.T. Muedi[2]. [1]Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD; [2]ARC-Grain Crops Institute, Potchefstroom, Republic of South Africa. *Presenter (talo.pastor-corrales@ars.usda.gov) We evaluated the reactions of 305 ADP common bean entries and 30 check cultivars to the bean rust pathogen (*Uromyces appendiculatus*) under field conditions in Cedara. The rust disease was quite severe throughout the field in all susceptible check cultivars. A total of 75 entries were resistant to rust, 99 entries were susceptible, and the rest were intermediate. The Mesoamerican *Ur-5* and *Ur-11* rust resistance genes were highly resistant, without any visible rust symptoms. On the other hand, the Andean *Ur-4* and *Ur-6* rust resistance genes were very susceptible.
3:45-4:00 PM	**How to Improve Root Rot Controlled Assays to Simulate Better the Conditions Found in Field.** Mosquera, G*., Jara, C., Cotes, C., Arredondo, V., Castellanos, G., and Beebe, S. Agrobiodiversity Research Area, International Center for Tropical Agriculture (CIAT). Cali, Colombia. *Presenter (G.M.Mosquera@CIGAR.ORG) Root rot diseases are becoming more relevant for several crops including beans. Different to foliar diseases, root rots imply additional parameters that should be take into account to assure good correlation between the results obtained under greenhouse and those observed under field conditions. Some of these parameters are being analyzed to adjust protocols designed to screen bean germplasm against root rot pathogens under greenhouse conditions, to identify sources of resistance.
4:00-4:15 PM	**Mapping QTL for Root Rot Resistance, Root Traits, and Morphological Traits in a Common Bean Recombinant Inbred Population.** Hagerty C.H* and J.R. Myers. Department of Horticulture, Oregon State University, Corvallis, OR. *Presenter (hagertyc@science.oregonstate.edu) We evaluated a Mesoamerican x Mesoamerican *P. vulgaris* RIL population for root rot resistance, and several snap bean processing-related traits. The RIL population was genotyped using the Illumina 10,000 SNP BARCBEAN6K_3 Beadchip through

	the BeanCAP. Our study yielded several QTL including QTL for *Fusarium solani* root rot, *Aphanomyces euteiches* root rot, root architecture, pod shape, and pod strings.
4:15-4:30 PM	**Genotyping-By-Sequencing (GBS) Enabled Mapping and Marker Development for the By-2 Potyvirus Resistance Allele.** Hart J.P.[1]* and P.D. Griffiths[1]. [1]Department of Plant Breeding and Genetics, Cornell University, Geneva, NY.*Presenter (jph248@cornell.edu) In light of recent snap bean virus-complex epidemics in the United States, there is enhanced relevance and value in the renewed characterization, evaluation, and potential deployment of multiple-potyvirus resistance conditioned by the *By-2* allele. We employed a GBS protocol, publicly available bioinformatics tools, and developed a novel strategy to identify and validate highly significant SNPs in our germplasm to within a 114kb region on chromosome 2 where several candidate genes are present. This research generates new knowledge and hypotheses in common bean-potyvirus interactions, develops important tools for future research, and enables new opportunities for marker-assisted gene pyramiding and the development of multiple-virus resistant common bean cultivars.
4:30-4:45 PM	**A Recombinant of *Bean Common Mosaic Virus* Induces Whole Plant Necrosis in an *I* Gene Bearing Line of Common Bean.** Feng, X., A.R. Poplawsky, and A.V. Karasev*. Department of PSES, University of Idaho, Moscow, ID. *Presenter (akarasev@uidaho.edu). We describe biological and molecular characterization of a new *Bean common mosaic virus* (BCMV) isolate, BCMV-RU1m (pathotype VII, serotype B), that is able to induce severe whole plant necrosis in bean cultivar Jubila carrying the *I* gene. The whole genome of BCMV-RU1m was cloned, sequenced, and for the most part found 98-99% identical to the non-necrotic BCMV isolate RU1-OR (also pathotype VII). Analysis of the nucleotide sequence for BCMV RU1m revealed that it originated through a recombination event between BCMV RU1-OR and a yet unknown potyvirus, with a *ca.* 1-kb fragment of an unknown origin in the RU1m genome likely linked to its ability to induce necrosis in beans carrying the *I* gene.

Monday, 28 October 2013 5:00 – 6:30 PM (authors with even numbers present)

Tuesday, 29 October 2013 5:00 – 6:30 PM (authors with odd numbers present)

P-01

***DREB* Genes as Candidates for Improving Drought Tolerance in Common Bean.** Konzen E.R.[1*]; Recchia G.H.[1]; Cassieri F.[1]; Caldas D.G.G.[1]; Berny J.C.[2]; Gepts P.[2]; Tsai S.M[1]. [1]Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, SP, Brazil. [2]Department of Plant Sciences, University of California, Davis, CA.*Presenter (erkonzen@cena.usp.br)

Drought episodes constantly affect common bean yield and therefore several breeding efforts have been started in order to develop drought tolerant cultivars. *DREB* (Dehydration Responsive Element-Binding) genes are strong candidates for marker-assisted selection (MAS) aimed at drought tolerance since they are frequently induced by water deficit treatment and SNP markers directly associated to tolerance have been reported for other species. We performed an *in silico* search and categorized 54 putative *DREB* genes for common bean. Four of these genes, named *PvDREB1*, *PvDREB2A*, *PvDREB5* and *PvDREB6B*, showed different expression profiles under dehydration conditions when analyzed by qRT-PCR. These genes were cloned and are being resequenced in a set of common bean genotypes in order to find SNPs among contrasting parents. These SNPs will be further converted to markers for mapping *DREB* genes in segregating populations, in an attempt to associate these markers to drought tolerance traits in common bean.

P-02

Population Development to Investigate Drought Adaptation Within the Mesoamerican Gene Pool of Common Bean. Berny J.C[*], A. Palkovic, M. Gilbert, and P. Gepts. Department of Plant Sciences, University of California, Davis, CA.*Presenter (jcberny@ucdavis.edu)

Drought is one of the major constraints to common bean productivity. Genetic improvement for drought adaptation within the domesticated germplasm has been relatively effective, but mostly derived from a single eco-geographic race. In addition, variation within the wild ancestor, which is potentially adapted to drought-prone environments, remains untapped. We are surveying the genetic variation within the Mesoamerican gene pool and mechanisms of drought adaptation through QTL analyses of newly developed complex populations. We are developing three backcross recombinant inbred populations between a single domesticated parent (SEA5) and three wild accessions that comprise a wide range in rainfall. To assess variation within the domesticated gene pool, we are developing a multiparent population with a modified 8-way cross, using elite germplasm from different races, market classes, and mechanisms of drought adaptation.

P-03

Estimates of Genetic Parameters in Common Bean (*Phaseolus vulgaris* L.) Under Drought Stress. Martins, V.S.[1], G.F. Lacanallo[1], D.S.Y. Nanami[1], V. Moda-Cirino[2], M.C. Gonçalves-Vidigal[1], and P.S. Vidigal Filho***.** **[1]**Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil, 87020-900; [2]Instituto Agronômico do Paraná, Londrina, Paraná, Brazil. [*]**Presenter** (psvfilho-@uem.br).

The parents and the generations F_1, F_2, BC_1 and BC_2 from the Perola (drought tolerant) × LP97-28 (low drought tolerance) cross, under water stress, were evaluated by estimates of genetic parameters for yield (PROD) weight of hundred seeds (M100S), number of pods per plant (NVP) and number of seeds per pod (NSV) of common bean. The results showed the predominance of additive gene effects and the genetic gain which magnitude value were 3.15, 6.64, 2.91 and 1.54%, respectively, for PROD, M100S, NSV and NVP.

P-04

Genetic Analysis and Yield Gain in Common Bean Segregant Populations Under Drought Stress.
Lobato, A.K.S.[1], P.S. Vidigal Filho[1*], G.F. Lacanallo[1], V.S.R. Martins[1], V. Moda-Cirino[2], and M.C. Gonçalves-Vidigal[1]. [1]Departamento de Agronomia, Universidade Estadual de Maringá, PR, Brazil, 87020-900; [2]Instituto Agronômico do Paraná, Londrina, Paraná, Brazil. [*]Presenter (psvfilho@uem.br)

The objective of this study was to evaluate the genetic control of grain yield and its primary components in the parental and F_1, F_2, BC_1 and BC_2 generations derived from the IPR-Uirapuru (drought tolerant) × LP 97-28 (low drought tolerance) cross, when submitted to drought stress conditions. The results showed predictable genetic gains of 43.5% for production, 15.7% for 100 seed weight, 34.1% for number of pods per plant and 16.1% for number of seeds per pod, demonstrating higher contributions of additive gene effects in the genetic control of the studied characteristics.

P-05

Identification of QTL for Drought Tolerance and Characterization of Extreme Phenotypes in the Buster X Roza Mapping Population. Trapp, J.[1*], Phillip Miklas[1], Carlos Urrea[2], Perry Cregan[3], [1]USDA-ARS, Prosser, WA; [2]University of Nebraska-Lincoln; [3]USDA-ARS, Beltsville, MD. [*]Student Presenter (jennifer.trapp@ars.usda.gov)

Terminal and intermittent drought limits dry bean production worldwide. The Buster/Roza RIL population has been screened for drought tolerance across multiple years/locations. QTL have been identified for yield response under stress and further characterization of the differential response to drought among RILs representing phenotypic extremes has been initiated.

P-06

Screening of Selected Andean Diversity Panel (ADP) Varieties of Common Bean (*Phaseolus vulgaris* L.) Under Low Fertility Stress in Tanzania. Eninka Mndolwa [*1], Phil Miklas[1] and Susan Nchimbi-Msolla[2] [1] USDA-Prosser, Washington [2]Sokoine University of Agriculture, Morogoro-Tanzania. *Presenter (ejmndolwa@yahoo.com).

The preliminary results for 95 ADP lines screened under low fertility soils in Morogoro region Tanzania 2012/2013 indicates that, there is variation among lines in yield and yield component data at ($P \leq 0.05$) also there is significant correlations between nodules and yield. This could be contributed to differences in genotypes since the environmental factors and the management of the crop was similar. These are preliminary results, further studies are still going on among the lines evaluated and the best performing lines will be selected then advanced in the breeding programme for fertility stress.

P-07

Association of Common Bean Endornaviruses with Increase in Seed Germination, Grain Yield, and Interaction with other Plant Viruses. Khankhum J.[1], Aumpuchin P.[1] and Rodrigo Valverde[1*]. [1]Dept. of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA. [*]Presenter (ravalve@lsu.edu)
We conducted comparative studies between two lines of the common bean cultivar Black Turtle Soup, one infected with endornaviruses and the other virus-free. Seeds of the virus-infected line germinated

earlier, plants matured earlier, and grain yield was higher than the virus-free line. However, the virus-infected line was very susceptible to systemic infection by *Tobacco ringspot virus*.

P-08

Biocontrol of *Rhizoctonia solani* against *Trichoderma* spp.: Membranes and Dual culture. Influence of the Isolation *Rhizoctonia solani* and *Trichoderma* spp. on Germination of Bean. Mayo, S.[1]; González, O. [1]; Rodríguez, A. [1]; Campelo, M.P. [1]; Lorenzana, A. [1]; Gutiérrez, S. [2]; Casquero, P.A. [1*]. [1]Department of Agrarian Engineering and Sciences. Institute of Environment, Natural Resources and Biodiversity. [2]Department of Molecular Biology. University of León. Avenida de Portugal, 41; 24071 – León (Spain). *Presenter: (smayp@unileon.es)

It was evaluated the influence of the isolation *Rhizoctonia solani* on germination of bean along with the presence and/or absence of the biocontrol agent *Trichoderma* in the culture substrate.

P-09

Influence of the Isolation *Rhizoctonia solani* and *Trichoderma* spp. on Germination of Bean. Mayo, S.[1*]; González, O. [1]; Rodríguez, A. [1]; Campelo, M.P. [1]; Lorenzana, A. [1]; Gutiérrez, S. [2]; Casquero, P.A. [1]. [1.] Department of Agrarian Engineering and Sciences. Institute of Environment, Natural Resources and Biodiversity. [2.] Department of Molecular Biology. University of León. Avenida de Portugal, 41; 24071 – León (Spain). *Presenter: (smayp@unileon.es)

It was evaluated the biocontrol capability of 24 isolations of *Trichoderma* against *Rhizoctonia solani* by in vitro tests, such as the use of membranes and the dual culture.

P-10

Tolerance to Temperature and Salinity Of *Rhizobium* Isolates Obtained from Different Common Bean Genotypes. Cardoso, A. A.[1*], Andraus, M. P.[1], Ferreira, E. P. B.[2].
[1]School of Agronomy, Universidade Federal de Goiás, Goiânia, Goiás, Brazil. [2]Embrapa Arroz e Feijão, Santo Antônio de Goiás, Goiás, Brazil. *Presenter (aline.assiscardoso@gmail.com)

Aiming to evaluate the tolerance to salinity and temperature of *Rhizobium* isolates obtained from 11 genotypes of common bean cultivated in soil collected in the states of Goiás, Minas Gerais and Paraná, 114 rhizobia isolates and the three pattern strains SEMIA 4077, SEMIA SEMIA 4080 and SEMIA 4088 were tested under different temperature and salinity conditions on the laboratory of Soil Microbiology of Embrapa Rice and Beans. The isolates stemmed from genotypes 2 and 8 presented more bacteria which have grown under conditions of highest temperature and salinity. Genotype 2 was that amounted more bacteria among genotypes.

P-11

Analysis Of The Symbiotic System Bean-Rhozobia Under Water Stress Conditions In Greenhouse.
De Ron, A.M.[1]*, A.P. Rodiño[1] and M. Riveiro[2]. [1] Biology of Agrosystems, MBG-CSIC, Pontevedra, Spain. [2] Agricultural Experimental Station "Baixo Miño", Salceda de Caselas, Spain. *Presenter (amderon@mbg.csic.es)

The symbiotic system common bean-rhizobia is often influenced by the availability of water in the soil. To assess this influence, ten common bean landraces and breeding lines, some of them tolerant to drought, were inoculated with 10 *Rhizobium* strains (eight local and two reference ones) in greenhouse under two different conditions: irrigation and water stress. Aerial dry matter of the plant, root dry matter, nodule number and nodule dry matter were evaluated and the variation detected in these characters was analyzed by ANOVA.

P-12

QTL Analysis of Biological Nitrogen Fixation and Agronomic Traits in the Puebla/Zorro RIL Population.

Heilig, J.A.[1*] and J.D. Kelly[1]. Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, MI. [*]Presenter (heiligja@msu.edu)

Improved Biological Nitrogen Fixation (BNF) in dry beans would help to improve yields, increase the area where dry beans can be grown, and reduce dependence on N fertilizer inputs. A black bean RIL population resulting from a cross of the landrace selection Puebla 152 and the commercial variety Zorro was developed to study the genetics of BNF and transfer the enhanced BNF ability of Puebla 152 (Type III growth habit) into the efficient Zorro (Type II). RILs were genotyped using the SNP markers developed by the BeanCAP. Phenotypic data was recorded in the field, greenhouse, and lab. QTL for traits such as root biomass and distribution, biomass, and percent N derived from the atmosphere, which are associated with BNF have been identified. These QTL may serve as markers for further breeding of genotypes with enhanced BNF.

P-13

Maintenance of Biological Nitrogen Fixation On Common Bean Genotypes With Different Growing Cycles. Andraus, M. P.[1]*, Cardoso, A. A.[1], Ferreira, E. P. B.[2]. [1]School of Agronomy, Universidade Federal de Goiás, Goiânia, Goiás, Brazil. [2]Embrapa Arroz e Feijão, Santo Antônio de Goiás, Goiás, Brazil. *Presenter (michelandraus@gmail.com)

Aiming to evaluate the nodule activity of common bean genotypes with different growing cycles a field experiment was conducted at Embrapa Rice and Beans. It were evaluated common bean cultivars with early cycle, half-early cycle, normal cycle and late cycle, in a total of 22 cultivars. The seeds were inoculated with commercial inoculant composed by three *Rhizobium tropici* strains. At different phenological stages (V4, R5, R6, R7 and R8) two plants were collected from each plot. For each plant was determined leaf area (LA), and nodules activity (NA) in each of the phases. The cultivars showed peak of NA in phase R5, with subsequent decrease until complete senescence. The values of leaf area were increasing throughout the phenological stages, being highest in cultivars with normal cycle and late cycle.

P-14

Nodulation Response of Common Bean Genotypes with Different Growing Cycles. Ferreira, E. P. B.[1*], Andraus, M. P.[2], Cardoso, A. A.[2] [1]Embrapa Rice and Beans, Santo Antônio de Goiás, Goiás, Brazil. [2]School of Agronomy, Goiás Federal University State, Goiânia, Goiás, Brazil. *Presenter (enderson.ferreira@embrapa.br)

Aiming to evaluate the nodulation of common bean genotypes with normal and late growing cycles a pot experiment was conducted under greenhouse conditions at Embrapa Rice and Beans. Seeds of 9 normal cycle genotypes and 2 late cycle cultivars were inoculated with commercial inoculant composed by three *Rhizobium tropici* strains. Evaluations of number of nodules (NN), nodules dry mass (NDM) and nodules activity (NA) were done at different phenological stages (V4, R5, R6, R7 and R8). Greater values of NN and NA were found at V4, R5 and R6 stages and NDM at R6 stage. Cultivars Pérola (normal cycle) and Vereda (late cycle) showed the highest NN and BRS Executivo (normal cycle) the lowest one. There was not observed significant difference for NDM and NA among cultivars.

P-15

Phenotyping Root and Shoot Traits in Common Bean (*Phaseolus vulagris* L.) using RILs. F.J. Ibarra-Perez[1], J.G. Waines[2] and B. Edahie[2] [1]CE Cotaxtla, INIFAP, Carretera Veracruz-Córdoba Km. 34, Veracruz, Mexico. [2]University of California Riverside, Riverside, CA, 92521-0124.
*Presenter (Ibarra.francisco@inifap.gob.mx)

Relatively little effort has been devoted to the selection of desirable root traits in common bean (*Phaseolus vulgaris* L.) breeding programs, mainly due to the lack of appropriate screening techniques to evaluate large segregating populations or recombinant inbred lines (RILs). The phenotyping of the root system architecture was undertaken using a series of 120 RILs from the cross Zorro / Puebla 152 grown up to plant maturity under glasshouse conditions.

P-16

Population Structure and Genetic Diversity of Common Bean Accessions (*Phaseolus vulgaris* L.) from Brazil. Valentini, G.[1*], L.D. Moiana[2], N.N.A. Mindo[2], P.S. Vidigal Filho[1] and M.C. Gonçalves-Vidigal [1]Departamento de Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brazil, 87020-900; [2]Instituto Agronômico do Paraná, Londrina, Paraná, Brazil. [2]Instituto de Investigação Agrária de Moçambique. Av. das FPLM, 2698. Maputo, Mozambique. [*]Presenter (Giseli.Valentini@ars.usda.gov)

The objective of this study was to analyze the genetic structure of common bean accessions from South and Midwest regions of Brazil using microsatellite molecular markers distributed throughout the genome. Genetic diversity and population structure results revealed the formation of two major groups, Andean and Mesoamerican. Admixture was observed between these two groups. The Mesoamerican group consisted of five sub-populations with a high level of dissimilarity among them.

P-17

Potential Gain from Selection in Heirloom Dry Beans. Swegarden H.R.[1*] and T. Michaels[1]. [1]Department of Horticulture, University of Minnesota, St. Paul, MN. *Presenter (swega001@umn.edu)

As part of a larger effort to breed dry beans for organic systems, we are evaluating within-line variability and selecting superior sublines from fourteen, genetically diverse heirloom populations. Our evaluations this growing season focused on morphological characteristics (e.g. days to flowering, canopy height, seed yield/plant, etc.) and will later include molecular diversity estimates. Initial data indicate that heirloom dry beans maintain significant variability in morphological and agronomic traits, which suggests an opportunity to make significant gains from selection.

P-18

The New Grain Legumes Working Group (GLWG) in the European Association for Research on Plant Breeding (Eucarpia). De Ron, A.M.[1]*, J. Vollmann[2], B. Uzun[3] and B. Boller[4]. [1]Biology of Agrosystems, MBG-CSIC, Pontevedra, Spain. [2]Dept. Crop Sciences, University of Natural Resources and Life Sciences, Vienna, Austria. [3]Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya Turkey. [4]Fodder crop breeding, Agroscope, Zurich, Switzerland. *Presenter (amderon@mbg.csic.es)

EUCARPIA is a non profit organization aiming at the promotion of scientific and technical co-operation in all fields of plant breeding in order to foster its further development. The Association has 11 sections and a number of working groups focusing on particular crop species and cross-cuttings topics. Within the Oil and Protein Crops Section was created the Grain Legumes Working Group (GLWG) focused to food and feed legumes. Special attention will be paid to the common bean, since it is the major protein crop for direct human consumption.

P-19

Association Mapping of Agronomic Traits Using Dry Bean Breeding Populations. Agarwal, C.[1*], J.M.Osorno[1], P. McClean[1] and S. Mamidi[1]. [1]Department of Plant Sciences, North Dakota State University, Fargo-ND 58108. [*]Presenter (chiti.agarwal@my.ndsu.edu)

Association mapping using the bean breeding pipeline could help to explain the genetic basis of many complex traits in this economically important species. The main focus of this analysis is to map genomic regions associated with 100-seed weight, plant height, days to maturity and seed yield using 6000 SNPs. Advanced yield trials and preliminary yield trials from the NDSU bean breeding program were evaluated in field trials grown in 3 different environments in 2012. The best statistical model with a minimum of false positives and minor allele frequency will be selected after controlling population structure and relatedness. This research will help to identify markers that are associated with agronomical important traits in dry beans within and among market classes. These markers could then be incorporated in breeding programs to improve cultivars in a MAS scheme.

P-20

Lima Bean QTL and Marker Discovery to Support Breeding for Nematode and Lygus Resistance. Dohle S.[1*], K. Ngo[2], A. Palkovic[1], and P. Gepts[1].[1]Department of Plant Sciences, University of California Davis, CA; [2]Genome Center, University of California Davis, CA. [*]Presenter (smdohle@ucdavis.edu)

A physical linkage map of lima bean (*P. lunatus*) containing thousands of SNPs was developed based on synteny with common bean (*P. vulgaris*) using next generation sequencing. The sequenced lima bean varieties are being used to develop a recombinant inbred population resulting from inter-gene pool crosses between a Mesoamerican small-seeded vine type, UC-Haskell, with tolerance to *Lygus*, and an Andean large-seeded bush type, UC-92, with resistance to *Meloidogyne incognita*. This linkage map in association with the RI population will be used for QTL and marker discovery. Concurrently, reciprocal backcrosses are being conducted to facilitate the development of advanced lines with multiple resistances in a market background.

P-21

Rogues for pod traits in Snap Bean (*Phaseolus vulgaris*). Al-Bader, N.* and Myers J.R. Department of Horticulture, Oregon State University, Corvallis, OR. *Presenter (albader@onid.orst.edu)

Seed companies spend tens of thousands of dollars every year removing off types from seed lots of snap beans. They are found in all varieties but the kind of off type or rogue, and frequency varies. Among traits that have greatest economic consequence are suture strings and oval (as opposed to round) pods. We initially collected 95 off types from 11 breeding lines and cultivars in the field in 2012 that exhibited one or more of the traits of interest. We focused primarily on off types with suture strings and/or oval pod shape. The latter is often associated with higher pod fiber. For almost half of the selections, the off type was not found in the progeny and we concluded that the variation initially observed was not heritable. However, 46 of these selections did transmit the off type to the progeny and continued to segregate after three generations of selfing for one or both of the rogue traits. It appears that the original selections with heritable off types were initially heterozygous as would be expected for a spontaneous mutation. Genotype by sequencing (GBS) will be used to compare parental lines with off type lines to identify polymorphisms associated with the off type.

P-22

A SNP-Based Linkage Map of Snap Bean (*Phaseolus vulgaris*). Davis, J.W.[1*], J. Myers,[1], D. Kean[1], N. Al Bader[1], B. Yorgey[2], P. Cregan[3], Q. Song[3], and C. Quigley[3]. [1]Department of Horticulture and [2]Department of Food Science and Technology, Oregon State University, Corvallis, OR. [3]Soybean Genomics and Improvement Lab, Beltsville Agricultural Research Center – West, USDA, ARS, Beltsville, MD. *Presenter (davisjo@hort.oregonstate.edu)

A linkage map of snap bean has been constructed for a recombinant inbred population developed from the cross 'Minuette' × 'OSU 5630' using single-nucleotide polymorphism (SNP) markers. Minuette is from the Andean center of domestication whereas OSU 5630 is a bush blue lake green bean from the Mesoamerican center of origin. The framework map consists of 754 SNP's in 19 linkage groups covering 994 cM. The linkage groups ranged from 3 to 118 SNP's each and have been assigned corresponding chromosome (Pv) numbers based on the origin of SNP marker sequences. All eleven *P. vulgaris* chromosomes were represented by these linkage groups, although several were found to be in two or three segments. Additional marker (SSR's, RAPD's) and QTL data from previous work will be incorporated into this map.

P-23

Quantitative Trait Loci Analysis of Symbiotic Nitrogen Fixation in Common Beans. Farid, M.[1*], R. Khanal[1], W. Xie[1], R. Stonehouse[2], H. J. Earl[1], K. P. Pauls[1], K. Bett[2], and A. Navabi[1]. [1]Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program; [2]University of Saskatchewan. *Presenter (mfarid@uoguelph.ca)

Despite the inherent ability of legumes to fix atmospheric nitrogen, the actual symbiotic N_2 fixation (SNF) of dry bean (*Phaseolus vulgaris* L.) is relatively low compared to other legumes. Breeding bean varieties with improved N_2 fixation is expected to improve dry beans productivity and promote the development of low-input cropping systems. The objective of this study is to examine the variation in N_2-fixation and related traits in a recombinant inbred line population of a cross between high and low N_2-fixing genotypes and to identify quantitative trait loci for SNF and related traits.

P-24

SNP Marker Development to Improve Marker Assisted Selection at CIAT Bean Breeding Program. Soler-Garzón A.[1]*, Gil J. [1],Beat K.[2], Buendia H.F. [1] and Raatz B. [1]. [1]Bean Molecular Genetics, CIAT, Palmira, Colombia. [2] ETH Zurich, Zurich, Switzerland. *Presenter (a.soler@cgiar.org)

Common bean is an important food legume particularly for smallholder farmers in developing countries, where it is an essential due to its high protein and micronutrient contents. Breeding at CIAT aims to develop improved varieties with superior resistance to abiotic and biotic stresses and higher micronutrient levels. Marker assisted selection (MAS) is utilized to accelerate the breeding process and to increase efficiency. SNP markers are developed that can be analyzed in a gel-free system to replace SSR and SCAR markers. Marker conversions have been achieved for markers for BCMV, CBB, ALS, and bruchid resistance. A protocol for seed DNA extraction is being improved to be able to genotype plants before bringing them to the field. As genotyping is getting ever cheaper and easier, while field phenotyping becomes the most resource limited activity, seed DNA extraction has a big potential to improve breeding in future.

P-25

Using Growing Degree-days to Estimate Phenology and Development in Common Bean. Colbert R.W.*and J.M. Osorno. Department of Plant Sciences, North Dakota State University, Fargo, ND. *Presenter (raphael.colbert@ndsu.edu)

Growing degree-days (GDD) measurements allow predicting more accurately crop developmental stages than calendar days, as temperature varies across years and locations. Two common bean (*Phaseolus vulgaris* L.) populations derived from inter-pool crosses [Negro Jamapa x ICA-Calima (RIJC) and Stampede x Redhawk (RISR)] were evaluated in field trials at Hatton and Prosper, ND from 2011 to 2013. The RISR population showed late vegetative development but early flowering time compared to the RIJC population and a novel approach for predictions of specific phenologic stage will require a gene-based crop model including GDD and quantitative trait loci.

P-26

Characterization of a Common Bean (*Phaseolus vulgaris* L.) Homolog of an Anti-yield Gene. Qi,Y,Z[1]*, S. Rothstein, K.P. Pauls. Department of Plant Agriculture, University of Guelph,ON,CA. *Presenter (yqi@uoguelph.ca)

AT1G74730 is an anti-yield gene from *Arabidopsis* coding for a transcription factor whose level of expression value is inversely related to plant maturity and seed yield. The current study was initiated to characterize the function of an AT1G74730 homolog in common bean. The correlation between the expression of the gene and field yield will be tested and complementation tests with *Arabidopsis* knock-out mutant plants and the bean AT1G74730 homolog will be conducted.

P-27

Pursuit (Imazethapyr) Tolerance in Post Emergent Dry Beans. Smith, T.H.[1*], A.J. Burt, T. Rupert [1], and A. Navabi [1]. [1] Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program. * Presenter (thsmith@uoguelph.ca)

The objective of this study was to examine the response of dry beans to post emergent applications of the herbicide Imazethapyr, also known as Pursuit, to determine breeding opportunities. Experiments were conducted in the growth room as well as in the field. Treatments included increasing levels of post emergent applications inside, as well as the recommended soybean rate on dry beans in the field. Dry bean plants exhibiting tolerance were selected in the field, showing differences in Pursuit tolerance do exist and offering breeding opportunities and challenges for the future.

P-28

Genetic Improvement of Protein Quality in Edible Beans with Adaptation to Manitoba. Hou, A.[1], Marsolais F.[2,*], Pajak A.[2] and R.L. Conner[1]. Agriculture and Agri-Food Canada, [1]Morden Research Station, Morden, MB; [2]Southern Crop Protection and Food Research Centre, London, ON *Presenter (Frederic.Marsolais@agr.gc.ca)

Protein quality in beans is limited by the suboptimal levels of sulphur-containing amino acids, methionine (Met) and cysteine (Cys). The germplasm line SMARC1N-PN1 lacks major seed storage polypeptides. This leads to increased total Cys (up to 70%) and Met content (about 10%) and decreased levels of *S*-methylcysteine as compared with the corresponding wild-type line. A cross was made between SMARC1N-PN1 (S) and the navy cultivar Morden003 (M) to generate an $F_{2:8}$ population of 185 recombinant inbred lines (RIL). Protein profiles classified them into four groups according to genetic inheritance at the phaseolin and lectin loci. A few of the MS lines had high legumin concentration. Sulphur amino acids were quantified in a subset of lines. The molar concentration of Met plus Cys was increased by 16% in SS as compared with MM lines. One SS line stood out with nearly 50% higher *S*-methylcysteine than the group average. The RIL population will be grown at multiple locations and amino acid levels further evaluated.

P-29

Association of Slow Darkening Gene 'sd' with Grain Quality Traits in Carioca Bean. Alvares R.C.[1*], Melo P.G.S.[1], Pereira H.S.[2], Melo L.C.[2] and Miklas, P.[3]. [1]Universidade Federal de Goiás. [2]Embrapa Arroz e Feijão, Goiás-Brazil. [3]USDA-ARS, Prosser, WA. [*]Presenter (renataalvares08@hotmail.com)

Carioca bean seed darkens during storage becoming less acceptable to consumers. The SSR-1158 marker linked to sd gene that controls the delay of grain darkening in pinto bean was associated with slow darkening trait segregating in two carioca bean RIL populations (BRSMG Madrepérola x BRS Estilo and BRSMG Madrepérola x BRS 9435 Cometa) from Embrapa Arroz e Feijão breeding program. Cooking time after 90 days of storage was not influenced by variability for seed darkening. These and other results will be discussed.

P-30

Phenotypic Association of Parameters Commonly used to Predict Canning Quality of Dry Beans (*Phaseolus vulgaris* L.). Khanal R.[12*], A. Burt[1], L. Woodrow[2], and A. Navabi[12]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada. [2]Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada (AAFC), 2585 County Road 20, Harrow, ON, N0R 1G0, Canada. *Presenter (rkhanal@uoguelph.ca)

Dry bean *(Phaseolus vulgaris* L.) is the most important grain legume in human diets and in many countries it is predominantly produced for canning industry where they are prepared for consumption as canned beans in sauce. Canning quality of dry beans determines the acceptability of bean varieties by consumers and industry; hence, the bean varieties must be evaluated for canning quality parameters before they released as improved varieties. A better understanding of association among different canning quality parameters may be useful for selection of bean varieties with high canning quality.

P-31

The Transcriptome of Developing Pods of Navy Beans. Astudillo-Reyes C.*[1] Fernandez A .C and K.A. Cichy[2] [1]Plant Soil and Microbial Sciences Department, Michigan State University, East Lansing, MI, USA [2]USDA-ARS Sugarbeet and Bean Research Unit, East Lansing, MI, USA. *Presenter (astudil2@msu.edu)

The transcriptome of developing pods of Albion and Voyager navy beans were sequenced and characterized to identify genes important in zinc and iron transport to the seed. A relatively small number of genes (542) were differentially expressed between Albion and Voyager including ferritin, iron regulated transporter like protein (ZIP), zinc-induced facilitator (ZIF) and heavy metal associated (HMA) family genes.

P-32

Influence of Fe, Zn, and Cd on Uptake and Translocation of Mineral Elements in Common Bean. M. McDonald[1*], H. J. Longtin, T. Kawalski[1], V. Kalavacharla[2], and K. G. Hossain[1] Mayville State University, Mayville, ND 58078; [2]Delaware State University, Dover, DE 19901. *Presenter (megan.mcdonald.1@mayvillestate.edu)

Common bean is a valuable source of essential minerals and to estimate the influence of Fe, Zn, and Cd on mineral concentration and translocation, a replicated trial of three genotypes of this species were conducted in greenhouse with increased concentrations of Fe, Zn, and Cd. Our objectives were to estimate the influence of Fe, Zn, and Cd on human essential minerals and their translocation through different tissues of common bean. At grain filling stage, root, stem, and pod were analyzed for 20 mineral elements and assessed for the influence of Fe, Zn, and Cd on uptake and translocation mineral elements in common bean.

P-33

Genotypic Diversity for Potassium Efficiency in Common Bean. Grusak M.A.[1]*. [1]USDA-ARS Children's Nutrition Research Center, Dept. of Pediatrics, Baylor College of Medicine, Houston, TX. *Presenter (mike.grusak@ars.usda.gov)

Poor soil fertility (including limited potassium [K] availability) is a major problem in many common bean growing regions of Africa, leading to sub-optimal yields. Because we are interested in developing new, higher yielding bean cultivars for African farmers, we have worked to identify K-efficient Andean bean lines (more tolerant of limited K supply) that could be deployed directly, or used in bean breeding programs. For these experiments, diverse Andean lines were selected to assess expansive leaf growth (leaf area) in response to limited availability of K. Plants were grown hydroponically on a complete nutrient solution until full expansion of the unifoliate leaves and then were maintained on control K (1.2 mM), 300 µM K, or 50 µM K for 10 days. Our leaf area measurements demonstrate that broad genetic diversity exists for K efficiency in Andean bean lines. Genome-wide association mapping will be conducted in an attempt to find quantitative trait loci associated with enhanced K efficiency.

P-34

Seed Mineral Concentrations in Diverse Bean CAP Bean Lines. Grusak M.A.[1]*, McClean P.E.[2], Brick M.A.[3], Despain B.[4], Kelly J.D.[5], Miklas P.N.[6], Osorno J.M.[2], Porch T.G.[7], Urrea C.A.[8]. [1]USDA-ARS CNRC, Houston, TX; [2]North Dakota State University; [3]Colorado State University; [4]Archer Daniels Midland; [5]Michigan State University; [6]USDA-ARS, Prosser, WA; USDA-ARS, Mayaguez, Puerto Rico; [8]University of Nebraska. *Presenter (mike.grusak@ars.usda.gov)

As part of our Bean Coordinated Agricultural Project, we were interested in characterizing seed mineral concentrations in diverse lines, as well as assessing possible genotype by environment effects. In the summer of 2012, 300 Bean CAP lines were grown at four locations (2 replicates each) under control conditions, and 96 of these lines were grown at five locations in drought versus control fields. Yield data were also collected. All samples have been ground, digested, and analyzed for minerals using inductively coupled plasma-optical emission spectroscopy. Results will be presented for seed mineral concentrations for the population as a whole and amongst market classes, demonstrating the diversity that exists across these lines. We also will present correlations across environments, with a particular focus on drought stress effects.

P-35

Variability in Seed Mineral and Protein Concentration in an Andean Bean Diversity Panel. Katuuramu D.N.[1*] and K.A. Cichy[2]. [1]Department of plant, soil, and microbial sciences, Michigan State University, East Lansing, MI. [2]USDA-ARS, Sugarbeet and Bean Research Unit, East Lansing, MI. [*]Presenter (katuuram@msu.edu)

An evaluation of 250 Andean bean lines revealed seed iron and zinc levels ranging from 41.2-114 and 19.4-54.8 µg g^{-1}, respectively. Protein concentration varied from 16.4 to 30.7 %. Red mottled and cranberry types had higher levels of Fe and Zn than beans from the other market classes.

P-36

Investigating Genotype by Environment (GxE) Interactions in Navy Bean Performance Trials in Ontario.

Burt, A.J. *, R. Khanal, and A. Navabi. Agriculture and Agri-Food Canada / University of Guelph Bean Breeding Program. *Presenter (aburt@uoguelph.ca)

Evaluating variety performance through testing in multiple locations and years is essential to making decisions for variety registrations. Interactions of genotype with environment (GxE) profoundly complicate the identification of superior varieties. Data from 23 years of the Ontario Pulse Crop Committee variety registration and performance trials was examined with site regression analysis (SREG) and shifted multiplicative model cluster analysis (SHMM) to separate and interpret the effect of environments and GxE in Ontario performance trials.

P-37

Monitoring Anthracnose Severity and Virulence in Ontario: Implications for Breeding and Research.

A.J. Burt[1*], K.P. Pauls[1] and A. Navabi[1]. [1]Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program. *Presenter (aburt@uoguelph.ca)

Anthracnose, caused by *Colletotrichum lindemuthianum*, is a major disease of common bean (*Phaseolus vulgaris* L.). Race 73 had a major impact on navy been growers in 2003 and has been assumed to be the predominant form of anthracnose in Ontario since. Cultures from infected seed and scouted fields collected in 2011 and 2012 have been analyzed to determine the range and virulence of anthracnose present in Ontario. Strategies and progress in breeding for resistance will be discussed.

P-38

Analysis of Diverse *Colletotrichum lindemuthianum* Isolates of Common Bean (*Phaseolus vulgaris* L.) from Mato Grosso State, Brazil. Felipin-Azevedo, R., M.C. Gonçalves-Vidigal[*], G.F. Lacanallo, M.C.M. Souza, S.A. Lima, M.P. Caixeta, and P.S. Vidigal Filho. Departamento de Agronomia, Universidade Estadual de Maringá, PR, Brazil, 87020-900. [*]Presenter (mcgvidigal@uem.br)

Thirty *Colletotrichum lindemuthianum* isolates from Mato Grosso state were characterized using the 12 common bean differential cultivars. This work allowed the identification of races 1, 8, 9, 10, 24, 64, 65, 72, 73 and 81 of *C. lindemuthianum*. Among these races, 1, 8, 9, 10, 24, 64, 72 and 73 were identified for the first time in this State. In addition, this was the first world report of race 24. Cultivars Perry Marrow, Kaboon, PI 207262, TO, TU, AB 136 and G 2333 were resistant to all isolates.

P-39

Molecular Characterization of Common Bacterial Blight Pathogen Strains Showing Differential Pathogenicity. Xie, W[1*], C. Cintora [1], G. Perry[1], S. Ramcharan[1], B. L. Zhang[2], K. Yu[2], K. P. Pauls[1], and A. Navabi [1,2]. Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program; [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1; [2] Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, Ontario, Canada N0R 1G0. *Presenter (wxie@uoguelph.ca)

Common bacterial blight (CBB), caused by *Xanthomonas campestris* pv. *phaseoli (Xcp)* and its fuscan variant *Xanthomonas fuscans* subsp. *fuscans (Xff),* is a damaging disease of common bean (*Phaseolus vulgaris* L.) throughout the world. Two *Xcp* strains and two *Xff* strains, collected locally, showed differential pathogenicity on a set of bean genotypes. Single colony strains from these isolates were characterized in DNA sequence level to identify candidate effector genes which might cause differential levels of pathogenicity.

P-40

Race Structure of *Pseudomonas syringae* pv. *phaseolicola* from Dry Bean Fields in Western Canada. Chatterton S.[1*], P. M. Balasubramanian[1], D. L. McLaren[2], R. L. Conner[3], and R. J. Howard[4]. [1]Lethbridge Research Centre, Agriculture and Agri-Food Canada (AAFC), Lethbridge, AB; [2]Brandon Research Centre, AAFC, Brandon, MB; [3]Morden Research Station, AAFC, Morden, MB; and [4]Crop Diversification Centre South, Alberta Agriculture and Rural Development, Brooks, AB. *Presenter (syama.chatterton@agr.gc.ca)

Bacterial diseases of dry bean, such as common blight and halo blight can significantly impact production in western Canada. The objectives of this study were to assess the incidence of multiple bacterial diseases on dry beans in southern Alberta using a multiplex PCR diagnostic assay and to determine the prevalent halo blight races in western Canadian dry bean fields. Results to date indicate that *Pseudomonas syringae* pv. *phaseolicola* isolates from southern Alberta bean fields belong to race 2, while isolates from Manitoba bean fields belong to race 2 or 6. Assessing the virulence of race 2 and 6 isolates to dry bean lines with resistance to common bacterial blight is currently underway.

P-41

Recombinants of *Bean common mosaic virus* (BCMV) and Genetic Determinants of BCMV Involved in Overcoming Resistance in Common Beans. Karasev A.V.[1]*, X. Feng[1], A.R. Poplawsky[1], and J.R. Myers[2]. [1]Department of PSES, University of Idaho, Moscow, ID; [2]Department of Horticulture, Oregon State University, Corvallis, OR. *Presenter (akarasev@uidaho.edu).

In order to understand the genetic determinants of pathogenicity for *Bean common mosaic virus* (BCMV), the whole genome was cloned and sequenced for the BCMV strains US10 and RU1-OR (pathotype VII), and also for the strain RU1p (pathotype VI). Inspection of the nucleotide sequences for BCMV RU1-OR and US10, and closely related sequences BCMV RU1p, RU1d, and RU1-W (all pathotype VI) revealed that BCMV RU1 isolates originated through a series of recombination events between US10 and a yet unknown parental genome, resulting in changes in virus pathology. The data obtained suggest that a fragment of the US10 genome in the P1-HC-Pro region may be involved in its ability to overcome the BCMV resistance in beans conferred by the *bc-2*^{2} gene.

P-42

Enhancement of Dry Bean Production by Soil Ripping. H. F. Schwartz*, M. A. Brick, J. B. Ogg and M. S. McMillan· Colorado State University, Fort Collins, CO; *Presenter (howard.schwartz@colostate.edu)

A two-year study compared the performance of pinto bean varieties with different growth habits when inter-row ripped during early vegetative growth to enhance root vigor, production efficiency and return to growers. Type II Croissant and Stampede were compared to Type III Montrose grown as 2 lines (15 cm apart) per 75 cm wide bed at 173000 plants per hectare under furrow irrigated conditions in Colorado. Yields averaged more than 3200 kg per hectare, depending on the variety and ripping treatment in 2012; with 2013 results to be reported later. On average, in 2012, soil compaction was 20 percent less in ripped than non-ripped treatments. During 2013, an additional stress comparison across ripping treatments was made on the effects of irrigation every 7 versus 14 days from flowering until crop maturity. Plant biomass, first node height and yield component differences will be presented for the two-year study.

P-43

Genotyping-by-Sequencing of 25 Marker Loci Linked to the *Phg-2* Locus in Six Common Bean Varieties Reveals a High Frequency of INDEL Markers. Miller T.[1]*, A. Namusoke[2], A. Namayanja[2], P. Gepts[1]. [1]Department of Plant Sciences, University of California, Davis, CA; [2]National Crop Resources Research Institute - Namulonge, Kampala, Uganda. *Tamara Miller (timiller@ucdavis.edu)

The African Bean Consortium, involving five Eastern Africa countries seeks to introgress resistance genes for five major diseases into preferred common bean varieties using phenotypic and marker-assisted selection. *Phg-2*, which confers resistance to Angular Leaf Spot, is one gene that is a target for disease resistance breeding; however, the SN02 marker used to select this locus, is monomorphic among parental cultivars in Uganda. In order to find an alternative marker linked to SN02, we used the PhaseolusGenes database to locate linked STS, SSR, SCAR, SNP, and INDEL markers and tested them by PCR and sequencing to find polymorphisms between resistant and susceptible cultivars. Our analysis via sequencing revealed that although most of the markers tested were monomorphic between parents, there was a high frequency of unreported INDEL polymorphisms. These results confirm the potential of INDEL markers as an untapped source of polymorphisms in marker-assisted breeding.

P-44

Analysis of Complex Mendelian Segregations for the Resistance to Anthracnose in the RIL Population Xana/Cornell49242. Campa A.[1], C. Rodriguez-Suárez[2], R. Giraldez[3], J.J. Ferreira[1*]. [1]Área de Cultivos Hortofrutícolas, SERIDA, Asturias, Spain. [2] Instituto de Agricultura Sostenible, CSIC, Apdo. 4084, E-14080 Córdoba, Spain [3]Área de Genética, Dpto. Biología Funcional, University of Oviedo, Spain. *Presenter (jjferreira@serida.org)

Inheritance of the resistance against five isolates of *Colletotrichum lindemuthianum* (classified as races 3, 6, 7, 19 and 73) was analyzed in a recombinant inbred population obtained from the cross Xana x Cornell49242. Segregations for resistance to races 6 and 73 fitted to a 1 resistant (R): 1 susceptible (S) ratio, expected for one resistance gene. Segregations for resistance to races 3, 7 and 19 showed a good fit to a 5 R: 3 S ratio, expected for three independent genes, two of them with a complementary mode of action. Reaction against the races 3, 7 and 19 exhibited a close co-segregation. Linkage analysis based on the genetic map developed in this population suggest that linkage groups Pv01, Pv02, Pv04 and Pv11 are involved in the resistant reaction.

P-45

Black Bean (*Phaseolus vulgaris* L.) Germplasm Rich in Anthracnose Resistance. Hou A.[1*], R.L. Conner[1], P. Balasubramanian[2] and J.G. Boersma[1]. Agriculture and Agri-Food Canada, [1]Morden Research Station, Morden, MB; [2]Lethbridge Research Centre, Lethbridge, AB. *Presenter (anfu.hou@agr.gc.ca)

One hundred and sixty black bean accessions originating from twenty countries were introduced from the USDA *Phaseolus* Germplasm Collection and evaluated in the field during 2009 - 2013 at the Morden Research Station. Significant variation was observed in agronomic traits including photo-period sensitivity, flowering date, growth type, maturity, lodging resistance, seed size and yield. Artificial inoculation in growth chambers identified 47 accessions that were resistant to anthracnose race 73, and

46 accessions resistant to both races 73 and 105. Identification of the genotypes with desirable seed characteristics, high yield potential and resistance to anthracnose provides much-needed public breeding materials for black bean cultivar development in Canada.

P-46

Genetic Analysis of the Reaction to Thirteen *Colletotrichum lindemuthianum* Races in the RIL Population AB136/ MDRK. Campa A., N. Trabanco, E. Pérez Vega, J.J. Ferreira*. Área de Cultivos Hortofrutícolas, SERIDA, Asturias, Spain. *Presenter (jjferreira@serida.org)

Previous analysis showed the high complexity of the resistance inheritance to *Colletotrichum lindemuthianum* in the bean genotype AB136, one of the twelve differential cultivars used in the race characterization of this fungus. In this work, we investigated the inheritance of the reaction to thirteen isolates classified as different races in a recombinant inbred population derived from the cross AB136 x MDRK. The genetic analysis was supported by a linkage map which included 120 loci distributed along the eleven linkage groups. Results revealed that the AB136 genotype carries, at least, one complex cluster of race-specific resistance genes located on the linkage group Pv07.

P-47

Identification of Anthracnose Resistance Sources in Common Bean (*Phaseolus vulgaris* L.). Mindo, N.N.A[1], P.S. Vidigal Filho[2], G. Valentini[2], L.L. Sousa[2], R. Felipin-Azevedo[2] and M.C. Gonçalves-Vidigal[2*]. [1]Instituto de Investigação Agrária de Moçambique. Av. das FPLM, 2698. Maputo, Mozambique. [2]Dep. Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brazil. 87020-900. *Presenter (mcgvidigal@uem.br).

A total of 104 accessions of common bean from the Nupagri Germplasm Bank were evaluated with races 2 and 65 of *C. lindemuthianum*. Ten plants of each cultivar were inoculated, and the procedure was repeated twice. After a 48 h incubation period in mist chamber, seedlings were evaluated for their disease reaction using a scale of 1 to 9, seven days after inoculations. Results revealed that 51 plants were resistant to race 2 and 28 were resistant to race 65. Considerably higher level of resistance to both races was recorded in 11 Andean accessions and 10 Mesoamerican.

P-48

Molecular Characterization of Anthracnose Resistance to Race 73 in the Navy Bean Variety Bolt. Vazin, M.[1*], A. J. Burt[1], W. Xie[1], C. Gillard[2], K. P. Pauls[1], K. Bett[3] and A. Navabi[1]. [1]Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program; ; [2]University of Guelph, Ridgetown Campus; [3]University of Saskatchewan. *Presenter (vazinm@uoguelph.ca)

Anthracnose, caused by *Colletotrichum lindemuthianum*, is a major disease of common bean (*Phaseolus vulgaris* L.). A population of 126 $F_{4:6}$ recombinant inbred lines of a cross between the resistant navy bean variety Bolt and the susceptible line H4784A-29844 was evaluated for resistance to anthracnose race 73 in growth room trials and in the field in four environments and genotyped with genome-wide SNP markers. Leads from a QTL-based approach identified four candidate genes near the locus of *Co-1*, the likely R-gene in Bolt. Results of the molecular characterization will be presented.

P-49

Anthracnose Genetic Resistance in Common Bean Cultivar Paloma. Castro, S.A.L.[1*], D.S.Y. Nanami[1], A.A.T. Frias[1], R. C. Franzon[1], G.F. Lacanallo[1] and M.C. Gonçalves-Vidigal[1]. [1]Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil, 87020-900. *Presenter (sandralima.bio@hotmail.com)

The genetic resistance in Paloma cultivar was characterized in the F_2 population from the Paloma × Cornell 49-242 cross. Segregation fitted a ratio of 3R:1S, which indicates the presence of a single dominant gene in Paloma, conferring resistance to race 2047 of *Colletotrichum lindemuthianum*. Alellism tests were conducted and revealed that the resistant gene in Paloma is independent from the previously identified genes of Andean and Mesoamerican gene pools.

P-50

Inheritance and Allelic Relationships of Anthracnose Resistance in Common Bean Amendoim Cavalo. Nanami, D.S.Y.[1*], A.A.T. Frias[1], S.A.L. Castro[1], J.C. F. Elias[1], G.F. Lacanallo[1], M.C. Gonçalves-Vidigal[1]. [1]Dep. Agronomia, Universidade Estadual de Maringá, PR, Brazil, 87020-900. [*]Presenter (daninanami@hotmail.com)

The objectives of this work were to conduct allelism tests and evaluate anthracnose resistance inheritance in Amendoim Cavalo cultivar, which is resistant to *Colletotrichum lindemuthianum* races 2, 7, 65, 73, 89 and 2047. The segregation in F_2 population Amendoim Cavalo × Mexico 222 fitted a ratio of 3R:1S, indicating that a single dominant gene in Amendoim Cavalo is conferring resistance to race 73. Results indicated that the resistance gene in Amendoim Cavalo is inherited independently from those previously characterized.

P-51

Genetic Analysis of Anthracnose Resistance in Jalo Pintado 2 Dry Bean Cultivar. Frias, A.A.T[1], S.A.L. Castro[1], D.S.Y. Nanami[1], M.C.M. Souza[1*], M.C. Gonçalves-Vidigal[1] and M.Z. Galván[2]. [1]Dep. Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brazil. 87020-900. [2]Consejo Nacional de Investigaciones Científicas y Técnicas, CONICET, La Plata, Argentina. [*]Presenter (maria.martiniano@ipa.br)

The Andean common bean cultivar Jalo Pintado 2, resistant to races 2, 7, 9, 31, 65, 73, 95, 453 and 2047 of *Colletotrichum lindemuthianum*, was crossed with susceptible cultivar Cornell 49-242 (race 73), and also with resistant cultivars Michigan Dark Red Kidney, Corinthiano, Jalo Listras Pretas, Jalo Vermelho and Pitanga. The segregation ratio observed in F_2 population from Jalo Pintado 2 × Cornell 49-242 cross was 3R:1S, demonstrating the presence of a single dominant gene in Jalo Pintado 2, conferring resistance to race 73. The allelism tests indicated that the gene in Jalo Pintado 2 is independent from those previously characterized.

P-52

Common Bean White Mold Resistance Sources Identified by Greenhouse Screening in Brazil. Ferreira, L.U.[1], P.G.S. Melo[1], M. Lobo Junior[2], A. Wendland[2], H.S. Pereira[2], L.C. Melo[2], L.C. Faria[2] and T.L.P.O. Souza[2*]
[1]Universidade Federal de Goiás (UFG), Goiânia, GO 74001-970, Brazil; [2]Embrapa Rice and Beans, Santo Antônio de Goiás, GO 75375-000, Brazil. [*]Presenter (thiago.souza@embrapa.br)

White mold (WM) incited by *Sclerotinia sclerotiorum* is a major disease problem for the common bean crop worldwide, including in Brazil. WM can cause severe yield and seed quality losses, which dramatically reduce farmer incomes. As a basic and continuous step of breeding efforts aiming to develop resistant cultivars, 39 bean lines from different market classes were screened for WM reaction at greenhouse using a modified straw test method. Bean genotypes were grown in a completely randomized design with six replications composed by one plant each. Plants were inoculated at the fourth/fifth node, about 35 days after seedling emergence (R5 stage), using the *S. sclerotiorum* isolate SS 1370, the most virulent one maintained by Embrapa Rice and Beans. The inoculum (mycelial plugs) was grown for 72 h on PDA medium at 21,5º C. After inoculation, plants were kept under greenhouse at 28°C and relative humidity above 85%. WM severity was scored on a 1 to 9 scale, where 1= no symptoms and 9= dead plants. The results revealed significant genetic variation for WM reaction among the 39 screened common bean lines (ANOVA, F test at 1% probability), which were grouped on five resistance levels according to Skott-Knott test at 5% probability. Cultivar BRS Cometa and the advanced line CNFC 9500, both carioca seeded genotypes, in addition to CIAT variety K0407, showed to be potential WM resistance sources for Brazil. These lines presented mean infection rates of 2.6, 3.1, and 2.8, respectively. The obtained results are agreed with previous reports from field screening realized in Brazil.

P-53

Inheritance of White Mold Resistance in Othello X A 195 and A195 X G122 Crosses. Viteri, D.M.[*] and S.P. Singh**.** Plant, Soil and Entomological Sciences Department, University of Idaho, Kimberly Research & Extension Center, 3793 North 3600 East, Kimberly, ID 83341-5076. * Presenter (dviteri@uidaho.edu)

White mold is a devastating disease of common bean in cool and wet production regions. Partial white mold resistance is found in small- and large-seeded common bean, wild bean, and *Phaseolus* species of the common bean secondary gene pool. Inheritance of resistance in large-seeded Andean dry bean genotypes A195 and G 122 will be described.

P-54

Association Mapping of White Mold Resistance in a Panel of North American Breeding Lines and Cultivars Representing the Middle American Gene Pool. Oraguzie O.B.[1*], Bello M.H[2], McClean P.E.[3], Cregan P.[4], Miklas P.[2] [1]Crop Science Department, Washington State University, WA. [2]USDA-ARS, Prosser, WA. [3]Plant Science Department, NDSU. [4]USDA-ARS, Beltsville for generation of the SNPs. *Presenter (bathanson@yahoo.com)

Host resistance and avoidance can limit losses due to white mold (WM) disease. A genome-wide association study using a 6K SNP array examined straw test and field reaction to white mold for 268 dry bean lines from the BeanCAP panel. The coefficient of membership (*Q*) values generated in 'STRUCTURE' will be used in TASSEL as covariates for determination of marker-locus-trait associations.

P-55

Analysis of Variation for White Mold Resistance in the Bean CAP Snap Bean Panel. Arkzwazee, H.[1]*, J. Davis[1], P. Miklas[2], S. Moghaddam[3], and P. McClean[3], and J.R. Myers[1]. [1]Depart. Horticulture, Oregon State University, Corvallis OR [2]USDA-ARS, Vegetable and Forage Crop Production Unit, Prosser, WA; [3]Dept. Plant Sciences, North Dakota State University, Fargo, ND. *Presenter (haidarh@onid.orst.edu)

White mold disease caused by *Sclerotinia sclerotiorum* is one of the most devastated diseases that infect snap and dry beans; in severe season the yield loses reach 100%. We assessed the Bean CAP snap bean panel consisting of 134 determinate cultivars and breeding lines for resistance to white mold in the field and using the straw test in the greenhouse. Reported here are the results from the first field evaluation in 2012; data from the greenhouse and field screen in 2013 await analysis. A set of lines in the panel exhibited high levels of resistance; in some cases as good as the resistant checks and was repeatable over years. Association mapping of resistance revealed three potential regions in the bean genome that condition resistance.

P-56

Sources of Physiological Resistance to *Sclerotinia sclerotiorum* in *Phaseolus vulgaris* Lines from Bulgaria. Sofkova, S.[1*] and I. Kiryakov[2]. Department of Plant Breeding, Variety Maintenance and Introduction, Vegetable Crops Research Institute "Maritsa" (VCRI), Plovdiv, Bulgaria. [2] "Dobrudzha" Agriculture Institute, General Toshevo, Bulgaria. * Presenter (svetlas_76@yahoo.com)

White mold disease, caused by *Sclerotinia sclerotiorum (Lib.) de Bary* harms bean production *(Phaseolus vulgaris L.)* in temperate North regions of Bulgaria. The purpose of this work was to identify genotypes with physiological resistance to *S. sclerotiorum* among advanced breeding lines of the VCRI bean breeding program. Among 90 genotypes evaluated by straw test rating scale, 33 sources of physiological resistance (rates 1 - 3) and 43 sources of intermediate resistance (rates 4 - 6) to *S. sclerotiorum* were identified.

P-57

Combined Resistance to Bacterial Wilt and Fusarium Wilt in Common Bean Genotypes Derived from a Segregating Population. Papa, G.G.[1], L.C. Melo[2], T.L.P.O. Souza[2], J.G.C. da Costa[2], L.C. Faria[2], H.S. Pereira[2] M.V.C.B. Cortês[2], A.S. Moreira[2], F.J. Gonçalves[2], M. Lobo Junior[2], M.I.S. Oliveira[2], E.P.B. Ferreira[2], G.F. Theodoro[1] and A. Wendland[2*]
[1] Universidade Federal de Mato Grosso do Sul, Campo Grande, MS 79070-900, Brazil;
[2] Embrapa Rice and Beans, Santo Antônio de Goiás, GO 75375-000, Brazil. [*]Presenter (adriane.wendland@embrapa.br)

Bacterial wilt (*C. flaccumfaciens* pv. *flaccumfaciens* - *Cff*) and Fusarium wilt (*F. oxysporum* f. sp. *phaseoli* - *Fop*) present similar symptoms derived from the obstruction of xylem vessels. A mapping population obtained by crossing Ouro Branco (resistant) x CNFP 10132 (susceptible), contrasting for bacterial wilt was evaluated for both diseases. The 12 more resistant genotypes of the generation F5:7 were inoculated in Embrapa Rice and Beans greenhouse by injecting 20 uL of bacterial suspension (10^8 UFC.mL^{-1}) of isolates Cff33 and Cff25, ten days after planting. The inoculation of suspension of 10^6 conidia.mL^{-1} of the isolates Fop101 and Fop102 was made by dipping cut roots during 5 min with subsequent transplant. The control was also inoculated with water. Evaluations were made at 15, 18 and 20 days after inoculation with *Cff,* and 21 days after inoculation with *Fop*, using severity scales of 1 = no symptoms to 9 = dead plants. Data were submitted to analysis of variance and means compared by Skott-Knott test at 5% probability. Plants were considered resistant when the mean rate was at 1 to 3. The more resistant genotypes for both diseases were identified as OBxCNFP 10132.42, OBxCNFP 10132.27 (clear grains) and OBxCNFP 10132.66, OBxCNFP 10132.162 (black grains) as well presented the morphological characteristics and commercial grain favorable to consumers.

P-58

Inheritance of High Levels of Resistance to Common Bacterial Blight Caused *by Xanthomonas axonopodis* Pv. p*haseoli* in Common Bean (*Phaseolus vulgaris* L.). Guachambala Cando[1], M.S., M. Zapata[1], J.S. Beaver[1*] and T.G. Porch[2] [1]Department of Crop and Agro-Environmental Sciences, University of Puerto Rico, Mayagüez, Puerto Rico, [2]USDA-ARS Tropical Agriculture Research Station, Mayagüez, Puerto Rico. [*]Presenter (james.beaver@upr.edu)

The inheritance of high levels of resistance to common bacterial blight with the pathogenic strain *Xap* UPR 3353 was evaluated in a population derived from a cross between breeding line PR0313-58, which has moderate levels of resistance, and VAX 6, which has high levels of resistance to common bacterial blight. Common bacterial blight evaluations were conducted in the field and greenhouse on F_2 plants and $F_{2:3}$ lines. The results suggest that in this population two putative dominant complementary genes confer high levels of resistance to bacterial blight.

P-59

Evaluation of the Tepary Bean (*Phaseous acutifolius*) Ciat Germplasm Collection for Response to Common Bacterial Blight and *Bean Common Mosaic Necrosis Virus.* Ana Vargas[1*], Timothy Porch[2], James Beaver[1] [1]University of Puerto Rico, Dept. of Crops and Agroenvironmental Sciences, Mayaguez, PR 00681; [2]USDA-ARS-TARS, 2200 P.A. Campos Ave, Suite 201, Mayaguez, PR 00680;
*Presenter (ana.vargas2@uprm.edu)

Developing resistance to viruses, specifically BCMV, BCMNV and BGYMV, will be critical for expanding tepary bean production. Few evaluations of the international tepary collection at CIAT have been conducted to evaluate their response to abiotic and biotic factors. This study evaluated the response of the tepary collection to common bacterial blight and to *bean common mosaic necrosis virus* using controlled greenhouse evaluations and found variability in response to both pathogens.

P-60

Screening of the USDA Core Collection of Common Bean for Resistance to Halo Blight
Ghising, K.[1]*, J.M. Osorno[1] K.McPhee[1] J.Pasche[2], and R.Lamppa[2] [1]Dept. of Plant Sci., North Dakota State Univ., [2]Dept. of Plant Path., North Dakota State Univ., Fargo, ND 58108.
*Presenter (Kiran.ghising@my.ndsu.edu)

Halo blight, caused by *Pseudomonas syringae* pv. *phaseolicola* (*Psp*) is an important seed-borne bacterial disease of common bean (*Phaseolus vulgaris* L.), and could cause significant yield loss, especially on susceptible cultivars. A subset of 283 accessions of *P. vulgaris* from the USDA-NPGS core collection was evaluated for reaction to *Psp* race 6 in the growth chamber. Of the 283 accessions evaluated, twenty-one percent of accessions with a mean disease score of 1-3 were classified as highly resistant to *Psp* race 6. However, PI 533259 (a black bean from Mexico) displayed the highest level of resistance to *Psp* race 6 with a mean disease score of 1. The observation suggests that PI 533259 could be a useful source of resistance to *Psp* race 6.

P-61

QTL Analysis for Fusarium Root Rot Resistance in Snap Bean Under Greenhouse Conditions. Bello, M.H[1*], Hagerty, C.H[2], Myers, J.R[2], Porter, L[1], and Miklas, P.N[1]. [1]USDA-ARS, Vegetable and Forage Crop Production Unit, Prosser, WA. [2]Department of Horticulture, Oregon State University, Corvallis, OR.
*Presenter (marco.bello@ars.usda.gov)

Fusarium root rot (*Fusarium solani* f. sp. *phaseoli*) is a major disease of common bean worldwide. Reaction to Fusarium root rot in a snap bean RIL population (RR6950/OSU5446) that was previously genotyped on a Illumina 10K SNP chip, was evaluated by inoculation with a highly virulent strain of the pathogen under greenhouse conditions. QTL associated with disease severity and root biomass were detected on chromosomes Pv2, Pv9, and Pv11.

P-62

SSR DNA Markers Linked With Broad-Spectrum Rust Resistance in Common Bean PI 310762 Discovered by Bulk Segregant Analysis Using a Large Set of SNP DNA Markers. Shin, S-H.[1,2], Q. Song[1], P.B. Cregan[1], M.A. Pastor-Corrales[1*]. [1]Soybean Genomics and Improvement Laboratory, ARS-USDA,

Beltsville, MD; [2]Upland Crop Research Division, NICS, RDA, 441-857 Seodun-dong Gwonseon-gu Gyeonggi-do, Republic of Korea. *Presenter (talo.pastor-corrales@ars.usda.gov)

The Mesoamerican common accession PI 310762 was resistant to 89 of the 90 races of the rust pathogen used in this study. PI 310762 was also was resistant to all races that rendered susceptible all known and mapped rust resistance genes in common bean. The objective of this study was to identify simple sequence repeat (SSR) DNA markers linked to the rust resistance gene in PI 310762. These markers were discovered by bulk segregant analysis (BSA) using a large set of SNP DNA markers.

P-63

Development of Tools for *Macrophomina phaseolina* Evaluation and for Genetic Improvement of Resistance in Common Bean. Porch, Timothy[1*], James Beaver[2], Sara Colom[2], Ana Vargas[2], Consuelo Estevez de Jensen[2], [1]USDA-ARS-TARS, 2200 P.A. Campos Ave, Suite 201, Mayaguez, PR 00680; [2]University of Puerto Rico, Dept. of Crops and Agroenvironmental Sciences, Mayaguez, PR 00681 *Presenter (timothy.porch@ars.usda.gov)

Ashy stem blight (*Macrophomina phaseolina*) causes significant yield reduction in the tropics and subtropics, often in association with drought stress. A collection of *M. phaseolina* isolates was assembled in Puerto Rico for the study of diversity and virulence using a novel greenhouse inoculation technique and field evaluation. The response to controlled inoculation of a RIL population and the Andean Diversity Panel was evaluated with the goal of genetic improvement of resistance.

P-64

Routes of Indole Acetic Acid Synthesis in Beans. Hernandez, JL* Sanchez-Perz MI and Quiroz-Velasquez JD; Experimental Biotechnology Lab. Centro de Biotecnologia Genomica IPN. *Presenter (jhernandezm@ipn.mx).

The indole acetic acid synthesis is produced in plants using four pathways called dependent TRP-D Tryptophan, another pathway called independent TRP-I Tryptophan, deriving to kynurenine and after to anthranilic acid and at the end to indole acetic acid. It was studied the pathways for IAA synthesis on Pinto Saltillo bean. These substances are detected by HPLC. In bean Tryptamine and IAN pathway was detected. The indol acetaldoxine and indol pyruvic acid pathways are absents. The kynurenine pathway it was detected and also anthranilic acid from the alternative pathway TRP-I.

P-65

Growth Stimulation of Flor de Mayo Bean Treated with *Trichoderma* spp. Hernandez, JL* García-Olivares, JG and Quiroz-Velasquez JD; Experimental Biotechnology Lab. Centro de Biotecnologia Genomica IPN. *presenter (jhernandezm@ipn.mx).

Frequently *Trichoderma* spp is used as phytopathogen controller, however has show to produce plant grow promoters such indolyacetic acid. The above experience, it was inoculated on seeds of Flor de Mayo bean with 16 native strains of *Trichoderma* spp from Tamaulipas and Texas frontier. Data are obtained to 30 days after seeding and was founded that five *Trichoderma* strains stimulate root growth or foliage. Other strains apparently have no effect on the bean plants.

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