BIC

2017 Biennial Bean Improvement Cooperative Meeting

October 29 - November 1, 2017

East Lansing, Michigan

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2017 Bean Improvement Cooperative Program

Sunday, October 29, 2017

6 p.m.	**Registration and Opening Reception**	**Red Cedar**

Monday, October 30, 2017

7 a.m.	**Breakfast**	**Big Ten B**
8 a.m.	Welcome from President Phil Miklas	**Big Ten C**
	Opening Sessions	**Big Ten C**
8:15 a.m.	New Plant Phenotyping and Analytics Platforms for Improved Grain Legumes *David Kramer, Michigan State University*	
9:15 a.m.	Advances in abiotic and biotic research of common bean including new tools and strategies *Stephen Beebe, International Center for Tropical Agriculture (CIAT)*	
10 a.m.	**Break**	**Big Ten C Lobby**
	Abiotic Session – Moderator Andrew Wiersma, Michigan State University	**Big Ten C**
10:30 a.m.	Analysis of the OAC-Rex Genome Reveals the Location of Interspecific Introgression from Wild Tepary Bean (Phaseolus acutifolius) *Gregory Perry, University of Guelph*	
11 a.m.	Transcriptome Analysis of Common Bean (Phaseolus vulgaris L.) under Elevated Temperatures *Ali Soltani, Michigan State University*	
11:30 a.m.	Effects of High Night Temperature Stress on Reproductive Structures of Lima Bean (Phaseolus lunatus) *Emmalea Ernest, University of Delaware*	
12 p.m.	**Lunch**	**Big Ten B**
	Biotic Session – Moderator Juan Osorno, North Dakota State University	**Big Ten C**
1 p.m.	QTL Mapping for Seed Weight and Resistance to Acanthscelides obtecus in Common Bean *Kelvin Kamfwa, University of Zambia*	
1:15 p.m.	A Repeatable Protocol for Fusarium Root Rot Phenotyping of Common Bean *Julie Pasche, North Dakota State University*	
1:30 p.m.	Characterization of Common Bean Landrace Beti-10 for Angular Leaf Spot Disease Resistance in Tanzania *Luseko Amos Chilagane, Sokoine University of Agriculture*	
1:45 p.m.	ALS pathotype specificity in common bean – Genome-wide association studies and application in breeding for disease resistant cultivars *Michelle Nay, ETH Zurich*	
2 p.m.	Rust-proofing dry edible beans in North Dakota *Cecilia Monclova, North Dakota State University*	
2:15 p.m.	Waterlogging and Root Rots: The value of Phaseolus genetic diversity for combined stress tolerance *Gloria Mosquera, International Center for Tropical Agriculture (CIAT)*	
2:30 p.m.	Development and Characterization of an Infectious cDNA Clone of Bean common mosaic virus *Alexander Karasev, University of Idaho*	
2:45 p.m.	Virulence diversity of Colletotrichum lindemuthianum in Guatemala and GWAS to identify genomic regions associated with anthracnose resistance in common bean *Carlos Maldonado Mota, North Dakota State University*	

3 p.m.	**Poster Session and Reception: Featuring Odd Numbered Posters**	**Lincoln**
	Agronomics/Fertility Session – Moderator Kelvin Kamfwa, University of Zambia	**Auditorium**
4:30 p.m.	Symbiotic Nitrogen Fixation in the Mesoamerican Genepool of Common Bean (Phaseolus vulgaris L.) *Jennifer Wilker, University of Guelph*	
4:45 p.m.	Genetic Diversity and Association Studies of Nitrogen Fixation in Common Bean under Low Nitrogen Field Condition *Marwan Diapari, Agriculture and Agri-Food Canada*	
5 p.m.	Genome-Wide Association Study for some agronomic traits in common Andean bean *Daniel Ariza-Suarez, International Center for Tropical Agriculture (CIAT)*	
5:15 p.m.	Genetic Architecture of Photosynthate Allocation and Remobilization in Pods of Common Bean (Phaseolus vulgaris L.) under Drought Stress *Jorge Carlos Berny-Mier y Teran, UC Davis*	
5:30 p.m.	Using High Temperatures to Assist in Screening Phaseolus spp *Jesse Traub, Michigan State University*	
5:45 p.m.	Field Screening and Selection of Common Bean Carioca Seeded Progenies with Multiple Resistance to BCMNV, BGMV and CPMMV *Thiago Souza (Souza TLPO), Embrapa Rice and Beans*	
6 p.m.	**Networking and Dinner on Your Own**	

Tuesday October, 31, 2017

7 a.m.	**Breakfast** **Registration**	**Big Ten B** **Big Ten C Lobby**
	Quality Session – Moderator Carlos Urrea, University of Nebraska Lincoln	**Big Ten C**
8 a.m.	Little Beans, Big Opportunities: Leveraging the Power of Food Industry Collaboration to Promote Healthier Diets *Janice Rueda, ADM*	
8:30 a.m.	Sensory Characteristics of Andean Dry Beans *Amber Bassett, Michigan State University*	
8:45 a.m.	Nutritional Profile and Consumer Acceptability of Fresh Pastas With Different Bean Varieties as the Main Ingredient. *Sharon Hooper, Michigan State University*	
9 a.m.	Bean purchasing preferences among low-income Hispanic and non-Hispanic women *Donna M Winham, Iowa State University*	
9:15 a.m.	Genetic Characterization of the Non-Darkening Trait in Common Bean *Mohammad Erfatpour, University of Guelph*	
9:30 a.m.	QTL Analysis of Cooking Time in an Andean Recombinant Inbred Line Population *Matthew Berry, Michigan State University*	
9:45 a.m.	Evaluating Specialty Succulent Lima Beans (Phaseolus lunatus) as Alternative Crops in Delaware *Gordon Johnson, University of Delaware*	
10 a.m.	**Break**	**Big Ten C Lobby**
	Genomics Session – Moderator Phil McClean, North Dakota State University	**Big Ten C**
10:30 a.m.	Investigating Differential Expression of Stress- Responsive Genes in the Same Common Bean (Phaseolus vulgaris) Genotype Grown in Two Different Locations (DE and NE) *Isaac Fisher, Delaware State University*	
10:45 a.m.	Integrated Transcriptomic and Epigenomic Approaches to Understanding Biotic and Abiotic Stresses in Common Bean *Venu (Kal) Kalavacharla, Delaware State University*	
11 a.m.	Development of a repeatable system for bean transformation and/or gene editing *Jose Luis Moreno, International Center for Tropical Agriculture (CIAT)*	

11:15 a.m.	Fine mapping of genes conferring resistance to rust and anthracnose of common bean *Oscar Hurtado, USDA-ARS Beltsville*	
11:30 a.m.	Why Wax Beans Lack Carotenoids *Jim Myers, Oregon State University*	
11:45 a.m.	Identification and characterization of a pectin acetylesterase from the seed coat of common bean (Phaseolus vulgaris) *Frédéric Marsolais, Agriculture and Agri-Food Canada*	
12 p.m.	**Lunch**	**Big Ten B**
	Nutrition Session – Karen Cichy, Michigan State University	**Big Ten C**
1:15 p.m.	Beneficial effects of common bean on adiposity and lipid metabolism *Henry J. Thompson, Colorado State University*	
1:40 p.m.	Sustainable Iron Biofortification of Beans via Enhanced Iron Bioavailability; The USDA-ARS Approach to Improving Fe Nutrition from Beans and Bean Products *Raymond P. Glahn, Cornell University*	
2 p.m.	Total dietary fiber content of dry bean, dry pea, chickpea, and lentil cultivars using the Integrated Dietary Fiber Assay (AOAC 2011.25) *Mark A. Brick, Colorado State University*	
2:15 p.m.	Evaluation of Genotype-by-Environment Interactions for Agronomic, Cooking Time, and Nutritional Quality Traits in Common Bean Accessions Grown On-farm in Uganda *Dennis Katuuramu, Michigan State University*	
2:30 p.m.	**Break and Poster Reception: Featuring Even Numbered Posters**	**Lincoln**
	International/Diversity – Moderator Susan Nchimbi Msolla, Sokoine University	**Big Ten C**
4 p.m.	Bean improvement in the Eastern Africa bean corridors: Challenges and Opportunities *Clare Mukankusi, International Center for Tropical Agriculture (CIAT) Uganda*	
4:15 p.m.	Genetic Diversity of the Guatemalan Climbing Bean Collections *Maria Gabriela Tobar Pinon, North Dakota State University*	
4:30 p.m.	Identification of virus infecting cultivated and wild Phaseolus in the Central-West Region of Mexico *Elizabeth Chiquito-Almanza, Jorge Acosta, National Institute of Forestry, Agriculture and Livestock Research*	
4:45 p.m.	Spatial and Temporal Scales of Range Expansion in Wild Phaseolus vulgaris *Paul Gepts, UC Davis*	
5 p.m.	**Business Meeting**	**Big Ten C**
6 p.m.	**Bean Improvement Cooperative Award Banquet**	**Huntington Club at MSU Stadium**

November 1, 2017

7 a.m.	**Continental Breakfast**	**Lincoln Lobby**
8 a.m.	W3150 Business Meeting	**Room 106**
10 a.m.	**Break**	**Lincoln Lobby**
10:30 a.m.	Phaseolus Crop Advisory Committee Meeting	**Room 106**
11:30 a.m.	BIC Genetics Committee Meeting	
12 p.m.	BIC Meeting Concludes	

Additional November 1, 2017 Opportunities

Legume Tour Frankenmuth Michigan

10:30 a.m.	**Board Bus**	**Hotel Lobby**
12 p.m.	Lunch—Saginaw Valley Research and Extension Center	
1 p.m.	Tour: • Saginaw Valley Research & Extension Center • Everbest Organics	
5:30 p.m.	Bus Returns from Frankenmuth	

7th International Legume Root Diseases Workshop

7 a.m.	**Continental Breakfast**	**Lincoln Lobby**
8 a.m.	Introduction and Session 1	Lincoln
10 a.m.	**Break**	**Lincoln Lobby**
10:30 a.m.	Sessions 2 and 3	Lincoln
12:30 p.m.	**Lunch**	**Brody Café**
2 p.m.	Breakout Sessions	Lincoln Room 106
3:45 p.m.	**Break**	**Lincoln Lobby**
4:15 p.m.	Summary and Conclusions	Lincoln

Oral Presentation Abstracts

Opening Presentations

New Plant Phenotyping and Analytics Platforms for Improved Grain Legumes

Kramer DM[1], Kamfwa K[2], Kuhlgert S[1], TerAvest D[1], Weebadde P[3], Hoh D[1], Osei-Bonsu I[1,4], Onziga ID[4,5]; Kanazawa A[1], Tessmer O[1], Savage L[1], Cruz JA[1], Zatzke C[1], Kelly J[6]*

[1]Department of Biochemistry and Molecular Biology and MSU-DOE Plant Research Lab, Michigan State University; [2]University of Zambia; [3]PhotosynQ LLC; [4]CSIR-Crops Research Institute, Ghana, [5]National Crop Resources Research Institute, Namulonge, Uganda; [6]Plant Soil and Microbial Sciences, Michigan State University

It is estimated that to feed the projected 9.1 billion people by 2050, we will need to increase food production by 70% worldwide *and by a staggering 200% in developing countries*. Meeting these needs will require unprecedented rates of improvements of crops and crop production. Unfortunately, many of the cutting-edge tools for crop improvement tools are expensive, time consuming, difficult to use, and thus have not been fully implemented for the diverse or specialty crops and smaller farms. Consequently, the vast majority of regions and markets urgently need innovative approaches to accelerating crop improvement. The presentation will describe new enabling technologies designed to overcome these limitations by dramatically lower the barriers to access for scientific tools, data and analytics, thus enabling a broader use of the promising, cutting edge crop improvements approaches. The technologies include: PhotosynQ.org - Community -driven plant phenotyping platform and data analyses platform for agriculture; MultispeQ – A PhotosynQ-enabled tool for field phenotyping; and Dynamic Environmental Phenotype Imager (DEPI)- A platform for high-throughput plant phenotyping under simulated environmental conditions. I will describe how the integration of sophisticated, yet inexpensive and easy to use, phenotyping tools and cloud-based analytics can accelerate the mapping of genetic loci that can guide the breeding of elite varieties. I will also describe how the ability to measure many related phenotypes allows for the basic understanding of the processes that allow some varieties to outperform others. To illustrate these capabilities, I will describe several ongoing projects using these platforms to improve common bean varieties by developing location-, environment- and management-specific common beans in Zambia, Uganda, USA and other locations. Finally, I will describe our vision for the future of these platforms, for assessing soil and other environmental properties, early predictions of yield, disease nutrient deficiencies etc., and how researchers in the audience can contribute and benefit.

Notes

Advances in Abiotic and Biotic Research of Common Bean Including New Tools and Strategies

Beebe S[1], Rao I[2], Polania J[1], Barrera S[1], Cajiao C[1], Rivera M[1]*

[1]CIAT, International Center for Tropical Agriculture,A.A. 67-13, Cali, Colombia (s.beebe@cgiar.org) [2]Peoria, Illinois, USA

Common bean (*Phaseolus vulgaris* L.) is especially sensitive to abiotic stress of high temperatures, drought, and edaphic constraints. Much of this sensitivity is expressed in the wild ancestor which is likely the source of these defects. Sister species of common bean evolved for adaptation to environments where abiotic stress was prevalent, and thus express tolerance to some of these factors. *P. coccineus* tends to partition more biomass to roots, and thus has genes for root vigor and tolerance to edaphic constraints. however, its progeny may show less tendency to convert fully to a reproductive phase, and thus may partition less to pods and grain. Tepary bean (*P. acutifolius*) on the other hand evolved in a semi-arid environment in which rapid seed development was necessary for survival. Tepary bean and its close relative, *P. parvifolius*, may have genes for superior partitioning to grain, which may result in better grain yield. Crosses with tepary bean may be facilitated by bridging genotypes that are cross fertile with both tepary and common bean. This would open many options to access genes for heat and drought tolerance, disease resistance, and possibly insect resistance.

Notes

Oral Presentation Abstracts

Abiotic

Analysis of the OAC-Rex Genome Reveals the Location of Interspecific Introgression from Wild Tepary Bean (*Phaseolus acutifolius*)

Perry GE[1], Munholland S[2], Reinprecht Y[1], Dinatale C[2], Diaz-Castro E[1], Xie W[1], Morneau E[1], Crosby W[2], Pauls KP[1]*

[1]University of Guelph, Department of Plant Agriculture [2]University of Windsor, Department of Biology

The navy bean variety, OAC-Rex, was the first common bacterial blight-resistant cultivar released in North America. The disease is endemic in all regions where beans are grown, and can cause significant yield loss in infected plants. The disease is caused by the pathogen *Xanthomonas axonopodis* pv. *phaseoli* and *X. fuscan* subsp. *fuscans, and as there is limited resistance found in Phaseolus vulgaris, an interspecific hybridization between P. vulgaris and Phaseolus acutifolius was used to bring over strong resistance into common dry bean. Our previous work to sequencethe OAC-Rex genome (Perry et al., 2013) and partially sequence the genome of P. acutifolius* accession PI440795*, gave us the opportunity to determine the locations and sizes of P. acutifolius-derived DNA intogressed into OAC Rex.* Using a pseudochromosome-level assembly of the OAC-Rex genome, combined with the previously released sequences for the *P. vulgaris* lines G19833, and Bat93, along with a contig-level assembly of *P. acutifolius* accession PI440795, we identified a total of 1.4Mb that was uniquely shared between OAC-Rex and PI440795, distributed over all 11 chromosomes. Although the majority of these sequences were from non-coding regions, a total of 114 fragments were found to fall within annotated genes, and 97 of these were found to have identifiable gene ontologies. When these regions were mapped back onto the OAC-Rex pseudochromosomes, 4 sequences were discovered to reside within the major CBB-resistance QTL on chromosome 8; including a 1Kbp fragment located in a previously identified polymorphism in a NiemannPick-like gene, which is conserved between OAC-Rex and PI440795 but is different from those seen in G19833 and Bat93. This type of fragment analysis provides a rapid means for identifying potential regions of introgression from *P. acutifolius* into *P. vulgaris*. Additionally, the identification of unique genic and intergenic regions that are common to the two species can help to pinpoint important genes that may have agronomic value in cultivated beans.

Notes

Transcriptome Analysis of Common Bean (*Phaseolus vulgaris* L.) under Elevated Temperatures

Soltani A[1], Weraduwage SM[2], Porch T[3], Sharkey TD[2,4,5], Lowry D[1,5]

[1] Michigan State University, Department of Plant Biology, East Lansing, MI. [2] Michigan State University, MSU-DOE Plant Research Laboratory, East Lansing, MI. [3] United States Department of Agriculture, Mayaguez, PR. [4] Department of Biochemistry and Molecular Biology, East Lansing, MI. [5] Plant Resilience Institute, East Lansing, MI.

Heat is one the most important abiotic stresses that impacts crop production worldwide. With global climate change, heat will lead to greater crop losses in the 21st-century. Elevated temperature adversely affects several physiological pathways that ultimately results in reduced yields. Dry bean (*Phaseolus vulgaris* L.) is particularly susceptible to heat stress. Establishing a better understanding of the dynamic responses of this important crop to heat stress will facilitate the development of new varieties with improved tolerance to elevated temperatures. Three genotypes from the kidney market class, including Sacramento, Redhawk, and NY-105, were grown under control (29/20℃) and heat stress (32/25℃) conditions. Eight replicates from each genotype were subjected to each treatment condition. We analyzed gene expression by fitting linear models with the program EdgeR. In addition to gene expression, we quantified photosynthetic parameters with a LI-COR 6800 and MultiSpeQ. The number of stomata were counted on the abaxial and adaxial leaf surfaces, while leaf area, chlorophyll content, nutrient content, and seed set were quantified on all plants. We observed that seed set rate under heat stress was the highest in Sacramento (24.6 ± 18.4) and lowest in Redhawk (0.0). Sacramento possessed the highest number of stomata per leaf area (186.4 ± 16.2), compared with NY-105 (158.6 ± 13.0) and Redhawk (150.2 ± 9.9). Stomatal conductance was higher in Sacramento and NY-105 under heat conditions. However, the most susceptible genotype (Redhawk) did not exhibit this stomatal response. We also performed mRNA-seq analysis on the samples and a drastic change in gene expression was observed in plants under elevated temperature. Interestingly, the most tolerant genotype, Sacramento, has a distinct expression profile in both treatment conditions. The results of this study will help illuminate the physiological responses of common bean to elevated temperatures and will facilitate the development of new heat tolerant varieties.

Notes

Effects of High Night Temperature Stress on Reproductive Structures of Lima Bean (*Phaseolus lunatus)*

Ernest EG, Wisser RJ, Johnson GC*

Department of Plant and Soil Sciences, University of Delaware (emmalea@udel.edu)

Heat stress reduces yields of May and early June-planted lima bean (*Phaseolus lunatus*) in the Mid-Atlantic Region of the US. High night temperatures during flowering and seed development can reduce or delay pod set, resulting in delayed harvest, lower yield and split pod sets. Breeding heat tolerant baby and Fordhook type lima beans is one 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 in order 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.

In more recent experiments, heat sensitive genotypes exhibited a number of physiological changes while under heat stress, some of which may 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. Ovule number was not affected by heat stress, indicating that some aspects of reproduction are not affected in heat sensitive genotypes. Other aspects of reproduction, such as stigma receptivity, may be problematic in some heat sensitive genotypes, but not others. As evidence, in one heat sensitive genotype grown under heat stress conditions, mature seed was obtained in 40% of flowers hand pollinated with pollen from a heat tolerant genotype that had been grown in ideal conditions. Only 3% of self-pollinated flowers on the same heat stressed plants produced mature seed. In a different, more heat sensitive genotype, mature seed was produced in only 10% of similar hand pollinations, compared to no mature seed from self-pollinated flowers.

Vegetative growth was not reduced by high night temperatures. Plants grown under stressed and unstressed conditions produced similar shoot dry weights. Heat sensitive plants produce more leaves and stems under high temperature conditions, compensating for the reduction in seed weight.

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.

Notes

Oral Presentation Abstracts

Biotic

QTL Mapping for Seed Weight and Resistance to *Acanthoscelides obtectus* in Common Bean

Kamfwa K[1], Beaver JS[2], Kelly JD[3], and Cichy KA[4]*

[1]Dep. of Plant Sciences, University of Zambia, Lusaka, Zambia (kelvinkamfwa@gmail.com) [2]Department of Department of Agro-Environmental Sci., University of Puerto Rico, P.O Box 9000, Mayagüez, Puerto Rico 00681. [3]Dep. of Plant, Soil and Microbial Sciences, Michigan State Univ., 1066 Bogue St., East Lansing, MI 48824. [4]USDA–ARS, Sugar beet and Bean Research Unit, Michigan State Univ., 1066 Bogue St., East Lansing, MI 48824.

The common bean weevil, *Acanthoscelides obtectus*, is an important post-harvest pest. To expand the current knowledge of resistance to *A. obtectus*, QTL analysis was conducted using a mapping population of 210 $F_{4:5}$ recombinant inbred lines derived from a cross of AO-1012-29-3-3A and Solwezi, which are resistant and susceptible, respectively, to *A. obtectus*. This population was genotyped with 5300 SNP markers, and evaluated for seed weight and resistance to *A. obtectus*. A total of five QTL for seed weight were identified on Pv04, Pv05, Pv07, and Pv10. Two QTL for resistance to *A. obtectus* were identified on Pv04 and Pv10. The QTL for resistance to *A. obtectus* on Pv04 was previously reported as the APA locus whereas the resistance QTL on Pv10 is new. The QTL for resistance to *A. obtectus* on Pv04 co-localized with the QTL for seed weight. Once markers linked to the identified QTL for resistance are validated, they could potentially be used in marker-assisted breeding to accelerate development of common bean varieties resistance with to *A. obtectus.*

Notes

A Repeatable Protocol for Fusarium Root Rot Phenotyping of Common Bean

*Zitnick-Anderson K[1], Modderman C[1], Hanson LE[2], and Pasche JS[1]**

[1]North Dakota State University, Department of Plant Pathology (Julie.Pasche@NDSU.edu) [2]USDA-ARS, East Lansing, MI

Pathogens within the *Fusarium solani* species complex (FSSC) cause root rot on common bean worldwide. Infection of root tissue by these pathogens results in destruction of the vascular system, reducing seed yield. While integrating cultural management practices including crop rotation, planting high-quality seed and cultivation can reduce severity of Fusarium root rot, the most effective method of managing the disease is incorporating resistance. A crucial step in developing resistant varieties is a repeatable protocol to screen for pathogen resistance under controlled conditions. However, phenotyping for Fusarium root rot often results in a lack of adequate disease pressure and inconsistent results. A protocol was developed utilizing a watering regime that allowed for the soil matric potential to decrease until just above wilting point before soil was saturated to field capacity. Temperature and humidity were tightly regulated in a walk-in growth room throughout the experiment. Five genotypes were evaluated using five plants per replicate and three replicates per trial. The inoculation experiment was repeated four times. When the hypocotyl arch broke the soil surface, soil was saturated to field capacity and five mL of a macroconidial suspension consisting of nine FSSC isolates pathogenic on common bean was dispensed directly to the base of each plant added within 30 minutes of watering. Plants were rated for symptoms of root rot 14 days after inoculation on a 1 to 9 scale, where 1 represents no disease. Ratings were transformed into a disease severity index (DSI). Results indicate the DSI from each of five genotypes evaluated over 4 trials could be combined based on Levene's test for homogeneity of variance. Additionally, across the four trials, a consistent rank from susceptible to resistant was observed for three of five control genotypes. VAX3 was consistently the most resistant genotype with an average DSI of 16%. Percent DSI for the two genotypes exhibiting interchanged rankings, Talon and Dynasty, was not significantly different in any of the trials. These two genotypes were considered intermediate based on mean DSI of 28% across the four trials. Cabernet was more susceptible than these two with a mean DSI of 38%, and Montcalm was consistently most susceptible to Fusarium root rot, with a mean DSI of 50%. This protocol for consistent, repeatable phenotyping will pave the way to identify reliable sources of resistance to Fusarium root rot.

Notes

Characterization of Common Bean Landrace Beti-10 for Angular Leaf Spot Disease Resistance in Tanzania

Chilagane LA[1], Msolla SN[1], Kusolwa PM[1]*

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Angular leaf spot (ALS) is an important disease of common bean in Tanzania. For durable resistance there is a need to pyramid genes for resistance from diverse backgrounds. This work aims at characterizing ALS resistance in the Tanzanian landrace Beti-10. Crosses were made between Kablanketi (Susceptible) vs Beti-10 (Resistant) and Beti-10 vs Mexico 54 and their reciprocals and their F_2 used for studies of inheritance and allelic relationship. F_2's segregation results for Kablanketi/Beti-10 (χ^2 = 0.061, *P* = 0.806) and Beti-10/Kablanketi (χ^2 = 3.776, *P* = 0.052) indicate that single dominant gene controls resistance to ALS in Beti-10 and no maternal influence to was observed. F2 segregation in Beti-10 vs Mexico 54 cross shows that, the genes responsible for ALS disease resistance in these genotypes are different. This study opens room for Beti-10 landrace in addition to Mexico 54 to be used for breeding against ALS disease in Tanzania.

ALS Pathotype Specificity in Common Bean – Genome-wide Association Studies and Application in Breeding for Disease Resistant Cultivars

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[1] ETH Zürich, Switzerland, Molecular Plant Breeding (michelle.nay@usys.ethz.ch)

[2] CIAT Cali, Colombia, Bean Program

The common bean disease Angular Leaf Spot (ALS) causes high yield losses in the tropics and subtropics. ALS resistant cultivars are available, but due to the high diversity of the pathogen, efficient and durable resistance is difficult to achieve.

To study ALS pathotype specificity, a panel of 321 common bean lines was evaluated with single isolates of the pathogen in the greenhouse and with mixes of isolates on field sites in Colombia. The lines of the panel were genotyped-by-sequencing and genome-wide association studies (GWAS) were conducted to find resistance loci. Preliminary results suggest a major locus at the end of chromosome eight, which coincides with the mapping interval of the characterized resistance locus Phg-2. This locus also played a major role in ALS resistance of bean pods in one field trial. SNPs associated with ALS resistance will be tagged by molecular marker for use in marker-assisted selection in breeding programs.

Notes

Rust-Proofing Dry Edible Beans in North Dakota

Monclova C[1], Markell SG[1], Osorno JM[2], Acevedo M[3] and Pasche JS[1]*

[1] North Dakota State University Department of Plant Pathology (Cecilia.monclovasant@ndsu.edu) [2] Department of Plant Sciences, North Dakota State University [3] Cornell University, Department of International Programs

Dry bean rust caused by *Uromyces appendiculatus* is primarily controlled using genetic resistance, but the pathogen has overcome many utilized resistance genes. Race identification using the standard differential set indicated 90% of the 70 *U. appendiculatus* isolates collected in North Dakota during 2015 and 2016 were race 20-3, reported for the first time in the state in 2008. This race is virulent on resistant genes *Ur-3, Ur-6,* and *Ur-7*. The 20-3 virulence phenotype expressed on PC-50 (*Ur-9, Ur-12*), Early Gallatin (*Ur-4*) and Mexico 235 (*Ur-3+*) ranged from hypersensitive to small-intermediate pustule sizes (0.2 to 0.4mm), suggesting greater diversity in the pathogen population than is reported in current 20-3 race nomenclature. Some breeding lines belonging to the pinto (~20%), black (~40%), navy (~10%), and kidney (~40%) market classes were identified as resistant to hypersensitive virulence phenotype of race 20-3. Genetic evaluation of the pathogen population is currently underway.

Waterlogging and Root Rots: The Value of Phaseolus Genetic Diversity for Combined Stress Tolerance

Mosquera GM, Cotes CA, Arredondo VE, and Beebe SE*
International Center for Tropical Agriculture (CIAT), Agrobiodiversity Research Area. (g.m.mosquera@cgiar.org)

Climate change is an important factor that is affecting production and distribution of beans affecting directly plant development and also indirectly by influencing changes in disease patterns. By 2020, an increase in precipitation would be expected in many African countries, and under these conditions root rot diseases will be favored. In order to address these limitations, it is necessary to use new genetic variants that could be used by breeding programs to develop better varieties resilient to climate change. Wild bean relatives are a useful resource that must be explored more extensively, since they harbor genes important for bean adaptation to diverse environments, and can be used to improve cultivated beans with superior performance against abiotic and biotic stress.

We are reporting results obtained from phenotyping a set of 100 accessions from *Phaseolus vulgaris*, 40 *Phaseolus coccineus*, 10 *Phaseolus dumosus*, 15 *Phaseolus costaricensis* and one *Phaseolus albescens*, to find waterlogging tolerance and Pythium resistance. These accessions were inoculated under greenhouse conditions with one strain of *Pythium myriotylum*, either in combination to waterlogging or Pythium under normal soil moisture.

We were able to identify several *Phaseolus* accessions that showed to be resistant to *P. myriotylum* and waterlogging. Accessions with combined resistance to both limitations were used in crosses with two bean genotypes developed by CIAT breeding program, SMR 138 and BFS 142, which have good agronomic characteristics. Populations are being advanced in order to transfer the resistant into elite lines to obtain better varieties.

Notes

Development and Characterization of an Infectious cDNA Clone of *Bean Common Mosaic Virus*

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A full-length cDNA clone of *Bean common mosaic virus* (BCMV) isolate RU1-OR was assembled in a pUC-derived plasmid; it was subsequently cloned into a binary vector and stabilized in *Agrobacterium tumefaciens*. This RU1-OR cDNA clone was tested for infectivity in *Nicotiana benthamiana* and *Phaseolus vulgaris* following agro-inoculation. The clone was found infectious in *N. benthamiana* producing asymptomatic systemic infection, and in common bean expressing symptoms similar to the wild-type RU1-OR isolate. This BCMV-RU1 clone replicated in *N. benthamiana* and in common bean at the same level as the wild type RU1-OR control, and was easily detected by ELISA and RT-PCR in upper, uninoculated leaves. Infectivity in common bean is under investigation.

Virulence Diversity of *Colletotrichum lindemuthianum* in Guatemala and GWAS to Identify Genomic Regions Associated with Anthracnose Resistance in Common Bean

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Anthracnose, caused by *Colletotrichum lindemuthianum* (Sacc. and Magnus) Briosi and Cavara is a fungal disease that affects dry bean worldwide. Seed yield loses sometimes reach 100% when the seed is infected and conditions favor the disease. The breeding program of ICTA in Guatemala has a germplasm collection of climbing beans from the highland regions. Climbing beans in Guatemala represent the main source of protein for the habitants of this region (9.4 kg/ person/year). However, climbing beans are significantly affected by anthracnose and there is no knowledge about the races present in the region. Using the set of differential lines, a race characterization of samples collected in Guatemalan Highlands was made and 6 races were found: 556, 585, 897, 1609, 1993, and 3981, also, resistance to anthracnose for race 73 from North Dakota was evaluated, which is one of the most predominant races in the U.S. Approximately 10% of 369 climbing bean accessions showed no symptoms (score of 1). GWAS results using 78754 SNP markers indicated that genomic regions for resistance to *C. lindemuthianum* exist in Pv07.

Notes

Oral Presentation Abstracts

Agronomics/Fertility

Symbiotic Nitrogen Fixation in the Mesoamerican Genepool of Common Bean (*Phaseolus vulgaris* L.)

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The 300 genotype Mesoamerican Diversity Panel (MDP) and 20 AAFC-UofG Mesoamerican cultivars were grown at three low-nitrogen field sites in Ontario and Puerto Rico from 2014-2016. Various agronomic and symbiotic nitrogen fixation (SNF)-related parameters were measured in the field and post-harvest (including: yield, days to flowering and maturity, leaf chlorophyll content, nodule size and number). Nitrogen fixing capacity, quantified by calculating percent nitrogen derived from the atmosphere (%Ndfa), was assessed by analyzing nitrogen content in the seed using gas-chromatography mass-spectrometry. SNP genotyping was used to identify SNPs in 284 genotypes and a Genome Wide Association (GWA) analysis was performed to identify genomic regions associated with Symbiotic Nitrogen Fixation (SNF) in bean.

Genetic Diversity and Association Studies of Nitrogen Fixation in Common Bean Under Low Nitrogen Field Conditions

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Common beans are generally considered poor nitrogen fixers. Optimization breeding technology related to genetic improvement in symbiotic nitrogen fixation (SNF) is investigated using marker-trait association study. We have genotyped a population of 129 Canadian germplasm entries using BARCBean6K_3 array. The population has been planted in low nitrogen soil at London RDC in summer 2016 and 2017. Population structure analysis classified the population into Mesoamerican and Andean clusters and grouped with the expected standard genotypes. The Mesoamerican group showed higher nitrogen fixation than the Andean group. The highest nitrogen fixer was SVM_Taylor_Hort, Montecarlo_15059, and Seafarer. Association mapping analysis identified two loci that are associated with 15N content in seeds.

Notes

Genome-Wide Association Study for Some Agronomic Traits in Common Andean Bean

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Common bean breeding program at CIAT aims to develop improved beans that show resilience under adverse growing conditions. For this, it seeks to combine improved agronomic and seed traits by using gene discovery and marker assisted selection. However, the genetic basis underlying many of these traits is not completely understood. A genome-wide association study for four agronomic traits was conducted using 400 individuals from CIAT's elite Andean bean breeding panel. We used data from 8 previous breeding trials conducted yearly from 2013 to 2016 in two different locations under different irrigation managements. These lines were genotyped with 7729 SNP markers obtained from GBS data. Some QTLs for days to flowering and days to physiological maturity were found on chromosomes Pv01 and Pv11. In addition, some markers associated to yield were found on Pv07. Future work includes the validation of associated markers and the search for candidate genes to incorporate these results as a bean breeding genomic resource.

Genetic Architecture of Photosynthate Allocation and Remobilization in Pods of Common Bean (*Phaseolus vulgaris* L.) Under Drought Stress

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Common bean, the most important staple legume crop, is commonly affected by drought, reducing its productivity and seed quality. Photosynthate remobilization is one of the main mechanisms of drought tolerance and overall productivity. We evaluated a recombinant inbred population of the cross of ICA Bunsi and SXB 405, from the Mesoamerican genepool, to evaluate the effects on drought on its productivity and its components, as related to photosynthate remobilization. The population was grown for two years, under irrigated, terminal and intermittent drought in the first year, and irrigated and terminal drought in the second year.

We studied the pod harvest index (PHI), the partition of seed biomass to the whole pod biomass, its components, and phenology. There was a significant effect on the water regime and year effect on all the traits, at both the phenotypic and the QTL level. We found several QTLs for pod harvest index, including a major stable QTL in Pv07. Although the QTLs for yield were not stable across water/regime combinations, we detected 3 on the overall mean. We also found substantial epistasis evidence, explaining a considerable part of the variation for yield and PHI. The components of PHI co-localized differently, in some QTLs the variation was driven by either the pod wall, seed mass, or both. We found 8 QTLs for yield, 3 of which co-localized with PHI QTLs, underlying the importance of photosynthate remobilization in productivity.

Notes

Using High Temperatures to Assist in Screening *Phaseolus* spp.

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Heat stress negatively impacts the yield of common beans (*Phaseolus vulgaris* L.) and prevents their cultivation in certain areas. Furthermore, under field conditions, heat stress often coincides with and exacerbates the effects of drought stress. This research examined a variety of methods for screening large numbers of bean germplasm exposed to heat stress, using tepary bean (*Phaseolus acutifolius* A. Gray) as a stress tolerant check. Bean plants exposed to temperatures of 45 °C for two days showed signs of heat stress as measured by gas exchange, chlorophyll fluorescence, oxidative stress, and visual ratings. Gradually raising temperature was useful for screening a large group of germplasm for heat tolerance, but this heat tolerance only partially related to drought tolerance observed in the field. Plant breeders can utilize some of the methods described here to supplement field data and further characterize the stress tolerance of later generation bean lines.

Notes

Field Screening and Selection of Common Bean Carioca Seeded Progenies with Multiple Resistance to BCMNV, BGMV and CPMMV

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Common bean (*Phaseolus vulgaris* L.) is among the most consumed legume crops in the world, mainly because of its social and economic importance as well as its high nutritional value. Brazil is the world's largest producer and consumer country of common bean. Approximately 70% of beans consumed by Brazilians come from the carioca market class (light beige seeds with light brown stripes, nearly full elliptical shape, opaque, not shiny), making it the most popular commercial class in Brazil, although it has very restricted consumption in other countries. Despite the genetic progress obtained in the last decades, in average, the common bean crop still present a seed yield below its yield potential in Brazil. One of the factors that compromise the yield performance and reduce the commercial quality of seeds is its susceptibility to a large number of diseases. Among these diseases, viruses caused by *Bean common mosaic necrosis virus* (BCMNV), *Bean golden mosaic virus* (BGMV) and *Cowpea mild mottle virus* (CPMMV) are major concerns, mainly in Central Brazil. Seed yield losses ranging from 40 to 100% are being reported, depending on the rate of occurrence, time of sowing, time of plant infection, and cultivar choice. The main goal of the present work was to evaluate common bean elite progenies from the carioca market class in the field and select those with multiple resistance to BCMNV, BGMV and CPMMV. Two field nurseries were carried out at Embrapa Rice and Beans (Santo Antonio de Goias, GO, Brazil) during the rainy growing season of 2016 and the dry growing season of 2017. Thirty-nine elite progenies were evaluated, all harboring the transgenic event Embrapa 5.1 which confers resistance to BGMV, as well as three carioca seeded control cultivars (BRS Estilo, BRS FC402 and BRS FC401 RMD). Of these 39 progenies, 10 derived from the cross BRS Estilo × CNFCT 16206, on generations BC4F4:6 and BC3F5:7, and 29 from the cross BRS Sublime × BC3F1 (BRS Estilo × CNFCT 16206), on generations F3:6 and F4:6. Both nurseries were carried out in a randomized block design with three replicates, using the regular technologies recommended for the crop but without control of diseases and pests. The plots consisted of four 4.0-meter rows with 0.5 m between rows. The scoring scale used to evaluate virus severity ranged from 1 (absence of disease symptoms and signs of pathogens) to 9 (80-100% disease severity or plant death). Individual and combined variance analyses ($p < 0.01$) were performed using the F test. The comparison of means were accomplished by the Scott-Knott method ($p < 0.05$). The combined analysis for disease severity showed variability between progenies, environments, and the presence of G × E interaction ($P \leq 0.01$). As expected, this differential response of the progenies to the environments is because of the highest natural pressure of viruses in the dry growing season. All progenies showed effective resistance to BCMNV and BGMV, exhibiting mean severity scores of 1.0, whereas the conventional controls were susceptible to BGMV, exhibiting mean severity score ≥ 6.0. It was not possible to evaluate the severity of CPMMV in the control cultivars since the symptoms were totally confused or hidden by the symptoms of BGMV. For this reason, the severity of CPMMV was evaluated only in elite progenies. Twelve progenies showed mean score for CPMMV severity ≤ 3.0 and, therefore, they were selected as resistant to BCMNV (gene *I*), BGMV (event Embrapa 5.1) and CPMMV (resistance gene(s) under characterization). Individual plants were selected from these 12 progenies to develop carioca seeded inbred lines homozygous for the resistance to the three viruses. This breeding step is being aided by marker-assisted selection and artificial inoculation. The resulting inbred lines will be further tested in final field trials for a wide agronomic performance evaluation.

Notes

Oral Presentation Abstracts

Quality

Little Beans, Big Opportunities: Leveraging the Power of Food Industry Collaboration to Promote Healthier Diets

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Food is changing. With consumers looking for clean-label, nutrient-dense, sustainable products and large food companies looking to differentiate products and brands in the face of disruptive competition from upstarts, the humble dry bean has become the new rising star of food ingredients. However, success in the marketplace depends on much more than merely developing a delicious, healthy product, and there are several challenges food makers must overcome to develop and launch successful bean ingredient-based products. This presentation will show a model of industry and research collaboration designed to meet these challenges and result in large-scale change to the food supply to have a positive impact on human health.

Sensory Characteristics of Andean Dry Beans

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Dry beans are a nutrient-rich food that often require long cooking times, particularly without prior soaking. They also display a range of sensory characteristics. Sensory quality includes important traits considered when consumers select dry beans and when food companies include beans in their products, but these traits have largely been overlooked by breeders. In order to increase consumption of dry beans and access to the associated nutritional benefits and to encourage the use of beans in new products, flavor must be addressed.

Using the Andean Diversity Panel (ADP), we have developed a protocol to assess sensory characteristics in dry beans. Mattson cookers were used to determine cooking time for each genotype, and these cooking times were used to prepare beans for sensory evaluation. A trained sensory panel determined flavor and texture profiles of each genotype using 5-point scales. A texture analyzer with a 2mm cylindrical probe determined work to bite for each genotype and to support the texture data obtained from the panel. Following a second year of data collection, association mapping of flavor profiles and texture will identify genomic regions influencing these traits. This information can enable breeders to target specific flavor and texture profiles in their programs, as well as allow agronomic traits of dry bean varieties to be improved without sacrificing desirable flavor.

Nutritional Profile and Consumer Acceptability of Fresh Pastas With Different

Notes

Bean Varieties as the Main Ingredient

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Dry beans are traditionally utilized in the whole form (boiled or canned). However, long cooking times deter most time-constrained families from preparing beans on a regular basis. Discovering new applications for the use of dry beans as the main ingredient in conveniently prepared foods will help to incorporate the dry bean back into the daily routines of house-hold consumers. The dry bean is a natural resource of key dietary nutrients such as protein and iron, which is ideal for modern day ingredient development. In this study, whole bean flour was formulated into single variety fresh pastas and compared nutritionally to their boiled bean counterparts. Consumer sensory evaluations of six single bean variety pastas (white kidney, navy, otebo, cranberry, dark red kidney and black) along with two wheat controls were also conducted. Dry bean pastas retained the nutritional profile of boiled whole seeds with respect to protein, starch as well as iron concentrations. They are also nutritionally superior to wheat pasta with higher protein, iron and resistant starch concentrations (bean: 22 %, 58 ppm, 3.2% vs. wheat: 16%, 35 ppm, 1.2%), as well as lower total starch content (44% vs. 68%). Resistant starch (a component of dietary fiber) increased in the bean pastas when compared to their boiled whole seed counterparts, potentially lowering the glycemic properties. Varietal and genotypic differences were observed between the different color types and textures of dry bean pastas. No significant differences were observed among the bean pastas for the attributes of appearance, aroma, flavor, texture and overall acceptability when evaluated by 100 consumer panelists. Based on nutritional and consumer evaluations, single variety dry bean pastas have commercial potential in the market place as healthy gluten free pasta options. Dry bean based ingredients also have to potential to boost the nutrition labels of new food products.

Notes

A Repeatable Protocol for Fusarium Root Rot Phenotyping of Common Bean

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Pathogens within the *Fusarium solani* species complex (FSSC) cause root rot on common bean worldwide. Infection of root tissue by these pathogens results in destruction of the vascular system, reducing seed yield. While integrating cultural management practices including crop rotation, planting high-quality seed and cultivation can reduce severity of Fusarium root rot, the most effective method of managing the disease is incorporating resistance. A crucial step in developing resistant varieties is a repeatable protocol to screen for pathogen resistance under controlled conditions. However, phenotyping for Fusarium root rot often results in a lack of adequate disease pressure and inconsistent results. A protocol was developed utilizing a watering regime that allowed for the soil matric potential to decrease until just above wilting point before soil was saturated to field capacity. Temperature and humidity were tightly regulated in a walk-in growth room throughout the experiment. Five genotypes were evaluated using five plants per replicate and three replicates per trial. The inoculation experiment was repeated four times. When the hypocotyl arch broke the soil surface, soil was saturated to field capacity and five mL of a macroconidial suspension consisting of nine FSSC isolates pathogenic on common bean was dispensed directly to the base of each plant added within 30 minutes of watering. Plants were rated for symptoms of root rot 14 days after inoculation on a 1 to 9 scale, where 1 represents no disease. Ratings were transformed into a disease severity index (DSI). Results indicate the DSI from each of five genotypes evaluated over 4 trials could be combined based on Levene's test for homogeneity of variance. Additionally, across the four trials, a consistent rank from susceptible to resistant was observed for three of five control genotypes. VAX3 was consistently the most resistant genotype with an average DSI of 16%. Percent DSI for the two genotypes exhibiting interchanged rankings, Talon and Dynasty, was not significantly different in any of the trials. These two genotypes were considered intermediate based on mean DSI of 28% across the four trials. Cabernet was more susceptible than these two with a mean DSI of 38%, and Montcalm was consistently most susceptible to Fusarium root rot, with a mean DSI of 50%. This protocol for consistent, repeatable phenotyping will pave the way to identify reliable sources of resistance to Fusarium root rot.

Notes

Genetic Characterization of the Non-Darkening Trait in Common Bean

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In order to prevent the occurrence of postharvest darkening, the non-darkening trait has been introgressed into pinto and cranberry beans. The objective of this study was to characterize the genetic basis of non-darkening trait in common bean. A population of 128 F_5-derived RILs, derived from a cross between Wit-rood and 1533-15, was characterized for seed phenotype and genotyped with an Illumina BeadChip. A genetic linkage map was constructed using 1314 informative SNPs plus the phenotypic data for non-darkening and slow darkening traits, a STS marker ($OL4S_{500}$) and a SSR marker (Pvsd-0028), previously associated with the J gene and Sd gene, respectively. The map consisted of 11 linkage groups and was 1277.7 cM large. A major QTL for the non -darkening trait was flanked by $OL4S_{500}$ and SNP ss715647913 on chromosome 10. The region, which spanned 8.7 cM, explained 50.3% of the phenotypic variation for seed coat darkening. Forty-four candidate genes were identified in the QTL interval. A library of amplicons was prepared from the candidate genes and resequenced using an Illumina MiSeq System. This presentation will discuss the results obtained from the amplicon sequencing and polymorphisms, potentially, associated with the non-darkening trait.

QTL Analysis of Cooking Time in an Andean Recombinant Inbred Line Population

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Dry beans (*Phaseolus vulgaris*) are an inexpensive and nutrient dense food high in protein, fiber, and vitamins. However, lengthy cooking times are required prior to consumption. Research into the environmental effects on cooking time in beans is abundant, but a dearth of information exists on the genetic causes behind cooking time differences. A recombinant inbred line (RIL) population was developed by crossing ADP0027 (PI146755) and ADP0037 (PI661767). ADP0037 cooks twice as fast, has a lower percentage of seed coat, and has a higher hydration capacity compared to ADP0027. The RIL population of 161 lines was grown in Arusha and Morogoro in Tanzania during the 2016 season. A range of cooking times (28-125 min), seed coat percentages (8-12%), and hydration capacities (17-57 g water/100 g seed) were observed in the population. In addition, a QTL analysis with 2427 SNP markers was performed and for cooking time from Morogoro were discovered on linkage groups Pv03, Pv09, and Pv10. From the Arusha location, QTL were discovered on linkage group 11 with the largest QTL being responsible for nearly 20% of the variation observed for cooking time.

Notes

Evaluating Specialty Succulent Lima Beans (*Phaseolus lunatus*) as Alternative Crops in Delaware

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Lima bean (*Phaseolus lunatus*) is the most widely grown vegetable crop in Delaware. Green seeded baby lima bean types predominate (over 95% of the crop). In addition, three specialty lima beans are also grown on limited acres: a speckled type, a light colored butterpea type, and a large seeded green Fordhook type. These specialty lima beans currently represent less than 5% of the lima beans grown in Delaware. The University of Delaware initiated a breeding program 12 years ago, focusing on green baby lima beans and green Fordhook types. In the breeding program, diverse lima bean germplasm is used for crosses and a wide variety colors, forms, and qualities result in the progeny. While the focus of the program is on green types, there is potential for developing and introducing new specialty types adapted to Delaware. We currently have a grant project seeking to identify and evaluate new specialty lima beans from the Delaware breeding program to be grown as succulent lima beans for freezing and canning. In addition, specific selections from US and international germplasm collections are being increased and evaluated.

Objectives of the project are:

- To evaluate specialty succulent types already developed as offshoots of the UD green baby lima breeding program in large strip trials in grower/ processor fields including an improved Jackson Wonder speckled type, a mixed green and speckled type, a white type, a red type as well as other promising types.
- To evaluate additional fixed breeding lines from the UD breeding program not previously evaluated and selected germplasm from USDA and other sources with potential as specialty limas in small plot field trials. Promising varieties will then go to grower/processor strip trials.
- To evaluate a collection of diverse lines maintained by the UD lima bean breading program for cooking and eating characteristics for use in further breeding of specialty limas. Types that are non-bleeding (that do not release soluble colors into the cooking water) are sought as well as those with desirable texture (that are not grainy or mealy) and taste (buttery, nutty, other positive flavors) for use in breeding new succulent specialty lima beans. This material, because of its diverse sources from germplasm collections, consists mainly of vining pole types. An offshoot of this objective would be the identification of pole lima types from this diverse material that could be grown as specialty lima beans by small farmers.
- To evaluate consumer acceptance of specialty succulent lima beans from the UD breeding program. A current limitation to the growth of the lima bean industry in Delaware, and the US as a whole, is overall demand. Quality characteristics of identified specialty succulent lima beans impacting consumer acceptance will be evaluated such as color bleeding, texture, and taste parameters using sensory and taste panels.

Notes

Bean purchasing preferences among low-income Hispanic and non-Hispanic women

Donna M. Winham, DrPH, RD, Food Science and Human Nutrition, Iowa State University, Ames IA

There is limited research on consumer purchasing preferences for dry or canned beans in the United States. This knowledge can be useful in directing crop improvements and seed characteristics that are of importance to consumers in general as well as niche markets.

Two similar face-to-face surveys were administered to low income women in Arizona in 2011, and in Iowa in 2016. The study purpose was to describe purchasing patterns, determine preferred characteristics of dry beans and canned beans, and assess attitudes and perceptions towards beans in the diet. Both groups of women were aged 18-65, and were eligible to participate in a Federal government assistance program such as the Expanded Food and Nutrition Education Program (EFNEP), the Special Supplemental Nutrition Program for Women and Children (WIC), or the Supplemental Nutrition Assistance Program (SNAP). The target audience was Hispanic and non-Hispanic white women. Participants completed survey on questions on Hispanic ethnicity, and the Bidimensional Acculturation Scale (BAS) that categorizes individuals by cultural affiliation as Hispanic-dominant, bicultural, or English-dominant. The English-dominant category included non-Hispanic white women too.

The participants in both studies shared similar characteristics in terms of age, number of children in household, income, and education. Hispanic-dominant women tended to have less education, more children, be in a relationship, and have greater food security regardless of income. Hispanic-dominant women consumed beans significantly more often than bicultural or English-dominant colleagues (p=.000). Almost 100% of the Hispanic-dominant women purchased dry beans. Preferred dry bean characteristics by percent mentioned for each state sample were: price, always buy this brand, quality, taste of beans, nutritional value, color of beans, cook quickly, brand, and shape (Iowa only). These characteristics by acculturation status were markedly different. Hispanic-dominant women in both Arizona and Iowa had similar rankings for the characteristics, but a higher percentage were interested in all of these traits, e.g. 43% concerned about price, but only 28% English-dominant interested in price. For the cook quickly trait, 25% (Iowa) and 21% (Arizona) of the respondents felts this was important. Twenty-eight percent of the Iowa Hispanic-dominant women were concerned about bean shape, but only 1% of the English-dominant women thought this was important.

The majority of Arizonans did not prefer to buy beans from a specific country (67%), but 29% preferred a Latin American country. The Iowa respondents were asked if they would like to buy dried beans from Iowa. Forty-percent said yes. Latina women in Arizona (32%) and Iowa (52%) bought canned beans less often than English-dominant women (81% Arizona; 70% Iowa).
English-dominant women in both states reported that dry beans take longer to prepare than their bicultural or Hispanic-dominant peers. Additional data on the responses to questions about difficulty of preparing foods with beans, and cultural affinity and beans will be presented.

In conclusion, significant differences in bean purchasing, preferences, and attitudes exist across low-income Hispanic and non-Hispanic white women. Identification of the barriers, attitudes, and current consumption patterns can elucidate ways to resolve these problems.

Notes

Oral Presentation Abstracts

Genomics

Investigating Differential Expression of Stress- Responsive Genes in the Same Common Bean (*Phaseolus vulgaris*) Genotype Grown in Two Different Locations (DE and NE)

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Common bean is an important food crop and it is consumed worldwide for its essential nutrients. Abiotic stress factors such as drought affect the growth and development of plants, and it is a major risk for common bean production and yield reduction. Our aim is to analyze epigenetic control of gene expression in common bean during drought in multiple locations. We cultivated the same genotype of common bean in Nebraska and Delaware within the same season. Each location had two different plots, fully irrigated rows and rows with irrigation ceasing once flowering began. Total RNA isolated from leaf, root, and pod tissue was used to synthesize cDNA. Differential expressions of stress responsive genes have been identified in drought-treated and control samples and between the two locations using reverse transcriptase PCR. Our findings provide a basis for future work in understanding genotypes that can best tolerate drought in different locations.

Integrated Transcriptomic and Epigenomic Approaches to Understanding Biotic and Abiotic Stresses in Common Bean

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We are interested in understanding biotic and abiotic stress tolerance in plants. Common bean is one of the important food legumes in the world due to the agricultural, economic, and health benefits it provides. However, biotic and abiotic factors affect the production of this crop causing significant yield loss. Our goal is to understand the epigenetic and epigenomic mechanisms involved in the regulation of biotic and abiotic stress responses in plants- since gene expression is controlled by a combination of epigenetic factors including small RNAs, DNA methylation, and histone modifications. We are interested in profiling a combination of these mechanisms to understand heat, drought, salinity, and plant biotic stress interactions. We present recent research from the DSU Molecular Genetics and Epigenomics Lab in the development and use of novel integrated transcriptomic and epigenetic profiling tools in several crop plants using common bean (*Phaseolus vulgaris* L.) as a model species.

Notes

Development of a Repeatable System for Bean Transformation and/or Gene Editing

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To obtain a reproducible transformation and genome editing protocol for common bean (Phaseolus vulgaris) we used *Agrobacterium tumefaciens* to introduce marker genes (GUS + hptII), and Cas9/sgRNA + hptII constructs targeting three genes (PDS, and stachiose and raffinose synthases) into cultivars Chauchachuga, Ica Quimbaya and Calima. The protocol developed was based on those reported for soybean. Transgenic shoots of Chauchachuga expressing the Gus gene in trichomes were visualized in vitro; eight seedlings were regenerated from them, from which two survived transfer to pots. Also, two plants of Ica Quimbaya showed PCR bands after amplification of the Gus gene. In terms of genes targeted with CRISPR/Cas9, two Ica Quimbaya regenerated plants, and three from cultivar Calima, were positive for the PCR-amplification of Cas9 and hygromycin. Currently several plants are being transferred to biosafety greenhouses to develop larger leaves for Southern blots and detect the number of genes inserted, and to advance to the next generation for cleaning potential chimerism of T0 plants. Our results indicated that a soybean-based protocol for transferring and/or editing genes in common beans may be feasible, though it requires further refinement for improving efficiency.

Fine Mapping of Genes Conferring Resistance to Rust and Anthracnose of Common Bean

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Current molecular markers linked to rust and anthracnose resistance genes in common bean often yield false positive and false negative results. In an effort to improve the effectiveness of the molecular markers linked to these genes, we are combining accurate phenotyping of these genes with specific races of the bean rust pathogen with the power of high-throughput genotyping using the SNP chip BARCBEAN6K_3, bulk segregant analysis, haplotype identification from resequenced bean lines, and customized SNP marker development (KASPs) to determine the precise physical location for each of the loci under study. Specifically, we have initiated the fine mapping of Andean *Ur-4* and Mesoamerican *Ur-3*, *Ur-5*, and *Ur-14* rust resistance genes. In addition, we are fine mapping Mesoamerican *Co-3[4]* and the recently discovered Andean *Co-AC* anthracnose resistance gene that confers broad resistance to highly virulent Mesoamerican races of the rust pathogen. Tightly linked markers are being validated on set of wide diverse common bean lines and cultivars. The markers developed through this approach will significantly reduce time and labor associated with the current phenotypic detection of these rust and anthracnose disease resistance genes.

Notes

Why Wax Beans Lack Carotenoids

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The yellow pod or wax bean trait (*y*) of snap beans was first described in the 19th century. It is among the genes used to construct the first pre-molecular marker linkage maps in common bean. In a map constructed in 1996 with RFLP markers using a wax bean by wild bean cross, *y* was mapped to the distal end of Pv02. We were able to refine the location of *y* using two biparental populations ('Unidor'/'OSU5630' and 'Serin'/'OSU5630') and through association mapping in the Bean CAP Snap Bean Diversity Panel (SBDP) that had been characterized for pod color and carotenoid levels. The data from these three sources all point to a relatively narrow region of Pv02 harboring the gene conditioning pod color. The interval bracketed by SNPs in this region contains approximately 43 gene models. Using RNA seq data to identify those genes with highest expression in flowers and pods, we found a pentatricopeptide repeat (PPR) protein to meet this criteria. PPR proteins are modular RNA-binding proteins that often control gene expression in organelles and in the null form may produce an albino phenotype. Data from the Bean CAP SBDP revealed that despite their pale yellow color, wax beans have the lowest levels of carotenoids. Our hypothesis is that a PPR protein targeted to pod chloroplasts is a defective version of *y* that interferes with chlorophyll synthesis and carotenoid accumulation.

Identification and Characterization of a Pectin Acetylesterase from the Seed Coat of Common Bean (*Phaseolus vulgaris*)

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Common bean is rich in dietary fibre, a major component of which is pectin present in the seed coat. Pectin is produced as an esterified polymer in the Golgi apparatus, which can be de-esterified after it is secreted. The enzyme pectin acetylesterase participates in this process. De-esterification can change the structural properties of the cell wall. Esterification decreases calcium binding and gelation of pectin. A gene designated *PAE1* was characterized which encodes a major pectin acetylesterase in the seed coat. This gene is differentially expressed at all stages of seed development between germplasm lines SARC1 and SMARC1N-PN1, with transcript levels higher in SMARC1N-PN1 by 5- to 16-fold according to microarray data. The transcript was found to accumulate specifically in the seed coat, and the difference in expression between genotypes was confirmed by quantitative RT-PCR. Protein accumulation was observed in seed coat extracts of SARC1 and SMARC1N-PN1 by Western blot, with levels higher in SMARC1N-PN1 by approximately 2-fold. Initial velocity of pectin acetylesterase in seed coat extracts was higher by approximately 3-fold in SMARC1N-PN1. The acetate content of purified pectin from seed coats was 2.8 fold higher in SARC1 than SMARC1N-PN1. The difference in pectin acetylesterase expression is associated with an insertion of 150 base pair insertion in the promoter of SARC1. SMARC1N-PN1 was found to have a decreased seed water uptake and germination as compared with SARC1, particularly in older seeds.

Notes

Oral Presentation Abstracts

Nutrition

Beneficial Effects of Common Bean on Adiposity and Lipid Metabolism

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In developed countries which are at the epicenter of the obesity pandemic, pulse crop consumption is well below recommended levels. In a recent systematic review and meta-analysis of 21 randomized controlled clinical trials, pulse consumption was associated with improved weight control and reduced adiposity, although the underlying mechanisms were a matter of speculation. Common bean (*Phaseolus vulgaris*, L.) is the most widely consumed pulse crop and was the focus of this investigation. Using outbred genetic models of dietary induced obesity resistance and of dietary induced obesity sensitivity in the rat, the impact of bean consumption was investigated on the efficiency with which consumed food was converted to body mass (food efficiency ratio), body fat accumulation, adipocyte morphometrics, and patterns of protein expression associated with lipid metabolism. Cooked whole bean as well as a commercially prepared cooked bean powders were evaluated. While bean consumption did not affect food efficiency ratio, bean reduced visceral adiposity and adipocyte size in both obesity sensitive and resistant rats. In liver, bean consumption increased carnitine palmitoyl transferase 1, which is the rate limiting step in long chain fatty acid oxidation and also resulted in lower levels of circulating triglycerides. Collectively, our results are consistent with the clinical finding that pulse consumption is anti-obesogenic and indicate that one mechanism by which cooked bean exerts its bioactivity is oxidation of long chain fatty acids.

Sustainable Iron Biofortification of Beans via Enhanced Iron Bioavailability; The USDA-ARS Approach to Improving Fe Nutrition from Beans and Bean Products

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For over 15 years, the common bean has been a crop officially targeted for enhancement of Fe content (ie. biofortification) and considered a vehicle for alleviating iron deficiency anemia, the leading nutritional deficiency worldwide. This biofortification approach (breeding for Fe content) assumes that increased density of Fe in the seed, leading to greater Fe content in the diet will have substantial net increase in Fe absorption and thus nutritional benefit. In recent years, in vitro and in vivo (animal and human efficacy) studies have demonstrated that increasing Fe density in beans can result in improved Fe nutrition; however, such effect could be limited in impact due to the seed coat polyphenolics and unsustainable increases in Fe content due to environmental interactions. Alternatively, research indicates that identifying varieties with enhanced Fe bioavailability could have greater and possibly more sustainable effect as Fe bioavailability in beans is linked to traits such as seed coat color and cooking time. For example, the figure below demonstrates sustainable increases in Fe bioavailability in certain varieties of yellow beans selected for fast cooking. These effects are significantly greater than increases already known to result in measurable nutritional benefits in human efficacy trials. This presentation will demonstrate the USDA-ARS approach of increasing Fe bioavailability, not merely content, to develop beans and other staple food crops that will enhance the nutritional quality of Fe in food systems and in food products. Research funded entirely by USDA-ARS.

Notes

Total Dietary Fiber Content of Dry Bean, Dry Pea, Chickpea, and Lentil Cultivars Using the Integrated Dietary Fiber Assay (AOAC 2011.25)

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The health benefits of dietary fiber (DF) in food crops have been well documented. However, the consumption of DF worldwide is lower than recommended, and the gap between actual consumption and recommended intake represents an unrecognized health risk. To better advocate for an increase in pulse consumption, the content of DF in pulse crops using the consensus definition is needed. Total dietary fiber was measured in 26 cultivars of dry bean, 11 cultivars of dry pea, 13 cultivars of lentil and 24 cultivars of chickpea, each grown in two locations, using the AOAC 2011.25 method. The total dietary fiber (TDF) content was among pulse crops was 25.5% for dry bean, 24.6% for dry pea, 20.1% for lentil, and 21.8% for chickpea. The TDF among cultivars ranged from 24.1 to 27.4% for dry bean, 20.1 to 30.6% for dry pea, 17.6 to 21.6% for lentil, and 15.8 to 25.8% among chickpea cultivars. Dietary fiber content in pulse crops varied significantly among cultivars while location of production had little effect. These results indicate that all four pulse crop have high TDF and genetic diversity should be adequate to improve DF in these pulse crops. Consumption of 2 to 3 servings per day of any of these pulse crops would eliminate the dietary fiber gap that exists today. This data will also contribute to update the content of dietary fiber in pulse crops using the consensus method AOAC 2011.25.

Notes

Evaluation of Genotype-by-Environment Interactions for Agronomic, Cooking Time, and Nutritional Quality Traits in Common Bean Accessions Grown On-farm in Uganda

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Common bean is an important source of protein and micronutrients and a target for iron biofortification programs. Biofortification has potential to address micronutrient malnutrition especially when plant based staples are widely grown and consumed. However, the efficacy of biofortified crops to address human malnutrition can further be improved by understanding the genotype x environment interaction for seed mineral concentration and ensuring high mineral bioavailability. Common bean genotypes with high iron and zinc concentrations, high iron bioavailability and fast cooking time phenotypes were identified through screening of the Andean Diversity Panel. A subset of 15 nutritionally superior genotypes were identified and evaluated in farmers' fields along with local check genotypes in a participatory variety selection for two field seasons (2015 and 2016). Nine farmer groups each comprised of about 30 farmers participated in the field research. The growers were from districts representing three agro-ecological zones in Uganda that are important for dry bean production and consumption. A majority of the farmers preferred genotypes with upright architecture, many and longer pods, had red mottled or yellow grain color, and were high yielding especially under hostile growth conditions of too little or too much water. Seed yield across locations over the two growing seasons ranged from 400 to 2,050 kg ha^{-1}. ADP0445 (Chijar) from Puerto Rico was the most productive across locations and seasons. For the post-harvest preference scores 80% of the farmers selected genotypes ADP0001 (Rozi Koko) and Chijar (both red mottled), and ADP0468 (PI527538) and ADP0512 (Ervilha) (both yellows) as the most desired accessions. Cooking time was relatively stable across locations and yellow colored genotypes ADP0521 (Cebo, Cela) and Ervilha generally cooked fastest. Based on the data from 2015 and 2016 field trials, common bean genotypes nutritionally superior to the local checks and exhibiting good adaptation to the Ugandan bean production conditions were identified.

Notes

Oral Presentation Abstracts

International/Diversity

Bean Improvement in the Eastern Africa Bean Corridors: Challenges and Opportunities

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The CIAT breeding program aims to develop elite lines with multiple traits responding to the complex production constraints and market demanded traits of bean clients (producers, consumers and processors) in Africa. The East Africa region is the highest bean producing region in Africa with three of the PABRA member countries (Ethiopia, Tanzania and Uganda) being among the leading global producers and are a highly prioritized commodity in this region. Red mottled beans, yellow beans and sugar beans are the most preferred types in these countries with the exception of Ethiopia and Madagascar where white beans rein. Other bean types are still grown though at lower levels. Bean breeding in PABRA has been organized to respond to clients' needs using the bean corridor approach. Four bean corridors are defined for seven East African countries; they include; EAREM (East Africa red mottled bean corridor; Kenya, Uganda, Rwanda), EAYEBEAN (East Africa yellow bean corridor; W Tanzania and Burundi), ETREBEAN (Ethiopia bean corridor), Madagascar bean corridor (Madagascar). Market driven breeding approaches promoted in the corridors and product profiles for each country developed. Capacity building is conducted in response to the identified priority of each corridor. Bean breeders are urged to work with untraditional partners (private sector) to help respond to the gaps in bean access. Positive results have been noted such as the inclusion of untraditional traits in breeding pipelines such as short cooking time, canning quality and Fe and Zn content that are demanded by the market in addition to resilience traits. Enhanced interest in beans as a commercial crop is leading to development of financial products such as crop insurance to respond to the private sector needs. Though the corridor approach offers great opportunities for breeders to reach more users as well as get feedback on their products and in so doing become more market driven, it requires tracking the cost and efficiency of breeding program as viable businesses. Modern data management and estimation of genetic gains are some of the areas being emphasized.

Notes

Genetic Diversity of the Guatemalan Climbing Bean Collections

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Common bean (*Phaseolus vulgaris* L.) is the most important legume crop for human consumption in the world. In Guatemala, it occupies 17.8% of the available production area. Beans are also the primary source of protein in the daily diet in the country, where 8 out of 10 native children of 5 years-old or younger suffer from chronic malnutrition, the highest level in Latin America. For this reason, food security plays a key role in the development of a healthy country. At this point, bean breeders are challenged to increase seed yield while maintaining seed quality and breeding for diseases resistance. Guatemalan climbing beans have been suggested to represent race Guatemala, a new race in the Middle American gene pool. Interestingly, these beans are grown in the highlands of Guatemala where poverty is the highest, and it may represent a source of new alleles for bean improvement. The objectives of this research were to evaluate and describe the population structure, genetic diversity, and genetic differentiation of two Guatemalan climbing bean collections of 369 and 260 accessions respectively. Also to perform a genome-wide association study (GWAS) to map important agronomic traits. 102,343 single nucleotide polymorphisms (SNPs) were used for the analysis. Population structure was analyzed using STRUCTURE 2.3.4, principal component analysis, and a maximum-likelihood tree. Genetic diversity was analyzed estimating the expected heterozygosity (H_e) and polymorphic information content (PIC). All population structure analyses showed that the Guatemalan collections are strongly differentiated when compared to races Mesoamerica and Durango-Jalisco. PIC and H_e showed that Guatemalan accessions were the most diverse. GWAS identified new loci associated with important traits such as rust (*Uromyces appendiculatus*) resistance and local adaptation. These results demonstrate that Race Guatemala is represented by Guatemalan climbing beans and is a potential source of alleles for breeding programs.

Notes

Identification of Virus Infecting Cultivated and Wild *Phaseolus* in the Central-West Region of Mexico

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During 2013/2015 leaf samples from wild *Phaseolus* spp (WB) and cultivated common bean *Phaseolus vulgaris* (CB) plants with and without symptoms of virus damage were collected in the Mexican states of Guanajuato, Jalisco and Nayarit. The aim was to identify the viruses infecting bean plants in this area of Mexico, as well as its distribution. Virus identification was performed by high throughput sequencing and assembly of total small RNAs (small RNA sequencing and assembly; sRSA). Total RNA from different CB and WB samples was used to construct 53 sRNA libraries: 26 from CB (*P. vulgaris*), and 27 from WB that included samples from *P. vulgaris*, *P. coccineus* and *P. leptostachyus*. In the libraries from CB we identified six virus species: *Bean common mosaic virus* (BCMV), *Bean common mosaic necrosis virus* (BCMNV), *Cowpea mild mottle virus* (CPMMV), *Phaseolus vulgaris endornavirus 1* (PvEV-1), *Phaseolus vulgaris endornavirus 2* (PvEV-2), and *Bean golden yellow mosaic virus* (BGYMV). Likewise, in the libraries of WB four virus were identified: BCMV, BCMNV, PvEV-1 y *Peanut mottle virus* (PeMoV). All identified viruses were confirmed by PCR or RT-PCR. While in all the libraries of CB the viral sequences were identified, only six libraries of WB presented these sequences. In total, nine complete genomes and 36 partial genomes of the identified viral species were reconstituted throughout alignment with a related virus genome. These sequences and the virus isolates will be useful for understanding viral genomic diversity and their biological characteristics. With the exception of BGYMV, all the virus species identified are seed borne. Due to controversies with respect to seed transmission of CPMMV, more studies are needed to assess the phytosanitary risk of this virus. BCMV and BCMNV represent high phytosanitary risk due to a high rate of transmissibility; whereas PvEV-1 and PvEV-2, considered non-pathogenic, and PeMoV with a transmissibility rate below 3%, represent low risk. The abundance of these viruses in cultivated beans suggests the absence of genetic resistance or varietal deterioration combined with the repeated use of grain as seed; thus, among other traits, new cultivars must include resistance against these viruses, along with production practices that enhance healthy and vigorous plant development and the control of vectors.

Notes

Spatial and Temporal Scales of Range Expansion in Wild *Phaseolus vulgaris*

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The wild progenitor of common-bean has an exceptionally large distribution from northern Mexico to northwestern Argentina, unusual among crop wild progenitors. This research sought to document major events of range expansion that led to this distribution and associated environmental changes. Through the use of genotyping-by-sequencing (~20,000 SNPs) and geographic information systems applied to a sample of 246 accessions of wild P. vulgaris, including 157 genotypes of the Mesoamerican, 77 of the southern Andean and 12 of the Northern Peru-Ecuador gene pools, we identified five geographically distinct subpopulations. Three of these subpopulations belong to the Mesoamerican gene pool (Northern and Central Mexico, Oaxaca, and Southern Mexico, Central America and northern South America) and one each to the Northern Peru-Ecuador (PhI) and the southern Andean gene pools. The five subpopulations showed distinct distributions for temperature and rainfall resulting in decreased local potential evapotranspiration (PhI and southern Andes groups) compared to the two Mexican groups. Three of these subpopulations represent long-distance dispersal events from Mesoamerica into northern Peru-Ecuador, southern Andes, and Central America and Colombia, in chronological order. Of particular note, is that the dispersal to Northern Peru-Ecuador markedly predates the dispersal to the southern Andes (~400 Ky vs. ~100 Ky), consistent with the ancestral nature of the phaseolin seed protein and chloroplast sequences observed in the PhI group. Seed dispersal in common bean can be, therefore, described at different spatial and temporal scales, from localized, annual seed shattering to long-distance, evolutionarily-rare migration. The temporal and spatial divergences of the PhI group, including the existence of ancestral versions of both phaseolin and cpDNA and a metabolome more similar to those of *P. dumosus* and *P. coccineus* indicate this group is a diverged taxon from *P. vulgaris*, henceforth called *P. debouckii*.

Notes

Poster Presentation Abstracts

P1: Influence of High Temperature on Bean Reproductive Biology

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The common bean (*Phaseolus vulgaris* L.) is one of the important basic crops in Brazil and is a major source of vegetable protein, carbohydrates, vitamins and iron. Due to its origin in high altitude regions, it is sensitive to high temperatures. This study is to investigate the effect of high temperature stress on twelve genotypes: studying their reproductive biology, monitoring the number of flowers, pollen grain viability, meiosis process, pod setting, production compounds and grain yield. The plants were grown in a controlled chamber with temperature maintained at 25-20^{o}C (day and night) for control and 37-26^{o}C for heat stress. The experimental design was a 2x12 factorial with 6 replicants. Temperature and genotype factors affected most of the parameters and high temperature resulted in lower flower production, lower pod formation and consequently lower grain yield.

P2: Advanced Interspecifiv Hybrids of Common Bean and Tepary Bean Without Embryo Rescue

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The productivity of common bean is currently limited due to night high temperatures, while global warming is expected to exacerbate this limitation. The limited variation of heat tolerance requires exploration, the development and use of species in the secondary and tertiary gene pool. Tepary beans (*Phaseolus acutifolius* A. Gray) have different traits that confer adaptation to hot and dry climates and are an attractive option for broadening the genetic base of common bean. However, hybrids between common and tepary bean show poor chromosome pairing during meiosis, require embryo rescue and consecutive backcrosses to obtain viable plants, limiting the possibilities to increase the diversity. From 2015-2016 we obtained, trough embryo rescue, interspecific backcross families (F_4) (typically common bean phenotype) derived from a cross between tepary (G40264) (*Phaseolus parvifolius* Freytag) and two common bean lines (INB 834 and INB 841). Two years of crosses and generational advances allowed identifying families as potential parents for cross directly with tepary beans. Currently we have obtained advanced interspecific F1 of different tepary beans and interspecific families without embryo rescue.

Notes

P3: Sources of Resistance to *Colletotrichun Lindemuthianim* in Common Bean Landraces from Brazil

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We investigated resistance sources in common bean germplasm to *Colletotrichum lindemuthianum*. One hundred and four common bean accessions from Nupagri germplasm bank, with Andean and Mesoamerican origins, were phenotyped using *C. lindemuthianum* races 65 and 3481. Forty accessions were resistant to race 65, from which 23 were Andean and 17 were Mesoamerican. Regarding race 3481, we observed 42 resistant accessions, which 27 were Mesoamerican and 15 were Andean. Nineteen out 104 accessions were resistant to both aforementioned races. The pathogenicity index of races 65 and 3481 in these accessions were estimated in 61.54% and 59.61%, respectively.

P4: Evaluation of Common Bean Lines for Heat Tolerance and Web Blight Resistance

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In the lowland, humid tropics web blight caused by *Thanatephorus cucumeris Frank* (Donk) can cause significant reductions in yield and quality of common bean seed. In Central America and the Caribbean, high temperature can reduce the yield of beans planted during the summer months. During 2015 and 2016, 644 lines from different bean breeding programs were screened in the field at Isabela, Puerto Rico for heat tolerance and web blight resistance. Thirty-seven lines were identified with web blight resistance having mean scores ≤ 4.5 during both growing seasons based on the CIAT (1-9) disease rating scale. During the summer of 2017, these heat tolerant and web blight resistant lines and F_7 lines from the third cycle of recurrent selection for web blight resistance were evaluated in field trials planted at Isabela, Puerto Rico and Zamorano University in Honduras. Results from the field trials will be presented.

Notes

P5: Improving Color Retention and Canning Quality Traits in Black Beans through QTL Mapping

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Black beans are healthy, affordable, and gaining in popularity. Since black beans are commonly eaten as canned products, canning quality is crucial to both industry standards and consumer preferences. Unfortunately, the canning process often creates substantial color loss, transforming the beans from dark black to an undesirable faded brown color. Genotypes with superior color retention and favorable agronomics have been identified within Michigan State University's dry bean breeding program, providing opportunity for genetic improvement. For this study, crosses were made between elite black bean genotypes with contrasting color retention. After canning, two of the parents remain a striking, dark black color, while three of the parents take on a faded, brownish coloring. RIL populations of approximately 150 individuals were developed through SSD and phenotyped for canning quality traits in advanced generations. Individual RILs were processed using a small-scale canning procedure and evaluated for canning quality traits such as color retention, overall appearance, and texture. Post-canning color and appearance measurements were determined by a trained sensory panel and digital imaging, and texture was calculated as the force needed to completely pulverize a 100g sample of canned, rinsed beans. Evaluation data from the two RIL populations segregating for color retention will be used in QTL mapping to identify regions of the dry bean genome associated with canning quality traits. Because phenotyping canning quality traits is a time- and labor-intensive process, associated QTL and linked markers may allow more efficient germplasm screening and incorporation of these traits in breeding programs.

Notes

P6: Generating a Reference Genome for Tepary Bean *(Phaseolus acutifolius)*: A Highly Heat Tolerant Species

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Tepary bean (*Phaseolus acutifolius* A. Gray), native to Mexico, the Southwest U.S., and parts of Central America, is highly tolerant to heat and drought. Tepary bean has been domesticated and used as a source of introgressions into common bean conferring biotic and abiotic stress tolerance. Access to genomic resources for tepary bean would be informative to not only common bean breeders interested in accessing tepary germplasm but also to a wide range of biologists interested in mechanisms of stress tolerance. Currently, transcriptomic and genetic diversity datasets are available for some tepary bean accessions and access to a robust genome sequence, annotation, and diversity datasets would enable comparative analyses between common and tepary bean and identification of loci that confer heat tolerance. The accession G40001, parent of a biparental recombinant inbred population, was selected to serve as the reference genotype. Currently, efforts are underway to generate a high quality genome assembly of G40001 using long read technologies. To date, RNA from a set of 12 developmental stages from G40001 has been isolated and mRNA-sequencing will be performed for use in genome annotation and generation of a gene expression atlas. This will be complemented with gene expression data from leaves and flower buds under heat stress to annotate genes involved in heat tolerance. For comparison, we are generating an NRGene assembly of W6 15578, a wild tepary bean accession. Furthermore, a small diversity panel of 54 accessions will also be subjected to whole genome re-sequencing to reveal the extent of sequence diversity in tepary bean. An update on the tepary genome project will be presented.

Notes

P7: The Legume Federation Resources for Common Bean

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There are many online resources available for common bean and other warm-season legumes. We will describe tools from the Legume Information System (LIS) and Legume Federation projects (https://legumeinfo.org, https://legumefederation.org).

A Geographic information system (GIS) viewer for visualizing germplasm collections globally against high-resolution maps for beans, cowpea, and other legumes.

Interactive genetic map viewer, cmap-js, with QTL traits compiled from a large number of QTL studies.

- InterMine instances for common bean.
- Genome browsers for both *Phaseolus* genome assemblies.
- Sequence search tools for *Phaseolus* genomes and gene modes, including tools for visualizing sequence matches.
- Gene family viewers for legume species.
- Synteny viewer for exploring genome-wide and gene-focused synteny across the legumes.

We will also describe how to contribute data for inclusion into these or related resources. This includes the collection of GWAS data to be displayed on a common reference genome framework.

Notes

P8: Current Situation of the Bean Germplasm Collections in Spain

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Since 1995, there is a cooperative program in Spain for the conservation, regeneration and characterization of plant genetic resources, including the common bean (*Phaseolus vulgaris* L.). The national collection is at the National Plant Genetic Resources Center of the National Institute for Agricultural and Food Research and Technology (CRF-INIA, Alcalá de Henares, Spain) with 4418 accessions of common bean. In the Misión Biológica de Galicia of the National Spanish Research Council (MBG-CSIC, Pontevedra, Spain) there is also a collection including 2014 accessions, some of them shared with the national collection at the CRF-INIA. The MBG-CSIC contributed to the cooperative program for the conservation, regeneration and characterization of the national common bean germplasm collection since its origin, and leaded it in the period 1995-2002.

In Spain there is a great variability in the types of common bean cultivated by small farmers, therefore, in the collection missions by the CRF-INIA and the MBG-CSIC many different varieties are being collected and the national collection increases continuously that makes regeneration necessary to maintain the viability of the seeds.

In the last years (2013-2016), 429 accessions were regenerated in the MBG-CSIC experimental farm, and the results of this regeneration are presented in this work. An average of 114 seed/ accession were sown and 7.3 g were harvested in average for each seed sown; 102 accessions were unproductive, 30 yielded less than 100 g and 134 yielded more than 1000 g, in the four years considered. In a collection mission carried out in 2014, 45 accessions were collected in small farms and were grown in 2015 and 2016, 14 of them yielded more than 1000 g and nine were unproductive.

Taking into account the age of the CRF-INIA seeds planted in those years and the harvest obtained, it can be assumed that there is a certain process of genetic erosion in the Spanish collection of common bean. In addition, the fact that some accessions collected from farmer fields were non-yielding could also be an indicator of genetic erosion on the farms themselves.

P9: Investigating the Positions of the Anthracnose Resistance Genes at the Beginning of the Bean Chromosome Pv04

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Until now, seven anthracnose resistance loci were mapped at the beginning of the bean chromosome Pv04; *Co-3* from Mex222, *Co-z, Co-y* from JaloEEP558, *Co-9* from BAT93, *Co-10* from Ouro Negro, *Co-15* from Corinthiano and *Co-16* from Crioulo 159. The genes *Co-9* and *Co -10* were considered alleles of the same locus and renamed as *Co-3*[3] and *Co-3*[4]. In this work, we investigated the genetic and physical position of genes conferring resistance to anthracnose races 6, 38, 39 and 357 in the RIL population Xana x BAT93 (145 lines). For this purpose, a fine map of the beginning of chromosome Pv04 was developed including 26 SNPs obtained through Genotyping by Sequencing, 3 InDel, 2 SSR specifically designed from sequence and, several markers reported to be closely linked to previously described anthracnose resistance genes. Results can contribute to clarify the complex scenery of the resistance genes previously mapped at the beginning of Pv04.

Notes

P10: Genetic Diversity Gathered in a Common Bean Panel Established for Genome-Wide Association Studies

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Genome-wide association studies (GWAS) strongly depend on factors related to Panel design. In this work, we describe a diversity Panel of 308 lines established from the SERIDA bean collection. Type (landrace or elite), form of consumption (dry or snap) and previous genetic knowledge of materials were the three main aspects considered to constitute this Panel. It includes 213 local accessions, most of them from the Spanish core collection in which 65 seed phenotypes were described. A total of 60 lines derive from elite cultivars of snap bean consumption. The panel also includes well-known bean genotypes as anthracnose differential cultivars, parents of RIL populations, or the sequenced genotypes BAT93 and G19833. The Panel was characterized with 9974 SNP markers obtained through Genotyping by Sequencing. The genetic diversity gathered in this Panel was studied through cluster and principal component analysis. Results can contribute to optimize the design of this Panel for future GWAS.

P11: Exploring the Genetic Control of Pod Traits in Common Bean Using Genome-Wide Association Study

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Depending on pod traits, some bean genotypes can be harvested for consumption as snap beans before the seed development phase. In this work, a genome-wide association study (GWAS) in a common bean panel consisting of 308 snap and dry bean lines was conducted to explore the genomic regions involved in genetic control of 14 morphological pod traits. Genotyping by sequencing (GBS) was used to generate 5990 SNP distributed along the 11 bean chromosomes for the analysis. The general linear model (GLM) and mixed linear model (MLM) implemented in TASSEL V5 were used to detect QTL conditioning pod traits. Significance thresholds were determined using Bonferroni correction from the α-level of 0.05. Results revealed many significant genomic regions influencing genetic control of pod traits in common bean.

Notes

P12: Response of Two Common Bean Genotypes to Different Inoculation Ways and Cells Concentration on the Rhizobial Inoculant

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The objective of this work was to evaluate the effect of different doses and ways of inoculant application on nodulation, growth and grain yield of common bean. The field experiment was conducted in a randomized complete block design with 4 replicates, using the genotypes BRS Notável and BRS Esplendor. The treatments were composed by the combination of three inoculation ways (seed inoculation with peat, seed inoculation in furrow and furrow inoculation), and four cells concentrations ($1x10^8$, $1x10^{10}$, $1x10^{12}$ and $1x10^{14}$ cells mL^{-1}). Nodulation (number of nodules and nodule dry mass), plant growth (root dry mass and shoot dry mass) and production components (number of pods, number of grains and grain yield) were assessed. On general, the furrow inoculation with $1x10^{12}$ cells mL^{-1} provided better nodulation and plant growth, resulting in a grain yield about 3300 and 3500 kg ha^{-1}, respectively, for the genotypes BRS Notável and BRS Esplendor.

Notes

P13: Development of Genetic and Genomic Tools for Lima Bean Breeding (*Phaseolus lunatus*)

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The objective of the University of California, Davis, lima bean breeding program is to develop Large and Baby Bush- and Viny-type dry bean varieties with lygus (*Lygus hesperus* or Western Tarnished Plant Bug) and nematode (*M. incognita*) resistance. In contrast with common bean (*P. vulgaris*), however, lima bean has very few, if any, genetic stocks and molecular tools such as DNA maps and markers to facilitate future breeding efforts. This research project resulted in the development of a Recombinant Inbred (RI) population of Lima bean (n ~ 230), use of Simple Sequence Repeat markers for rapid confirmation of hybrids, and field-based phenotypic data correlated with yield, in the presence or absence of lygus insect pressure. The population was developed from two contrasting cultivars belonging to conspecific Andean and Mesoamerican gene pools currently grown in California, UC Haskell (Mesoamerican) and UC 92 (Andean). UC 92 is a bush determinate, large-seeded lima with tolerance to nematode *Meloidogyne* sp. UC Haskell is a vine-type, small-seeded ("baby") lima bean, which has shown partial lygus tolerance. First, we created a physical SNP map based on assumed synteny with common bean based on Illumina Hiseq sequencing of RESCAN libraries prepared after DNA digestion with the restriction enzyme *Nla*III and barcoding of sequences of the two parents. The putative SNP location was based on alignment of sequences with at least 5X coverage with the common bean genome sequence from Andean variety G19833 v.1.0 created in 2012. This SNP-based physical map currently has ~50,000 SNPs spread across all 11 chromosomes. Thus, the UC Haskell – UC 92 cross maximized the genotypic and phenotypic diversity of the population. The population has been shared with the Genetic Resources Program at the International Center for Tropical Agriculture (CIAT) in Palmira, Colombia. Second, a genetic linkage map containing 516 SNP markers for Lima bean was developed using 139 F_5:$_6$ RI lines developed from reciprocal crosses of UC Haskell and UC 92. The SNP markers were obtained after Genotyping-By-Sequencing using the ApeKI protocol. The map consists of 13 linkage groups, with two chromosomes each represented by two linkage group (Pl5 and Pl10), indicating that additional markers are needed to saturate this map. This linkage map in combination with field phenotypic data was used for composite interval mapping of 27 significant QTLs for germination rate, seed weight, yield, flowering time, inflorescence position, and hydrogen cyanide potential. Of particular note, is a single QTL on one of the Pl05 linkage groups for HCN (cyanide) content in first trifoliolate leaves with a LOD score of 15, which explains 44% of the phenotypic variation. Using current California cultivars as parents for genetic tools expedites the development of basic lima bean genetics and biology information to improve lima bean breeding for California growers.

Notes

P14: Can One Fungicide Control White Mold and Anthracnose in Dry Bean?

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Anthracnose, a devastating seed-borne dry bean disease caused by *Colletotrichum lindemuthianum*, is managed by genetic, cultural and chemical controls. Foliar fungicides are an important tool to manage in-season disease outbreaks. Various rates of nine registered or experimental fungicides were evaluated in four small plot replicated experiments over two years. Picoxystrobin, azoxystrobin and pyraclostrobin (FRAC group 11) and thiophanate-methyl (group 1) were highly efficacious, metconazole and prothioconazole (group 3) and fluazinam (group 29) were moderately efficacious, while fluxapyroxad, fluopyram and penthiopyrad (group 7) were ineffective. Fluopyram+prothioconazole (ProPulse®) and fluazinam (Allegro®) are highly efficacious for the control of white mold in dry bean, but these products appear to differ in their control of anthracnose. Since the timing of fungicide application is similar for white mold and anthracnose, identifying a product that was superior for both pathogens would minimize strobilurin fungicide use, reduce production costs, and provide a new tool for resistance management.

P15: Genotype by Cropping System Selection Criteria for Bean and Maize Intercrops Identified by Farmers in Northern Province, Rwanda

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Common bean (*Phaseolus vulgaris* L.) and maize (*Zea mays* L.) intercropping systems are grown by smallholder farmers worldwide and provide multiple ecosystem services, but few bean genotypes are developed specifically for these systems. In Rwanda, climbing bean farmers consider crop production choices in terms of diverse and healthy food, market services, land-use efficiency, risk, and cultural services; services the traditionally grown intercrop systems provided. In order to improve genotypes for these multi-service cropping systems, breeding efforts may need to consider genotype performance in the competitive intercrop and high stress environments typical of smallholder low-input systems. Fifty-nine interviews with farmers were conducted to understand farmer knowledge about bean traits for intercrops agronomic trials were conducted to determine if there are specific bean phenotypes that are associated with improved performance. Six climbing bean genotypes were evaluated for yield and phenotypes in a sole crop (SC) and an intercrop (IC) with maize on two research stations and seven farms in northern Rwanda. The greatest sources of variation were environment or cropping system and there were genotype by environment interactions for yield and all component traits. Bean yields were reduced in the IC but maize yields were not. Average bean yields on-station ranged between 3.2-3.8 mt/ha in the SC and 1.3-2.1 mt/ha in the IC. There were few differences in bean yield between the genotypes in the SC, but in the IC, RWV2070 yield was higher ($P>0.0001$) than other genotypes. On-station pods per plant indicated RWV2070 was the best cultivar in the IC. The IC environment increased biotic stress but was less affected by abiotic (seasonal) stresses than the SC. Bean yields were reduced in both systems on-farm, and contrary to the station data, there was no evidence that RWV2070 was a superior genotype in either cropping system. The 59 interviews confirmed the relevance of pods per plant as a competitive genotype indicator, but more importantly they revealed farmers consider multiple bean attributes that improve performance in an intercrop: trait-based competitive abilities including plant architecture, intrinsic competitive ability, and environmental adaptation. Results indicate there are genotypes that have greater competitive ability than others in an intercrop, selection for phenotypic plasticity or specialized environments is necessary to identify these competitive genotypes, and farmer knowledge provided key insights into selection criteria for competitive bean genotypes. Adoption of improved bean genotypes will require meeting the multi-service expectations of smallholders and genotype selection in diverse environments, including both the abiotic and the cropping system.

Notes

P16: A High-Density SNP Consensus Map Reveals Segregation Distortion Regions (markers/chromosomes) in Common Bean

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In order to verify the presence of segregation distortion regions (SDRs) in common bean, a high-density consensus map was constructed, using single nucleotide polymorphism (SNP) markers, by merging genetic map developed from 110 recombinant-inbred lines (RILs) population from California Dark Red Kidney (CDRK) × Yolano (CY population) cross. RILs were genotyped using the BARCBEAN6K_3 BeadChip. Chromosome regions with obvious segregation distortion were identified in the map. A total of 3,277 SNPs out of 5,392 SNP markers segregated in this population and the final map spanned 936 cM in genetic distance with an average interval of 0.3 cM. The number of markers that showed distorted segregation was 653 (20%) in the CY population. Most of the distorted markers (449) were mapped on chromosomes Pv01 (CDRK alleles in excess) and Pv10 (Yolano alleles in excess) in the consensus map, which accounted for 14% of mapped markers. Further, distorted markers clustered in the SDRs of most chromosomes, except on chromosomes Pv03 and Pv04.

P17: Co-Segregation of Recombinant Inbred Lines of the California Dark Red Kidney X Yolano to Races 73 and 3481 of *Colletotrichum lindemuthianum*

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The reaction of a total of 107 RILs from cross California Dark red Kidney × Yolano were evaluated. A segregation of 55 resistant lines and 52 susceptible lines to races race 73 and 3481 (χ^2= 0.084; p = 0.7718), fitted in a ratio of 1R:1S, proving the action of a single dominant gene in AND 277 cultivar. These results showed that these RIL's co-segregated to both inoculated races, suggesting that a gene present in CDRK confers resistance to both races 73 and 3481 of *C. lindemuthianum.*

Notes

P18: The Isolation and Characterization of Bio-Based Nanoparticles and Their Uptake and Translocation in *Common Bean Tissue*

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Application of nanoparticle has opened a large scope of novel application in the fields of biotechnology and agricultural industries because of its high surface area, high reactivity, tunable pore size, and particle morphology. However, majority of the nanotechnology based research and their applications have been conducted using the nanoparticles of synthetic origin. In recent years, interest in use of nanoparticles derived from bio-based polymers has accelerated because of its renewable and biodegradable properties. We have been isolating nanoparticles from wheat bran with a goal to encapsulate bio-based nanoparticle with health related micronutrients and deliver it to common bean plant. A dye labelled bio-based compatible nanoparticle was applied to germinating seeds of common bean and the uptake and translocation of nanoparticles into different tissues was studied. The nano-encapsulated health related nutrients could efficiently enhance nutrient content of food crops, release the nutrients on-demand, and control release of chemical fertilizers.

P19: Dry bean germination under cold and wet conditions

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Sustained cold weather and saturated soil conditions present challenging germination environments for dry bean production in western Canada. In order to improve the commercial productivity of dry beans, varieties should possess the ability to germinate during the lengthy period of harsh Spring climate. In this study, a large number of early-maturing dry bean varieties and plant introduction accessions were tested under controlled environmental conditions at 10 °C and saturated soil moisture. They were compared with those under optimal germination conditions at 24 °C. In general, commercial varieties showed better germination ability than most of the PI accessions. Under the cold and wet conditions, seeds frequently rotted and did not germinate. In the lines that did germinate, emergence was usually non-uniform and slow, taking as long as 3 weeks. Selections were made for the lines that germinated uniformly and having seeds that remained viable under cold and moisture stress conditions.

Notes

P20: Improving anthracnose resistance in early maturing dry beans

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Anthracnose, caused by *Colletotrichum lindemuthianum*, is a serious dry bean disease. The major races of the pathogen in western Canada include 73 and 105. To develop dry bean varieties with durable resistance, crosses were made between two navy beans, Morden003 and SMARC1N-PN1. Morden003 has been identified to have resistance to races 73 and 105, while SMARC1N-PN1 is resistant to race 73, but susceptible to race 105. Molecular mapping with SNP markers has located the resistance genes in Morden003 in the vicinity of *Co-3* on chromosome 4, while the resistance gene in SMARC1N-PN1 is located on the lower arm of chromosome 1. Field tests of 180 recombinant inbred lines derived from Morden003/SMARC1N-PN1 have identified superior lines that are early-maturing and have desirable agronomic characteristics, which possess multiple resistance genes to races 73 and 105 of *C. lindemuthianum*. The resistance materials will be useful for future short-season dry bean variety development.

P21: Sequencing the Complex Genome of the Bean Rust Pathogen (*Uromyces appendiculatus*)

Hurtado-Gonzales OP, Diaz-Valderrama J, Aime C, Pastor-Corrales MA

Uromyces appendiculatus is the causal agent of the rust disease of common bean (*Phaseolus vulgaris*). The extensive virulence diversity of this pathogen makes it difficult to achieve durable resistance. Hundreds of virulent strains of *U. appendiculatus*, known as races, have been reported. Remarkably, this virulence diversity mirrors the diversity of the common bean. Races of this pathogen obtained from large-seeded beans from the Andean gene pool infect only or mostly Andean beans. Conversely, races recovered from Mesoamerican beans infect beans from both host gene pools, albeit they prefer Mesoamerican beans. It is also significant that, like its common bean host, the diversity of Mesoamerican races is greater than the diversity of Andean races. The similarities between the virulence diversity of *U. appendiculatus* and the genetic diversity of *P. vulgaris* suggest that the rust pathogen has undergone parallel evolution with its common bean host. That is, Andean races coevolved with Andean common beans and Mesoamerican races would have coevolved separately with Mesoamerican common beans. Little is known about the genomic structure and the genetic basis of virulence diversity and evolution of the rust pathogen or -about the mechanisms that drive rust-bean interactions.. Here we report the development of genomic resources for this pathogen by initially conducting whole genome sequencing of two races, one Andean (race 5-0, previously known as race 38) and one Mesoamerican (race 31-1, or race 53). Spores from race 5-0 and 31-1 were increased in common bean cultivars Early Gallatin and Olathe, respectively. High-quality and high-molecular weight DNA was obtained from each race for next-generation sequencing (NGS). NGS libraries of 500 bp inserts were paired-end sequenced at 150X with mate-pair libraries of 2Kb and 5Kb inserts. After removing the adapter sequences and trimming poor quality bases, a total of 320 M and 307 M reads were generated for the Andean and Mesoamerican races respectively. Discovar software was used for de novo assembly and BESST for scaffolding, resulting in genomes assemblies of 587.6 Mb and 546.7 Mb at a k-mer of 90 for the Andean and Mesoamerican races. N50s were 78Kb and 50.5Kb for races 5-0 and 31-1 respectively. Scaffolds larger than 10Kb were examined for presence of SSRs using the QDD pipeline. Detected SSRs were cross blast- to identify polymorphic SSRs between the two races. A subset of 93 polymorphic SSRs are being tested on a collection of 43 rust races from different parts of the world. A subset of these races are being sequenced for detection of SNPs. The information generated here will help to conduct comparative and phylogenetic studies of the bean rust pathogen. The results from these studies should provide insights into the signatures and mechanisms of race evolution, the development of tools for the identification of specific races, the surveillance of new races, and they may also provide information that common bean breeders may use to develop common bean cultivars with effective rust-resistance.

Notes

P22: Promising Black-Seeded Common Bean Breeding Lines Resistant to BCMV, BCMNV and BGYMV with Adaptation to Terminal Drought and Acid Soils of Tropical Southeastern Mexico

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Productivity of the dry bean crop is low in tropical environments of southeastern Mexico, due to the effect of different biotic and abiotic factors that substantially reduce grain yield. The biotic factors include by far fungal (angular leaf spot, rust and web blight) and viral (BCMV, BCMNV and BGYMV) diseases. The most important abiotic factors are the presence of terminal drought that occurs frequently after flowering and the presence of acid soils where common beans are cultivated. Recombinant breeding lines, derived from different crosses, were assessed to determine their adaptation to bean production environments of tropical southeastern Mexico. A field trial, composed of 12 previously selected breeding lines and two checks, was assessed across ten environments during 2016 and 2017 growing seasons. Four promising breeding lines were identified that possess high yield potential and adaptation to abiotic stresses, which carry the *I*, *bc-3* and *bgm-1* genes identified by molecular markers.

P23: Identification and Characterization of *Slow Darkening* Gene in Pinto Bean (*Phaseolus vulgaris* L.)

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Postharvest darkening of seed coat in pinto bean (*Phaseolus vulgaris* L.) is an undesirable trait that affects its market value. Darkening is comparatively more rapid in the adapted cultivars like CDC-Pintium than the newly developed slow darkening cultivar 1533-15. A single gene, *slow darkening* (*Sd*), is responsible for the slow darkening in pinto beans and the trait co-segregates with two simple sequence repeat (SSR) markers. The objective of this research is to identify and characterize the *Sd* gene to understand the slow darkening mechanism in pinto bean seed coat. A search for *Sd* within the linkage distance from the SSR markers has identified a basic helix-loop-helix (bHLH) transcription factor gene, *PvbHLH333,* on chromosome 7 as a candidate gene. Our complementation assay showed *PvbHLH333* is able to rescue the *tt8* mutant phenotype in Arabidopsis suggesting that *PvbHLH333* is the orthologue of *AtTT8* which regulates proanthocyanidin biosynthesis in Arabidopsis.

Notes

P24: A Saturated Genetic Linkage Map of Common Bean (Phaseolus vulgaris L.) Developed Using Genotyping by Sequencing (GBS)

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High-density linkage maps are valuable tools to uncover the genetic basis of complex quantitative traits. Our goal was to construct a high-density genetic map to facilitate the identification of markers associated with cooking time in common bean. We used genotypic data of the F6 recombinant inbred line population developed from two Andean lines from Tanzania ADP0027 x ADP0037 to construct a genetic map. The map was constructed from single nucleotide polymorphism (SNP) markers that were genotyped using a Genotyping by Sequencing **(**GBS) protocol reported by Schröder *et al* 2016 with the Taqa1/MseI enzyme combination for library construction. A total of 48,244 markers were identified in 146 RILs and their parents. The SNPs were filtered by alignment quality, minor allele frequency, and percentage of missing data. In total 2,427 markers were assigned to 11 linkage groups with a map length of 1,137 cM and a mean distance between markers of 0.58 cM. Overall, the map has 175 SNPs in coding (114 Synonymous, and 61 Missense), and 2,252 in non-coding regions.

References

Schmutz, J., McClean, P. E., Mamidi, S., Wu, G. A., Cannon, S. B., Grimwood, J., … Jackson, S. a. (2014). A reference genome for common bean and genome-wide analysis of dual domestications. *Nature Genetics*, (November 2013). http://doi.org/10.1038/ng.3008

Schröder, S., Mamidi, S., Lee, R., McKain, M. R., McClean, P. E., & Osorno, J. M. (2016). Optimization of genotyping by sequencing (GBS) data in common bean (Phaseolus vulgaris L.). *Molecular Breeding*, *36*(1), 1–9. http://doi.org/10.1007/s11032-015-0431-1

P25: Resistance to *Bean Common Mosaic Necrosis Virus* Conferred by the *bc-1* Gene Affects Systemic Spread of the Virus

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Bean common mosaic necrosis virus (BCMNV) isolates belong to two pathogroups (PG), PG-III and PG-VI, which are distinguished in common bean due to the inability of the PG-III isolates to overcome the *bc-1* recessive resistance alleles. Three isolates of BCMNV were typed on a set of twelve bean differentials, with two, 1755b and TN1a, assigned to PG-VI, and one, NL8-CA, assigned to PG-III. Isolate NL8-CA (PG-III) and both PG-VI isolates replicated normally in inoculated leaves of the common bean cultivars from host groups 2, 3, and 9 carrying *bc-1* alleles. Only PG-VI isolates were able to systemically infect the same cultivars. Apparently, the phenotypic differences among PG-III and PG-VI isolates of BCMNV in common bean cultivars from host resistance groups carrying *bc-1* alleles, were due to restricted systemic movement of the PG-III isolate, and suggested a role of the recessive *bc-1* gene in interfering with systemic spread of BCMNV.

Notes

P26: Prediction of Genetic Potential of Common Bean Segregant Populations for Slow Seed Darkening

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The objective of this study was to predict the genetic potential of common bean segregant populations for slow seed darkening. Twelve common bean genotypes were divided into two groups, thus group I - two genotypes with slow seed darkening and group II - ten genotypes with regular seed darkening, which were both crossed according to the partial genetic diallel design. In 2010, segregant populations F3:4, F4:5 and their parents were evaluated at the locations of Santo Antônio de Goiás and Ponta Grossa in different seasons. Seeds were harvested and stored under uncontrolled temperature and humidity conditions for 155 days. The evaluation of seed darkening was performed individually on 120 progenies for each population, using a grade scale of 1 (very light colored grains) to 5 (very dark colored grains). It was used the methodology of Jinks and Pooni for predicting the genetic potential of the populations, which allows an estimating probability of each population and originates lines surpassing a determined standard. In this case, BRSMG Madrepérola cultivar has shown slow seeds darkening. The result demonstrated that the probability estimates ranged from 0.035 to 34.89%, hence the best population was BRSMG Madrepérola x IPR Siriri.

P27: Evaluation of Protein, Starch and Dietary Fiber in Dry Bean

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Protein, starch and dietary fibre are major seed components of dry bean and important to human health. Seeds of over 350 dry bean germplasm and cultivars of diverse market classes were assessed for these major compositions. The average seed protein content in dry bean was approximately 25% DW, but some germplasm lines had over 35% protein content. Total starch contents in dry bean varied from 22% to 40% with an average of 32%, in which amylose contents in starch granules ranged between 17% and 42%. Dietary fiber contents in dry bean ranged from 10% to 28% with an average of 21%. Based on overall analytic results, we selected five genotypes as parents and made 16 cross combinations to develop recombinant inbred lines (RILs) for molecular characterization to identify dry bean lines with high protein and dietary fibre.

Notes

P28: Comparative Annual Grain Legume Root Architecture

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Grain legume production is fundamental to many smallholder and subsistence farmers and to local and regional economies. Productivity is constrained primarily by water and phosphorus availability, which typically have contrasting availabilities in the soil profile when both are limiting. Root architecture is important for increasing water and phosphorus acquisition but tradeoffs may mitigate the benefits of breeding for single stress environments. Panels of common bean (*Phaseolus vulgaris)*, tepary bean *(Phaseolus acutifolius)*, cowpea (*Vigna unguiculata)*, soybean (*Glycine max)*, chickpea (*Cicer arientinum)*, and groundnut (*Arachis hypogaea)* were evaluated for a variety of root architectural characteristics. A smaller collection including lima bean (*Phaseolus lunatus)* and faba bean (*Vicia faba)* and minor *Phaseolus* species were also evaluated. We found that legume root systems can be placed on a root system architecture (RSA) spectrum and grouped into root architectural categories corresponding to epigeal or hypogeal germination. We identified inverse relationships between investment in different root classes and between indicators of deep and shallow exploration. Bean and tepary showed particularly strong tradeoffs while chickpea and groundnut show less pronounced tradeoffs. These tradeoffs may be formed by interactions between resource availability, resource acquisition strategy and life strategy in a given domestication environment. Using an economic analysis to understand the advantages and disadvantages of various root architectures may help to maintain and expand the range of these important food security grain legumes. We highlight instances of dimorphic root architectures that may co-optimize resource acquisition in environments with contrasting resource availability profiles.

Notes

P29: Genetics of Phenotypic Variation and Genotype by Environment Interactions in the Cooperative Dry Bean Nurseries

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Common bean (*Phaseolus vulgaris*) yields have been improved by multiple long-term breeding efforts across the world. One example of such an effort is the Cooperative Dry Bean Nursery (CDBN), an ongoing 60+ year collaboration across the United States and Canada. CDBN collaborators have collected phenotypic data for a suite of agronomic traits for over 500 common bean varieties grown in 84 locations. Despite yield improvements, large genotype-by-environment interactions (GxE) persist in common bean. Though genomics-assisted breeding tools and methodological frameworks to study GxE are rapidly improving, accurate phenotyping in relevant field conditions remains a major limitation of these analyses. Major phenotyping efforts such as the CDBN, when combined with genomic data, offer unparalleled opportunities to determine how major genetic factors affect genotype by environment interactions.

In collaboration with current common bean sequencing efforts, we sequenced 314 varieties from the CDBN and established a genome-wide association mapping population. We obtained monthly weather data associated with each CDBN trial year at each site, and performed a principal components (PC) analysis on all weather variables. The first two PCs explained 39.1% and 22.6% of the variance, and loaded strongly with temperature and precipitation variables, respectively. These PCs separate the CDBN trial years and locations into seven geographic regions (Figure 1). To reduce the location complexity in this dataset, we determined trait averages for each variety within these seven geographic regions for yield, days to flowering, days to maturity, and plant height.

We used TASSEL on the CDBN panel to test for genomic regions that were differentially associated with phenotypes in the seven geographic regions within the CDBN, or genomic regions with GxE. Overall, there was little overlap in the top SNPs associated with phenotypes between the different geographic regions, implying there is substantial GxE associated with specific genomic regions within this dataset. We discuss these associations, as well as two ways we attempted to increase the power to detect pleiotropic variants in this dataset. First, we discuss using multivariate models to associate phenotypes expressed in multiple environments simultaneously. Second, we discuss the incorporation of pedigree information and genotypes of 115 additional varieties within the pedigree to improve the relationship matrix of the CDBN varieties.

Notes

P30: Gene Expression and Physiological Comparison between Tepary and Common Bean under High Night Temperature Stress

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Temperature controls the metabolic rate in plants and can affect yield. Common bean (*Phaseolus vulgaris*), the most important edible legume world-wide, is susceptible to heat stress in the reproduction phase, especially the micro- and mega-sporogenesis stage. However, its sister species, tepary bean (*Phaseolus acutifolius*) is native to the Sonoran Desert and is resistant to heat. We compared physiological aspects of Amadeus (small red) and G40001 (tepary) under control (29°C day/20°C night) and night temperature stress (32°C day/27°C night) conditions. Half of the plants were exposed to heat stress starting at 11 days before anthesis and physiological measurements were taken at two time points: 1) five days after stress (DAS) from the 1st trifoliate, 2) 11 DAS, at flowering time, from the 7th or 8th trifoliate. Leaf discs and flower buds were sampled for gene expression analysis at the flowering stage (11 DAS). Pollen viability tests revealed 95% pollen viability in both species under the control conditions; however, under heat stress, 95% of Amadeus pollen grains were non-viable yet only 25% for G40001. Stomatal conductance, photosynthesis, photosynthesis/ respiration, and leaf internal CO_2 level were higher in common bean at five DAS regardless of the treatment. Under heat stress, the values increased in Amadeus but decreased in G40001. Interestingly, this pattern was reversed in tepary bean at 11 DAS and G40001 showed an increase in the values of measured photosynthesis-related traits under the heat stress. These results indicate the leaves that develop under high night temperature show an altered physiological response at flowering time in tepary bean but not in common bean.

P31: Population Structure between Accessions of Common Bean from the Pernambuco State, Brazil

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This work provided selection of useful SNPs for high-throughput common bean genotyping using GBS, followed by population structure and genetic diversity analyses among accessions through Principal Component analysis. The evaluated accessions belong to IPA Bean Germplasm Bank, while traditional cultivars were collected in the producing areas of Pernambuco. The genotyping identified 30,529 high-quality SNPs, which were distributed in 11 linkage groups. The amount of SNPs per chromosome ranged from 1,731 to 3,853. Population structure analysis showed that accessions were divided into two well defined groups, at K = 2 it was observed 26 accesses of the Andean gene pool and 60 from the Mesoamerican one. At K = 3 the Mesoamerican accessions were divided in two subpopulations with great presence of alleles mixture between the two groups. GBS analysis data confirmed a narrow genetic base in the accessions from Andean gene pool, while a broad diversity was found in those originally from Mesoamerican gene pool.

Notes

P32: Narrowing the Introgression Interval Associated With The Type II Growth Habit Phenotype in Modern Durango Genotypes

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The growth habit of Pinto, Great Northern, and other race Durango common beans (*Phaseolus vulgaris* L.) was restructured over the last 25 years. Breeders converted prostrate Type III growth habit varieties into varieties with an upright Type II growth habit. The Type III architecture created a humid environment optimum for disease and required two passes during harvest. The new upright Type II architecture is currently the industry standard and requires only a single pass to combine the crop. It also aids with reducing humidity in the canopy which in turn reduces disease incidences of diseases such as white mold. In this research, the phenotypic effects of the conversion were assessed in a Durango Diversity Panel (DDP; n=182) consisting of historic and newly released pinto, great northern, pink, and medium red bean genotypes. A two-location, two-year field trial established that canopy height, the major phenotypic difference between Type II (tall) and Type III (short) varieties, was correlated with growth habit (r= -0.63**). The correlation (r=0.80**) between canopy height and stem diameter suggested Type II plants compensate for the tall plant by developing a thicker stem. The DDP was resequenced (~8X), and ~789,469 SNPs were defined. Diversity scans (100kb non-overlapping windows) within the pinto and great northern populations identified a shared ~600kb Pv07 (34.6Mb – 35.2Mb) region with a high diversity ratio ($\pi_{Type\ III}/\pi_{Type\ II}$) suggesting this region contains a genetic factor that was jointly introduced into these two market classes. A search for appropriate candidate genes within this region is underway.

Notes

P33: General and Specific Combining Ability Analysis fir Evaluation of Common Bean Under Drought Stress

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Water deficit occurs frequently in the common bean producing regions of the world, causing reduction in yield, yield components and biomass accumulation. The effects of water deficit on common beans have been widely studied and depend on the frequency, duration and intensity of stress and the developmental stage of the crop. The objetive of this study was selecting common bean parents to be used in a breeding program aiming on drought tolerance. The parents general and specific combining ability (GCA and SCA) were evaluated under drought conditions employing partial diallel mating design. The experiment was conducted in greenhouse and the hybridizations were performed between group I, composed of three tolerant parents (IAPAR 81, BAT 477 and SEA 5) and group II consisting of nine cultivars widely sown by producers. In this last group, three cultivars were from Mesoamerican origin - carioca type (BRS Estilo, IPR Campos Gerais and IAC Alvorada), three from Mesoamerican origin - black type (IPR Uirapuru, IPR Nhambú and BRS Esteio) and three from Andean origin (IPR Garça, DRK 18 and BRS Radiante). The experimental design was a randomized block, with four replications. The 12 parents and 21 F_1 progenies obtained from hybridizations were grown until R5 phenological stage at 80% of pot capacity (PC) and then subjected to water deficit (30% PC), for 20 days. At the physiological maturity stage (R9) the agromorphological characteristics: plant height (PH), number of nodes (NN), number of pods per plant (NP), seeds per pod (SP), seeds per plant (SPP), grain yield and total dry biomass (TB) were evaluated. The values of GCA and SCA indicated the presence of additive and non-additive effects on those traits genetic control and that the hybrid combinations obtained showed significant differences. Under water deficit conditions, GCA estimated for group I showed that BAT 477 presented the best results, with positive values for all agromorphological characteristics. For group II, IAC Alvorada, IPR Uirapuru and BRS Esteio, Mesoamerican cultivars, showed increased for all agromorphological traits too. In relation to the SCA under drought conditions, the hybrid combinations IAPAR 81/ IPR Campos Gerais, IAPAR 81/IPR Garça, SEA 5/BRS Radiante, BAT 477/ BRS Estilo and BAT 477/DRK 18 presented greatest increases in grain yield and total dry biomass. The choice of parents for formation of segregating populations is crucial for the success of breeding programs. In this sense, the results of this study indicated that BAT 477 genotype should be considered an important parent in the development of cultivars for drought tolerance.

Notes

P34: Total Phenolys, Condensed Tannins, Flavonoids, Phytates and Antioxidant Activity in *Phaseolus Vulgaris* of Andean Origin

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Common bean is an economically and socially important crop in many countries and contributes to human food supplying essential nutrients. *Phaseolus* breeding searchs different sources of genetic variability to increase the nutritional value of cultivars. The antioxidant activity (AA) is associated with several phenolic compounds and phytate [1,2]. The objective of this study was to identify the variability of these components in Andean beans genotypes of different colors. Fifteen genotypes cultivated in the 2016 rainy season in Guarapuava, PR, Brazil, were evaluated (Table 1). Total phenols, condensed tannins, flavonoids contents, and AA were determined following the methodologies of Heimler, et al. (2005). Phytate content was determined by procedure described in Oomah et al., 2008.

Among the evaluated genotypes there was a high variation in phytate contents (10.21 to 16.58 mg/g) regardless of the beans colors. White beans showed low total phenols, condensed tannins, flavonoids and AA. LPSIA0907 and LPSIA0938 showed high contents of phenols, condensed tannins, flavonoids and AA (5.09 and 5.86 mg/mg DPPH). Positive correlations between phenolic compounds and AA were observed, suggesting the participation of these compounds in AA. The AA of red and cranberry beans ranged from 6.89 to 11.48 mg/mg DPPH and from 6.58 to 6.47 mg/mg DPPH, respectively. The genetic variability found among the genotypes can be alternative source of genetic improvement for nutritional characteristics.

Key words: phenolic common bean, genetic variability, cranberry.

1. Oomah, B.D.; Blanchard, C.; Balasubramanian, P. Phytic Acid, phytase, minerals, and antioxidante activity in Canadian dry bean (*Phaseolus vulgaris* L.) cultivars. J. Agric. Food Chem. 2008, 56, 11312–11319.

2. Heimler, D.; Vignolini, P.; Dini, M.G.; Romani, A. Rapid tests to assess the antioxidant activity of *Phaseolus vulgaris* L. dry beans. J. Agric. Food Chem. 2005, 53, 3053-3056.

Notes

P35: Genome Wide Association Study (GWAS) for White Mold Resistance in Snap Bean

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Common bean is one of the most widely produced legumes worldwide. White mold, caused by *Sclerotinia sclerotiorum* (Lib.) de Bary, is considered one of the most important diseases that can cause up to 100% yield loss under certain conditions in bean fields. Genome wide association study (GWAS) was conducted to detect markers significantly associated with white mold resistance in two panels of snap bean cultivars. The objectives were: 1) to verify previously reported QTLs detected in other populations and studies, 2) to detect novel QTLs associated with white mold resistance and 3) to identify new sources of resistance to this disease in snap bean. Two populations of snap bean were used in this study: Bean CAP (Coordinated Agriculture Project) Snap Bean Diversity Panel (SBDP) (n = 137) and the Snap Bean Association Panel (SnAP) consists of 376 cultivars and breeding lines. The Bean CAP was evaluated for reaction to white mold in the field for two years (summer 2012 and 2013). The SnAP was screened for white mold reaction in the greenhouse only using the seedling straw test. The population was genotyped using genotyping by sequencing (GBS) for which 40,023 SNPs were generated. GWAS was analyzed using the R package FarmCPU. One-hundred forty-six significant SNPs that were associated with white mold were detected on all 11 common bean chromosomes. Twenty significant SNPs was detected for the seedling straw test while 126 significant SNPs were detected in one or both years; 51 SNPs in 2012 and 75 SNPs in 2013. The 146 significant SNPs grouped into 40 regions. The regions overlapped with 13 previously identified QTL (WM1.1, WM2.2, WM3.1, WM3.3, WM5.5, WM6.1, WM6.2, WM7.1, WM7.4, WM7.5, WM8.1, WM8.3 and WM9.3) that were found in bi-parental populations. Also, the associations in the present study overlapped with 13 significant markers that were associated with white mold detected by GWAS in a dry bean panel. NY6020-5 and Unidor were the most outstanding snap bean cultivars in the field tests for both years while Homestyle and Top Crop were the most resistant snap beam cultivars in the straw test.

Notes

P36: Occurence and Genetic Diversity of Several Viruses in Common Bean Plants Grown by the Small Scale Farmers in Tanzania

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Common bean (*Phaseolus vulgaris* L.) is the most important grain legume in developing countries especially in Africa and America. It has been estimated that common beans provide about 15% of total daily calories and 36% of total daily protein (Todorović *et al*., 2008). It is therefore not only grown for cash but also plays a nutritional role. Common beans may be intercropped or grown in rotation with non-leguminous crops such as maize and potato thereby playing role in improvement of soil fertility. Tanzania is among the top ten major producers in sub -Saharan Africa but the yield of common bean in Tanzania is still 500kg/ha because most of farmers are still using unimproved seeds such as Kablanketi which have low yields, but the yield of improved varieties for example Mshindi, Pesa, Lyamungu 90, Uyole 98, Uyole Njano ranges from 1000 to 1500kg/ha. Apart from abiotic and improper agronomic practices, low yields are caused by fungal, bacterial and viral diseases. Diseases of common beans caused by viruses have not been studied extensively in Tanzania mainly due to lack of diagnostic and detection tools. Thus a survey to document symptoms and collect samples for detection of viruses was carried out in 2015 in four agro-ecological zones. Samples were collected from four agro-ecological zones in Tanzania. Total RNA was extracted using the CTAB method with modifications. Then the next generation (deep sequencing of small RNAs) and Sanger sequencing techniques were employed to detect and characterize viruses, which infect common bean in Tanzania. The *denovo* assembly of small RNAs were achieved using a velvet assembler programs. In a survey, during collection of diseased leaf samples, symptoms were also observed and recorded. The symptoms recorded included mosaic, vein banding, rugosity, leaf curl and leaf malformation. NGS has revealed that viruses infecting common beans in Tanzania belong to at least four families, namely *Potyviridae*, *Bromoviridae*, *Tombusviridae* and *Endornaviridae*. It was further revealed that at molecular level, isolates of *Bean common mosaic virus* (BCMV) are diverse while a single strain of BCMNV was detected in all agro-ecological zones. It was found that viruses are distributed in all zones where they cause devastative disease symptoms such as leaf curl, mosaic, rugosity and malformation. From this study it was noted that viruses from various families are infecting beans in each agricultural zone of Tanzania and this has implication on breeding programs for management of viral diseases in Tanzania. The challenge of breeding for virus diseases resistance may be posed by the genetic diversity of BCMV.

Reference

Todorović, J., Vasić, M., Todorović, V., 2008. Dry and spring bean.Grafomark, Institute of Field and Vegetable Crops, Novi Sad, Faculty of Agriculture, Banja Luka, Serbia and BiH., 333 p.

Acknowledgments

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Notes

P37: Interaction of *Fusarium solani* species complex and Soybean Cyst Nematode on Root Rot Severity in Dry Bean

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Members of the *Fusarium solani* species complex (FSSC) and soybean cyst nematode (*Heterodera glycines*; SCN) are pathogens that co-exist in dry bean fields in the North Dakota-northern Minnesota dry bean production region. This region has the largest dry bean production in the United States. SCN has been spreading throughout the region and is a new threat to dry bean. These two pathogens infect roots, suggesting the potential of a disease complex. To study the interaction of SCN (HG type 0) with FSSC 11 (isolate 91-113-3), a pathogenic member of FSSC on dry bean, greenhouse studies were conducted on two kidney bean varieties, Montcalm and Rosie, using combinations of a low and a high level of pathogen inoculums. Montcalm was susceptible to Fusarium root rot while Rosie had moderate resistance. Plants were grown in Containers (164-ml volume) in 150 g of La Prairie silt loam. Greenhouse temperatures ranged from 22° to 25° C and plants were illuminated for 16 h/day with natural light and high-pressure sodium lamps (1,000 µE·m–2·s–1). Three Fusarium inoculum levels (0, 10^3 and 10^5 conidia/cm^3 of soil) and three SCN egg levels (0, 10^3 and 10^4/plant) were tested in all combinations and plant height was measured after 4 weeks and root rot severity (1 to 7 scale; RRS) and dry root weight were recorded after 6 weeks. Montcalm showed higher RRS compared to Rosie (mean of 3.9 to 2.7 and 3.8 to 3.5 at low and high FSSC 11 levels, respectively). Severity in Montcalm was significantly greater only at the highest SCN level when combined with the highest level of FSSC 11 (RRS 5.6) compared to FSSC 11 alone or the other pathogen combinations with RRS ranging from 3.9-4.7. There was no root rot on plants growing only in the presence of SCN in either variety. On the other hand, the root rot resistant variety Rosie showed significantly higher RRS with both the low and high level of inoculum of both pathogens compared to plants infected with FSSC 11 alone. For example, at the high Fusarium level alone RRS was 3.5 while with SCN at either egg level, RRS was 4.3 to 4.5. There were no consistent effects of the interaction of the two pathogens on plant height or root weight. Results indicated infection by SCN can increase dry bean root rot caused by FSSC 11 and can reduce the genetic resistance to FSSC 11 in a moderately resistant variety. This is the first report to study the interaction of these two important pathogens in dry bean. The results have important implications for dry bean root rot management strategies.

Notes

P38: Variation among edible podded PI accessions for pod and seed sugar concentrations

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We developed and evaluated over two years (2015 and 2016) a diverse sub-core of 94 Plant Introductions (PI) characterized as snap beans, Romano-types, and other beans eaten as edible immature pods, and 20 dry bean PI accessions. In addition checks included a kidney bean (Montcalm, Andean gene pool) as well as 8 cultivars represented the various market classes consumed as edible green pods currently grown commercially in the United States.

Large positive Spearman rank correlations were observed between years for glucose (0.89), fructose (0.73) and sucrose (0.62) concentrations. Over years, a large positive correlation (r=0.85**) was observed between the simple sugars Glucose and Fructose. In contrast a large negative correlation was observed between the disaccharide sucrose with both monosaccharides, glucose (r=-0.67) and fructose (r=-0.68). Glucose concentration had a mean of 16.1 mg g-1 dry weight, and ranged from near zero to over 40mg g^{-1} dry weight. P.I accessions with high concentrations of sucrose were generally both heirloom and modern commercial snap beans cultivars, e.g. Provider, Eagle, Cascade, Hystyle and BBL47. Fructose concentration had a mean of 42.2 mg g-1 dry weight, and ranged from near zero to over 70mg g^{-1} dry weight. Sucrose had a much lower concentration of 7.9 mg g-1 dry weight, and ranged from near zero to 14 mg g^{-1} dry weight.

P39: Gene Action and Inheritance of Resistance to Common Bacterial Blight in Common Bean

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Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv *phaseoli* (Xap) (Smith) Vauterin, Hoste, Kosters & Swings and its fuscans variant *X. fuscans* sbsp. *fuscans* (Xff), is an important disease of dry beans (*Phaseolus vulgaris* L.). Although several sources of resistance to CBB have been identified, the disease remains a major challenge in dry bean production worldwide. The study was initiated using two crosses between South African market class cultivars (Teebus-RCR 2/Teebus-RR 1, and RS 7/Tygerberg) to investigate the mode of gene action governing inheritance of resistance to CBB, estimate the heritability, and establish the significance of maternal effects in CBB resistance. Both additive-dominant and epistatic gene effects were detected in both crosses. Heritability of CBB resistance was moderate and maternal effects were significant in both crosses. This implies that backcross breeding, recombinant breeding, delayed selection and choosing a resistant parent as a female parent could yield positive results in CBB resistance breeding programs if these parents are to be used.

Notes

P40: Responses to selection of yield traits among climbing common bean genetic pyramids developed to manage multiple tropical diseases

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Despite high yield potentials of climbing beans, production is still low in tropical highlands due to several diseases. Therefore, resistance genes; fungal (Co4^2, Co5, P*ythium ultimum*, Phg-2) and viral (*I* and bc3) were pyramided using SCAR markers at CIAT. Pyramided bean populations and differentials were, evaluated in high and mid altitude districts of Uganda (Kabale and Kawanda) and Tanzania (Maruku and Kitengule) in 2016 and data collected on yield traits and diseases. Mean, flowering time was 48 days and 27.4g/100 seeds for pyramids. Pod load per plant ranged from 17 – 28 pods, above the best parent (21 pods for G2333) due to trangressive segregation. Pyramids were resistant to field Angular leaf spot (ALS), Anthracnose and BCMNV. ALS race 63:63 was present at all locations except Kabale. Anthracnose races were; 63:31 - Maruku, 39:14 - Kitengule and 8:15 - Kabale. Superior pyramided lines need further evaluation for yields in the tropics.

P41: Target SNPs Identified for CBB Resistance Marker Development in Dry Bean

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Common bacterial blight (CBB) on dry edible bean (*Phaseolus vulgaris*) is caused by *Xanthomonas axonopodis* pv. *phaseoli* (*Xap*) and is a worldwide disease. Lesions can occur on leaves, stems, pods and seeds causing reductions in seed quality and yield losses up to 50% due to loss of photosynthetic area. *Xap* is seed-borne and planting resistant varieties is a key management component. Host resistance is controlled by minor and major QTL identified across all eleven chromosomes of *P. vulgaris*. Phenotypic and genotypic data were collected for over 700 NDSU breeding lines across 9 market classes. Unifoliate and trifoliate leaves were inoculated under greenhouse conditions and evaluated on a 1 to 9 disease rating scale two weeks post inoculation. Targeted sequencing was conducted on all lines. Twenty-seven percent of breeding lines exhibited a resistant phenotype (disease rating of 3.5 or less) at the unifoliate and trifoliate growth stages. The highest and lowest proportion of lines exhibiting resistance were observed in the small red (57%) and navy (4%) market classes, respectively. Within the lines exhibiting resistance at the unifoliate stage, 16% did not have either SAP6 or SU91, two markers commonly used during marker assisted selection for *Xap* resistance. Neither SAP6 nor SU91 were present in 22% of the lines exhibiting trifoliate resistance. Preliminary association mapping indicates multiple genomic regions previously implicated in CBB resistance are present in the NDSU preliminary breeding lines, including regions on Pv1, Pv2, Pv3, Pv4, Pv5, Pv10, and Pv11. SNPs within these regions will serve as targets for developing suitable markers useful for marker assisted selection across genotypes from different genetic backgrounds.

Notes

P42: Ability of Great Northern Beans in Remediating High Cholesterol and Other Metabolic Effects Induced by a High Fat Diet

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Great northern beans are considered a rich source of nutrients, including protein, fiber, prebiotics, mineral, vitamin and other micronutrients. Many of these components (in isolation) have been showed to reduce LDL levels. However, research on the cholesterol lowering properties of great northern beans in response to a high fat diets do not exist. Therefore this study investigated the ability of great northern beans to reduce low-density lipoprotein cholesterol and other cholesterol markers in plasma and liver of hamsters fed an high fat diet and potential mechanism(s) responsible for the response. This study was achieved using four groups of eleven male hamsters each were fed four different diets, including a normal fat, high fat and high fat diets supplemented with great northern bean at 5 % (w/w) or bean hull at 0.5 % (w/w) for four weeks. The whole bean and hull were fully characterized before incorporation into the diet. The bean supplemented diet for both the whole bean and hull substantially reduced both plasma and liver cholesterol with a concomitant increase in fecal excretion of neutral sterols and bile acids. Animals fed the bean based diets presented with down-regulated small intestinal Niemann-Pick C1 like 1 (NPC1L1), acyl-coenzyme A: cholesterol acyltransferase 2 (ACAT2) and microsomal triacylglycerol transport protein (MTP), while up-regulated hepatic hepatic 3-hydroxy-3-methylglutaryl CoA reductase (HMGR), lanosterol 14α-demethylase (CYP51) and low-density lipoprotein receptor (LDLR) and small intestinal ATPbinding cassette transporters sub-family G member 5 (ABCG5). The underlying mechanism for cholesterol lowering effect of the bean was the induction of fecal cholesterol excretion via the suppression of small intestinal NPC1L1 and ACAT2 expression (refer below). An increase in the expression of hepatic HMGR and CYP51 and small intestinal ABCG5 that occurred for the bean fed hamsters also indicates that the supplemented diets maintained cholesterol homeostasis. Moreover, liver weights and average weight of the animals fed high fat diets supplemented with whole beans were similar to that of the low fat diet. This research is thus expected to aid bean breeders in producing great northern beans cultivars capable of consistently lowering cholesterol and other metabolic disorders.

Notes

P43: Climbing Bean Breeding for High Iron Content and Disease Resistance

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Climbing beans are the farmer preferred growth type in some regions in ES Africa and LAC (dominant in Rwanda and Colombia), due to higher yields and resilience. Anthracnose and BCMV are diseases that cause major yield losses in common bean, affecting production. In this study new climbing bean populations were generated (coded ENF, CGA, NCC) to combine high Fe and disease resistance. In trials in Darien and Popayan lines were identified with yields above 4000 kg / ha combining BCMNV and Anthracnose resistance. Double and triple crosses between parents with virus and anthracnose resistance, high seed iron and good agronomic traits were employed. Among the NCC population genotypes combining yields of up to 5500 kg/ha and seed Fe content of 90 ppm were identified. Evaluations validate the usefulness of SNP markers bc-3 and I genes for BCMNV and Co-3 for anthracnose as a selection tool for field resistance. These results show the genetic potential of the lines which are now being tested in target regions to be delivered to smallholder farmers.

P44: Advances in Climbing Bean Breeding and Marker Development for Breeders

Raatz B. et al, International Center for Tropical Agriculture, Andean bean breeding Program

Climbing beans are the farmer preferred growth type in some regions in ES Africa and LAC, mainly utilized by smallholder farmers. The latest climbing bean populations generated at CIAT combine high seed Fe content and disease resistance. In trials at locations Darien and Popayan lines were identified with yields above 3500 kg/ha combining BCMNV and Anthracnose resistance. In another population genotypes combining yields of above 3500 kg/ha and seed Fe content of 90 ppm were found. SNP markers tagging *bc-3* and *I* genes for BCMNV and *Co-3* gene for anthracnose were validated and used as a selection tool for filed resistance. Further examples for marker design from genotypes G21212, G104747 and G2333 based on sequencing data will be presented, and first data from the new outsourcing genotyping platform established by the “excellence in breeding” platform project that is now available for breeders.

P45: Bean Paste Quality of Selected White and Yellow Genotypes as a New Food Application

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Otebo beans grown in Michigan are exported to Japan for the production of bean paste, which is used in confectionary. Bean paste has a possibility of being used in the US market because of the increasing interest in gluten-free products and health-promoting food. However, the suitability of other white market classes for bean paste is unknown. In this study, three Otebo, three white and one yellow bean genotypes were tested for paste making quality, namely paste yield, color, texture and sensory profile (Figure 1). The seed quality traits were also analyzed for correlation with paste quality in order to identify traits that can be used in phenotypic screening for this end use. Both sensory evaluation and color measurement showed that the sweetened paste of the yellow bean retained white color better than others. It showed the potential of this yellow genotype for bean paste production in terms of color.

Notes

P46: Genome-Wide Association and Fine-Mapping of the Bct Allele for Resistance to *Beet Curly Top Virus* in Snap Bean

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Beet curly top virus (BCTV) (family *Geminiviridae*) is a curtovirus vectored by the beet leafhopper *Circulifer tenellus* (Baker) that causes serious crop damage in common bean. The most effective control of BCTV in bean is genetic resistance. The SCAR marker SAS08 (Larsen and Miklas, 2004) linked with *Bct* gene has been used in snap bean breeding programs for marker-assisted selection for resistance to BCTV, but new genomic tools provide the opportunity to fine map the locus. *Beet curly top virus* interaction phenotypes were obtained through agroinoculation of the SnAP with a proprietary infectious clone. Genotyping-by-sequencing of the 376 cultivars of the Snap bean Association Panel (SnAP) provided 23,304 SNPs to further elucidate the genetic basis of *Bct* by GWAS and fine mapping. These efforts revealed a resistance allele (*Bct*) at a single locus on Pv07 just 6 kb away from SAS08. Eight putative candidate genes were identified in a 48 kb region. Sanger sequencing of an uncharacterized locus, Phvul.007G036300, revealed a single SNP that was 99.5% predictive of the *Bct* resistance allele in the SnAP as compared to 94% predictive for the SAS08 SCAR marker. This SNP provides a more rapid and breeder-friendly molecular marker for *Bct* in snap beans.

P47: A QTL for Common Bacterial Blight Resistance on Chromosome Pv07 is Detected in Multiple Common Bean RIL opulations

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Common bacterial blight (CBB), caused by *Xanthomonas campestris* pv. *phaseoli* Smith (Dye) and X. *fuscans sbsp. fuscans* sp. nov., is a severe disease limiting common bean production and quality worldwide. Previous studies have identified markers associated with various QTL for resistance to CBB (reviewed by Singh and Miklas, 2015). Forty-nine recombinant inbred lines (RIL) from OT11-9/OV1-38 (O38) and 79 RIL from DOR364/XAN176 (DX) were screened in the greenhouse with inoculated leaves scored from 1 = no symptoms to 9 = completely diseased. Genotyping was performed using 5398 SNP BARC_3 Ilumina bead-chip. The QTL detected on Pv07 explained 33% of phenotypic variation in O38 population and 8% in DX population. The QTL region is positioned between 3.9 – 4.2 Mb (Pv07) where there is a cluster of 31 Cysteine-rich RLK genes. These genes are related to basal resistance toward bacterial pathogens by recognizing bacterial flagellin. Examination of other RIL populations (DOR 476/SEL 1309; BAT 93/Jalo EEP 558; Othello/VAX 3; and VAX 1/ICA Quimbaya) segregating for CBB resistance revealed the same physical position on Pv07 exhibiting a QTL (7 to 50% PVE) for resistance.

Notes

P48: Genetic Transformation of Common Bean (*Phaseolus vulgaris* L.)

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Stable transformation of common bean has been successful, to date, only for pinto beans using biolistic-mediated transformation, and regeneration from meristem-containing embryo axes remains the main approach to get stable transformation. In this report, we summarize a 5-year effort to develop a stable transformation system for common bean cultivars using *Agrobacterium tumefaciens*-mediated transformation. Embryogenic calluses and somatic embryos were induced from embryo axes but optimization of the parameters to further develop somatic embryos are still needed. Preculture of embryo axes on shoot induction medium for 6-8 weeks prior to stable transformation enhanced shoot production. Three strains of *A. tumefaciens* GV3101, LBA4404, and EHA105 were efficient in gene delivery. However, *A. tumefaciens* infection in stable transformation was associated with reduction in the survival rate of the infected explants. Optimal parameters for stable transformation, including using precultured explants, a low *A. tumefaciens* concentration, and a short co-cultivation time, that resulted in transgenic plants of 'Pinto Olathe' and 'Merlot' with herbicide resistance after 10-week selection. The results demonstrated stable transformation of common beans using *A. tumefaciens*. Potential use of transient/stable transformation for genome editing of common bean is discussed.

Notes

P49: General and Specific Combining Abilities as an Efficient Approach to Select Parents and Superior Populations for Resistance to White Mold in Common Bean

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White mold (WM), caused by fungus *Sclerotinia sclerotiorum*, is one of the most destructive diseases that affect the common bean (*Phaseolus vulgaris* L.) crop in the world, mainly in North and South American countries, including the United States, Canada, Argentina, and Brazil. Yield and seed quality losses up to 100% have been observed in these areas. This work reports on the selection of common bean parents and populations resistant to WM based on estimates of general combining ability (GCA) and specific combining ability (SCA) for WM severity in three environments (field nurseries) in Brazil. Partial diallel crosses were performed between parents from two groups: GI) three sources of partial resistance to WM identified abroad, and GII) nine Brazilian cultivars and elite lines. Twenty-seven populations were obtained and advanced in bulk up to F_6 generation, when they were screened for WM severity in three field nurseries in Brazil (Oratórios-MG, Viçosa-MG, and Goianira-GO). GCA and SCA estimates were obtained by the Griffing model IV. Significant effects of populations (P) and of interaction between populations and environments (P × E) for WM severity were shown by the combined analysis of variance. The overall mean of WM severity considering the combined analysis of the 27 populations in the three field nurseries ranged from 2.83 to 5.03, in contrast with the mean severity of 7.21 presented by the susceptible control cultivar BRS Requinte. The results also showed the existence of variability for WM severity among parents from GII but not among the parents from GI, indicating that the selection should focus on cultivars and elite lines. In general, the GI parents contribute with favorable alleles for resistance to WM in the tested populations, but the genetic effects depend of the environment. K-59, in Oratórios-MG and Viçosa-MG, and K-407, in Goianira-GO, contributed to increase the resistance to WM in the tested populations. Considering the GII parents, BRS Executivo and BRS Esplendor performed better across the three environments. The populations identified as most promising to be explored to obtain common bean lines resistant to WM were K-59/BRS Executivo, PI204717/BRS Campeiro, PI204717/Jalo Precoce, K-59/BRS Radiante and K-407/ BRS Cometa, which presented significant and negative effects of the SCA.

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Notes

P50: Fungicide Sensitivity and Population Structure of *Sclerotinia Sclerotiorum* Isolates from Brazil, Argentina, and the U.S.

Miorini TJJ, Pannullo A, Higgins RS, Everhart SE, Steadman JR

Sclerotinia sclerotiorum is a necrotrophic fungal pathogen of more than 400 plant species. One method of disease control is fungicide applications. Although *S. sclerotiorum* is predicted to have low risk of resistance development based on expected population genetic variability, intensive use of fungicides, can select for fungicide resistance. An understanding of fungicide sensitivity and structure of *S. sclerotiorum* populations is needed. To address this, we selected 120 isolates from soybean (n=96) and dry bean (n=24) that were collected in Brazil (n=100), Argentina (n=5), and the U.S. (n=15). To characterize fungicide sensitivity, a discriminatory dose (DD) was obtained for a set 23 isolates to determine sensitivity (EC_{50}) to 8 fungicides. The average and standard deviation (SD) of EC_{50} of each fungicide was used to create a single DD for assessments. Subsequently, the EC_{50} was determined for isolates in the 90^{th} percentile of growth. Resistance factors (RF) were calculated in three ways: the highest EC_{50} was divided by 1) baseline of 23 isolates, 2) difference between maximum and minimum EC_{50} in the baseline, and 3) two times the SD. Reduced sensitivity for boscalid was found and RF_1 was highest (5.39). Reduced sensitivity to both dicarboximide fungicides was also found, however, RF_3 yielded highest values (14.1 for iprodione and 13.40 for procymidone). Overall, results showed a low frequency of reduced sensitivity isolates, nevertheless repeated application of fungicides with the same mode of action, such as procymidone and iprodione, should be avoided. A subset of 95 isolates from soybean was genotyped using 11 SSR loci and identified a total of 84 unique multilocus genotypes (MLG). Loci had an average of six alleles, where the population in Brazil had 26 private alleles, Nebraska had seven, and Argentina had two. There was significant difference in populations subdivided by state (AMOVA $p<0.01$) and by country ($p<0.001$). Despite clonal population structures, results suggest higher levels of genetic diversity in South America may allow fungicide resistance to emerge with intensive fungicide use.

Notes

P51: Search for Resistance to Bean Rust in Nebraska, Zambia and Uganda: Field and Greenhouse Tools

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Bean rust is a common disease in Africa and the Americas. The pathogen, *Uromyces appendiculatus,* has both distance urediniospores for dissemination and survival teliospores that contribute to its ability to cause significant yield losses in dry beans. Fungicides can help manage bean rust, but timing is critical and costs reduce profits. Thus disease resistance is the most cost effective management option. The bean rust pathogen has many races that need to be identified to facilitate breeding for resistance. To identify the races in greenhouse environments, bean lines with specific rust resistance genes are inoculated with urediniospores from fields and responses are recorded. Another method uses bean plants with specific resistance genes placed in fields with bean rust. This mobile nursery is a set of differential bean lines at the primary leaf stage in a plastic tray. When placed in a field with rust, the plants will be naturally inoculated. Placing the nursery in a mist chamber with high humidity for 12-16 hours then transferring to a screen house or greenhouse for 14 days allows rust to develop. Bean lines identified with resistance to local races can be crossed with locally adapted bean varieties. Rust resistance genes of Mesoamerican origin are typically resistant to Andean rust races and Andean origin genes are resistant to Mesoamerican rust races. This low cost technology available for breeders will facilitate development of new bean germplasm with rust resistance and new bean varieties for local small farm and large farm growers that yield well and beans that cook in a shorter time, and have more nutrients.

Notes

P52: Molecular and Culture Based Tools for Accurate Identification of Root and Crown Rot Primary Fungal *Pathogens of Dry Beans in Different Countries*

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Root/crown root (RCR) has emerged as an important production constraint of beans in Africa and the Americas due to various factors such as climate change effects and lack of genetic resistance to target pathogen(s), In Africa, in addition, factors such as lack of certified seed and proper soil management have exacerbated yield losses due to RCR. Molecular and culture based methods were compared to identify the RCR fungal pathogen(s). RCR bean samples were collected from 2013-2015 at the breeder nursery sites and farmer fields in Nebraska, Zambia and Mozambique. Diseased and healthy interface tissue was either cut for direct plating on agar media or ground for DNA extraction from homogenates used for blotting onto FTA® cards. DNA extracted from FTA® cards and root tissue were used for metagenomics analysis by the Illumina System and 454 pyrosequencing of small subunits of the rRNA gene and PCR amplification with specific primers. Isolates from cultures were identified by morphology and sequences of the ITS rRNA region and the elongation factor gene and tested for pathogenicity. Multivariate analysis was used to compare results of the methods. Analysis of DNA from plant tissue and ground tissue extracts spotted on FTA cards identified *F. oxysporum*, *F. solani* and other species of the Fusarium complex as the most abundant reads and Operational Taxonomic Units (OTU) in the three countries. *Fusarium* spp. were also detected in over 70% of the samples analyzed by conventional PCR using specific primers and also had the highest frequency of recovery (>0.8) from culture. Over 90% of the Fusarium species recovered were pathogenic. Identification of a different primary pathogen associated with RCR in Nebraska, Zambia and Mozambique provides evidence and isolates to use in screening for RCR resistance and incorporating in bean breeding.

P53: Reduction in Root Secondary Growth as a Strategy for Phosphorus Acquisition

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We tested the hypothesis that reduced root secondary growth of dicotyledonous species improves phosphorus acquisition. Functional-structural modeling in *SimRoot* indicates that in common bean (*Phaseolus vulgaris),* reduced root secondary growth reduces root metabolic costs, increases root length, improves phosphorus capture, and increases shoot biomass in low phosphorus soil. Observations from the field and greenhouse confirm that under phosphorus stress, resource allocation is shifted from secondary to primary root growth, genetic variation exists for this response, and reduced secondary growth improves phosphorus capture from low phosphorus soil. Under low phosphorus in greenhouse mesocosms, genotypes with reduced secondary growth had 39% smaller root cross sectional area, 60% less root respiration, 27% greater root length, 78% greater shoot phosphorus content, and 68% greater shoot mass than genotypes with advanced secondary growth. In the field under low phosphorus, these genotypes had 43% smaller root cross sectional area, 32% greater root length, 58% greater shoot phosphorus content, and 80% greater shoot mass than genotypes with advanced secondary growth. Secondary growth eliminated arbuscular mycorrhizal associations as cortical tissue was destroyed. These results support the hypothesis that reduced root secondary growth is an adaptive response to low phosphorus availability and merits investigation as a potential breeding target.

Notes

P54: Effect of drought on bean cooking time and water absorption using germplasm selected for root rot resistance for Mozambique and Zambia

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Root rot and crown rot of dry beans has becoming a limiting factor in Mozambique and Zambia. *Fusarium* spp. were identified as the major pathogens associated with root rot crown disease in Zambia and Mozambique. Bean cooking time is a major concern in Africa because longer cooking time requires use of more energy resources. Based on common dry bean trials planted in Zambia and Mozambique in 2015, we assembled a common root rot trial of 22 entries to be planted in both countries. This trial was also planted at Mitchell, NE in 2016 to explore the effect of drought on cooking time for the above entries. This was accomplished by comparing the cooking time of beans grown under drought and non-drought conditions. The lines were grown in replicated trials in adjacent irrigated (non-stressed, NS) and non-irrigated (drought-stressed, DS) plots. Both NS and DS blocks were irrigated until flowering to ensure good plant establishment and normal vegetative growth. Thereafter, the stressed block was not irrigated. After beans were harvested and stored for four to five months, a Matson Bean cooker was used to evaluate the effect of drought on cooking time. Seed from each plot was processed separately using the following procedures. A 60-seed sample was soaked in distilled water overnight (16 h). Initial seed weight was recorded. Distilled water was added to the cooker and heated to 98°C, then 24 of the pre-soaked seeds were placed in the template in the cooker to align the seeds with the plungers. Final seed weight was recorded and water absorption was calculated. An observer recorded the time when the beans were placed in the cooker and when 80% were cooked (indicated by the plungers dropping). Some sources of root resistance grown under DS took longer to cook and had less water absorption than grown under NS conditions.

P55: Characterization of Nested Association Mapping Population in Dry Bean

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Understanding the genetic bases of different traits agronomic and quality traits are important for efforts to breed improved lines in common bean. A Nested Association Mapping (NAM) population of $F_{4:5}$ recombinant inbred lines (RILs) was created with the cultivar Ex Rico 23, and 10 founder lines (Apex, Compass, Cruiser, Mist, Envoy, OAC Rex, Rexeter, T9905, Gryphon, Laser) that span the genetic diversity of Ontario Mesoamerican germplasm. The NAM population was evaluated for different agronomic traits in the field (including: flowering time, maturity, and yield) in four environments. It will be genotyped using Genotyping by Sequencing (GBS). The results of the phenotypic characterization will be presented.

Notes

P56: Waterlogging Tolerance in Wild Accessions of Common Bean (*Phaseolus vulgaris* L.) and Related Species

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North Dakota (ND), with approximately 38% of the national production, is the top producer of common bean in the United States. However, 35% of ND lands producing common bean are located on floodplains. The effect of waterlogging and associated abiotic and biotic factors results in 16-20% yield losses annually. Previous research has identified some waterlogging tolerant common bean genotypes; however, testing wild accessions and closely related species under waterlogging conditions is important for identifying accessions harboring tolerance. This study will also aid in understanding morphological and physiological adaptations related to waterlogging tolerance in common bean. With the inclusion of GWAS, this study will also attempt to detect waterlogging tolerance alleles that have yet to be identified in or incorporated into modern genetic material. The objective of this study is to identify waterlogging tolerant genotypes from wild accessions of common bean and closely related species that might be useful as parental sources in ND dry bean breeding programs. Moreover, the data generated in this study will be used to elucidate the evolutionary patterns of waterlogging tolerance among wild and domesticated bean accessions, as well as related species. For this study, a set of 348 dry bean accessions provided by the United States Department of Agriculture, and composed of 137 runner beans (*P. coccineus)*, 9 tepary beans (*P. acutifolius)*, 94 year-long beans (*P. dumosus* Macfady), and 100 wild beans (*Phaseolus vulgaris* L. var. *aborigineus* (Burkart) Baudet) and 5 (*P. vulgaris* L.) were used to identify differences in waterlogging tolerance among accessions. A greenhouse experiment was set up in a Repeated Augmented Split Block Design. Genotypes were tested under waterlogging and normal irrigation with two replicates for each genotype and treatment. Each replicate was subdivided into 10 blocks, each including 23 test entries and 5 checks. Genotypes were randomly assigned to blocks. Waterlogging and normal irrigation treatments will be applied for ten days to previously irrigated plants at the start of the V2 phenological stage. After draining and harvesting plant material, the following traits are measured: chlorophyll content (SPAD*unit), stomatal conductance (mmol m^{-2} s^{-1}), photosynthetic efficiency (Fv/Fm), leaf area (cm^2/ plant), adventitious rooting (scored from 0 to 5), total weight (TW, g), shoot weight (SW, g), root weight (RW, g) and hypocotyl length (HL, cm).

P57: Races of *Colletotrichum lindemuthianum* in Common Bean from Parana State

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The objective of this study was to characterize isolates of *Colletotrichum lindemuthianum* from different regions of Paraná State, Southern of Brazil. Nineteen isolates were obtained, through monosporic isolation process, and evaluated according to their virulence using the set of anthracnose differential cultivars of common bean. Thirteen races were identified: 1, 9, 17, 24, 25, 27, 72, 73, 81, 89, 95, 339 and 345. Interestingly, all of them were classified as Mesoamerican. This is the first occurrence report of race 24 in Paraná State, and race 345 in the world.

Notes

P58: Relationship of Root Architecture with Total Plant Biomass and Seed Yield in Common Bean (P*haseolus vulgaris* L.) Under Glass House Conditions

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Research on root architecture in common bean (*Phaseolus vulgaris* L.) has been neglected for 150 years. The objective of this study was to characterize root architecture of ten bean lines including landraces, old and modern cultivars adapted to seed production in USA and Mexico. Plants were grown to maturity in a sand/turface medium in polyethylene bags supported by PVC tubes, 100 cm x 10 cm diameter, in a cooled glass house under well water conditions. Above ground, characters including shoot biomass and yield components were recorded. Root traits consisting of root biomass from 0 to 30 cm and 30 to 100 cm, and length of the longest root were recorded. Hypothesis tested included: 1) seed yield is correlated with total biomass, 2) seed yield is correlated with total root biomass, 3) seed yield is correlated with total shallow or deep root biomass, 4) seed yield is correlated with total plant biomass.

P59: Pre-Germination Flooding Tolerance of Middle American Dry Bean Genotypes

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Worldwide, flooding occurrences have increased in frequency over the last several decades. Seed germination is dependent upon oxygen and therefore, germination stages of crops tend to be particularity sensitive to flooding. Dry bean (*Phaseolus vulgaris* L.) is the most economically important edible legume species and it is also one of the most sensitive crops to flooding. Previous studies have shown that pigmented dry bean genotypes (black, small red, and pink) are more tolerant to flooding at germination stages compared to unpigmented (navy and great northern) genotypes. To further understand the mechanism (s) of tolerance, genotypes from the Middle American Diversity Panel (MDP) were separated based on seed coat color and screened for pre-germination flooding tolerance. The screenings were performed in greenhouse conditions as a randomized complete block design (RCBD) with a split-plot arrangement, the treatments (non-flooded and flooded) as the main plots and genotypes as the subplots. For the unpigmented genotypes, 85 genotypes were subjected to 3h of pre-germination flooding stress and screened for germination rate (GR; percent germinated out of 10 seeds planted), plant height (PH; cm), root (RW), shoot (SW), and total weights (TW; g) 14 days after planting. Significant treatment effects were detected for GR and GR ranged from 23-100% with an average of 89% for the non-flooded treatment whereas it ranged from 0-93% with an average of 14% for the flooded treatment. 'Royalty' (a cream-colored seed tolerant check) had a GR of 93% in the flooded treatment which was significantly higher than the second most tolerant genotype, 'Verano' with a GR of 63%. Genotype-by-treatment interactions were significant for all traits except PH which suggests that the different response of genotypes to pre-germination flooding stress can lead us to tolerant genotypes. The ten most tolerant and ten most susceptible genotypes will be analyzed for protective metabolic enzymatic activity that could be involved in the pre-germination flooding tolerance.

Notes

P60: Assessment of Dry Beans (Phaseolus Vulgaris L.) Tolerance to Soybean Cyst Nematode (Heterodera Glycines Inchinohe) and the Effects of Biological and Chemical Controls in a Controlled Enviroment

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Soybean cyst nematode (*Heterodera glycines* Ichinohe; SCN) is a major pest of soybean (Glycine max (L.)) production worldwide. SCN also impacts dry bean (*Phaseolus vulgaris* L), an important plant source of protein in worldwide. One Andean (kidney bean) and one Mesoamerican (black bean) cultivar were evaluated for SCN tolerance with and without treatment with biological nematicides *Pasturia nishizawae* and *Bacillus firmus*, as well as the chemical nematicide fluopyram, at various concentrations. These treatments, along with resistance and susceptible soybean cultivars were planting in autoclaved sand in a controlled environment for 30 days. The female index (FI=the average number of females on the test plant / the average number of female number on Lee 74 x100) of SCN and the dry weights of above ground plants were measured. Kidney bean was more susceptible with a higher FI than black bean. Only seed treatment *B.firmus* + fluopyram reduced the FI of kidney bean, but there was no response was measured in black bean.

P61: Characterization and Distribution of an Emerging Race of Anthracnose in Michigan

Awale H, Bornowski N, Wright EM, Varner GV, Kelly JD

Anthracnose (*Colletotrichum lindemuthianum*) is a fungal pathogen of beans that can cause significant economic loss when field conditions are conducive to infection. The pathogen is classified into a race structure based on its virulence on a set of differential cultivars, each with an assigned binary value. Numerous isolates collected from Michigan fields have been characterized in recent years and consistently characterized as Race 73. A number of resistant varieties have been developed by deploying the *Co-1* gene, which confers resistance to the previously known races present in Michigan, including Race 73.

In 2017, a severe infection of anthracnose was observed in a field of Zenith black beans in Alcona County, in Northern Michigan. Infected plants were collected, DNA was isolated from leaves and the NDSU-IND_50.2219 marker on Pv01 was used to confirm the presence of the *Co-1* gene. A fungal isolate was cultured from an infected pod on Mathurs Agar and increased until sufficient quantity of sporulating plates were obtained to inoculate the complete set of differential cultivars with a spore suspension. The race of the isolate was determined by summing the binary value associated with each of the susceptible differentials.

A survey of the bean growing region of Michigan was made by sampling thirty-seven infected fields. Both resistant and susceptible varieties across six market classes and eight counties were sampled. Nine samples were chosen for initial study based on geographic location to better understand the distribution of the race that overcomes the *Co-1* gene. Isolates were made by culturing infected pods and then inoculating the differential series to determine the race of the isolate. The remaining samples will be characterized in the future. The information from this survey will be useful to guide variety selection by growers based on what race is present in their region. It will also help inform breeding decisions for deployment of additional anthracnose resistance genes in future bean cultivars.

Notes

P62: Development and Application of 50K Versus 6K Beadchip SNP Assays in Soybean May Provide a Reference for Developing SNP Assays in Common Bean

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We developed two Illumina Beadchip assays, SoySNP50K and BARCSoySNP6K containing >50k and 6k single nucleotide polymorphisms (SNPs) in soybean, respectively. The assays could efficiently characterize thousands of DNA variations in a large number of samples in less than a week. The markers in the assays were carefully selected based on their position and flanking sequence specificity in the genome, polymorphism rate among accessions, and genotyping quality. With the SoySNP50K BeadChips, we have already completed the analyses of large numbers of germplasms and breeding lines created by soybean breeders. These include the entire USDA Soybean Germplasm Collection with approximately 20,000 accessions. The datasets are sources for the detection and mapping of quantitative trait loci and genes in the germplasm via association mapping, the construction of haplotype blocks, and determination of LD decay in the soybean genome. It is known that the recombination event in the soybean genome is low, breeders usually don't need a large number of markers to characterize the progeny from a bi-parental cross. Evaluation of too many markers will not only increase the cost but also generate redundant information. In order to efficiently map the genes in the bi-parental crosses, we developed a new breeder's tool –BARCSoySNP6K BeadChip containing 6k markers, these markers were carefully selected from SoySNP50K based on their position in the genome and haplotype map, polymorphism among accessions, and quality of assay on 20,000 accessions. Analysis of progeny from two large families genotyped with SoySNP50K containing 50,000 SNPs vs. the BARCSoySNP6K showed that position of the markers along linkage maps, position of seed size quantitative trait loci (QTL) and number of unique bins were consistent based on the two tools, however, the rate of redundant markers were dramatically reduced with the BARCSoySNP6K. We also observed that this tool has the same efficiency and resolution to identify genes controlling traits as that of whole genome sequencing approach in most populations created by breeders with population size less than 350.The BARCSoySNP6K is an excellent tool for the detection of QTL and for assessing genetic diversity in the families derived from bi-parents. The work on soybean may serve as a reference to common bean.

Notes

P63: The Rhizosphere Microbiome as an Auxiliary Breeding Component in Common Bean Against *Fusarium Oxysporum*

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The rhizosphere microbiome plays a key role in plant growth and health, providing a first line of defense against root infections by soil-borne pathogens. Here, we investigated the composition and metabolic potential of the rhizobacterial community of different common bean (*Phaseolus vulgaris*) cultivars with variable levels of resistance to the fungal root pathogen *Fusarium oxysporum* (*Fox*). For the different bean cultivars grown in two soils with contrasting physicochemical properties and microbial diversity, rhizobacterial abundance was positively correlated with *Fox*-resistance. Pseudomonadaceae, Bacillaceae, Solibacteraceae and Cytophagaceae were more abundant in the rhizosphere of the *Fox*-resistant cultivar. Network analyses showed a modular topology of the rhizosphere microbiome of the *Fox*-resistant cultivar, suggesting a more complex and highly connected bacterial community than in the rhizosphere of the *Fox*-susceptible cultivar. Metagenome analyses further revealed that specific functional traits such as protein secretion systems and biosynthesis genes of antifungal phenazines and rhamnolipids were more abundant in the rhizobacterial community of the *Fox*-resistant cultivar. Metatranscriptome data revealed that community assembly in the rhizosphere follows niche-based mechanisms, presenting lower diversity and distinct community structure comparing to the bulk soil. In comparison with the susceptible plant, the microbiome of the *Fox*-resistant cultivar presented high expression of genes affiliated to the family Paenibacillaceae, a group known by its antifungal activity. The *Fox*-resistant cultivar also presented high expression of genes related to metabolism of nutrients and specific functional traits related to pathogen suppression, such as motility and chemotaxis, and phenazine and colicin V. Network analysis showed similar results to the metagenome approach, revealing a more complex community in the *Fox*-resistant cultivar and pointed the genus *Paenibacillus* as a keystone species in the microbiome. Our findings suggest that breeding for *Fox*-resistance in common bean have co-selected for other unknown plant traits that support a higher abundance of specific beneficial bacterial families in the rhizosphere with functional traits that support a more complex rhizosphere microbiome and reinforce the first line of defense against the pathogen.

Keywords: rhizosphere microbiome, plant-microbe interactions, metagenome, metatranscriptome

Notes

P64: Adaptability and Stability of Elite Lingeages and Common Bean Cultivars of Different Commercial Classes for the Three Seasons of Cultivation in Minas Gerais, Brazil

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This work aimed to identify elite lineages and cultivars of different commercial classes with better agronomic performance, adaptability and productivity stability at different growing seasons in the state of Minas Gerais, Brazil. The experiments were carried out in the cities of Sete Lagoas, Uberlândia, Janaúba and Jaíba, in the seaons of "water", "dry" and "winter" seasons between the years of 2010 and 2013. The analysis of adaptability and stability of lineage productivity was performed by the method of Annicchiarico (1992). The lineage CNFRx 15275 showed high productivity, adaptability and stability in all growing seasons.

P65: Towards Understanding the Effect of Pathogen and Salinity on Root Rot Disease in Common Beans

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Root rot diseases of common beans are often caused by fungi belonging to the *Fusarium* and *Rhizoctonia* genera. These biotic factors cause significant common bean yield reductions through weakened root systems and poor plant stands. Additionally, abiotic factors such as salinity disrupts plant growth and development, as well as disturbs the nitrogen-fixing, symbiotic interaction between common bean and bacteria. Salinity also affects fungal mycelial production, conidial formation and spore germination. To have a comprehensive view of how these pathogens and salinity affect the bean crop, we want to dissect the effect of salinity on these pathogens when grown in culture. Our objective was to evaluate the effect of salinity on the mycelial growth of fungi when grown in sodium chloride (NaCl)-amended potato dextrose agar (PDA) plates. The root-rot-causing fungal pathogens used were one isolate each of *F. solani* f. sp. *phaseoli* and *F. graminearum* and three isolates of *R. solani*. The isolates were subjected to low (50 mM), medium (150 to 250 mM) and high (400 mM) salt concentrations. At Day 3, 6 and 10 after subculture, mycelial growth was measured at two perpendicular points across the colony. Longitudinal data analysis in R was performed to determine the optimal salt concentration affecting each strain and determine ideal time points for data collection. Initial results suggest that the root pathogens can tolerate low salt concentrations where mycelial growth is no different from the control (no salt added). At medium salt concentrations, these isolates have a varied response to the added salt at Day 3, with most isolates showing significant growth reductions starting at 150 mM. Taking into consideration the differential growth rates of these pathogens across species and isolates, we found that at Day 6, some isolates only show significant growth reduction at 400 mM. Effect of salinity on radial growth can be observed as early as Day 3.

Notes

P66: Identification and Characterization of Root Rot Pathogens of Dry Bean in Michigan

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A root rot survey of 29 dry bean fields in seven counties was conducted from 2014-2017 in Michigan. A total of 280 oomycete, 725 *Fusarium* spp., and 213 *Rhizoctonia solani* isolates were recovered from diseased seedlings. Identification of oomycetes based on sequencing of the ITS region using rDNA, identified 24 *Pythium* spp., *Phytophthora gonapodyoides* and *Phytopythium vexans*. The translation elongation factor-1α gene was utilized to assign Fusarium isolates into *Fusarium solani*, *F. oxysporum*, *F. graminearum*, and *F. incarnatum-equiseti* species complexes. The *F. solani* species complex represented 56% of the isolates identified (n=304), followed by the F. *oxysporum* species complex at 24%. Further species level identification of isolates belonging in *F. solani* species complex clade 2 were made using the intergenic spacer region of rDNA. *Fusarium brasiliense*, *F. cuneirostrum*, and *F. phaseoli* comprised 43, 41, and 16%, respectively of the 76 isolates identified. This is the first report of *F. brasiliense* being isolated in the US and associated with root rot of dry bean. *Rhizoctonia solani* anastomosis groups were determined using RFLP of the ITS region of rDNA. Multinucleate AG2-2 was detected in the highest abundance, however AG1-1a, AG4, AG5, and AG11 were also identified. Seedling pathogenicity assays were conducted to evaluate a subset of isolates representative of each genera of root rot causing pathogen groups on black bean 'Zorro' and red kidney bean 'Red Hawk'. There were five *Pythium* spp. that reduced emergence, while root dry weight of 'Red Hawk' and 'Zorro' was reduced significantly by 13 and 9 *Pythium* spp., respectively. Results from the pathogenicity assays showed isolates within AG2-2 were the most virulent causing seed rot and severe root rot. Isolates within the *F. solani* and *F. oxysporum* species complexes caused the most severe root rot on both seed types. *Fusarium solani* isolates caused more rot of the tap root, whereas, some of the *F. oxysporum* isolates caused severe root stunting and interveinal necrosis of foliage.

Notes

P67: Efficacy of a Succinate Dehydrogenase Inhibitor Against Clade 2 Members of the *Fusarium Solani* Species Complex

Witte, Alexander, Michigan State University

Fungi within clade 2 of the *Fusarium solani* species complex (FSSC) include pathogens causing severe diseases on legume plants worldwide. In North and South America, members of the FSSC clade 2 species are the causal agents responsible for significant yield loss in dry beans and soybeans as a result of causing bean root rot and sudden death syndrome, respectively. The objectives of this study were to evaluate the *in vitro* sensitivity of FSSC clade 2 pathogens to the succinate dehydrogenase inhibitor (SDHI) fungicide fluopyram, and to demonstrate soybean seed treatment efficacy of an SDHI when challenged with high levels of FSSC inoculum.

Applying fungicide seed treatments to soybean and dry bean has become an important method in Fusarium disease management. To test fungicide efficacy prior to field trials, it is useful to conduct sensitivity assays *in vitro*. The poison plate assay is considered the "gold standard" technique for determining fungicide sensitivity. Currently, the sensitivity of 90 isolates among *Fusarium tucumaniae, F. crassistipatum, F. cuneirostrum, F. solani, F. phaseoli, F. brasiliense, F. azukicola,* and *F. javanicum* has been evaluated using a poison plate assay. Fluopyram was amended into half-strength potato dextrose agar at a final concentration of 0, 0.5 1.0, 3.0, 5.0, 7.0, 10.0, and 50.0 µg ml^{-1}. Isolates were aseptically transferred to 3 replicate plates for evaluation of fungicide dose responses. Preliminary results show that EC_{50} values (effective concentration which reduces mycelia growth by 50%) for 76 isolates screened was less than 3.0 µg ml^{-1}, indicating that fluopyram inhibits mycelia growth across seven Fusarium species. Only one species, *F. javanicum*, was found to be significantly less sensitive to fluopyram (EC_{50} > 50.00 µg mL^{-1}).

Field trials have demonstrated the efficacy of fluopyram-treated soybean seeds in preventing root rot and soybean sudden death syndrome (SDS) caused by *Fusarium virguliforme* in Michigan. However, it remains unclear how effectively fluopyram inhibits growth in other members of FSSC found in North and South America. A growth chamber seedling assay is being conducted to challenge seed treated with ILeVO (Bayer Crop Sciences, a.i. fluopyram) with inoculum from 5 SDS-casuing Fusarium species (*F. virguliforme, F. tucumaniae, F. crassistipitatum, F. cuneirostrum,* and *F. phaseoli*.) This research aims to provide valuable information on Fusarium disease management.

Notes

P68: Mycelial Compatibility, Pathogenicity/Aggressiveness and Oxalic Acid Production by *Sclerotinia sclerotiorum* on Bean Plants

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Mycelial compatibility groupings (MCGs), pathogenicity/aggressiveness, and virulence factors such as oxalic acid (OA), are used to study the diversity of *Sclerotinia sclerotiorum* within a region. The objectives of this study were to determine MCGs, aggressiveness, and OA production on *Phaseolus lunatus* (lima bean), *P. vulgaris* (common bean), and *Glycine max* (soybean) among isolates of *S. sclerotiorum*. MCGs were determined by pairing 25 isolates, collected from different locations and crops, in all possible combinations on Diana Sermons (DS) medium. Each isolate was also paired with itself and with a control (pure PDA plug). Mycelial reactions were recorded after 7 days and grouped as (i) incompatible when an apparent line of demarcation was observed between the confronting paired isolates, and as (ii) compatible if there was no line of demarcation. Chi-square analysis was used to determine the frequency of occurrence of compatibility vs. incompatibility. Aggressiveness was evaluated by inoculating one week old cultures of *S. sclerotiorum* grown on PDA on top of cut stems of one month old lima, soy-, and common bean plants using sterile drinking straws. The inoculated plants were incubated for 8 days in the greenhouse. The development of lesions was evaluated using a 1-9, Modified Petzoldt and Dickson Scale where: 1 = no lesion and 9 = lesions that extended beyond the third node from the straw. Lesion size was also measured in cm. Data were analyzed using PROC MIXED in SAS with block as a random factor and treatment as a fixed factor. To further test virulence of the isolates, OA from infected tissues was quantified using a diagnostic kit (BioVision). A total of 82% of the mycelial reactions were incompatible whereas 18% were compatible. There was a significant difference (X^2 = 131, P<0.01) between the frequency of the two reactions. The isolates that were scored as incompatible were subcategorized into 12 MCGs. There was no correlation between the crop of origin or location of origin of isolates, and their MCG. All the isolates were compatible with themselves. Aggressiveness (lesion size) of *S. sclerotiorum* varied significantly among the crops (P=0.019), but not among cultivars. The estimates of lesion size were 5.6 cm, 6.0 cm, and 8.0 cm for lima, soy-, and common bean, respectively. OA was not significantly different among the crops nor among the isolates. However, there were significant differences among cultivars.

Spearman Correlation Coefficients showed weak correlation between lesion size and OA production. This may indicate that low levels of OA produce large lesions on susceptible crops/cultivars and higher levels of OA are necessary for production of large lesions on resistant crops/cultivars. Alternatively it may indicate that the role of OA in lesion production is more complex than previously thought.

Notes

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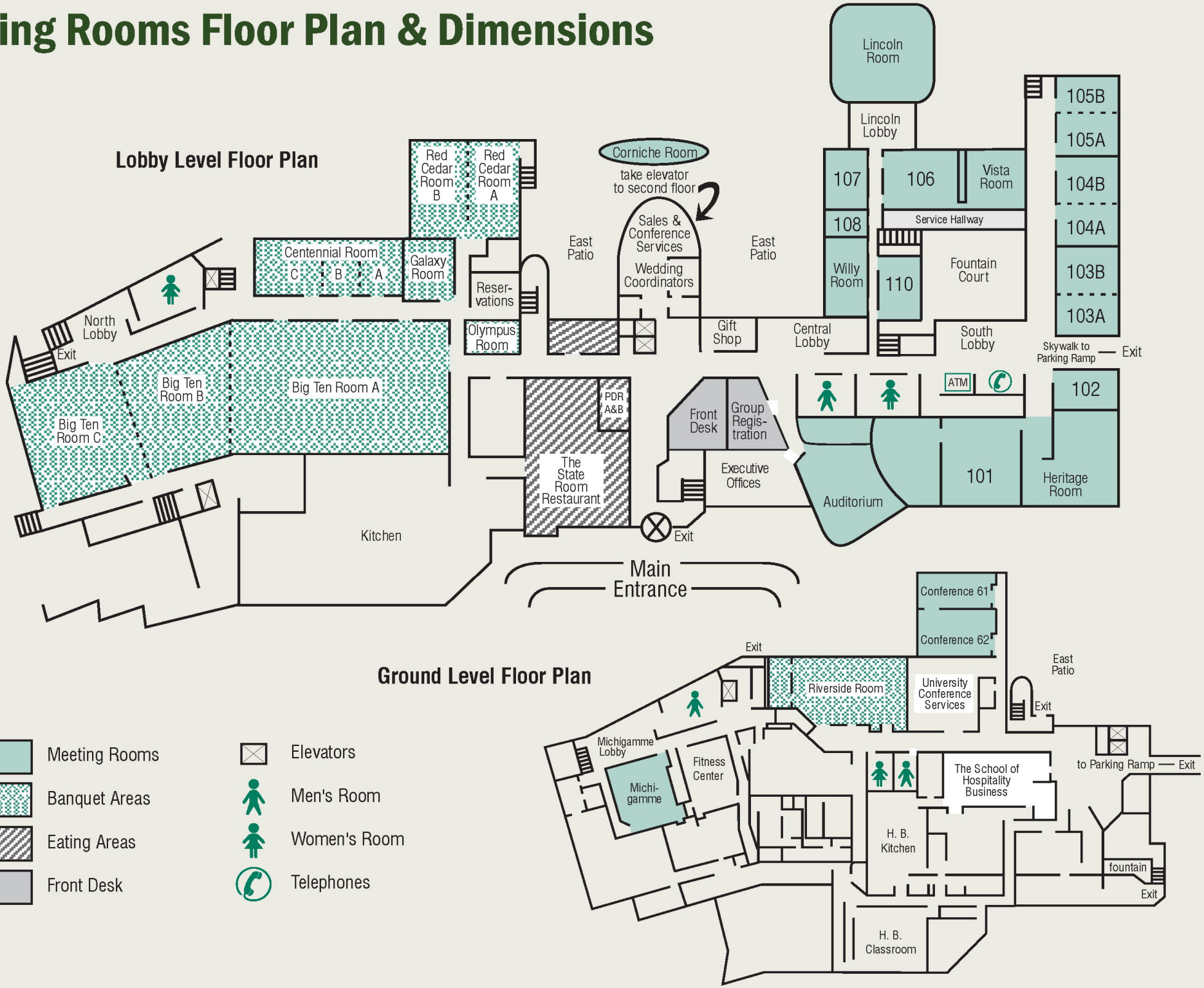
Meeting Rooms Floor Plan & Dimensions

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