2019 Biennial

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Fargo, North Dakota

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Welcome to the Radisson Hotel, Fargo, North Dakota
Bean Improvement Cooperative
2019 Biennial Meeting

Your Local Hosts:

Juan Osorno, Dry Bean Breeder, Dept. of Plant Sciences, North Dakota State University
Phil McClean, Dry Bean Genetics, Dept. of Plant Sciences, North Dakota State University
Julie Pasche, Diseases of Dry Bean, Pulse and Lentil Crops, Dept. of Plant Pathology, North Dakota State University
Nonoy Bandillo, Pulse Breeder, Dept. of Plant Sciences, North Dakota State University
Mike Grusak, Center Director, USDA-ARS Edward T. Schafer Agricultural Research Center

SUNDAY, NOVEMBER 3, 2019

4 – 6:00 PM	**Registration**	**Atrium**

* Student Presenter

MONDAY, NOVEMBER 4, 2019

7:00 AM	**Breakfast Buffet**	**Atrium**
8:15 AM	**Welcome**	**Cityscape Ballroom**

Symposium: Global Bean Research – Fostering International Collaborations

Moderators: Juan Osorno and Kristin Simons

8:30 AM	Frazier-Zaumeyer Distinguished Lectureship: Bean Production and Improvement in Central America	Juan Carlos Rosas
9:15 AM	Frazier-Zaumeyer Distinguished Lectureship: Production and Genetic Improvement of Beans in the Caribbean	James Beaver
10:00 AM	**Coffee Break**	**Atrium**
10:30 AM	Embrapa Common Bean Breeding Program: Main Objectives and Opportunities for Collaborations	Thiago Souza
11:00 AM	Common Bean Breeding in Africa: Current State and Future Perspectives	Stephen Beebe
11:30 AM	The Strange Case of Common Beans	Roberto Papa
12:00 PM	Status and Landscape of Snap Bean Breeding Research Worldwide	Jim Myers
12:30 PM	**Lunch Buffet**	**Atrium**
2:00 PM	Creating Greater Awareness of Pulses to Improve Food Security, Environmental Sustainability, Research Funding and International Trade	Cindy Brown
2:30 PM	Breeding for the Common Bean Value Chain	Phil McClean

Abiotic Stress

Moderators: Jim Heitholt and Shalu Jain

3:00 PM	Genetics of common Bean Response to High Temperature Stress	Timothy Porch
3:15 PM	Identification and Introgression of Tepary Beans as a Novel Source of Drought and Heat Adaptation in Elite Common Bean Backgrounds	Santos Barrera*

* Student Presenter

MONDAY, NOVEMBER 4, 2019

Abiotic Stress *continued*

Cityscape Ballroom

3:30 PM	Effects of High Night Temperature Stress on Reproductive Structures of Lima Bean (*Phaseolus lunatus*) and the Distribution of These Effects in the Genepool	Emmalea Ernest

3:45 PM	**Coffee Break**	**Atrium**

Human Nutrition

Cityscape Ballroom

Moderators: Mike Grusak and Jennifer Trapp

4:15 PM	Redefining Iron Nutrition from the Common Bean: Evidence For Moving From Biofortification to Biodelivery	Raymond Glahn
4:30 PM	Genotype by Environment Impact on Common Bean Yield and Nutrient Composition	Rosemary Bulyaba*
4:45 PM	On-farm Evaluation for Iron Concentration and Iron Bioavailability of the Fast Cooking Manteca Yellow Bean (*Phaseolus vulgaris* L.) in Uganda	Jason Wiesinger
5:00 PM	Formulating White and Yellow Beans (*Phaseolus vulgaris* L.) into Heat Treated Flour Ingredients Enhances the Iron Bioavailability of Bean-Based Spaghetti Pastas	Jason Wiesinger

5:15 PM	**Poster Session**	**Prairie Rose Room & The Loft**
6:30 PM	**Dinner on your own**	

TUESDAY, NOVEMBER 5, 2019

7:00 AM	**Breakfast Buffet**	**Atrium**

Biotic Stress

Cityscape Ballroom

Moderators: Julie Pasche and John Posch

8:00 AM	Exploring Common Bean Early Response to *Fusarium brasiliense* in a Mesoamerican x Andean population	Miranda Haus
8:15 AM	Natural Infection of Fungal, Bacterial and Viral Pathogens to Dry Bean Genotypes	Papias Binagwa*

* Student Presenter

TUESDAY, NOVEMBER 5, 2019

Biotic Stress *Continued*

Cityscape Ballroom

8:30 AM	Identification of Resistance Genes of Common Bean Line MAIII - 16.153 to *Pseudocercospora griseola*.	Paula Furtado de Pádua*
8:45 AM	QTL-based Sequencing to Identify Candidate Genes Associated with White Mold Resistance in Common Bean (*Phaseolus vulgaris* L.)	Atena Oladzad
9:00 AM	Multi-Parent Advanced Generation Inter-Cross Population for Improvement of Genetic Resistance of Dry Bean to White Mold: WM-Magic	Edgar Escobar*
9:15 AM	Interaction of *bc-u* Gene with Recessive Resistance Genes in Different Genetic Backgrounds for Control of Bean Common Mosaic Virus and Bean Common Mosaic Necrosis Virus	Alvaro Soler-Garzon

9:30 AM **Coffee Break & Poster Session** **Prairie Rose Room & The Loft**

10:30 AM	Gene Mapping and Marker Development Using Your Breeding Program: A Case Study on Common Bacterial Blight	Kristin Simons
10:45 AM	Mining the Common Bean Middle American Diversity Panel to Discover Genetic Factors for Resistance to the Most Prevalent Rust Races in North Dakota	Shalu Jain
11:00 AM	Reaction of Tepary, Common Bean, and Interspecific Accessions to Races of the Bean Rust Pathogen that Overcome All Common Bean Rust Resistance Genes	Carlos Urrea
11:15 AM	Identification of Race-Specific Resistance QTL for Anthracnose in Common Bean	Kelvin Kamfwa

11:30 AM **Lunch – Radisson Restaurant and various downtown locations**

Genomics/Gene Discovery

Cityscape Ballroom

Moderators: Kirstin Bett and Maria Muñoz-Amatriain

1:15 PM	Tools for Visualizing and Analyzing Genotype, Genetic, and Genomic Information for *Phaseolus*	Steven Cannon
1:30 PM	Integration of Anthracnose Resistance loci and RLK and NB-LRR - Encoding Genes in *Phaseolus vulgaris* L. Genome	Mariana Vaz Bisneta*

* Student Presenter

TUESDAY, NOVEMBER 5, 2019

Genomics/Gene Discovery *Continued*

Cityscape Ballroom

1:45 PM	Development and Validation of a Marker Linked to the *Ur-4* Rust Resistance Gene In Common Bean	Oscar Hurtado-Gonzales
2:00 PM	Exploring the Epigenomic State of Sodium Bisulfite-Treated Common Bean (*Phaseolus vulgaris*) within the *Crg* and *Ur-3* Deletion Regions on chromosomes Pv10 and Pv11	Antonette Todd
2:15 PM	Evaluating Genomic Predictions for Semi-Quantitative Traits: Does GS Hold Promise Predicting Disease Resistances for Root Rots and CBB?	Bodo Raatz

2:30 PM	**Coffee Break & Poster Session**	**Prairie Rose Room & The Loft**

Other Traits of Economic Importance

Cityscape Ballroom

Moderators: Timothy Porch and Carlos Urrea

3:15 PM	Phenotyping Improvements and QTL Mapping of Color Retention Traits in Processed Black Beans	James Kelly
3:30 PM	Investigation of the Effects of the Seed Coat Non-Darkening Trait on Agronomic Traits in Pinto Bean Populations	Mohammad Erfatpour*
3:45 PM	A Multidrug and Toxic Compound Extrusion (MATE) Transporter, Pvmate8, is a Vacuolar Transporter of Proanthocyanidin Monomers and Involved in Seed Coat Darkening in Common Bean	Nishat Islam*
4:00 PM	Effects of Nitrogen Application on Nitrogen Fixation in Common Bean Production	Yarmilla Reinprecht
4:15 PM	Nitrogen Fixation of Dry Beans Bred for Hillside and Marginal Land Production in Honduras	Jennifer Wilker*

4:30 PM	**Business Meeting**	**Cityscapes Ballroom**
6:30 PM	**Awards Banquet**	**Cityscapes Ballroom**

* Student Presenter

WEDNESDAY, NOVEMBER 6, 2019

7:00 AM	**Breakfast Buffet**	**Atrium**
8:00 AM	W-3150 Multistate Project Annual Meeting	**Cityscapes Ballroom**
9:45 AM	**Coffee Break**	**Atrium**
10:15 AM	Phaseolus Crop Germplasm Committee (PCGC)	**Cityscapes Ballroom**
11:00 AM	BIC Genetics Committee	
12:00 PM	**Lunch on your own**	
2:00 PM	**BIC & NAPIA TOUR** NDSU Agricultural Experiment Station Research Greenhouse Complex NDSU Northern Crop Institute Brewhalla – Drekker Brewing Co.	**Bus departs**
4:00 PM	NAPIA Registration	
5:30 PM	NAPIA Board Meeting	
6:00 PM	NAPIA Reception	**Bus Returns**

* Student Presenter

POSTERS

P01 Current Status and Future Opportunities with the Pulse Crop Health Initiative

P02 KnowPulse: An Evolving Breeder-Friendly Web-Portal for Pulse Crops

P03 A Descriptive Sensory Evaluation and Volatile Quantification of a Diverse Green Bean Panel

P04 Genomic Shifts in Snap Beans under Different Agricultural Management Systems

P05 Cosmetic Stay-Green in Snap Bean:Understanding Deleterious Effects on Germination Rate

P06 SNP Markers Associated with Slow Darkening Trait in Carioca Common Bean

P07 Genetic Control for Slow Seed Coat Darkening of

P08 Slow Darkening Pinto Beans Exhibit Enhanced Iron Bioavailability across Multiple Production Environments in North Dakota

P09 Multiplex Quantitative Assay for Simultaneous Detection of Bacterial Blight Pathogens of Common Bean

P10 Screening Ontario-adapted Dry Bean Germplasm for Reactions to Bacterial Diseases

P11 Effectiveness of Recurrent Selection Aiming Anthracnose Resistance in Common Bean

P12 Relationship Among *Colletotrichum* spp. Strains Associated to Common Bean Anthracnose and Scab

P13 Genome-Wide Association Study Reveals Regions on Chromosomes Pv03 and Pv05 Related to Anthracnose Resistance in Common Bean

P14 Sources of Resistance to *Colletotrichum lindemuthianum* and *Pseudocercospora griseola* in Common Bean from Brazil

P15 Co-Segregation Analysis and Fine Mapping of Anthracnose and Angular Leaf Spot Disease-Resistance Genes in the Common Bean Cultivar California Dark Red Kidney

P16 Genome Wide Association Analysis Reveals Markers Tagging Anthracnose and Angular Leaf Spot Resistance Genes in Common Beans from Brazil

P17 Comparison of QTL for Resistance to Angular Leaf Spot and Rust in Tanzania versus South Africa for the Andean Diversity Panel and Rojo/CAL 143 RIL Population

P18 Genetic Progress after 18 Cycles of Recurrent Selection for Angular Leaf Spot Resistance in Brazil

* Student Presenter

P19 Fine Mapping the *Ur-6* Rust Resistance Gene in Common Bean

P20 Identifying Resistance in Andean Common Beans to the Rust Pathogen *Uromyces appendiculatus*

P21 Genome-Wide Association and Fine Mapping of *bgm-1* Gene and Other QTLs for Resistance to Bean Golden Yellow Mosaic Virus in Dry Beans

P22 *Pythium* Species Associated with Common Bean in North Dakota and Minnesota

P23 Investigating MAT Heterokaryons in Isolates of *Sclerotinia sclerotiorum* in Brazil

P24 Next Generation Sequencing Rapidly and Simultaneously Detects Many Airborne Plant Pathogens from Dry Bean Fields and Other Crops

P25 Common Bean Inbred Lines of the Black Commercial Group Selected for High Yield Potential, Early Cycle and Disease Resistance

P26 Computational Identification, Phylogenetic and Synteny Analysis of Receptor-like Kinases "RLK" and Receptor-like Proteins "RLP" in Legumes

P27 QTL Analysis of a Yellow *Phaseolus vulgaris* Recombinant Inbred Line Population for a Fast Cooking, Flavorful, and Flourishing Future of Dry Beans

P28 Genetic Study of Seed Hardness Trait in Dry Bean (*Phaseolus vulgaris*)

P29 Investigation of Marsh Spot Variation in Cranberry Beans in Manitoba, Canada

P30 Assessing Genomic Selection Prediction Accuracy for Yield and End-Use Quality Traits in Black Beans

P31 Iron Biofortification of the Common Bean: Assessment of Bean Iron Concentration and Iron Bioavailability from Markets and Breeder Collections in East Africa

P32 Development of Edible Bean Germplasm Lines with Improved Cysteine and Methionine Concentration

P33 Wyoming-Grown Peruvian Popping Beans: Sensory Analysis and Consumer Acceptance

P34 Molecular Mapping the Pinto Pattern Gene in the *C* Locus of Common Bean

P35 Speed Breeding in Dry Beans

P36 Exploring Genetic Improvements and Innovative Process Methods in Organic Dry Beans

P37 The Pulse Crop Database: Expanding the Cool Season Food Legume Database into a Resource for Pulse Crop Research and Improvement

* Student Presenter

SYMPOSIUM - GLOBAL BEAN RESEARCH – FOSTERING INTERNATIONAL COLLABORATIONS

Bean Production and Improvement in Central America

Rosas JC

Zamorano University, Francisco Morazan, Honduras

Presenting author: jcrosas@zamorano.edu

Beans (*Phaseolus vulgaris* L.) in Central America are produced mainly by small-scale farmers facing several constraints, including diseases and pests, low fertility soils, increased drought and temperatures, and limited access to good quality seed and other available technologies. The development of bean cultivars having improved disease resistance and better adaptation has been the main strategy to cope with these limiting factors. Adoption of improved bean cultivars has contributed to a slight increase in yield and helped to stabilize the consumption and price of beans in the region. The Bean Research Program (BRP) of Zamorano University is a regional program focused on the genetic improvement of common beans with an emphasis on the generation and dissemination of improved small red and black bean cultivars for Central America and the Caribbean (CAC). The emphasis of the BRP is on genetic improvement of beans having disease resistance, greater tolerance to drought, low soil fertility and high temperatures, enhanced biological nitrogen fixation and bio-fortification, using conventional breeding methods, participatory plant breeding, marker assisted selection and regional evaluation and validation through the CAC-Bean Regional Network. Collaboration of the Zamorano BRP with US universities, USDA-ARS, CIAT, USAID-CRSP and LIL programs, national bean research institutions and non-governmental organizations, has led to the release of more than 60 improved bean cultivars. These improved cultivars are used extensively by small-scale farmers in Central America and Haiti, representing a significant impact in food security and quality of life for rural families and consumers.

* Student Presented

Production and Genetic Improvement of Beans in the Caribbean

Beaver J

University of Puerto Rico, Mayaguez, PR

Presenting author: james.beaver@upr.edu

The Caribbean has a long tradition of producing and consuming common (*Phaseolus vulgaris* L.) and lima (*Phaseolus lunatus* L.) beans. Approximately 300,000 ha of dry beans are harvested in the region each year. Various strategies are used in the Caribbean to enhance the value of the bean crop. Beans are frequently produced in multiple cropping systems. Intensification and diversification of crop production increases income on small-scale farms and enhances food security. Although the Caribbean is not considered a center of genetic diversity of the common bean, germplasm from the region has proven useful for the improvement of the crop. Bean producers in the Caribbean face many challenges. Beans are planted in a diversity of soil types that present a wide range of edaphic constraints. The mountainous terrain on the islands results in beans being produced in different temperature regimes and rainfall distribution patterns. Increasingly frequent extreme weather events including tropical storms and hurricanes can cause major disruptions in bean production. Successful bean cultivars also need to adapt to a range of levels of technology and different cropping systems used to produce the crop. Finally, bean producers in the tropics generally face greater disease and pest pressure. A major constraint for bean producers in the Caribbean is the unavailability of high-quality seed of improved cultivars. In recent years, Central American and Caribbean breeding programs have focused on combining multiple virus resistance and other traits of economic importance. Improved crop management practices are also needed to increase the productivity of beans in the Caribbean.

Embrapa Common Bean Breeding Program: Main Objectives and Opportunities for Collaborations

Souza TLPO, Pereira HS, Aguiar MS, Costa JGC, Faria LC, Abreu AFB, Knupp AM, Magaldi MCS, Souza NP, Rodrigues LA and Melo LC

Embrapa Rice and Beans, Santo Antonio de Goias, GO, Brazil

Presenting author: thiago.souza@embrapa.br

Brazil is the largest producer and consumer country of common bean worldwide. In 2017, around 2.6 million tons of beans were harvested on 1.7 million hectares. Several commercial classes are grown in three distinct growing season, on the majority states of the country. The national market is shared in approximately 70% of carioca beans, 20% of black, and 10% of other commercial classes. The Embrapa common bean breeding program is one of the pioneers in Brazil, being developed for over four decades. From 1984 to 2019, 71 new varieties were released, which currently have 60% of the Brazilian seed market share. Embrapa breeding program objectives include the release of varieties adapted to different production systems and regions in Brazil, with high yield and production stability, besides commercial, culinary, nutritional and functional seed quality. In addition, resistance to major biotic and abiotic factors restricting production, efficiency in nutrient uptake and use, including efficiency in biological nitrogen fixation. Research and/or financial collaborations have been established with 31 research centers and institutions, including 10 Embrapa research centers, nine Brazilian state research institutes, nine universities and three international research institutions (CIAT, Cali, Colombia; USDA, Beltsville, EUA; and NARO, Kampala, Uganda). However, there is room, opportunity and interest in establishing partnerships to advance knowledge and the development of technical solutions to improve the common bean crop. The main goal of this talk will be to present an overview of the common bean breeding research conducted by Embrapa and its partners, focusing on the develop and release of varieties adapted to the distinct growing conditions in Brazil, highlighting the main commercial classes, target problems and traits. It will be also presented the current opportunities for research collaborations with the world scientific community.

* Student Presented

Common Bean Breeding in Africa: Current State and Future Prospectives

Beebe S [1]*, Mukankusi C* [2]*, Chirwa R* [3]

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[2] *CIAT, Kampala, Uganda*
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Common beans are the principal grain legume for human consumption in East and southern Africa, and with local importance in West Africa. Breeding objectives are similar to those in the tropics of the western hemisphere, with the exception of the prevalence of necrotic strains of potyvirus (BCMNV), the bean stem maggot (*Ophiomyia* sp.), and occasionally bean scab (*Elsinoe phaseoli*). The Pan African Bean Research Alliance (PABRA) is a consortium of bean researchers in 29 countries. PABRA is facilitated by CIAT and coordinates breeding across the region. Besides CIAT's breeding programs, another half dozen programs are active in national research institutions while line testing occurs in nearly all bean producing countries. Increasingly breeding is focused on markets for specific grain classes under Demand Led Breeding (DBL) and within the context of production-to-consumption bean corridors. Currently efforts are underway to modernize breeding programs, under the guidance of the Excellence in Breeding Platform (EiB) of the CGIAR, with mechanization, marker assisted selection, and breeding methods. Climate change will present particular challenges for bean production in the tropics, and climate analysis is on-going to determine the required levels of stress tolerance to maintain the viability of bean production in Africa.

* Student Presented

The Strange Case of Common Beans

Papa R

Dipartimento di Scienze Agrarie, Alimentari ed Ambientali, Università Politecnica delle Marche, via Brecce Bianche, 60131 Ancona, Italy

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Common bean and *Phaseolus* can be considered as a unique model for the study of crop evolution, and in particular, for an understanding of the convergent phenotypic evolution that occurred under domestication. At least seven independent domestication events occurred in *Phaseolus* species, which provides the possibility to unravel the genetic basis of the domestication process not only among species of the same genus, but also between gene pools within the same species. Along with this, other interesting features makes *Phaseolus* crops very useful in the study of evolution, including: (i) their recent divergence, and the high level of collinearity and synteny among their genomes;(ii) their different breeding systems and life history traits, from annual and autogamous, to perennial and allogamous; and (iii) their adaptation to different environments, not only in their centers of origin, but also out of the Americas, following their introduction and wide spread through different countries. In particular for *P. vulgaris* this resulted in the breaking of the spatial isolation of the Mesoamerican and Andean gene pools, which allowed spontaneous hybridization, thus increasing of the possibility of novel genotypes and phenotypes. Moreover, a key aspect of domestication is the convergent phenotypic evolution that is associated with the adaptation to a novel agroecosystem, and to human needs. The loss of seed shattering is a key trait in crop domestication, particularly for grain crops such as legumes. For wild plants, seed shattering is a crucial mechanism to achieve greater fitness, although in the agricultural context, this mechanism reduces harvesting efficiency, especially under dry conditions. Loss of seed shattering was acquired independently in different crop species by 'convergent phenotypic evolution', leading to similar low dehiscent and indehiscent phenotypes and to similar functional changes. In common bean the indehiscent mutation has been probably selected after domestication leading to the development of snap bean types. Acknowledgments: This work was supported by the EU, H2020 grant BRESOV

* Student Presented

Status and Landscape of Snap Bean Breeding Research Worldwide

Meyer J

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Snap beans share common lineages with dry beans, and research problems overlap, but many aspects of snap bean breeding and genetics related to their use as a vegetable are unique to the crop. They have been selected for low fiber, stringlessness and thick succulent pods. Yield is more complex because of the need to balance with quality. Types for processing have additional requirements such as round pod cross-section, white seed and concentrated pod set. Globally, snap beans are most consumed in developed temperate zone countries. The plant breeding landscape differs substantially from that of dry beans with more private sector cultivar development. Applied research in the U.S. is addressed by about 1 ¾ FTE in the public sector and even less in Europe. Two research tools that are providing a vehicle for cooperative research nationally and internationally are screening nurseries and diversity panels. Public programs offer yield and quality evaluation and disease screening nurseries. Public-private partnerships have also been important in facilitative applied research. The OSU breeding program has conducted research on root rots and flavor volatiles with private sector support. Recently developed diversity panels for conducting genome wide association studies (GWAS) are facilitating cooperative research. Two diversity panels have been developed: the Bean CAP Snap Bean Diversity Panel (SBDP) and the Snap Bean Association Panel (SnAP). The SBDP has been distributed to Africa and Europe as well as in the U.S. Genotypic data for these is available in the form of a 6K Illumina beadchip (SBDP) and via GBS (SnAP). Cooperators can obtain these panels and screen for traits of interest, then conduct GWAS to map these traits and identify useful germplasm. Future activities to enhance breeding efforts will include use of diversity panels to identify, characterize and map candidate genes for traits of greatest interest to the snap bean research community.

* Student Presented

Creating Greater Awareness of Pulses to Improve Food Security, Environmental Sustainability, Research Funding and International Trade

Brown C

Global Pulse Confederation, Dubai, UAE

Presenting author: cbrown@globalpulses.com

The Global Pulse Confederation is a small organization with a BIG mission. Our mission is to create greater aware of pulses in order to improve: [1] food security; [2] environmental sustainability [3] research funding, and [4] international trade. The Global Pulse Confederation brought greater awareness and attention to pulses via the successful 2016 UN International Year of Pulses and the recently declared UN World Pulses Day, which takes place February 10 of each year. Yet, despite important achievements resulting from these efforts, pulses remain an underutilized and underappreciated plant protein. While often labeled a "Superfood" for their ability to address both malnutrition and overnutrition, pulses still suffer from lack of awareness, lack of research investments and lack of support at governmental levels. Funding available for pulses research is a small fraction of the funding provided to cereals crops. And other government support available to pulses such as production subsidies is almost non-existent. Sixty years ago, one in three people of the world's 3 billion population suffered from malnutrition. Today, "only" one in eight people in the world suffer from malnutrition but a nearly equal number of people suffer from overnutrition. Obesity levels have skyrocketed in countries like the United States, Australia and Mexico as consumers have moved away from traditional healthy diets that featured pulses to eat more ultra-processed foods and meals at quick serve restaurants. Pulses are an important part of the solution to this problem. To meet UN sustainable development goal 2 of zero hunger and to bring rural farmers out of poverty requires thoughtful, proactive, and committed multi-stakeholder partnerships. To be successful, we must work together to reach out to governments and private sector members to make them aware of the benefits of pulses for sustainability and economic development. We must work together because the people growing most of the world's food are also often the most impoverished. They are small farm holders in Africa, Asia and Latin America struggling to produce crops on degraded lands that are also subject to the extreme impacts of ever worsening climate change. Working together we can encourage greater research investment about the environmental benefits of pulses for small farm holders. Working collaboratively, we can facilitate projects that provide improved pulse varieties and economic prospects to farmers. Working together we can help develop new markets and products that create pull through demand for pulses. Working together we can change the world.

* Student Presented

Breeding for the Common Bean Value Chain

McClean P

North Dakota State University, Fargo, ND, USA

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To increase the value of common bean, value chain participants should agree on an improvement path that satisfies their needs. For the large-scale, high-yielding production industry, the participant list includes the breeding organization, seed industry, the producer, buyers/sellers of the crop, packers and processing companies, and, of course, the final customer. For small-holder production, the value chain might only include the breeding organization and the producer who grows the crop for their family consumption or to be sold at a small local market. Here sustainable production over varying climate conditions is a major breeding objective. As we look to the future of the crop, the challenge for large scale production is increasing yield. The breeding goal for the smallholder farmer though is also high yield, but a yield that can be maintained at relative higher levels over time, under climate change conditions, and in environments not typically the target for large scale production. With these two distinct needs, a single improvement path does not seem reasonable and different value chain participants should be involved as new performance traits are considered. While these two focuses are important, it is also important to continually consider what future purposes, possibly unrealized, that common bean can be used. Modifying the crop in a manner that dramatically increases its demand will positively impact, economically or nutritionally, either value chain. Recent advances in understanding our crop, from a production and sustainability perspective, are identifying genes and genomic regions that can be targets for breeding, using either hybridization techniques or targeted gene modification. This presentation will 1) highlight the interactions required of members of different value chains to design future common bean varieties with higher value or new uses, and 2) describe techniques to produce those valuable varieties.

* Student Presented

ABIOTIC STRESS

Genetics of Common Bean Response to High Temperature Stress

Porch TG [1]*, Raatz B* [2]*, Hart JP* [3]*, Beebe S* [2]

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[2] *CIAT, International Center for Tropical Agriculture, Colombia*
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Presenting author: timothy.porch@usda.gov

The sensitivity of common bean to high temperatures (> 25^{o}C), primarily evident in failed reproductive development, threatens reductions in yield and production area due to a warming climate. Continued advances in genetic improvement of heat tolerance in common bean is critical for maintaining current production areas and for increasing yields of this food security crop. This study evaluates the genetic response to heat in a recombinant inbred line population, INB 841/RCB 593, genotyped using genotyping-by-sequencing (GBS), and then evaluated using QTL analysis. The field experiments were conducted under high ambient temperatures in Puerto Rico and under drought stress and non-stress in Colombia between 2013 and 2019 and evaluated for traits associated with vegetative and reproductive development, including yield and pollen shed and using high-throughput methods for measuring canopy temperature and canopy height. QTL were identified that could be used for understanding heat tolerance mechanisms, and for genetic improvement of this trait in common bean.

* Student Presented

Identification and Introgression of Tepary Beans as a Novel Source of Drought and Heat Adaptation in Elite Common Bean Backgrounds

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[2] *University of California-Davis, CA, USA*
[3] *University of California, Agriculture and Natural Resources, Holtville, CA, USA*
[4] *International Center for Tropical Agriculture (CIAT), Cali, Columbia*

* Presenting author: sybarreral@huskers.unl.edu

The increase of drought and higher temperatures due to climate change has negatively impacted production of several crops that are important for food security. A staple crop experiencing the consequences from these changes is the common bean, (*Phaseolus vulgaris* L.). Drought, heat, and some fungal diseases limit the productivity of common bean. Genetic solutions for these constraints can be found in a related species, the tepary bean (*Phaseolus acutifolius* A. Gray). The tepary bean is quite diverse and highly tolerant of abiotic constraints such as high and low temperatures, drought and salinity. Furthermore, tepary beans have shown resistance to biotic constraints including common bacterial blight, rust, fusarium wilt, powdery mildew, seed weevil and leafhoppers. Hybridization between tepary and common bean usually requires numerous pollinations, embryo rescue, and consecutive backcrosses to obtain viable offsprings. In this study, tepary bean accessions were evaluated for drought and heat tolerance at five locations. Potential drought and heat tolerant tepary parents were identified. Interspecific hybridization between the two species is a viable option to improve biotic and abiotic resistance in the common bean. In addition, with the bridging parents reported in the BIC 2017, we successfully obtained crosses with elite tepary beans, without the need of embryo rescue, thereby providing a novel genetic source for the bean breeding program at the University of Nebraska Lincoln.

* Student Presented

Effects of High Night Temperature Stress on Reproductive Structures of Lima Bean (*Phaseolus lunatus*) and the Distribution of These Effects in the Genepool

Wisser RJ [1]*, and Johnson GC* [2]

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Heat stress reduces yields of May and June-planted lima bean (*Phaseolus lunatus*) in the Mid-Atlantic Region of the US. High night temperatures during flowering and seed development reduce or delay pod set, resulting in delayed harvest, split pod sets and lower yield. Breeding heat tolerant small and large seeded lima beans is a goal of the University of Delaware lima bean breeding program. Greenhouse experiments were used to characterize the response of several lima bean genotypes to high versus ideal nighttime temperatures to better understand the mechanism by which high night temperatures reduce yield. Past experiments had indicated that higher amounts of pollen shed onto the stigma and style under heat stress are correlated with higher yield under heat stress, and that there is genotypic variation for this trait. Greenhouse and field experiments were used to screen a diversity panel for amount pollen shed under heat stress to determine if this phenomenon is widespread within the genepool. Heat sensitive genotypes exhibited a number of physiological changes while under heat stress, some of which likely interfere with reproduction and affect yield: lower in vitro germination of pollen collected from the pistil, extrusion of the stigmatic pad from the keel, and anther indehiscence. Other aspects of reproduction, such as stigma receptivity or seed development are impaired by heat stress in some sensitive genotypes, but not others. The correlation of pollen quantity and yield under heat stress is present genepool-wide. Heat sensitivity is not isolated to large-seeded Andean genotypes, but such genotypes exhibit heat sensitivity of the stigma and the style, which was not apparent in Mesoamerican types. In the University of Delaware lima breeding program, characterization of some of the physiological changes associated with heat sensitivity is being used to screen diverse germplasm and breeding lines in order to select for heat tolerance.

* Student Presented

HUMAN NUTRITION

Redefining Iron Nutrition from the Common Bean: Evidence for Moving from Biofortification to Biodelivery

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The common bean (*Phaseolus vulgaris*) has been formally targeted for biofortification for more than 15 years as beans are widely consumed, and relatively high in Fe content with sufficient variability to suggest that high Fe can be a tractable trait. However, recent studies indicate that the primary biofortification approach of breeding for high Fe concentration (ie. 85-90 µg/g) may not be sustainable as Fe content is profoundly influenced by environment and genotype by environment interaction. Recent reports also indicate that the basic assumptions of this approach are not met as the average bean Fe concentration of non-biofortified varieites in markets such as east Africa is approximately 70 µg/g, significantly higher than the assumed average of 50-55 µg/g and essentially identical to most varieties that have been released as biofortified. High Fe bean varieties are also known to have higher levels of polyphenolics and phytate that can lower fractional Fe bioavailability and negate the nutritional benefit. Moreover, bioavailability estimates that have guided the high Fe approach are potentially flawed due to the caveats of extrinsic isotopic labeling. “Biodelivery” may be the best term to describe an alternative approach to improve Fe nutrition from staple food crops that focuses on factors that enhance Fe bioavailability. Factors such as processing to disrupt the cotyledon cell wall releasing intracellular Fe, influence of other components in the diet or meal, and traits such as seed coat polyphenolic profiles that enhance Fe uptake rather than inhibit are part of the biodelivery approach. Biodelivery utilizes models such as the Caco-2 cell bioassay coupled with a poultry feeding model to identify, confirm and monitor nutritional gains. This presentation will summarize the history and evidence that supports this shift in approach, and suggest a path forward that redefines efforts to enhance Fe nutrition from beans.

* Student Presented

Genotype by Environment Impact on Common Bean Yield and Nutrient Composition

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Common bean (*Phaseolus vulgaris* L.) is a major staple crop in many households worldwide. Global consumption is on the increase annually due to the influences of consumer desire for protein-rich crops and greater interest in sustainable agriculture practices. This makes common bean a great target crop for alleviation of food insecurity and nutrition inadequacies, given its richness in protein and micronutrients such as iron and zinc. With a complete block design, we set up an experiment using four diverse common bean varieties planted at four locations, Iowa, Colorado, Michigan and Uganda for 2 subsequent years. The objective of the study was to determine to impact of environment on common bean yield overall, yield components and, grain nutritional composition, particularly Fe and Zn. We found yield and yield components such as pods per square meter, seeds per pod and seed weight to differ across location. Additionally, common bean mineral value of P, K, Mg and crude protein (CP) among others differed significantly amongst the varieties. Dark Red Kidney bean 'Montcalm' had 18.2, 6.9 and 4.1% greater P concentration (mg/kg) and 12.9, 8.6 and 4.9% more CP (g/kg) than Black Turtle 'Eclipse', Mayocoba (MY06326) and Great Northern beans (Taurus), respectively, whereas Great Northerns contained 21.3, 12.4 and 4.4% more Mg (mg/kg) than Dark Red Kidney, Mayocoba and Black Turtle beans, respectively. Overall, while we found soil nutrients such Mehlich-3 extractable Fe, Zn, K, P and properties such as pH and organic matter to differ greatly amongst our four experimental locations, we did not observe significant differences in common bean for the variety × elemental composition across these diverse environments. The ramification of these findings for human nutrition is great since the same seed in a different environment may provide variable amounts of micronutrients. Nutrient content of seed lines should be evaluated at specific sites to support human nutrition interventions.

* Student Presented

On-farm Evaluation for Iron Concentration and Iron Bioavailability of the Fast Cooking Manteca Yellow Bean (*Phaseolus vulgaris* L.) in Uganda

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Yellow and red beans (Phaseolus vulgaris L.) are rich in iron, and are important market classes sold in East Africa, especially in Uganda, where farmers select varieties based on yield and end-use quality traits such as seed color and cooking time. Recent evidence shows the fast cooking properties of the Manteca yellow bean are highly hereditable, but its iron and iron bioavailability have never been evaluated across multiple production environments. This study compared the iron concentrations and bioavailability of two Manteca genotypes (Ervilha, Cebo) to eight other white, yellow and red mottled genotypes, including farmer local check varieties (NABE15, Masindi yellow). Genotypes were produced across nine on-farm locations in Uganda over two field seasons (2015, 2016). Cooking time was standardized with a Mattson cooking device. Iron bioavailability was measured with a Caco-2 bioassay, which measures ferritin formation (ng ferritin/mg cell protein) as an indicator of iron uptake. Ferritin formations were standardized to a navy bean (cv. Merlin) reference control with each assay. Iron concentrations of cooked genotypes ranged from 41 to 97 ug/g, with a mean of 67 ug/g across the nine production environments. Iron bioavailability ranged from 8 to 116% of navy bean control. There was a significant negative association ($r = -0.438$, $p \leq 0.05$) between cooking time and iron bioavailability of the white, yellow and red beans produced in Uganda. The fast cooking white (Blanco Fanesquero) and Manteca beans consistently had the highest iron bioavailability (64–116% of control) across all locations in Uganda. Iron concentrations were highly variable across environments in Uganda, and there was no relationship between iron concentrations and iron bioavailability ($r = 0.09$, $p = 0.23$) in cooked seed. This study demonstrates the high iron bioavailability trait of fast cooking white and Manteca yellow beans are stable across different production environments in Uganda.

* Student Presented

Formulating White and Yellow Beans (*Phaseolus vulgaris* L.) into Heat Treated Flour Ingredients Enhances the Iron Bioavailability of Bean-Based Spaghetti Pastas

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Dry beans (*Phaseolus vulgaris* L.) are especially rich in iron, an important micronutrient for many children, adolescents and women worldwide. Beans are primarily sold as uncooked or canned whole seed products, but as more consumers learn about the health benefits of eating beans, food manufacturers are responding by producing beans into additive flour ingredients. Processing techniques can impact the physiochemical properties of beans, such as breaking the cotyledon cell walls, allowing digestive enzymes access to intercellular iron stores. This study evaluated the iron bioavailability of seven bean varieties with different seed coat colors (white, yellow, cranberry, red, black) after processing into spaghetti pastas, which were formulated with heat treated bean flour as the major ingredient (90% bean flour). Iron bioavailability was measured as ferritin formation (ng ferritin/mg of total cell protein) in a Caco-2 cell bioassay. After processing into spaghetti pasta, the iron bioavailability of white and yellow bean varieties (Snowdon, Alpena, Samurai, SVS 0863) increased significantly ($p \leq 0.05$), with values 3 – 4 times higher as compared to their boiled whole bean counterparts. The iron bioavailability of white and yellow bean-based pastas (16 – 32 ng ferritin/mg protein) was also significantly ($p \leq 0.05$) higher as compared to a durum wheat spaghetti (5.6 ng ferritin/mg protein). No improvements in iron bioavailability were observed after the cranberry (Etna), red kidney (Red Hawk) and black (Zenith) bean varieties were processed into spaghetti pasta. Iron bioavailability of bean-based pastas was not dependent on their iron or phytate concentrations, but rather appears to be associated with the breaking of the cotyledon cell walls after processing. Low iron bioavailability of the color bean varieties and their bean-based pastas (1.7 – 5.9 ng ferritin/mg protein) suggests that seed coat color compounds have a negative impact on the absorption of iron.

* Student Presented

BIOTIC STRESS

Exploring Common Bean Early Response to *Fusarium brasiliense* in a Mesoamerican x Andean population

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Common bean growth is severely limited by Fusarium root rot (FRR) and the extent of this limitation is dependent upon the host plants' gene pool. Over twenty years of research suggests that root architecture may be a means for resilience to FRR, but progress toward a root ideotype for FRR resistance has been slow. Here, we phenotyped resistant and susceptible lines of a previously screened RIL population to identify important root traits governing FRR resistance. We grew beans in vermiculite, inoculated with either mock or *Fusarium* liquid culture, and measured the whole root system for traits related to disease symptoms. We also compared our results to field conditions using shovelomics techniques for sampling the root crowns. We have found that it is not necessarily root traits, but the developmental progression of building roots that confer resistance. Specifically, the length of the unbranched apical zone (LAUZ) was significantly shorter in resistant lines. Roots that establish quickly are more likely to have FRR resistance than those that do not. Root architecture as a means for FRR resistance cannot be understood as a single trait, but must be considered as a network of root phenotypes.

* Student Presented

Natural Infection of Fungal, Bacterial and Viral Pathogens to Dry Bean Genotypes

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Fungal, bacterial and viral diseases are the major economical foliar diseases that cause yield losses between 40-100% to commonly grown dry bean (Phaseolus vulgaris L.) globally. Narrow genetic diversity in global germplasm of small-seeded bean varieties contributes to low production and failure to meet global demands which lead to food insecure. Development of foliar disease resistance bean genotypes results from complex interactions between numerous environmental factors and alleles of many or single genes. This study focused on determining the natural infection of disease-causing pathogens of angular leaf spot, powdery mildew, bacterial blight and bean common mosaic virus in different agro-ecologies with its response to grain yield effects. Diversity of 211 bean genotypes were tested at two different disease hot spot locations under randomized complete block design with two replications for two cropping seasons in Tanzania. From this collection, 63.50% of genotypes classified as Mesoamerican center of origin and 36.50% as Andean. Diseases severity was significantly different (p5.00. Results showed that the affected genotypes gave low yield of 2156.40mm and relative humidity of 90% at Lyamungo showed to create better environment for disease occurrence which was inversely proportional to the other site which showed low grain to yield probably because of flower abortion and terminal drought. The five genotypes, FEB 189, A774, NUA 16, KG 71-4 and DOR 766 showed trait of resistance and can be used on improving Mesoamerican gene pool because even their productivity showed to be higher of between 1710kg/ha to 2170kg/ha.

* Student Presented

Identification of Resistance Genes of Common Bean Line MAIII -16.153 to *Pseudocercospora griseola*

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The angular leaf spot (ALS) of the common bean caused by the fungus *Pseudocercospora griseola*, is one of the most important diseases of crop. The most effective strategy for ALS control is the use of genetic resistance that is quantitative with major and minor genes. Identification resistance genes is important for use in common bean breeding programs. The line MAIII-16.153 obtained from the recurrent selection program for ALS conducted by the Universidade Federal de Lavras in partnership with Embrapa has shown high resistance to different *P. griseola* strains. During the Common Bean Disease Workshop on Angular Leaf Spot and Root Rot, carried out in Skukuza, South Africa, in 2015, this line was indicated to compose the new international differential cultivars set for the ALS. However, there is no information about the resistance genes present in this line. To obtain this information, the line MAIII-16.156 was crossed with line BRS Horizonte (susceptible) and F1 and F2 generations were obtained. The F2 plants were assessed in four experiments. Two *P. griseola* strains, race 63-63 and 63-23, were inoculated in plants in V2 and V3 stages. Disease severity was assessed using scores scales. Segregation in the F2 revealed a gene of major effect, and that dominant allele is responsible for resistance in the line MAIII -16.153.

* Student Presented

QTL-based Sequencing to Identify Candidate Genes Associated with White Mold Resistance in Common Bean (*Phaseolus vulgaris* L.)

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White mold (WM) is a serious worldwide fungal disease of common bean caused by *Sclerotinia sclerotiorum* (Lib.) de Bary that is most damaging in cold and moist condition. Depending on the cultivar, the pathogen can cause yield losses ranging from 30% in the Central high plains of the United States to 100% in Argentina. *WM2.2*, previously mapped to a large interval on Pv02, is one of the nine WM meta-QTL with a major effect on WM resistance. The objective of this study was to narrow the interval of this QTL using QTL-based bulk segregant analysis. Both phenotypic and genotypic data from two RIL populations with different parental backgrounds were used to select subpopulations of resistant and susceptible lines for bulk DNA sequencing. The physical QTL interval for each RIL population was defined by counting the number of the SNPs within 10kb-2kb sliding windows that were completely polymorphic between the two bulks. Two QTL, *WM2.2a* (3.54-4.56 Mbp located in the euchromatic region) and *WM2.2b* (12.19 to 26.41 Mbp located in the heterochromatic region), were identified within the large genomic region originally associated with the *WM2.2* meta QTL. These two *WM2.2* QTL appear to be associated with different WM resistance mechanisms. *WM2.2a* region is most likely associated with pathogen avoidance while *WM2.2b* is associated with plant architecture and physiological resistance.

* Student Presented

Multi-Parent Advanced Generation Inter-Cross Population for Improvement of Genetic Resistance of Dry Bean to White Mold: WM-MAGIC

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White mold (*Sclerotinia scleriotorum* Lib. de Bary) is one of the most important diseases of dry bean in the U.S. with seed yield losses up to 100%. The use of resistant varieties is an effective strategy for controlling diseases. However, white mold resistance has been difficult to incorporate because of low heritability, cumbersome screening methods, few sources of resistance and inadequate breeding methods. A new Multi-parent Advanced Generation Inter-Crosses (MAGIC) population (n=1050) was created using eight founder parents (7 pintos and 1 great northern). The objectives of this research were to: 1) genetically map the factors controlling resistance in this population, and 2) develop inbred lines with combined resistance to white mold and good agronomic performance. A subset of 500 lines were selected and screened for white mold (strain 1980) using the seedling straw test method. Disease was visually scored using a 1-9 scale. Genotypes with values from 1 to 3 were considered resistant, 4 as intermediate resistance and 5 to 9 as susceptible. One line exhibited a higher level of resistance than the most resistant check (PC-50), and 19 lines (14 pinto and 5 great northern) had equal performance to PC-50. GWAS using quantitative, polynomial and binomial phenotypic distribution data, identified genomic regions associated with resistance on Pv01, Pv02, Pv04, Pv05, Pv07, Pv08, Pv10 and Pv11. Genomic intervals were considered significant if the P-Wald score for the peak SNP was greater than 3.1 for polynomial, 6.0 for binomial and 3.6 for quantitative distributions. Cumulative R2 values were 57% for binomial distribution using 13 genomic intervals, 41% for polynomial using 8 genomic intervals, and 40% for quantitative distribution using 11 intervals.

* Student Presented

Interaction of *bc-u* Gene with Recessive Resistance Genes in Different Genetic Backgrounds for Control of Bean Common Mosaic Virus and Bean Common Mosaic Necrosis Virus

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Bean common mosaic virus (BCMV) and bean common mosaic necrosis virus (BCMNV) are two related but distinct seed-borne potyviruses transmitted by aphid vectors. Four recessive genes, *bc-1*, *bc-2*, *bc-3* and *bc-u*, and the dominant *I* gene have been associated with BCMV and BCMNV resistance. Our objective was to further characterize interactions of *bc-u* gene with the other recessive resistance genes. The Durango Diversity Panel (DDP) and Snap Bean Association Panel (SnAP) were screened in the greenhouse for reactions to NL-3 (PG-VIa) and NL-8 (PG- III) strains of BCMNV. DDP subsets were also tested with US-6 (PG-VII) strain of BCMV. Whole genome sequencing (WGS) and Genotype by Sequencing (GBS) were used to identify SNPs in the DDP and SnAP. Other materials: Andean Diversity Panel (ADP), Othello/VAX1 and Othello/VAX3 RIL populations, and F2:3 families from multiple crosses among DDP lines were used to validate gene interactions. SNP markers, tagging each recessive gene, were developed and screened. GWAS and linkage mapping revealed the location of *bc-u* and *bc-2* recessive genes on Pv05 and Pv11, respectively, and narrowed the position of *bc-1* on Pv03 and *I* gene on Pv02. Many interesting and important interactions were observed: *I* and *bc-u* showed delayed top necrosis (TN) to NL-8; *I* and *bc-1* exhibited TN to NL-3 and vein necrosis (VN) to NL-8; and *I*, *bc-u*, and *bc-1* had VN to both NL-3 and NL-8. No alleles at the *bc-1* locus were observed. Two different *bc-u* loci, 3 Mb apart, interacted with *bc-2*. The *bc-u(a)* combined with *bc-2* exhibited resistance to BCMV US-6 strain but was susceptible to both BCMNV strains. The *bc-u(b)* with *bc-2* was resistant to BCMNV strains but was susceptible to US-6. This latter combination with *I* gene had a local lesion response to NL-3. No alleles at the *bc-2* locus were observed. 83% of Andean lines and most snap beans possess *bc-1* for resistance to NL-8 strain. The breeding goal for these backgrounds should be to incorporate the *bc-u(b)* gene.

* Student Presented

Gene Mapping and Marker Development Using Your Breeding Program: A Case Study on Common Bacterial Blight

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One of the biggest challenges a breeding program faces is the allocation of resources. Customer-driven demand puts an emphasis on cultivar development and release in the shortest time span possible. However, basic upstream research to identify underlying genetics and gene function provides invaluable knowledge that can be leveraged during cultivar development. Utilizing the same population for both cultivar development and functional genomics would allow consolidation of limited resources. This research looked at the suitability of using the population of genotypes in the advanced and preliminary yield trial stages of NDSU's dry bean breeding program for gene mapping and marker development. The breeding population, consisting of 823 genotypes in yield trials, was genotyped using GBS. For sequence analysis, the genotypes were divided by gene pool, Andean (130 genotypes) or Middle American (MA; 693 genotypes). Over 30,000 SNP were used in GWAS to identify genomic intervals associated with resistance to common bacterial blight (CBB). Both populations allowed the mapping of CBB resistance into genomic intervals. However, the most significant interval on chromosome Pv10, a region known to harbor CBB resistance, was considerably smaller in the MA population, 0.18 versus 1.11 Mb. The smaller interval consisted primarily of a family of *lipoxgenase* genes known to be involved in disease resistance allowing the identification of candidate genes suitable for future testing. Further analysis of the most significant SNP in the smaller interval indicated one allele could be used to reduce the number of CBB susceptible genotypes in the program by 55% with 96.8% efficiency. Another significant SNP from an interval on Pv07 could be used to remove 14% of the genotypes with 100% efficiency. These results indicate breeding populations can be used for gene mapping and marker development with the resulting markers being directly applicable to the breeding program.

* Student Presented

Mining the Common Bean Middle American Diversity Panel to Discover Genetic Factors for Resistance to the Most Prevalent Rust Races in North Dakota

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North Dakota produces approximately 35% of US common beans, most notably, pinto, black, great northern and navy market classes which belong to the Middle American (MA) gene pool. The appearance of new *Uromyces appendiculatus* (Pers:Pers) races which overcome the long-deployed *Ur-3* gene is threatening common bean production in North Dakota and elsewhere. In this study, greenhouse screening of races 20-3 and 27-7 (two prevalent races found in ND) was carried out on 290 lines from Middle American Diversity Panel to identify potential sources of genetic resistance. Approximately 21 and 26% of accessions were resistant to races 20-3 and 27-7, respectively. Genome wide association study was conducted using pustule diameter for each race and MA HapMap consisting 205,293 SNPs to detect the presence of race specific rust resistance genomic regions. Two genomic regions on Pv06 and Pv11 were present in the same genomic interval for both races. The peak SNPs on Pv11 mapped to a cluster of NLR genes on the distal end of the chromosome. Further analysis indicated that this genomic interval is possibly the *Ur-11* locus. The identified resistant genotypes and genetic factors are valuable resource to provide a higher level of resistance to races present is North Dakota and elsewhere.

* Student Presented

Reaction of Tepary, Common Bean, and Interspecific Accessions to Races of the Bean Rust Pathogen That Overcomes All Common Bean Rust Resistance Genes

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Host resistance is the most cost-effective strategy to control the bean rust disease of common bean. However, populations of the rust pathogen (*Uromyces appendiculatus*) comprise an extensive and shifting virulence diversity that renders susceptible all known rust resistance genes in common bean. Conversely, it has been suggested that certain tepary bean (*P. acutifolius*) accessions are broadly resistant to *U. appendiculatus*. To test this hypothesis, we selected, six Mesoamerican [13-2 (43), 15-3 (47), 22-6 (49), 31-1 (53), 31-22 (67), 22-52 (108) and two Andean [21-0 (72), 37-1 (84)] races *of U. appendiculatus* to inoculate 34 accessions of domesticated, wild, and interspecific accessions of tepary and common bean. Five common bean control cultivars with known single rust resistance genes (Ur-3, *Ur-4*, *Ur-6*, *Ur-11*), and Pinto 114 (the susceptible check without known resistance genes) were included. All control cultivars were susceptible to one more of the races of *U. appendiculatus* used in this study. Conversely, four domesticated accessions (G40142, G40148, G40161, and G40237A) and two improved lines (TEP 22 and TEP 23) of tepary bean were immune to all eight races. This type of reactions, with no visible symptoms, is extremely rare in rust resistance common beans; thus, these six tepary beans had unique type of reactions to all eight races used. Two domesticated (G40274 and G40279) and one wild (G40264) tepary bean accessions were also resistant to all eight races but these accessions exhibited either tiny pustules or hypersensitive reactions (HR) to the eight races. Both types of reactions are widespread in rust resistant common beans. In addition, one domesticated tepary bean (G40019), five interspecific lines (VAP 1, VAP2, VAP 3, INB 834, INB 841), and one common bean (SEF10) were resistant to the same five races but were susceptible to races 22-52 and 32-22. These results suggest the presence of new and unique rust resistance genes in tepary beans.

* Student Presented

Identification of Race-Specific Resistance QTL for Anthracnose in Common Bean

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Anthracnose caused by the fungus *Colletotrichum lindemuthianum* is a major disease of common bean (*Phaseolus vulgaris*). *C. lindemuthianum* is highly variable and exists in many races. Here, we present a report on the 40 races of *C. lindemuthianum* that we have characterized from the bean growing areas of Zambia. Also, we report on the results of the QTL mapping and Genome-wide association analyses that were conducted to identify the QTL for resistance to the 40 races of *C. lindemuthianum*.

* Student Presented

GENOMICS/GENE DISCOVERY

Tools for Visualizing and Analyzing Genotype, Genetic, and Genomic Information for *Phaseolus*

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Genome assemblies have been generated for most crops in the *Phaseoleae* tribe (several each for *Phaseolus*, *Vigna*, and *Glycine*). Similarly, dense genotyping (e.g. SNP chips) have also become commonplace. Methods for utilizing genomic and genetic information have generally lagged data creation. We will describe new on-line tools for investigating genotype data, mapped traits, genome assemblies, and homologies across genome assemblies within and between legume species. For genotype data, a new visualization and query tool called GCViT (Genome Chromosome Visualization Tool) allows a user to pick a set of accessions and see visually where there are similarities or differences (genomic variants) between accessions. This enables a user to visualize pedigree relationships or to track introgressions or other regions of interest. We will also show on-line tools for comparing and visualizing multiple genome assemblies for a species or group of closely related species, and for visualizing relationships among orthologous genes, and for quickly doing complex analyses of collections of genomic features. Lastly, we will raise some questions for researchers working in this field regarding how to manage and make accessible the rapidly-growing collection of genetic and genomic data for this important group of crops.

* Student Presented

Integration of Anthracnose Resistance Loci and RLK and NB-LRR-encoding Genes in *Phaseolus vulgaris* L. Genome

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Bean anthracnose (ANT), caused by *Colletotrichum lindemuthianum*, is responsible for severe yield losses and low quality of common bean grains. The most effective strategy to manage this disease is the use of resistant cultivars. There are currently more than 20 ANT resistance genes identified and mapped in common bean chromosomes. Besides that, quantitative resistance loci (QRLs) were described through genome wide association study (GWAS). Identification of pathogen responsive-genes and proteins on a molecular level provides a better understanding of metabolic pathways involved in ANT resistance. In this study, we investigated typical resistance proteins located closely to ANT resistance loci in the common bean reference genome. Among them, we checked for proteins with NB-LRR (NL) domain and kinase domain. The majority of resistance genes encode proteins that have a nucleotide-binding site (NB) and a series of carboxy-terminal leucine-rich repeat (LRR). In addition, proteins with kinase domain are known to operate as pattern-recognition receptors (PRRs) that recognize pathogen-associated molecular patters (PAMPs) and activate immune response. Based on common bean reference genome (version 2.1), the region of 0.5Mb upstream and downstream, of the physical position of each ANT resistance locus, was taken into account for candidate gene search. Thus, an integrated map of ANT resistance loci and candidate genes (encoding defense response-related proteins) was constructed. This map contains candidate genes for all ANT resistance genes and QRLs, previously described in the literature. A total of 265 NL proteins and 208 protein kinases were detected. These candidate genes may be useful for further studies to validate their function in ANT response, and to understand how they interact with metabolic pathways.

* Student Presented

Development and Validation of a Marker Linked to the *Ur-4* Rust Resistance Gene in Common Bean

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We report the use of fine mapping to develop tightly-linked DNA markers that accurately tag rust resistance genes. Fine mapping involves phenotyping and genotyping technologies, plus haplotype analysis of sequenced-based information. Phenotyping involved the inoculation of common bean plants with specific races of the bean rust pathogen. Then, bulk segregant analysis (BSA) was combined with high-throughput genotyping using the SNP chip BARCBEAN6K_3 (~5K SNPs), haplotype identification, and customized SNP marker development (KASPs) on recombinant families. We performed the fine mapping of *Ur-4*, a rust resistance locus present in Andean bean Early Gallatin, that confers resistance to 53 of 88 races of the rust pathogen maintained at ARS Beltsville. About 400 segregating F2 plants from the Early Gallatin x Mexico 309 cross were inoculated with races 6-15 (73) and 22-52 (108). A segregation ratio of 3:1 confirmed the presence of *Ur-4* as a single dominant gene (p=0.33). BSA analysis identified SNPs positively associated with *Ur-4* on a 1.69 Mb genomic region between SNPs at 24,229,643 bp and 25,913,633 bp on chromosome Pv06. Further evaluation of recombinant F2:3 families (570 plants) permitted to narrow the position of the *Ur-4* locus to a 200-kb region. Haplotype analysis of this region using 33 whole genome sequenced bean lines including Early Gallatin and Lark (also known to carry the *Ur-4* locus), allowed the identification of SNPs highly associated to the *Ur-4* locus. The KASP marker SS208 that was tightly linked to the *Ur-4* locus, was used to genotype 238 bean cultivars that included Andean and Mesoamerican dry and snap beans with and without the *Ur-4* locus, with *Ur-4* alone and in combination with other rust resistance loci. This validation revealed that the KASP marker SS208, unlike a previously identified molecular marker tagging *Ur-4*, was highly accurate for the identification of the *Ur-4* locus and without false positive or false negative results.

* Student Presented

Exploring the Epigenomic State of Sodium Bisulfite-Treated Common Bean (*Phaseolus vulgaris*) within the *Crg* and *Ur-3* Deletion Regions on chromosomes Pv10 and Pv11

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Common bean (*Phaseolus vulgaris*) is a nutritionally dense, low cost food cultivated throughout the world, particularly in Central and South America and Africa. Epigenetics is the study of modification of gene expression without changing the genetic code. Epigenomics is the genome-wide study of the effect of DNA methylation and histone modification on regulation of global gene expression. DNA methylation is a heritable modification that does not change the genetic code, but regulates gene activation and inactivation. In this study, one common bean resistant genotype Sierra, and three susceptible genotypes (Olathe, *crg*, and *ur3-Δ3*) were challenged with race 53 of the fungal rust pathogen (*Uromyces appendiculatus*). Genomic DNA isolated from leaves 0, 12, and 84 hours after inoculation was treated with sodium bisulfite which converts unmethylated cytosines to uracils, followed by sequencing to analyze methylation patterns. Previous work in our group identified a region on chromosome Pv10 correlating with a deletion in the rust susceptible *crg* mutant corresponding to the complements resistance gene (*Crg*) gene, required for resistance mediated by the classical *Ur-3* gene. Similarly, the *ur3-Δ3* genotype carries a deletion at the *Ur-3* locus on Pv11. In order to understand the epigenomic state of these regions, we began to identify sequence variation between non-bisulfite treated and bisulfite treated samples. We developed six gene-derived molecular markers that exhibit differential PCR amplification patterns among the four genotypes, particularly between rust resistant Sierra (amplification) and rust susceptible *ur3-Δ3* (no amplification). We believe that identifying methylated and unmethylated sites may help us to better delineate the deletion in both *crg* and *ur3-Δ3* on chromosomes Pv10 and Pv11 respectively, while helping to elucidate the epigenomic state of rust-inoculated Sierra, particularly in the R-gene containing regions on chromosomes Pv10 and Pv11.

* Student Presented

Evaluating genomic predictions for semi-quantitative traits: Does GS hold promise predicting disease resistances for root rots and CBB?

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Marker assisted selection has been implemented successfully by some breeding programs, using a small number of markers (1-3) that tag major disease resistance genes, to predict disease resistance of new recombinants. Only in few cases, identified major resistance genes explain the majority of observed variance, and the amount of genetic heritable variance explained by major disease resistance loci is usually not determined. Furthermore, in many studies on disease resistance no major genes are identified in QTL/GWAS experiments, which opens the question to what extent quantitative effects of minor genes contribute to disease resistance. Genomic selection has received a lot of attention as a new promising technology to predict quantitative traits based on a model incorporating genome wide markers. We evaluated to what extent genomic prediction models can capture resistance traits. A panel of 200 lines was evaluated for Pythium in the greenhouse and for plant survival in the field, with good heritabilities of 0.71 and 0.94 in greenhouse and field, respectively. Markers were obtained by GBS. While no major resistance genes were identified by GWAS, genomic predictions accuracies >0.7 were observed and training data from the greenhouse allowed to predict phenotypic response in the field. A panel of 341 breeding lines was evaluated with two strains of CBB at three time points. Markers were obtained by GBS. 4 QTL were observed by GWAS, depending on strain and evaluation conditions. Heritabilities were lower in this trial and genomic prediction accuracies reached >0.4. Genomic predictions look to be a promising supplement to marker assisted selection for disease resistance traits and should be evaluated further in breeding populations.

* Student Presented

OTHER TRAITS OF ECONOMIC IMPORTANCE

Phenotyping Improvements and QTL Mapping of Color Retention Traits in Processed Black Beans

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When black beans are hydrothermally processed prior to consumption, water-soluble anthocyanins are released from the seed coat, resulting in a faded brown color in the cooked product that is undesirable to consumers. Traditional methods of phenotyping for color retention and other quality characteristics of canned beans are time and labor intensive, necessitating improvements. Two half-sibling black bean recombinant inbred line (RIL) populations segregating for post-processing color retention were developed from lines exhibiting extreme phenotypes for this trait. The RIL populations were canned and evaluated for color retention and other quality traits via subjective and objective methods. Both populations were genotyped with the BARCBean6k_3 BeadChip microarray. Color retention measurements from trained panelists, a spectrophotometer, and digital images were compared to each other and mapped as separate traits. Major QTL for post-processing color retention were detected on three chromosomes and mapped to regions where color loci are located.

* Student Presented

Investigation of the Effects of the Seed Coat Non-Darkening Trait on Agronomic Traits in Pinto Bean Populations

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Seed coats in pinto bean turn brown during storage, due to autoxidation of proanthocyanidins. Pinto beans with less intense or non-browning seed coat phenotypes are classified as slow darkening and non-darkening, respectively, and are more desired in the market. Breeding for non-darkening seed coat varieties is believed to increase their market value but may adversely impact their agronomic performance. The objectives of this study were to: (i) investigate possible associations between the seed coat non-darkening trait and days to flowering, days to maturity, harvestability, yield, 100-seed weight, and hydration capacity, (ii) determine variance components and broad sense heritabilities for these traits. Three hundred and thirty-seven F4:7 pinto bean genotypes derived from crosses of two darkening pinto bean varieties, La Paz and Stampede, by two non-darkening breeding lines, 88 and 52, and their reciprocal crosses were grown in four different environments of south-west Ontario in 2016. Among the three colour parameters (L*, a*, and b*), the a*, which is related to the redness of seed coats, was selected as the main discriminative parameter between the darkening and non-darkening seed coat phenotypes. The Spearman's correlation coefficients between the a* parameter and days to maturity, 100-seed weight, and hydration capacity were rs = - 0.20 (P = 0.0002), rs = -0.39 (P = 0.0002), and rs = -0.21 (P <0.0001), respectively. There was no correlation between the a* parameter and other agronomic traits. Estimates of heritability were from 39% to 83% for days to flowering, 65% to 86% for days to maturity, 80% to 84% for 100-seed weight, and 59% to 72% for hydration capacity, across the population. For harvestability and yield, the estimates of heritability ranged from 21% to 54% and 29% to 69%, respectively. Additional studies are required to investigate the linkages between the gene responsible for the non-darkening seed coat trait and yield and seed size.

* Student Presented

A Multidrug and Toxic Compound Extrusion (MATE) Transporter, PvMATE8, Is a Vacuolar Transporter of Proanthocyanidin Monomers and Involved in Seed Coat Darkening in Common Bean

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In common bean (*Phaseolus vulgaris* L.), proanthocyanidin is responsible for the postharvest seed coat darkening. The precursors of proanthocyanidin polymers are synthesized in the cytoplasm and the polymerization occurs in the vacuoles. This indicates the involvement of vacuolar transporters in the pathway. In *Arabidopsis thaliana*, a vacuolar membrane-localized multidrug and toxic compound extrusion (MATE) like transporter named TRANSPERANT TESTA 12 (TT12) have been identified to transport epicatechin 3'-O-glucoside (E3'G) to the vacuole. Here, we report the identification of a vacuolar transporter PvMATE8 by comparing global gene expression profiles of two pinto bean cultivars CDC Pintium (regular darkening) and 1533-15 (slow darkening). *PvMATE8* show higher expression in CDC Pintium compared to 1533-15, localized in the vacuole and is able to rescue the tt12 mutant phenotype in *Arabidopsis thaliana*. Vacuolar uptake of E3'G by PvMATE8 is in progress.

* Student Presented

Effects of Nitrogen Application on Nitrogen Fixation in Common Bean Production

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The nitrogen fixing ability of common bean (Phaseolus vulgaris L.) in association with rhizobia is often characterized as poor and nitrogen fertilizers are commonly used in bean production to achieve high yields. However, the addition of nitrogen inhibits nitrogen fixation and plants cannot utilize all the nitrogen fertilizer that is applied to the soil, leading to runoff and groundwater contamination. The overall objective of this work is to reduce nitrogen fertilizer use in common bean production. This would be a major advance in profitability for the common bean industry and would significantly improve the ecological footprint of the crop. In the current work, 22 bean genotypes [including a non-nodulating mutant (R99)] were screened in plots at the Elora research station (University of Guelph) for their capacity to fix atmospheric nitrogen in the presence (R) or absence (NoR) of rhizobia and with 100 kg ha-1 nitrogen (N) or without nitrogen fertilization [no nitrogen (NoN)], added at planting. The genotypes were evaluated in replicated split-split-plot designs on nitrogen-poor soils over three years (2016, 2017 and 2018) for: nitrogen derived from atmosphere (Ndfa) in the seed, yield and a number of yield-related traits. Significant differences among genotypes were identified for all analyzed traits in all three years and the level of nitrogen significantly affected most of the traits, including Ndfa and yield. In contrast, application of rhizobia significantly affected only few traits [Ndfa, flowering, harvestability and leaf chlorophyll content (SPAD)] and the effect was inconsistent among the years. The RN/R ratio for the Ndfa data, indicated that nitrogen application reduced symbiotic nitrogen fixation (SNF) to different degrees in different bean genotypes. This variation suggests that SNF in common bean can be improved through breeding and selection for the ability of bean lines to fix nitrogen in the presence of reduced fertilizer levels.

* Student Presented

Nitrogen Fixation of Dry Beans Bred for Hillside and Marginal Land Production in Honduras

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Dry bean (*Phaseolus vulgaris*) is a diverse species grown worldwide. It is a critical source of protein and nutrition, and provides a livelihood for millions of smallholder farmers. Beans engage in symbiotic nitrogen fixation (SNF) with Rhizobia, but their nitrogen-fixing is generally low compared to other food legumes such as groundnut (*Arachis hypogaea*), pigeon pea (*Cajanus cajan*), soybean (*Glycine max*), cowpea (*Vigna unguiculata*) and bambarra groundnut (*Vigna subterranean*). The non-governmental organization Fundación para la Investigación Participativa con Agricultores de Honduras (FIPAH) works with local farmer groups (CIALs) to develop bean varieties through participatory plant breeding (PPB). Whereas, conventional bean varieties are developed using modern practices for producers farming good agricultural land and with access to inputs, FIPAH's PPB bean varieties are developed under the extreme growing conditions characteristic of smallholder farms in Honduras, including low soil fertility and very limited inputs. Here we test the hypothesis that Honduran PPB beans have a greater capacity for SNF than conventionally-bred bean varieties. Over 70 Honduran bean genotypes and 6 check genotypes (HON panel) were examined for agronomic performance and SNF capacity in four low-N field trials in Ontario, Canada and Honduras from 2014-16. The HON panel was genotyped to investigate genetic relatedness. Nitrogen fixation was quantified using the natural abundance method on seed samples. At each location, significant differences were found between genotypes for agronomic traits and for nitrogen fixing capacity. Varieties with the best nitrogen fixing capacity could be used by CIALs in further PPB efforts to improve this trait among local varieties and reduce the need for N inputs.

* Student Presented

POSTERS

P01: Current Status and Future Opportunities with the Pulse Crop Health Initiative

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The Pulse Crop Health Initiative (PCHI), administered through the USDA, Agricultural Research Service, Edward T. Schafer Agricultural Research Center in Fargo, ND was inaugurated in fiscal year 2018. The goal of the Initiative is to use cooperative research on pulse crops (dry beans, dry peas, lentils, and chickpeas) to provide solutions to the critical health and sustainability challenges facing the citizens of the United States and the global community. Expected outcomes of this Initiative are to discover and promote the health and nutritional benefits of regular pulse consumption, to enhance the sustainability of the global food supply through optimized production of pulses, and to increase the consumption of pulses through enhanced functionality of whole pulses and pulse ingredients in foods. The Initiative is guided by a Steering Committee that includes commodity group, food industry, health community, and ARS representatives. A comprehensive research plan has been drawn from a previously developed Pulse Health Initiative Strategic Plan, which arose from planning sessions that included industry, academic, and government representatives. Each year, proposed plans-of-work are solicited for cooperative projects that fall within the scope and priorities of the Initiative. These proposals are reviewed by independent scientific review panels and by stakeholder research committees. In fiscal year 2019, 46 proposals were received and 24 projects were approved for funding as part of the Initiative. In this presentation, we will provide an update on the breadth of the current projects, plans for future research priorities and opportunities, and information on how to contribute to this new Initiative.

* Student Presented

P02: KnowPulse: An Evolving Breeder-Friendly Web-Portal for Pulse Crops

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KnowPulse (doi:10.3389/fpls.2019.00965; http://knowpulse.usask.ca) is a publicly-searchable web-based resource for plant breeders and geneticists interested in pulse crops. It is built using Tripal and developed at the University of Saskatchewan, and provides project management tools for the pulse breeding programs. KnowPulse also provides public access to various tools for utilizing genomic and diversity data for chickpea, common bean, field pea and lentil. Genomic data can be accessed via our crop-specific JBrowse instances and BLAST databases. Genotypic data is summarized on marker pages and can be queried, resulting in a marker-by-germplasm table for comparison among genotyped lines. Phenotypic data is visualized through trait distribution plots available on trait, germplasm and experiment pages, as well as through the trait distribution tool. To enhance accessibility, species-specific “launchpads” are now available which provide access to summary charts, publications and searches for germplasm and genetic markers. KnowPulse is constantly evolving with data and tools added as they become available. Full integration of genetic maps and quantitative trait loci (QTL) data is under development.

* Student Presented

P03: A Descriptive Sensory Evaluation and Volatile Quantification of a Diverse Green Bean Panel

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Research performed in the 1960's and 1970's by Tex Frazier and Jim Baggett at Oregon State University identified three compounds important to green bean flavor: 1-octen-3-ol, linalool, and 3-hexen-1-ol. Subsequent research has identified hundreds of volatile compounds in green beans but has not correlated this to sensory data. To assist with breeding efforts and quality control in industrial processing, sensory was performed on a diverse collection of 205 green bean varieties in parallel with GC-MS analysis of volatiles. Twelve volunteers tasted the green beans over 16 sessions lasting four weeks. Samples were ordered in a resolvable incomplete block design and the data was analyzed in R using base functions and the lme4 package. GC-MS was done on a Shimadzu GCMS-QP2010 Ultra Instrument with a Stabilwax column. Eight descriptors were included in the sensory study: floral, sweet, fruity, bitter, sour, nutty, green, and beany. Statistically significant correlations were found between floral, sweet, and fruity indicating congruency. Bitter and sour were weakly correlated due to a common confusion between these two tastes. Bitter and beany were also correlated and were negatively correlated to floral, sweet, and fruity. Linalool was correlated to the floral descriptor and 1-octen-3-ol was correlated to the nutty descriptor. Linalool and 1-octen-3-ol were negatively correlated with each other. Eleven wax beans were also broken out from the collection, but the statistical power was low, and few significant correlations were found. The correlation between 1-octen-3-ol and nutty has not been reported before but is consistent with the known presence of this compound in hazelnuts, chestnuts, and almonds. The negative correlation between 1-octen-3-ol and linalool may represent a genetic or biochemical divide between bean varieties.

* Student Presented

P04: Genomic Shifts in Snap Beans under Different Agricultural Management Systems

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This research was designed to identify what kinds of genetic changes might be produced in snap bean populations due to natural selection in both organic and conventionally-managed production systems throughout the breeding cycle. We utilized two recombinant inbred snap bean populations, OR5630 x Black Valentine (ORBV) and Hystyle x Provider (HYPR), which were split after the F1 generation and grown in parallel organic and conventional systems from the F2 through F6 generations, resulting in four populations, two in each system. Systems treatments (organic and conventional) differed for seed fungicide treatment, fertilizers, herbicides, and other pesticides utilized. We hypothesized that selection in the systems would result in genomic shifts, and genotyped 94 families (in each population/system) in the F5 generation with the Illumina 6000 SNP BARCbean6k_3 Beadchip to give us insights into what effects these systems produced, with the goal of identifying patterns that could inform future breeding projects. Linkage maps were assembled for all four populations, and segregation distortion patterns and QTLs for important phenotypic traits were analyzed in each. There were observed differences in map size and recombination, and unique patterns of segregation distortion and QTLs produced from natural selection in each system. These differences support the use of direct selection (selection within the target environment) to capture the desired alleles and traits for each system.

* Student Presented

P05: Cosmetic Stay-Green in Snap Bean: Understanding Deleterious Effects on Germination Rate

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Most contemporary snap bean cultivars are white seeded because flavonoids in colored-seeded types affect processing quality. Another category of seed coat color is persistent color (pc), which is a member of the stay-green gene family. It is desirable in snap beans because the trait provides uniform, dark green pods. However, the pc trait has deleterious effects on germination. Fungicide treated seed of pc lines have levels of germination similar to fungicide-treated white-seeded beans. The objective of this research was to understand why germination is reduced in pc lines. One hypothesis is pc seeds may be more fragile than other seeds, thereby leaking solutes into the rhizosphere that attract pathogens. Alternatively, pc genotypes may have normal seed coats but are inherently higher in sugars. As a preliminary experiment, germination tests were performed in the lab with 40 cultivars, includes pc, white and colored types with untreated seed. No significant differences among cultivars was observed and the germination rates were relatively high. In the field, a lower germination rate for pc types was observed, and seedlings were infected with at least two soil borne pathogens. In a third experiment, three paired lines [OR91G-p/OR91G-pgri, OSU6523 (pc)/OSU6523 (p), and Spartacus (pc)/Ulysses (p)] were compared for water uptake rate. The pc beans had significantly more rapid water uptake than white-seeded genotypes. After imbibition, pc types exhibited approximately twice as many cracked seeds compared to white seeded types. We also examined seed anatomical structure of the different seed types and found that pc types had thinner testa than white and colored forms, particularly with regard to the osteosclereid layer. Thinner seed testa of pc genotype supports the hypothesis that pc seeds are more fragile, resulting in more rapid water uptake and greater solute leakage.

* Student Presented

P06: SNP Markers Associated with Slow Darkening Trait in Carioca Common Bean

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Carioca bean market class represents about 70% of the Brazilian consumption, and a significant challenge for the growers and the dealers is to deal with the darkening of bean color, which often occurs during storage of the seeds. The slow darkening (SD) of bean seeds are genetically controlled for a single recessive gene expressed in the seed coat through the maternal tissue. In the present work, we investigated the single nucleotide polymorphism (SNPs) markers associated with SD in the Carioca common bean line LP97-28. A total of 146 F2:6 recombinant inbreed lines derived from the Iapar 81 (regular darkening-SD) × LP97-28 (SD-RD) cross were developed. The F2:8 recombinant inbred lines (RILS) were cultivated in the field during 2017 year crop season, and the harvested seeds were stored in a cold room for 12 months (temperature 10 ± 2ºC and relative humidity of 48%). After this period, the lines were categorized into two groups: SD and RD lines. SNP genotyping of each RIL was performed with BARCBEAN6K_3 BeadChip. After filtering process, a total of 773 polymorphic SNP markers for the RIL population were selected for association analysis using Tassel 5.0 MLM model. The observed segregation for the 146 families derived the from the Iapar 81×LP97-28 cross was 83RD:63SD, which fitted to an expected segregation ratio of 1RD:1SD ($\chi 2$=2.74, P-value = 0.0979) for a single gene in a RIL population. Association analysis revealed that SNPs ss715643259 and ss715640487 were associated with SD loci at the positions 32,675,523 bp and 39,295,293 bp in the linkage group Pv07. Loci for SD located on Pv07 were described for Carioca market class and Pinto bean cultivars. Based on this knowledge, the use of molecular markers is a promising strategy to improve selection of Carioca genotypes exhibiting SD trait, as phenotypic selection for SD is a complex process that involves recessive inheritance and expression in maternal tissue.

* Student Presented

P07: Genetic Control for Slow Seed Coat Darkening of Carioca Bean

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Seed coat post-harvest darkening is a problem of great concern for bean producers. The objective of this research was to study the genetic control of seed coat post-harvest darkening of common bean line LP 97-28. Segregant populations F2:3 e F2:4 were obtained through SSD method (Single Seed Descent) of cross carioca type LP 97-28 (SD - slow darkening of seed coat) × cultivar Pérola (RD - regular darkening of the seed coat). A total of 193 F2:3 and 180 F2:4 progenies derived from the Pérola × LP 97-28 cross were evaluated in relation to the seed coat darkening trait. The results revealed a monogenic segregation adjusted to a 3RD:1SD (140RD:53SD) ratio for darkening seed trait in these families. These findings suggest that the slow darkening of seed coat is controlled by a recessive single gene SD present in LP 97-28 line. Interestingly, SD phenotype of 100% F2:3 families remained with the same in F2:4. In addition, 10 out 140 of F2:3 families with RD phenotype changed it to SD in F2:4. Thus, it is possible to assume that these plants have a heterozygous genotype in the previous generation. Therefore, future efforts of common bean breeding programs of Nupagri-UEM will focus to transfer the slow darkening gene of LP 97-28 into commercial cultivars.

* Student Presented

P08: Slow Darkening Pinto Beans Exhibit Enhanced Iron Bioavailability across Multiple Production Environments in North Dakota

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Pinto beans *(Phaseolus vulgaris* L.) are rich in iron, but are suspectable to postharvest darkening, which is an undesirable trait that lowers their market value overtime. Polyphenolic compounds in the seed coat, such as proanthocyanidins (condensed tannins) determine the color of beans, and are also associated with postharvest darkening in the pinto and cranberry market classes. Iron uptake assays in Caco-2 cells show that some precursor molecules to proanthocyanidins, including procyanidin B1 are strong inhibitors to iron absorption, while other precursors such as kaempferol 3-glucoside are strong promoters of iron uptake. Slow darkening (Sd) pinto beans do not accumulate proanthocyanidins in their seed coats, but the nutritional quality of iron nutrition from these varieties has not been evaluated after cooking. This study compared the iron content and iron bioavailability of 4 Sd pinto varieties to 3 regular darkening pintos across multiple production sites in North Dakota from field season 2019. Iron bioavailability (ie. iron uptake) was measured as ferritin formation (ng ferritin/mg of total cell protein) in a Caco-2 cell bioassay. Iron bioavailability was significantly ($p \leq 0.05$) higher in Sd pintos (20 – 45 ng ferritin/mg protein) as compared to regular darkening pintos (4 – 8 ng ferritin/mg protein). Iron bioavailability in the Sd pintos was consistently higher across all production sites and was not dependent on seed iron concentrations. Iron concentrations ranged from 60 - 78 µg/g and were not correlated with the higher Fe bioavailability of the slow darkening trait. Preliminary polyphenolic analysis revealed the concentrations of procyanidin B1 were significantly lower in Sd pintos as compared to other regular darkening pinto varieties across production sites. This study suggests that the Sd trait represents an opportunity to enhance the iron nutrition of beans by altering the biosynthesis of polyphenols that inhibit Fe uptake.

* Student Presented

P09: Multiplex Quantitative Assay for Simultaneous Detection of Bacterial Blight Pathogens of Common Bean

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Common Bacterial Blight (*Xanthomonas axonopodis* pv. *phaseoli* or *X. fuscans* subsp. *fuscans*), Brown Spot (*Pseudomonas syringae* pv. *syringae*), and Halo Blight (*P. s.* pv. *phaseolicola*) affect common beans worldwide. Bacteria are transmitted from infected seed, tissue or debris, leading to a reduction in seed quality and yield. Distinguishing these three diseases via foliage or seed symptomology can be difficult, depending on the stage and severity. A multiplex qPCR assay would enable the quantification of each pathogen in the complex simultaneously during disease diagnosis or seed certification. The objective of this research was to optimize a multiplex qPCR assay using previously developed PCR primers to quantify all four bacterial pathogens. Simplex PCR assays for *Xap*, *Xff*, and *Psp* amplified only the target bacteria among 27 target and non-target bacterial species tested for primer specificity. Non-target species were amplified with primers targeting *Pss*; therefore, optimization of this assay is ongoing. Amplification of serial dilutions from *Xap*, *Xff*, *Psp*, and Pss cultures in a multiplex assay produced standard curves with assay efficiencies of 90.9%, 93.1%, 94.4% and 91.5%, respectively. R2 values were 0.99 for all assays. Validation of the qPCR assay against traditional plating assays for *Xff*, and *Psp* from infected seed has been initiated. A significant positive Pearson correlation was observed between traditional plating methods and qPCR detection from seed grown in field trials in Oakes, ND in 2016 ($P<0.0001$; $r = 0.85$) and Fargo, ND in 2017 ($P<0.0001$; $r = 0.56$). Further evaluation and validation is needed to determine if the multiplex qPCR assay can be adapted for use in seed certification.

* Student Presented

P10: Screening Ontario-adapted Dry Bean Germplasm for Reactions to Bacterial Diseases

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In Ontario, breeding for tolerance to Common Bacterial Blight (CBB) caused by the pathogenic bacteria *Xanthomonas axonopodis* pv. *phaseoli* and *Xanthomonas fuscans* subsp. *fuscans* has been the primary focus of dry bean breeding programs. Recent disease surveys and field trial observations have indicated that bacterial disease symptoms have been showing up in cultivars that were considered to be tolerant or moderately tolerant to CBB. Using differential selective media, disease surveys of Ontario dry bean fields indicate that bacterial brown spot (BBS) caused by *Pseudomonas syringae* pv. *syringae* is the primary bacterial pathogen found on dry beans, other than CBB. This led to a need for the re-examination of bacterial disease tolerance in Ontario-adapted dry bean germplasm. The Dry Bean Breeding program at the Harrow Research and Development Centre has a long established CBB nursery. At the London Research and Development Centre (London, ON), BBS and Halo Blight (HB; caused by *Pseudomonas syringae* pv. *phaseolicola*) nurseries were established. This location was selected due to cooler growing conditions favouring BBS and HB disease infection. The nurseries were planted as seven seed hill plots and inoculated twice with a high pressure sprayer using known bacterial isolates that cause CBB, BBS and HB. Starting three weeks after initial inoculations (two weeks for BBS), the plants were rated once per week for a total of three ratings. This is the first year of data for this project and so the results should be considered preliminary, however it appears that bacterial disease tolerance to CBB generally translates for BBS in small seeded dry beans. In large seeded dry beans there appears to be some tolerance to BBS. These results need to be confirmed in further testing which will proceed next field season, as well as indoors where we are developing testing methods.

* Student Presented

P11: Effectiveness of Recurrent Selection Aiming Anthracnose Resistance in Common Bean

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Colletotrichum lindemuthianum, the causal agent of anthracnose in common bean, presents great evolutionary potential to overcome genetic resistance. Besides the large variability of physiological races that has already been identified, variability within races has also been reported. The objective of this study was to develop and evaluate the effectiveness of a recurrent selection program as an alternative to obtain common bean cultivars resistant to different isolates of *C. lindemuthianum*. A mixture of 45 F2 populations (S0 population), derived from the diallel cross of ten common bean lines, with variability for the reaction to different *C. lindemuthianum* isolates, was used to form the base population (Cycle 0). From Cycle 0, five cycles of evaluation, selection and recombination were carried out. In each cycle, S0 plants were selected for resistance to 65, 73, and 89 *C. lindemuthianum* races. About 40 S0:2 progenies from each selective cycle were obtained and the mean of anthracnose severity scores of these progenies of each cycle, for each isolate separately, were used to obtain the linear regressions equations. The percentage genetic progress achieved, for resistance to *C. lindemuthianum*, per cycle, compared to the mean of S0:2 progenies from Cycle I was upper to 7% for all races. It was observed that there was a progressive increase in number of resistant progenies to a greater number of *C. lindemuthianum* isolates from the first to the last selective cycle. Besides that, it is important to highlight that new sources of genetic resistance can be added in any cycle, so that the host can respond dynamically to the genetic variability of the pathogen. Therefore, the recurrent selection can be an effective breeding method to obtain common bean cultivars with broad spectrum of anthracnose resistance.

* Student Presented

P12: Relationship Among *Colletotrichum* spp. Strains Associated to Common Bean Anthracnose and Scab

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Colletotrichum and *Glomerella* (teleomorph) strains have been isolated from anthracnose and scab lesions on common bean in Brazil. The behavior of *Colletotrichum* strains has been evaluated by cytological, pathogenicity, sensitivity to the fungicides, sexual and asexual recombination analyses. Wide variability among strains has been observed for all traits evaluated. Molecular phylogeny analysis have been carried out and the most strains was grouped in *C. lindemuthianum* and *C. sojae* clades. These information provide insight about evolution of these species, virulence and can assist common bean breeding program.

* Student Presented

P13: Genome-Wide Association Study Reveals Regions on Chromosomes Pv03 and Pv05 Related to Anthracnose Resistance in Common Bean

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Common bean anthracnose, caused by *Colletotrichum lindemuthianum*, is a serious disease that, under disease-promoting conditions, can result in yield losses up to 100 percent. Genome-wide association studies (GWAS) identified regions associated to the resistance to different races of this pathogen in all bean chromosomes, except Pv09. The objective of this study was to perform GWAS for resistance to race 1545. For this, seedlings of 89 accessions were inoculated at a concentration of 1.2×10^6 conidia mL^{-1} and maintained under disease promoting conditions for 72 hours. Symptoms were evaluated ten days after inoculation. Accessions were genotyped through Genotyping by sequencing (GBS) approach wherein a total of 28,822 SNPs distributed over the 11 chromosomes were obtained. GWAS was carried out using mixed linear model (MLM). SNPs with p-value < 0.001 were considered significantly associated. Gene models, within 100Kb upstream and downstream of significant SNPs, were taken into account for candidate gene search on NCBI and phytozome. Data from GWAS indicated that resistance to race 1545 resides in Pv03 and Pv05. The SNP S03_13038972 explained 15.16% of the phenotypic variation. In the reference genome v1.0 this SNP is located in the position 13,038,972, where ten gene models are found. Among them, *Phvul.003G080900* that encodes a protein kinase. Five SNPs (S05_706152, S05_713832, S05_739138, S05_747744, S05_755558) explained 14.87% of the phenotypic variation each. These SNPs are located in a region of 49,406bp in Pv05 (from 706,152bp to 755,558bp) where 25 gene models are found. Out of them, three genes might act in the resistance response: *Phvul.005G008100* that encodes a PPR (Pentatricopeptide) repeat, *Phvul.005G008500* encodes an F-box and leucine-rich repeat protein 2/20, and *Phvul.005G009000* encodes a protein kinase. The current study revealed new sources of anthracnose resistance detected in Pv03 and Pv05, which could be useful for future breeding programs.

* Student Presented

P14: Sources of Resistance to *Colletotrichum lindemuthianum* and *Pseudocercospora griseola* in Common Bean from Brazil

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Anthracnose (ANT) and angular leaf spot (ALS) are seed-borne diseases of common bean (*Phaseolus vulgaris* L.) caused by the fungus *Colletotrichum lindemuthianum* and *Pseudocercospora griseola*, respectively. Finding new sources of resistance against these devastating diseases are top priorities in breeding programs as highly virulent races of these fungi often emerge. Pathogenicity of physiologically distinct races of *C. lindemuthianum* (9, 65, 73, 2047, and 3481) and *P. griseola* (31-23 and 63-39) were evaluated on 57 Andean and 58 Mesoamerican bean accessions representing different market classes grown in the Brazilian states of Paraná and Mato Grosso. We have identified three Mesoamerican and eight Andean accessions with resistance to all *C. lindemuthianum* races tested (9, 65, 73, 2047, and 3481), in addition to five Mesoamerican and 12 Andean accessions with resistance to four races. Furthermore, 13 MA accessions were found to be resistant to both *P. griseola* races (31-23 and 63-39). Additionally, 43.85% of the Andean accessions were resistant to both *P. griseola* races. The results show that both Andean and Mesoamerican bean cultivars evaluated in this study represent a high genetic variability in response to different races of these pathogens. Some of this genetic material will be valuable sources of resistance to ANT and ALS in future bean breeding efforts. A clear understanding of the nature and inheritance of these resistance sources will be critical to facilitate the transfer of resistance to different commercial cultivars of common bean.

* Student Presented

P15: Co-Segregation Analysis and Fine Mapping of Anthracnose and Angular Leaf Spot Disease-Resistance Genes in the Common Bean Cultivar California Dark Red Kidney

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Anthracnose (ANT) and angular leaf spot (ALS), caused by *Colletotrichum lindemuthianum* and *Pseudocercospora griseola*, respectively, are devastating diseases of common bean (*Phaseolus vulgaris* L.) in the world. The use of resistant cultivars is the most cost-effective strategy to manage these diseases; however, highly virulent isolates of these pathogens often emerge, threatening current resistance sources. A total of 110 RILs from the CDRK × Yolano cross (CY) were evaluated for co-segregation of resistance to races 73, 2047, 3481 of *C. lindemuthianum*, and 63-39 *of P. griseola*. Results indicate that CDRK carries a dominant locus that confers resistance to these four races. Co-segregation analysis further revealed that the ANT and ALS resistance loci in CDRK were tightly linked at a distance of 0.0 cM. We are provisionally calling this locus *Co-CDRK*/*Phg-CDRK*. Genetic mapping of the F10 RILs population placed the *Co-CDRK*/*Phg-CDRK* locus in a 245 Kbp genomic region flanked by SNP markers ss715645251 and ss715645248 on the lower arm of chromosome Pv01. By genotyping 19 F10 RILs from CY population using three additional markers we fine mapped the *Co-CDRK*/*Phg-CDRK* locus in a significantly smaller genomic region (33 Kbp) flanked by the STS marker CV542014 and the SNP marker ss715645248. This 33 Kbp harbors seven predicted genes based on the common bean reference genome. Because the *Co-CDRK* and *Phg-CDRK* resistance alleles are linked in cis, they can be selected with great efficiency using molecular markers.

* Student Presented

P16: Genome Wide Association Analysis Reveals Markers Tagging Anthracnose and Angular Leaf Spot Resistance Genes in Common Beans from Brazil

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Common bean production can be severely affected by the angular leaf spot (ALS) and anthracnose (ANT) diseases. The objective of this study was to evaluate the reaction of 115 Brazilian accessions from both gene pools (Andean and Mesoamerican) of common bean inoculated with races 9, 65, 73, 2047, and 3481 of *Colletotrichum lindemuthianum* and races 31-23 and 63-39 of *Pseudocercospora griseola*, followed by a genome-wide association study (GWAS). DNA samples from non-inoculated trifoliolate leaves of each accession were screened with 5,398 SNP markers using the BARCBean6K_3 Illumina BeadChip according to the Infinium HD Assay Ultra Protocol. For the phenotypic evaluations, 12 seedlings of each accession were inoculated with a concentration of fungal spores adjusted to 1.2 × 106 and 1.2 × 104 conidia mL^{-1} for *C. lindemuthianum* and *P. griseola*, respectively. ANT and ALS symptoms were scored using the disease severity scales (1 to 9). GWAS was performed by mixed linear model (MLM) using the Tassel software. Significant marker-trait associations were observed as follows: races 9 and 73 on chromosome Pv04, race 65 on chromosomes Pv04 and Pv06, and race 2047 on chromosome Pv10. Furthermore, quantitative resistance loci (QRL) associated with race 31-23 of *P. griseola* were found in chromosomes Pv01, Pv02, Pv06, and Pv11, whereas resistance to race 63-39 was mapped to Pv06 and Pv08. These findings will help bean breeding programs to effectively transfer ALS and ANT resistance genes to commercial cultivars.

* Student Presented

P17: Comparison of QTL for Resistance to Angular Leaf Spot and Rust in Tanzania versus South Africa for the Andean Diversity Panel and Rojo/CAL 143 RIL Population

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Angular leaf spot (ALS) and rust are major bean diseases worldwide. Genetic resistance provides effective control of these diseases. Traditionally, large-seeded Andean beans (red, red mottled, yellow, etc.,) are preferred in Eastern and Southern Africa but ALS and rust resistance in these market types is generally lacking in these production regions. We sought to identify and characterize effective resistance for these production regions in the Andean Diversity Panel (ADP) of ~400 accessions and in the bi-parental Rojo/CAL-143 (RC) population of 149 RILs. The red mottled CAL-143 (calima type) from CIAT is a known source of ALS resistance in an Andean background. The ADP and RC population were planted in replicated trials in Cedara, South Africa and in Arusha and Mbeya, Tanzania. Disease ratings were scored from 1 to 9 using the CIAT rating scale. GWAS was performed for disease reaction in the ADP using SNPs generated by GBS from different labs (USDA-Mayaguez, PR, and NDSU, Fargo, ND). The RC population was genotyped for SNPs by GBS and using the BARCBean6K_3 5398 SNP array. FarmCPU and mrMLM were used for detection of QTN in the ADP by GWAS. The RC map was generated by MapDisto and QTL analyses of two-factor genome scans was performed by rQTL. For the ADP in South Africa, ALS resistance QTL corresponding to *Phg-2* and *Phg-4* were most important whereas *Phg-1*, and QTL on Pv03 and Pv09 were most important in Tanzania. For ALS in the RC, *Phg-2* and QTL on Pv03 were detected in South Africa and QTL on Pv03, Pv05, and Pv09 were detected in Mbeya. Similarly for rust, different resistant QTL were detected in South Africa versus Tanzania. Novel QTL for rust resistance were detected on Pv03 in both the ADP and the RC population, and on Pv05 for the RC population. Different strategies for resistance gene deployment are necessary to combat endemic ALS and rust pathogen populations in Africa.

* Student Presented

P18: Genetic Progress after 18 Cycles of Recurrent Selection for Angular Leaf Spot Resistance in Brazil

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The angular leaf spot (ALS), caused by the *Pseudocercospora griseola* fungus is one of the main diseases that occur in common bean crop in Brazil. Control strategies include crop management, fungicides and genetic resistance. Some factors have increased the occurrence of disease, the use of fungicides, contaminated seeds, susceptible cultivars and high variability of pathogen. Therefore, the most feasible alternative for ALS control is by resistant cultivars. Thus, in 1998 a recurrent selection program was started in Minas Gerais State, Brazil, aiming at resistance to ALS. Initially, a partial diallel with seven carioca-type lines and ten sources of resistance to *P. griseola* was carried out, resulting in 29 segregating populations that constituted the cycle 0 (C-0) of recurrent selection program. In the F2 (S0) generation of C-0, the plants with the least symptoms of the disease were phenotypically selected and derived the S0:1 progenies. The best ones were recombined to obtain the first cycle (C-I). The process was repeated until cycle XVIII (C-XVIII) in 2018. The aim of this work was estimating the genetic progress (GP) obtained for pathogen resistance in these 18 recurrent selection cycles, as well as the grain yield. We assessed the ALS severity (9 scores) in progenies S0:1 of each recurrent selection cycle. In all cycles, the cultivars Pérola (resistant) and Carioca MG (susceptible) were used as checks. As the assessment of S0:1 progenies of each cycle was carried out in different years (2001 to 2019), the GP for resistance was estimated by the average of progenies of each cycle in relation to check Pérola and, for grain yield, in relation to both checks. The GP for ALS resistance was 1.35% and the grain yield response was 0.88% per cycle under conditions of natural occurrence of ALS. Thus, even after 18 cycles of recurrent selection for resistance to ALS, the selection has been efficient.

* Student Presented

P19: Fine Mapping the *Ur-6* Rust Resistance Gene in Common Bean

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Bean rust is caused by *Uromyces appendiculatus*. This pathogen is a serious threat to the farming of common bean (Phaseolus vulgaris L.) and completes its entire life cycle on common bean. *Ur-6* confers resistance to races of *U. appendiculatus* that overcome other resistance genes and is present within the Andean gene pool. Genotypes from this gene pool are commonly farmed is South America and Africa. In this study, we are fine mapping *Ur-6* in the common bean genome. To this end, we have screened the Middle American Diversity Panel with *U. appendiculatus* race 15-3 (previously named race 47), which identifies the presence/absence of the *Ur-6* gene. A genome-wide association study was performed using the Efficient Mixed-Model Association (EMMA) algorithm, and 129 SNPs were discovered to be highly associated with race 15-3 resistance ($p \leq 9.02E-05$). This preliminary analysis has identified a strong association of trait race 15-3 resistance with a gene cluster on the proximal end of chromosome Pv07. In addition, the resistance specificity is also being mapped in a F2 population generated from the cross of Golden Gate Wax (*Ur-6*) and UI-114 (no resistance genes).

* Student Presented

P20: Identifying Resistance in Andean Common Beans to the Rust Pathogen *Uromyces appendiculatus*

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Rust, caused by *Uromyces appendiculatus* (Pers:Pers) is an economically important disease of common beans (*Phaseolus vulgaris* L.) worldwide. Common beans of Andean origin are preferred in Eastern and Southern Africa and in Europe. In the US, approximately 10% of common beans produced are of Andean background; however, they are of higher value than beans of Middle American origin. Few US breeding programs focus on the development of Andean cultivars and the genetic base of this population is much smaller than Middle American beans; therefore, fewer genetic improvement have been made. To aid in breeding for resistance to *U. appendiculatus*, 49 accessions from the Andean Diversity Panel (ADP) were challenged with *U. appendiculatus* races 20-3 and 27-7 under greenhouse conditions. Race 20-3 is most frequent in North Dakota and is virulent on resistance genes *Ur-3*, *Ur-6*, *Ur-7* and the Montcalm gene. Race 27-7 is virulent on *Ur-3*, *Ur-4*, *Ur-5*, *Ur-6*, *Ur-7*, *Ur-9*, *Ur-12* and *Ur-13*. ADP accessions screened included cranberry, white kidney, light (LRK) and dark red kidney (DRK). Five ADP accessions were resistant to both 20-3 and 27-7. An additional 14 accessions were resistant to race 20-3. Fifty advanced LRK and DRK lines from the North Dakota Agriculture Experiment Station dry bean breeding program were evaluated against races 20-3, 27-7 and 29-3. Race 29-3 is virulent on *Ur-3*, *Ur-4*, *Ur-6*, *Ur-7*, *Ur-9*, *Ur-12* and the Montcalm gene. Five DRK breeding lines were resistant to all three races, 13 were resistant to 20-3 and 27-7 and six to race 29-3. Four LRK lines were resistant to all three races, six were resistant to 20-3, four to 29-3 and seven to 27-7. The identification of resistant germplasm of Andean origin provides valuable resources in the effort of developing resistance to *U. appendiculatus*. Additionally, the incorporation of resistance genes of Andean origin into Middle American beans can provide resistance to a broader range of *U. appendiculatus* races.

* Student Presented

P21: Genome-Wide Association and Fine Mapping of *bgm-1* Gene and Other QTLs for Resistance to Bean Golden Yellow Mosaic Virus in Dry Beans

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Bean golden yellow mosaic virus (BGYMV) (family *Geminiviridae*) is a begomovirus vectored by *Bemisia tabaci* (*Gennadius*) whitefly that causes severe yield losses (40 to 100%) in common bean. The most effective control of BGYMV is to combine genetic resistances in the host. Two SCAR markers developed 25 years ago have been used for marker-assisted selection (MAS) programs for BGYMV resistance. The marker SR2 is linked to the *bgm-1* gene on chromosome Pv03 and SW12 marker with a quantitative trait locus (QTL) on Pv04. Our objective was to improve MAS for BGYMV. QTL analysis was applied in two biparental recombinant inbred populations, DOR364/XAN176 and DOR476/SEL1309, and genome-wide association studies (GWAS) were conducted on a panel of 415 breeding lines developed by the International Center for Tropical Agriculture (CIAT) and a panel of 120 select lines/cultivars developed for abiotic stress evaluations (BASE 120 panel). Linkage mapping revealed *bgm-1* on Pv03 and three QTL for BGYMV resistance on chromosomes Pv04, Pv07 and Pv08 with phenotypic variation explained between 10 to 33 percent. GWAS revealed significant SNPs associated with bgm-1 and the same QTL on Pv04, Pv07, and Pv08, and a novel QTL on Pv09. Two candidate genes for *bgm-1* were identified, both related to geminivirus resistance. An indel marker was developed from one candidate gene and evaluated on multiple bean genotypes by melting temperature (Tm)-shift method. This marker was completely correlated with BGYMV resistance across more than 700 genotypes. These results enhance our understanding of the genetic mechanisms of resistance to BGYMV and provide improved MAS for resistance to BGYMV in common bean breeding programs.

* Student Presented

P22: *Pythium* Species Associated with Common Bean in North Dakota and Minnesota

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North Dakota and Minnesota rank number one and four in US common bean (*Phaseolus vulgaris* L.) production, respectively. *Pythium* spp., *Fusarium* spp., and *Rhizoctonia solani* Kühn cause devastating root rot in common beans worldwide. To effectively manage root rot, it is vital to understand which pathogens are most damaging in the region. A root rot survey conducted a decade ago in North Dakota and Minnesota established *Fusarium* and *Rhizoctonia* as important pathogens. However, *Pythium* spp. were not included in that survey. Many *Pythium* spp. are aggressive pathogens to common bean and non-pathogen species can serve as initial colonizers of young root tissue, creating an entry point for pathogens. Seed treatments including mefenoxam (metalaxyl) are commonly used to manage Oomycete pathogens in many crops. Mefenoxam resistance has been observed in some Pythium populations in the US. This resistance is not yet widespread but appears to be increasing in some regions. To date, mefenoxam resistant *Pythium* spp. have not been reported in association with common beans. The objectives of this research are 1) to establish which *Pythium* spp. are important pathogens in common beans in North Dakota and Minnesota by determining the prevalence, pathogenicity, and aggressiveness and 2) determine mefenoxam sensitivity of isolates collected. To date, 14 Pythium spp. have been morphologically and molecularly identified from 10 of 82 fields sampled in 2018 and 2019. Preliminary results indicate that species associated with common bean exhibit varying levels of aggressiveness and mefenoxam sensitivity. Understanding which species of *Pythium* are most aggressive and prevalent in North Dakota and Minnesota will aid in developing best management practices and steer breading programs toward developing varieties that are resistant to *Pythium* spp. important to the region.

* Student Presented

P23: Investigating MAT Heterokaryons in Isolates of *Sclerotinia sclerotiorum* in Brazil

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Sclerotinia sclerotiorum is a homothallic fungus (self-compatible), the resulting population is expected to be clonal with limited variability, but high genetic variability has been reported. Presence of an inversion in mating type (MAT) locus has classified isolates in positive inversion (Inv+) and inversion negative (Inv-). In this case, isolates form MAT homokaryon Inv+ or Inv-. However, it has identified MAT heterokaryon isolates. There is no information about this in isolates *S. sclerotiorum* from Brazil. Sample of 17 isolates were assessed to verify presence of MAT homokaryon Inv+ or Inv- and MAT heterokaryon. Specific primers were used for identification of Inv+ and Inv-. We found prevalence of Inv− MAT *S. sclerotiorum* isolates. In addition, it was observed only one MAT heterokaryon isolate. The presence of heterokaryon isolate is a potential to increase genetic variability within the population.

* Student Presented

P24: Next Generation Sequencing Rapidly and Simultaneously Detects Many Airborne Plant Pathogens from Dry Bean Fields and Other Crops

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In Alberta, Canada, monitoring the air for plant pathogens is a task currently performed independently by different commodity crop groups interested in specific diseases: rust in wheat, sclerotinia stem rot in canola, white mould in dry bean, and late blight in potato. While this "one pathogen one crop" approach has been successful, next generation sequencing (NGS) techniques make it possible to identify virtually all microorganisms in an air sample at once, and could help consolidate disease forecasting efforts. This research employs NGS methods to describe the changes in airborne microbial diversity (AMD) across space and time over the course of a growing season in Alberta. To assess the effect of spatial scale on AMD, spore samplers were placed in dry bean fields across the bean growing region from July to August. To assess the effect of crop type on AMD, spore samplers were also placed in canola, wheat, and potato fields. Samples will be sequenced using Illumina metabarcoding with primers designed to identify fungi, bacteria, and oomycota. In addition, Oxford Nanopore's portable DNA sequencer, the MinION, will be compared to the Illumina data to assess its performance for in-field use. Preliminary results show that, within five hours from sample collection to results, the MinION was able to detect common plant pathogens of dry bean including *Xanthomonas* spp., *Pseudomonas syringae*, and *Sclerotinia sclerotiorum*. In addition, many common airborne plant pathogens of other crops such as *Alternaria alternata*, *Botrytis cinerea*, *Colletotrichum graminicola*, *Puccinia graminis*, and L*eptosphaeria maculans* were also detected. The presence of *S. sclerotiorum* was confirmed in a qPCR assay, and MinION results will be further validated with Illumina sequencing. These preliminary findings suggest that NGS approaches could provide rapid diagnostics to enhance disease forecasting efforts for many pathogen-plant combinations, including white mould of dry bean.

* Student Presented

P25: Common Bean Inbred Lines of the Black Commercial Group Selected for High Yield Potential, Early Cycle and Disease Resistance

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Brazil produces annually around 3,1 million tons of common bean, which 20% are from the black group. This production is not sufficient to meet the demand, requiring an import of approximately 100,000 tons, mainly from Argentina and China. In order to developing new cultivars to meet this demand a multiple cross involving five parents from the Middle American gene pool (BRSCampeiro//IAPAR20/ EMPASC201/3/ IAPAR14/IAPAR31) carried out in 2006 in a greenhouse at IAPAR. In 2007, the F1 population was sown in Londrina (PR, Brazil) and the obtained F2 population (1,500 seeds) was sown in 2008 in Ponta Grossa (PR, Brazil) in which a single pod was collected from each plant. The seeds from all pods were bulked and random samples of 1,500 F3 seeds were taken. In 2008, in rainy season the progeny F3 was sown in Londrina and individual plants were selected. In 2009, in dry season, the F4 progenies was sown in Ponta Grossa and in the same year, in rainy season, the F5 progenies was sown in Londrina, where 52 superior progenies were selected and harvested in bulk. In 2010, the F6 progenies selected were evaluated for agronomic performance at Experimental Station in Irati (PR, Brazil), in a Federer augmented block design. Nine progenies that overcome controls yield, whit upright plant architecture, early cycle, disease resistance and high commercial and culinary quality were selected, bulk harvested and considered as breeding lines. These lines were evaluated in the preliminary trials in two seasons, in the year 2011/12 and after they were promoted to final trial, the value for cultivation and use, established in 2012/13, 2013/14, 2014/15 in rainy and dry seasons in 26 environments. In this trial LP11-117 line exceeded the yield of the control cultivars by 12.5% and its yield potential was 4,797 kg.ha-1. Based in the high agronomic performance it was submitted for registration as a new black common bean cultivar in 2018 and named IPR Urutau.

* Student Presented

P26: Computational Identification, Phylogenetic and Synteny Analysis of Receptor-like Kinases "RLK" and Receptor-like Proteins "RLP" in Legumes

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The plant cell wall is an active structure that mechanically connects cell tissues and controls the shape of the plant cell by sensing external stimuli and transmitting signals to the cytoplasm. The plasma membrane is enclosed by the cell wall and contains RLK and RLP proteins, which play a fundamental roll in cell to cell interaction and are crucial in plant growth, development, and immunity. To date, no published comparative genomic analysis explores RLK and RLP among legume genomes. This study evaluates the following legumes: soybean (*Glycine max* (L.) Merrill), common bean (*Phaseolus vulgaris* L.), barrel medic (*Medicago truncatula* L.), mungbean (*Vigna radiata* (L.) R. Wilczek), cowpea (*Vigna unguiculata* L. Walp), adzuki bean (*Vigna angularis*), and pigeonpea (*Cajanus cajan* L.), and the non-legumes: *Arabidopsis thaliana* (L.) Heynh, tomato (*Solanum lycopersicum* (L.) H. Karst), and common grape (*Vitis vinifera* L.). The research demonstrates that a computational logical approach for classifying the RLK/RLP is statistically well supported and can be used in other plant species. The analysis of RLK/RLP of the species evaluated suggests that about 2% are RLK and less than 1% of the proteins are RLP. The results suggest a dynamic evolution of RLK and RLP in the legume family, with 66% to 85% of RLK and 83% to 88% of RLP belonging to orthologous clusters. The remaining RLK and RLP proteins are classified as singletons. The ratio of the pairwise synteny blocks of RLK/RLP among legumes shows a 1:1 relationship. The exception is G. max, which shows an approximately 2:1 ratio due to its recent whole genome duplication. The other legumes show evidence of a similar proportion of plasma membrane proteins among the legume pairwise synteny blocks. Due to the economic relevance of legumes for human and animal consumption, this detailed analysis of these plasma membrane proteins in legume species brings a new source of information to legume breeding and genetic research communities.

* Student Presented

P27: QTL Analysis of a Yellow *Phaseolus vulgaris* Recombinant Inbred Line Population for a Fast Cooking, Flavorful, and Flourishing Future of Dry Beans

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Dry beans are a nutrient-rich food with diverse culinary attributes, but dry bean consumption in the United States remains low due in part to their often long cooking times and the preconceived notions held by consumers regarding their flavor. Cooking time and sensory quality are two important traits considered when consumers choose whether to purchase dry beans and which dry bean products to purchase. However, the process of evaluating germplasm for these consumer-valued traits is costly in time and resources, which limits the ability of breeders to incorporate these traits in their programs. This study uses QTL analysis to contribute to the growing understanding of the genetic control of cooking time and to lay the foundation for sensory quality improvement in dry bean breeding programs. In this study, a yellow dry bean (Phaseolus vulgaris L.) recombinant inbred line population of 244 genotypes including parents Ervilha and PI527538 were grown in Entrican, Michigan for two years. The population was evaluated for cooking time, flavor, and texture. Cooking times ranged from approximately 18 to 40 minutes. A trained sensory panel determined flavor and texture profiles of cooked samples using 5-point attribute intensity scales. The genotypes exhibited a range of attribute intensities with beany flavor having the largest range from 1.38-4.13. A genotyping-by-sequencing approach with an *Ape*KI digest was used to genotype the parents and RILs. QTL mapping of cooking time, flavor profiles, and texture identified genomic regions influencing these traits. This information will enable breeders to target faster cooking times and specific sensory profiles in their programs, as well as allow for selection on agronomic traits without sacrificing desirable cooking time and flavor. By addressing the barriers these traits pose, dry bean consumption and their suitability in new food products might improve allowing increased access to their associated nutritional benefits.

* Student Presented

P28: Genetic Study of Seed Hardness Trait in Dry Bean (*Phaseolus vulgaris*)

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High percentages of hard seeds under short season growing conditions is a serious concern in commercial production and food processing, which affects cooking time and canning quality in dry beans. This study aims to identify the genetic factors associated with seed hardness, and develop associated molecular markers to better understand and tag this trait for variety development. In our previous study using a recombinant inbred line population derived from a cross between hard- and soft-seeded parental lines, three QTLs were mapped to chromosomes 1, 2, and 7. The results demonstrated that multiple genetic factors are involved in the control of this complex trait. In a new effort, 192 genotypes from various market classes including black, navy, pinto, kidney, and cranberry beans are being evaluated for hard seed at two sites for three years. The preliminary seed hydration test results showed wide variation of seed hardness among those genotypes. Using the genome wide association study approach, new QTLs are expected to be identified and molecular markers will be developed.

* Student Presented

P29: Investigation of Marsh Spot Variation in Cranberry Beans in Manitoba, Canada

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Marsh spot is a common seed quality concern in cranberry common beans. There is very limited literature on marsh spot genetics and breeding. Marsh spot symptoms are strongly influenced by environmental conditions, but genetics of marsh spot resistance remains to be exploited. In the field evaluation of 24 varieties over two years in Morden, significant variation in severity was observed among the varieties. A cross was made between a resistant and a susceptible variety in 2013, and a recombinant inbred line population of 140 lines was developed through single seed descent in the greenhouse. The lines have been phenotyped for marsh spot severity in the field at Morden during 2017, 2018 and 2019. Genomic sequencing of the lines is being conducted and QTLs associated with the marsh spot resistance will be mapped in order to understand the genetic mechanism controlling marsh spot resistance in cranberry beans.

* Student Presented

P30: Assessing Genomic Selection Prediction Accuracy for Yield and End-Use Quality Traits in Black Beans

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Genomic Selection (GS) has been implemented in plant breeding to improve quantitative traits, increasing the genetic gain per unit time, and optimizing resource allocation in the breeding pipeline. Yield is considered a crucial trait to be improved in breeding and usually is included in GS studies. However, dry bean cultivars in the US must possess suitable end-use quality (color retention and appearance after canning) for release and consumer acceptability. Nevertheless, breeding for end-use quality traits is often considered a secondary target because of the amount of seed needed, labor and expenses. Without selection for end-use quality traits, many undesirable materials are advanced, expending additional resources. In the present study, we describe the initial assessment of the predictive ability of a genomic selection model for yield, seed weight, processed appearance, and color retention in 275 black dry beans using single nucleotide polymorphism (SNP) markers identified by Genotyping by Sequencing. Prediction accuracies were evaluated using cross-validation with ridge-regression best linear unbiased predictions (rrBLUP). The overall prediction accuracies were 0.42 (color retention), 0.43 (yield), 0.50 (appearance) and 0.52, (seed weight) when 50% of the population was used to create the model. Although the prediction accuracies are a standard method to determine the success of GS models, it is more important asses the power of the models to predict extreme values, and it has been reported that models with overall accuracies of 0.4 to 0.5 are able to select between 60 to 70% of the top individuals. Genomic selection could be integrated into dry bean breeding to made selections in a wide range of complex traits leading to more efficient and integral breeding programs.

* Student Presented

P31: Iron Biofortification of the Common Bean: Assessment of Bean Iron Concentration and Iron Bioavailability from Markets and Breeder Collections in East Africa

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For 20 years, the predominant approach for bean Fe biofortification is to breed for high Fe content. This approach is based on three assumptions: 1) the average Fe concentration in beans currently consumed in targeted regions is approximately 50 µg/g (dry weight), 2) a 40 µg/g increase (target value 90 µg/g) can be sustained through traditional breeding, and 3) iron bioavailability from the biofortified bean will not decrease substantially to negate the increase in Fe concentration. This study examined these assumptions via collection of 76 marketplace samples (East Africa Marketplace Collection; EAMC) of multiple color classes from locations in Uganda, Rwanda, Democratic Republic of Congo, Burundi, Ethiopia, Kenya and Tanzania. Because market samples can be a mixture of seed varieties within a market class, 95 samples from the Africa CIAT Collection, and another 65 samples from breeders in Ethiopia (designated Ethiopia Breeder Collection) were also evaluated that represent beans of common markets. The average EAMC bean Fe concentration was 72 µg/g, ranging from 52-93 µg/g, with a couple of outlying varieties at 105 µg/g (MAC9) and 129 µg/g (MAC49). The CIAT collection averaged 69 µg/g (range of 55-90 µg/g), and the Ethiopian collection averaged 65 µg/g (range of 51-87 µg/g). The 18 biofortified varieties within the EAMC averaged 73 µg/g (range of 55-94 µg/g), which is essentially equal to the overall mean (70 µg/g) and range (54-93 µg/g) of the non-biofortified bean varieties in the EAMC. Using a Caco-2 cell bioassay to measure Fe bioavailability, the biofortified varieties did not deliver any additional Fe relative to non-biofortified varieties. These results indicate that the assumptions of the high Fe bean breeding approach are not met in the typical East African market place. Furthermore, based on the Fe content and bioavailability data collected from this study, the biofortified bean varieties from these markets are providing no additional dietary Fe.

* Student Presented

P32: Development of Edible Bean Germplasm Lines with Improved Cysteine and Methionine Concentration

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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 F2:8 population of 185 recombinant inbred lines (RIL). Protein profiles classified them into four groups according to genetic inheritance at the phaseolin and lectin loci. Lines were tested under field conditions and their amino acid concentrations were evaluated. Two SS lines were recovered having a stable protein profile, 2-37 and 3-84. They had an increased Cys concentration, by approximately 30% and Met concentration, by approximately 15%, as compared with the parental Morden003 cultivar. They have been deposited at the Plant Gene Resources of Canada. SNP markers enabling to track phaseolin deficiency were validated using a KASP assay.

* Student Presented

P33: Wyoming-Grown Peruvian Popping Beans: Sensory Analysis and Consumer Acceptance

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American consumers fall short of dietary guidelines for a variety of nutrients including dietary fiber. Beans are a rich source of protein and fiber, starch and vitamins/minerals however, intake of dry edible beans and legumes is currently included in daily dietary patterns for only 14% of U.S. adults. Nuña beans (*Phaseolus vulgaris* L.) are a class of common beans originated in South America and cultivated in the highland areas of Peru, Ecuador and Bolivia. They are unique due to their characteristic of "popping" after exposure to heat, producing a toasted, soft-textured edible snack. Nuña bean preparation is energy-efficient with reduced requirements for fuel and cook time compared to other dry beans. Plant scientists have attempted to eliminate the photoperiod-sensitive gene present in traditional nuña beans, while retaining the popping gene to begin cultivation in the U.S. This study aimed to evaluate consumer perception of nuña beans grown in Wyoming. Temperate-adapted nuña beans advanced breeding lines from Colorado were field grown using conventional practices in Lingle, WY for consumer testing. Participants included staff, faculty, students, and community members. Samples were evaluated for appearance, flavor, texture, aroma, and acceptability using a 9 point hedonic scale. Additional questions included willingness to pay, previous knowledge, and intentions of adding popping beans to their diet. Willingness to pay and sensory attribute mean response main effects were calculated using analysis of variance. Participants (n=130) responded positively to sensory characteristics and consumer acceptability. Differences in sensory evaluation and willingness to pay were identified between groups of consumers. Intake of dietary fiber, as part of a plant-based diet, including dry beans, has been shown to promote healthy weight and chronic disease prevention. Options such as the popping bean may contribute to an increase in nutrient dense options for consumers.

* Student Presented

P34: Molecular Mapping the Pinto Pattern Gene in the *C* Locus of Common Bean

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Seed coat patterning genetics in common bean (*Phaseolus vulgaris* L.) began with Tschermak (1902) who determined a single dominant genetic factor, *M*, controlled the difference between solid color and mottled seeds. While Shull (1907) and Emerson (1909) observed that some mottled patterns were only observed in the heterozygous state, later research discovered dominant acting genes for mottled seeds. The mottling gene was mapped at a single locus referred to as the "complex *C* locus" (Lamprecht 1932; Prakken 1974) that consisted of several sub-loci that controlled not only the mottled seed coat pattern (M) but also the striped seed coat pattern (*St*), seed coat color expression (*C*), red seed color (*R*), and hypocotyl color (*Acc*). This model of a series of very tightly linked genes was consistent with previous results of Tjebbes (1931) and Lamprecht (1940) that demonstrated very tight linkage between the *St* and *R* and *C* and *St* gene pairs. Prakken (1977) provided subsequent confirmation that the *C* locus contains multiple tightly linked genes when he observed that F1 seed from crosses of pinto (dark mottled, *M*) and cranberry (red striped, *St*) beans expressed both the mottled and striped patterns in their respective colors. Using a combination of association mapping of the pinto pattern gene and genome and individual gene sequencing, the *C* locus mapped to the proximal end of chromosome Pv08. The gene is located within a cluster of MYB transcription factors genes. The MYB gene within the cluster that controls pinto pattern (*Mpi*, proposed) shares features with MYB repressors. Natural mutants of this gene are responsible for solid color red and pink beans of race Durango. Since the gene content of this cluster is similar, but not identical, among the Middle American and Andean clusters, and that the locus structure has been partially maintained in cowpea and soybean, this cluster appears to date at least to the origin of the Phaseoleae legumes.

* Student Presented

P35: Speed Breeding in Dry Beans

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Speed breeding is the rapid generation advancement of plant populations using increased plant growth temperatures and longer day lengths. This technique was pioneered primarily in cereals but has been adapted to rapidly advance plant populations in a number of plant species. The Agriculture and Agri-Food Canada Dry Bean Breeding Program based in Harrow, ON has developed speed breeding methodology using existing greenhouse facilities and making use of expertise onsite to lower generation times to less than eight weeks. Key to this system is maximizing greenhouse space usage and minimizing labour costs through high density planting using flood benches watered with hydroponic nutrient solution. Basic speed breeding principles were tested including harvesting immature bean pods three weeks after flowering, making use of LED lights to provide an improved light spectrum shortening plant internodes and reducing climbing. This also allowed for increased lighting fixture density based on the electrical capacity of the greenhouse providing a consistent 400 µmol m^{-2} s^{-1} for 22 hours/day. Plant growth temperatures were increased to 28℃ (day) and 26℃ (night) to speed plant growth. Several challenges were faced in developing the system, mostly associated with high density planting. Increased plant density does reduce seed yield of plants on the inside of the bench, however more than enough seed was produced for population advancement through single seed descent. Flood irrigation reduces labour costs, however it does increase chances of Pythium root rot. The pH of the hydroponic solution is also critical as pH levels lower than 6.0 led to nutrient uptake issues. The development of this system also has disrupted typical breeding program flow enabling for disease screening of populations at each generation; advancing from crossing to F5 rows in one year. This will save approximately three years in breeding time over previous approaches.

* Student Presented

P36: Exploring Genetic Improvements and Innovative Process Methods in Organic Dry Beans

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The consumer demand for organic dry bean (*Phaseolus vulgaris*) has been rising in the United States and globally. Organic dry bean products are appealing to consumers as nutrient dense foods that are rich in proteins and dietary fiber, and largely free of added ingredients. Currently, the major challenges in the production of organic beans include unsatisfactory seed quality, and unappetizing appearance, texture, and taste of their products. Seed coat cracking during harvest is a significant problem associated with organic bean seed quality. Bean processors have challenges in obtaining satisfactory quality of canned/processed organic bean products. The major objectives of our study include: 1) Developing and delivering better organic kidney bean germplasm through breeding under organic conditions; 2) Improving organic bean packaging quality though innovational retortable pouch processing method. A black bean variety trial, a kidney bean variety trial, and a breeding nursery were conducted in 2018 and 2019, along with a yellow bean trial in 2019 in organic fields. The bean lines from these trials are also being tested for end use traits including canning quality, seed coat check, cooking time, texture and taste. The early generation lines will be advanced and selected through those phenotypic evaluations. New pouch processing and packaging technology are being tested and optimized with all the experimental trials, to generate a method of bean processing by using shorter time with improved physical and sensory quality as well as providing convenience to consumers. The top yielding black bean lines from 2018 are advanced breeding lines from MSU (B17220) and USDA-ARS (BL1402-15), which also have best color retention in canning. The top yielding kidney bean line from 2018 was the MSU variety Snowdon. The kidney bean variety Red Hawk and K16136 (MSU advanced breeding line) ranked on top for canning appearance.

* Student Presented

P37 The Pulse Crop Database: Expanding the Cool Season Food Legume Database into a Resource for Pulse Crop Research and Improvement

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The Cool Season Food Legume Database (CSFL) is being expanded under National Research Support Project 10 (NRSP10, www.nrsp10.org) to include common bean, cowpea, pigeon pea, groundnut, lupin, and vetches. Renamed the Pulse Crop Database (PCD, www.pulsedb.org), the new online resource focuses on providing access to curated and integrated data and tools to enable pulse crop research, translation and improvement. PCD includes publicly available genomics, genetics and breeding data including genomes, genes, transcripts, genetic maps, markers, QTL, germplasm, phenotype and publications, with integrated tools to easily access, view, filter and download the data. PCD users can: view and compare genetic maps using the MapViewer tool; search markers by type, organism, and/or location; search genome sequences with BLAST; view genomes with JBrowse and the Synteny Viewer; and explore genome metabolic pathways using PathwayCyc. The Breeding Information Management System (BIMS) in PCD allows for management of breeding programs via private user accounts while also enabling access to publicly available pulse phenotype data downloaded from the GRIN database. BIMS works with the Android app Field Book for streamlined phenotype data collection and upload, or with spreadsheet templates provided for data upload. Once the breeding program data is in BIMS, the secure data can be viewed, filtered, analyzed, and archived and used to create templates for data entry. BIMS is being furthered developed to include genotype data upload and querying with more advanced analysis capability using high performance computing.

* Student Presented

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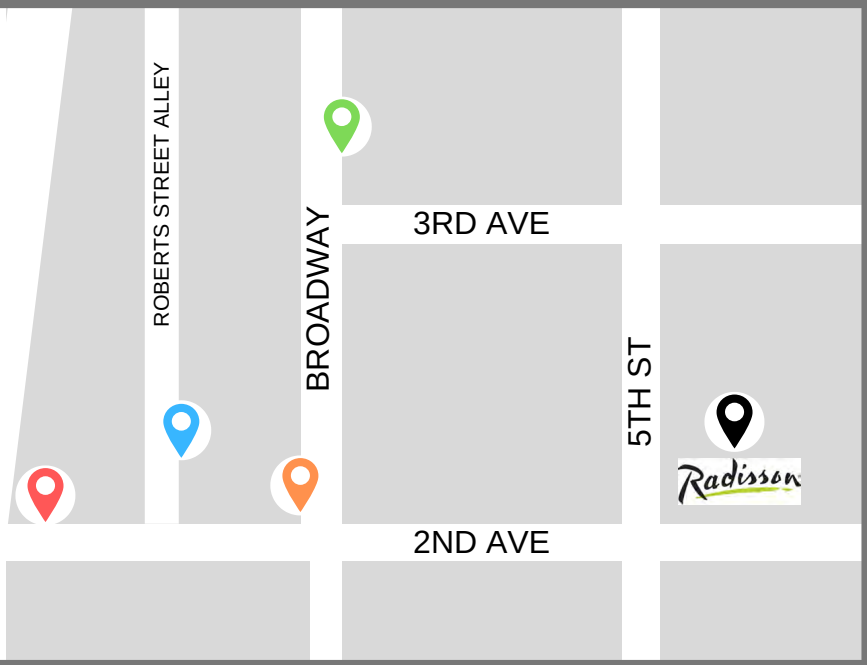

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