

# Common Bean Disease Workshop on Angular Leaf Spot and Root Rot

Protea Hotel Kruger Gate

Skukuza, South Africa

July 20-23, 2015

Organized by:

Deidre Fourie	Local host ARC, Republic of South Africa
Phillip Miklas	USDA-ARS, Washington State
Talo Pastor-Corrales	USDA-ARS, Maryland
Timothy Porch	USDA-ARS, Puerto Rico



# PROGRAM

## SUNDAY 19 JULY

- 16:00 - 18:00      **Registration**
- 19:00                **Meet and Greet Function**  
Sponsored by Syngenta

## MONDAY 20 JULY

07:00-08:30 Registration

**Session 1    Opening Session**  
Moderator:    Phil Miklas

08:30-09:00      **Welcome and introduction of participants**  
Deidre Fourie (ARC)

**Session 1    Angular Leaf Spot Pathology**  
Moderator:    Dr. Robin Buruchara

- 09:00:10:00 K1      **Keynote Address**  
A review of the angular leaf spot disease of common bean in Latin America and Africa and implications for improved disease management  
**M.A. Pastor-Corrales**, C. Jara, M. Galván, A. Wendland, and E.A. de Souza
- 10:00-10:15 T1      Towards genetic characterization of *Pseudocercospora griseola*, the causative agent of angular leaf spot of common bean in Tanzania  
**L.A. Chilagane**, S.N Msolla, T. Porch & L.M. Serrato-Diaz

- 10:15-10:30 T2 Importance and management of angular leaf spot in Ethiopia (T3)  
**A.H. Getachew**
- 10:30-10:45 Break
- 10:45-11:45 K2 **Keynote Address**  
Progress in Common Bean Breeding for Angular Leaf Spot Resistance  
**T.L.P.O. Souza**, M.C. Gonçalves-Vidigal, B. Raatz, C.M. Mukankusi, A.F.B. Abreu, L.C. Melo & M.A. Pastor-Corrales
- 11:45-12:00 Discussion
- 12:00-13:15 Lunch

<p><b>Session 2 Angular Leaf Spot Breeding and Genetics</b></p>
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<p>Moderator: Dr. Susan Nchimbi-Msolla</p>
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- 13:15-14:15 K3 **Keynote Address**  
Molecular Tools for Angular Leaf Spot Resistance  
**B. Raatz**, B. Keller, C. Manzanares, B. Studer, C. Jara, J. Gil, D. Solarte, V. Mayor, P. Izquierdo, C. Mukankushi, J.D. Lobaton & J. Duitama
- 14:15-14:30 T3 Progress in identifying sources of resistance to angular leaf spot (*Phaeosariopsis griseola*) in Malawi  
**R. Chirwa** & B. Chataika
- 14:30-14:45 T4 Genetics and breeding for ALS resistance in common bean  
**E.A. Souza**, A.F.B. Abreu, M.A.P. Ramalho, R. Pereira & S. Librelon
- 14:45-15:00 T5 Co-segregation analysis of resistance genes to angular leaf spot, anthracnose and rust in common bean  
**M.C. Gonçalves-Vidigal**, P.S. Vidigal Filho, G. Valentini, G.F. Lacanallo, L.L. Sousa, P. Gepts, P.B. Cregan, Q. Song & M.A. Pastor-Corrales
- 15:00-15:15 Break
- 15:15-15:30 T6 Resistance breeding against major diseases of common bean in Ethiopia  
**K. Tumsa**, B. Amsalu, K. Negash & A. Dagmawit

- 15:30-15:45 T7 Status resistance levels to angular leaf spot diseases for common bean (*Phaseolus vulgaris* L.) productivity in Burundi  
**E. Nduwarugira**, S. Nchimbi-Msolla, R. Capitoline & N. Népomuscène
- 15:45-16:00 T8 Genome resequencing for marker discovery in 16 common bean genotypes used in the African Breeding Consortium disease resistance breeding programs  
**T. M. Miller**, L. Chilagane, S. Nchimbi-Msolla & P. Gepts
- 16:00-16:15 T9 PhaseolusGenes database: from a marker database to a sequence database  
E. Arunga, A. Kabeja, C. Mukankusi, A. Namayanja, S. Nchimbi-Msolla, R. Otsyula, Y. Rezene & **P. Gepts**
- 16:15-16:45 Strategy Session (Major research themes)
- 16:45-17:45 Poster viewing (ALS) and Socializer
- 19:00 **Welcome Dinner with Traditional African Dancers**

<b>TUESDAY 21 JULY</b>
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- 08:15-08:45 Registration Desk Open
- 08:45-09:00 Opening

<p><b>Session 3: Root Rot Pathology</b> Moderator: Consuelo Estévez de Jensen</p>
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- 09:00-10:00 K4 **Keynote Address**  
A review of the root rot diseases of common bean with emphasis in Latin America and Africa  
**R. Buruchara**, C. Estévez de Jensen, G. Godoy, G. Abawi, J. Pasche, and M. Lobo Junior
- 10:00-10:15 T10 Screening Andean dry bean germplasm for root rot resistance and phenotyping *Pythium* species for pathogenicity and virulence  
**M.I. Chilvers**, J.L. Jacobs, D.R. Rossman, A. Witte, A.M. Byrne, A.M. & J.D. Kelly

- 10:15-10:30 Break
- 10:30-11:30 S1 **Special Presentation: Fusarium Population Biology**  
Diversity, ecology and evolution of soilborne fungal plant pathogens  
**M.M. Jimenez-Gasco**
- 11:30-11:45 T11 Diagnosis of fungal bean root rot pathogens using molecular and culture methods  
**G. Godoy- Lutz**, C. Mukuma, J. Steadman, S.V. Fernandes, K. Muimui, C. Joshua
- 11:45-12:00 T12 Species identification and diversity of Fusarium spp. causing common bean root rot in Brazil  
L. L. Silva-Abud, E. T. Barbosa, F. Yoshida, L. Ulhoa, A. Wendland,  
**M. Lobo Junior**
- 12:00-13:15 Lunch

**Session 4: Root Rot Breeding and Genetics**

Moderator: Celestina Jochua

- 13:15-14:15 K5 **Keynote Address**  
Breeding beans for root rot resistance  
**J.D. Kelly** & C. Mukankusi
- 14:15-14:30 T13 Root rots in beans: Generating knowledge and Resources for their control  
**C. Jara**, C. Cotes, V. Arredondo & G. Mosquera
- 14:30-14:45 T14 Morphological and molecular identification of Pythium spp. isolated from common beans infected with root rot disease  
**P.H. Binagwa**, C.K. Bonsi, S.N. Msolla & I.P. Ritte
- 14:45-15:00 Break
- 15:00-15:15 T15 Identification of root rot resistant germplasm for Mozambique and Zambia  
**C.A. Urrea**, C. Jochua, K. Muimui, J. Steadman, S. Fernandes, G. Godoy, C. Mukuma, K. Eskridge, E.V. Cruzado & M.A. Pastor-Corrales
- 15:15-15:30 T16 Selection for combined resistance to bean root rots and angular leaf spot diseases and potential yield increase on beans in Western

Kenya **R. M. Otsyula** & M. Wambulwa

15:30-16:30 Poster Viewing (Root Rots)

19:00 **Bush Boma Dinner**

<b>WEDNESDAY 22 JULY</b>
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08:00-08:30 Registration Desk Open

<b>Session 5: Research Planning</b> Moderator: Phil Miklas and Tim Porch
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08:30-09:30 Review and organize major research themes  
Two Groups: ALS & Root Rot

09:30-09:45 Break

09:45-12:00 Plant pathology/Plant breeding research objectives, research plan  
Four groups : ALS pathology, ALS breeding, Root rot pathology and  
Root rot breeding

12:00-13:30 Lunch

13:30-14:15 Research Plans – ALS Pathology (M.A. Pastor-Corrales)

14:15-15:00 Research Plans – ALS Breeding (T.L.P.O. Souza)

15:00-15:15 Break

15:15-16:00 Research Plans – Root rot Pathology (R. Buruchara)

16:00-16:45 Research Plans – Root Rot Breeding (J.D. Kelly)

16:45-17:45 General Poster Session

19:00 **Dinner – Banquet; Awards Ceremony**  
Sponsored by Dry Bean Producers Organization  
**Special Presentation:**  
Dr. Chavonda Jacobs-Young, Administrator of USDA-ARS

## THURSDAY 23 JULY

### Session 6: Updates on other pathogens

Moderator: Dr. Roy Scott

- 08:30-09:00 T17 Breeding for resistance to BCMV and BCMNV in common bean  
**P.N. Miklas**, J. Hart, T. Porch & J. Beaver
- 09:00-09:30 T18 Genes conditioning resistance to rust the rust pathogen of common bean and a protocol for monitoring local races  
**M.A. Pastor-Corrales** & J.R. Steadman
- 09:30-10:00 T19 Anthracnose update  
**J.D. Kelly**, G. Zuiderveen & B.A. Padder
- 10:00-10:30 Break
- 10:30-11:00 T20 Breeding for resistance to common and halo bacterial blights in common bean  
**P.N. Miklas** & D. Fourie
- 11:00-11:30 T21 Breeding for bruchid resistance into farmers' preferred common bean (*P. vulgaris*) varieties: Developments and Challenges.  
**P.M. Kusolwa**, M.W. Mwatawala, S.N. Msolla, G. Kananji, G.M. Tryphone, J.R. Myers & J. Beaver
- 11:30-12:00 Closing remarks
- 12:00 Lunch – Picnic in the Garden
- 13:00 Afternoon – free time
- 19:00 **River Boma Dinner**

## ABSTRACTS OF TALKS

### KEYNOTES

#### **K1. Review of the angular leaf spot disease of common bean in Latin America and Africa and implications for improved disease management**

**M.A. Pastor-Corrales<sup>1</sup>, C. Jara<sup>2</sup>, M. Galván<sup>3</sup>, A. Wendland<sup>4</sup>, and E.A. de Souza<sup>5</sup>**

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The fungus *Pseudocercospora griseola* (PG) is the causal agent of the recurrent and often devastating Angular leaf spot (ALS) disease of common bean in Latin America and Africa. Conclusive evidence of the virulence diversity of PG was not reported until 1979. The initial virulence diversity studies of PG were conducted using different sets of common bean differential cultivars, thus these studies could not be compared. A new set of differentials was created at CIAT in the early 1990s that contained six Andean and six Mesoamerican cultivars. These differentials have been used ever since then to conduct most published PG virulence studies. Today PG is known to possess high levels of virulence and genetic diversity and its reported virulence diversity within and between countries of Latin America and Africa is very extensive. Yet this diversity segregates into two major and distinct groups that mirror the diversity of their common bean host. One group is composed of PG isolates collected from large-seeded common beans from the Andean gene pool that infect only or mostly Andean common beans. The second group consists of isolates collected from small and medium-seeded beans from the Mesoamerican gene pool that infect common beans from both gene pools. Similarly, many studies of the genetic diversity of *P. griseola* using DNA markers have also segregated the diversity of PG into the same Andean and Mesoamerican groups. Mounting evidence is accumulating to favor the hypothesis that Andean and Mesoamerican PG isolates have undergone parallel co-evolution with Andean and Mesoamerican common beans respectively. Although host resistance is the most cost-effective strategy to manage the ALS disease, achievement of effective resistance is complicated by the extensive virulence diversity of PG. For instance, several virulence diversity studies have revealed that many PG isolates in several states of Brazil, as well as in Argentina, and countries of Central America, infect all of the present set of differential cultivars. These results, underlining the broadness of the virulence diversity of PG, suggest the need for a new set of differential cultivars. Moreover, these results also suggest the need to combine genes of Mesoamerican and Andean origin in the development of common bean cultivars, which would confer broad spectrum and effective resistance to the extensive virulence diversity of PG. To date, only three genes that confer specific resistance to PG isolates have been named and mapped on the linkage map of common bean. All in all, the results here described have implications for the development of common bean cultivars with effective ALS resistance. These improved cultivars would contribute greatly to the sustainable, cost-effective, and environmentally-friendly production of dry beans in Latin America and Africa.

## **K2. Progress in common bean breeding for angular leaf spot resistance**

**T.L.P.O. Souza**<sup>1</sup>, M.C. Gonçalves-Vidigal<sup>2</sup>, B. Raatz<sup>3</sup>, C.M. Mukankusi<sup>4</sup>, A.F.B. Abreu<sup>1</sup>,  
L.C. Melo<sup>1</sup> and M.A. Pastor-Corrales<sup>5</sup>

<sup>1</sup>Programa de Melhoramento do Feijão, Embrapa Arroz e Feijão, Santo Antonio de Goiás, GO, Brazil; <sup>2</sup>Departamento de Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brazil; <sup>3</sup>CIAT, Bean Program, Cali, Colombia; <sup>4</sup>CIAT, Bean Program, Kampala, Uganda; <sup>5</sup>Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD, USA. E-mail: [thiago.souza@embrapa.br](mailto:thiago.souza@embrapa.br).

One of several factors that undermine common bean (*Phaseolus vulgaris* L.) yield and its stability worldwide is the high number of destructive diseases that affect this crop, causing significant yield losses. Among these, is the angular leaf spot (ALS) disease caused by *Pseudocercospora griseola*. ALS is currently a major destructive fungal disease affecting the common bean crop in South America and Africa. Yield losses up to 80% have been reported in these areas. Genetic resistance is the most effective, easy to use, ecological and economical management strategy to control ALS and it is particularly important for yield stability in low input agriculture. However, progress in breeding for resistance to this disease has been difficult compared with other diseases of common bean. The high virulence diversity of *P. griseola* and the recurring discovery of new races of this pathogen are challenging for the development and release of ALS resistant cultivars. Therefore, the main goal of this keynote address is to summarize the global progresses, achievements and challenges faced when breeding common bean cultivars with effective and durable ALS resistance. The main topics in this presentation will include an overview of the named and mapped as well unnamed mapped genes that confer ALS resistance, the genomic characterization of resistance loci, the identification of molecular markers linked to resistance loci and their effective use for marker-assisted selection. In addition, it will be presented and discussed the breeding efforts to develop ALS resistant cultivars for Africa and Brazil. It is hoped that this keynote address will generate the necessary discussion and actions to formulate regional and international strategic research plans to facilitate breeding for improved and sustainable resistance to ALS.

### K3. Molecular tools for angular leaf spot resistance

**B Raatz**, B Keller, C. Manzanares, B. Studer, C. Jara, J. Gil , D. Solarte, V. Mayor, P. Izquierdo, C. Mukankushi, J.D. Lobaton and J. Duitama

<sup>1</sup>Centro Internacional de Agricultura Tropical (CIAT), A. A. 6713, Cali, Colombia; <sup>2</sup>ETH Zürich, Switzerland; <sup>3</sup>CIAT Kawanda, Uganda; [b.raatz@cgiar.org](mailto:b.raatz@cgiar.org)

Angular Leaf Spot (ALS) causes major common bean production losses in low input farming systems in the tropics. We report on the activities in genetics and molecular breeding for ALS at the CIAT bean program. A major resistance locus from the resistance source G5686 ALS4.1<sup>GS, UC</sup> was finemapped to a 418 kbp region harboring 36 candidate genes. Among these, 11 serine/threonine protein kinases arranged in a repetitive array constitute promising candidate genes for controlling ALS resistance. Evaluation of different pathotypes revealed that this major resistance locus for Andean pathotypes (like pathotype 15–44) has no effect on Mesoamerican pathotypes (e.g. pathotype 1–55), whereas the G5686 allele from QTL ALS10.1<sup>DG, UC, GS</sup> shows the opposite behavior, only conferring resistance to Mesoamerican pathotypes. Evaluation of crosses G5686 x U00297 in Uganda, confirmed usefulness of ALS10.1<sup>DG, UC, GS</sup> and the Mesoamerican the *Phg-2* locus on chromosome 8 for tagging ALS resistance. We report on the ongoing characterization of the *Phg-2* locus from resistance source G10474. SNP based Tms markers were developed and evaluated in marker assisted breeding at CIAT. Furthermore, GWAS studies in a breeding population confirm the importance of this locus. Re-sequencing of several common bean genotypes produced a large amount of genomic resources that can be applied for molecular breeding. Whole genome sequencing (WGS) data from G5686 and G10474 produces a large quantity of specific SNPs. Three different types of SNP based markers were designed based on these SNPs and genotyping of a common bean panel shows that these markers are superior in specificity and can be used to tag valuable alleles in marker assisted selection. We suggest an online bean community data base to collect next generation sequencing (NGS) data, to form a comprehensive data set which can be used to identify specific and diagnostic polymorphisms for marker design.

#### **K4. A review of the root rot diseases of common bean with emphasis in Latin America and Africa**

**R. Buruchara**, C. Estévez de Jensen, G. Godoy, G. Abawi, J. Pasche, and M. Lobo Junior, C. Mukankusi.

The importance of root rot diseases of common bean in Africa and Latin America has increased in the last two decades, constraining production of beans, the most important leguminous crop and a leading source of human dietary protein, particularly in Africa. Common bean, also plays a significant role in the sustainable livelihoods of smallholder farmers and their families, providing both food security and income. The effects of root rots range from reduced plant stand, yellowing of leaves, stunted plants, uneven growth, wilting, and reduced yield especially in marginal soils. Occurrence and severity are associated with reduced land holdings which are intensely used, and high production intensity of beans. The most prevalent diseases include *Pythium*, *Fusarium* and *Rhizoctonia* root rots, Southern blight and *Fusarium* wilt. The corresponding causal fungal pathogens either occur individually or as a complex of two or more depending on locality and environmental conditions. The increasing importance and distribution of root rots, necessitated development of an understanding of the pathogen complex and to accurately diagnose the components responsible for the diseases in different geographical and bean production areas. Understanding these aspects is a pre-requisite in developing more efficient and effective disease management strategies. This review focuses on the progress so far made in understanding the etiology, distribution and relative importance of the disease complex causing root rots and how this has been translated in developing crop and soil management approaches that have immediate and long term effects. It also identifies gaps and strategies to enhance this understanding, particularly in Africa and Latin America.

## **K5. Breeding beans for root rot resistance**

**J. D. Kelly, and C. Mukankusi**

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International Center for Tropical Agriculture (CIAT), P. O. Box 6247, Kampala, Uganda*

Breeding for resistance to root rot(s) dates back nearly 100 years and success has largely been restricted to Mesoamerican beans. Root rots are considered one of the major production constraints for beans in eastern Africa being responsible for the most significant yield losses. Sources of resistance have been identified among both the domesticated and wild *Phaseolus* spp. however, introgressing resistance into large seeded Andean beans has been a challenge. Progress in breeding for root rot resistance and the impact of improved varieties on the livelihoods of the rural communities in eastern Africa is highlighted. Despite this progress, bean root rot(s) are still ranked high as the major contributor to yield losses. Breeding methodologies and the integration of new technologies to achieve higher levels of resistance will be discussed. The use of molecular tools offers an opportunity to enhance selection for resistance as phenotypic selection is greatly influenced by the screening environment. However, molecular tools will not completely address this challenge of integrating quantitatively inherited traits like resistance to Fusarium root rot (*Fusarium solani* f. sp. *phaseoli*) into future varieties. A singular focus on resistance needs to be expanded to include root traits that contribute to disease avoidance as an overall strategy to improve bean root health and enhance productivity under challenging environmental and management conditions.

## SPECIAL PRESENTATION : Fusarium Population Biology

### S1. Diversity, ecology and evolution of soilborne fungal plant pathogens

**M.M. Jimenez-Gasco**

*Department of Plant Pathology and Environmental Microbiology,  
The Pennsylvania State University, University Park, PA 16802. [jimenez-gasco@psu.edu](mailto:jimenez-gasco@psu.edu)*

Much of the current knowledge on the population biology and ecology of soilborne fungal plant pathogens has been derived from research focused on fungal-plant interactions that result in disease. However, the ecology and diversity of these fungi when not engaged in disease has been virtually ignored in plant pathology. I will discuss examples that involve the plant pathogenic, soilborne fungi *Fusarium oxysporum* and *Verticillium dahliae*. These fungi are well-known plant pathogens that also have a cryptic life as endophytes and saprobes. Using a population biology approach and tools based on next generation sequencing technologies I will discuss ecological and evolutionary scenarios for the emergence and evolution of plant pathogenicity. We found that endophytic *F. oxysporum* are extremely diverse and some seem to be adapted to a given host plant. We have also identified *V. dahliae* endophytic to plants previously considered to be non-hosts that are often used as rotational crops. We conducted Genotyping-by-Sequencing (GBS) on *V. dahliae* isolates representative of host, geographic origin, pathotype, and vegetative compatibility group (VCG), and found clear evidence of recombination widespread among clonal lineages. The extent and patterns of recombination observed suggest that clonal lineages arose by sexual reproduction. The potential dual role of these fungi, pathogenic on certain plants and endophytic on others, raises interesting questions about the biology, ecology, persistence, and spread of these fungi, which have very important potential implications in disease management in agroecosystems.

**T1. Towards genetic characterization of *Pseudocercospora griseola*, the causative agent of angular leaf spot of common bean in Tanzania.**

**L. A. Chilagane<sup>1</sup>, S. N. Msolla<sup>1</sup>, T. Porch<sup>2</sup> and L. M Serrato – Diaz<sup>3</sup>**

<sup>1</sup>Department of crop Science and Production, Sokoine University of Agriculture, P. O. Box 3005 SUA CHUO KIKUU Morogoro, TANZANIA, <sup>2</sup>Tropical Agriculture Research Station, 2200 P.A. Campos Ave., Suite 201 Mayaguez, PR 00680, <sup>3</sup>Department of Biology, University of Puerto Rico, P.O.Box 23360 San Juan, PR 00931-3360  
[lusekochilagane@yahoo.co.uk](mailto:lusekochilagane@yahoo.co.uk)

Angular leaf spot caused by the fungus *Pseudocercospora griseola* is one of the most important diseases of common bean in Tanzania, and in Africa at large. Breeding for resistance to this disease is reported to be complicated due to the variable nature of the pathogen. In Tanzania, no thorough attempt has been done to evaluate the variability of this pathogen so as to come up with proper strategies for breeding for durable resistance. This work aims at discovering the variability of this pathogen at the molecular level by characterization of three genes of the pathogen. *P. griseola* isolates were collected in two growing seasons, 2013 and 2014, in major common bean production regions of Tanzania. Isolation, purification and DNA extraction from 129 pure isolates were completed, followed by amplification of the Internal Transcribed Spacer of rRNA (*ITS*), partial Small Sub Unit (*SSU*) and Actin (*ACT*) genes using primers ITS5 and ITS4 for ITS region, NS1 and NS4 for SSU region and ACT-512F and ACT783R for actin gene. The amplified PCR products were purified and the three genes sequenced directly from PCR product after purification. Subsequently, a phylogenetic analysis comparing the isolates, based on the sequences in these three genes is to be completed. Concurrent work is underway to compare isolates from Honduras, Guatemala and Puerto Rico with the intention of doing combined analysis to compare isolates from Tanzania and these other regions. Corresponding author:

## **T2. Importance and management of Angular leaf spot (*Phaeoisariopsis griseola*) in Ethiopia**

**<sup>1</sup>Getachew Ayana, <sup>2</sup>Kidane Tumisa and <sup>3</sup>Behailu Atero**

<sup>1,2</sup> Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Center, P.BOX 436, Adama, Ethiopia and <sup>3</sup>Ethiopian Institute of Agricultural Research, Jimma Agricultural Research Center .PO. Box 192 Jimma, Ethiopia

Common bean (*Phaseolus vulgaris*. L) production and productivity in Ethiopia is constrained by different biotic and abiotic factors. Diseases caused by different fungal and bacterial pathogens are among the major biotic factors. Angular leaf spot (ALS) (*Phaeoisariopsis griseola*) is one of the most important fungal diseases causing significant yield losses. Management ALS mainly focuses on the use the least susceptible varieties, different cultural practices such as crop rotation and deep plough and application of an effective fungicide during early critical growth stages. In order to identify appropriate management option for ALS a field experiment were carried out involving commonly release bean varieties in Ethiopia and supplementary fungicide sprays at specific crop growth stages. A factorial combination of common bean varieties and supplementary fungicide sprays (Tebucnazole at a rate of 2 liter/ha) at three critical bean growth stages (V4, R5 and R 6) arranged in randomized block design. The study was done under natural epidemic condition. This report presents results of field experiment during main cropping season in the years of 2009 to 2012. In the fists two years (2009 to 2010) the common bean varieties used were Awashmelka, Goberasha and Mexican 142 and during 2011 and 2012 Awash-1, Awashmelka and Nasser common bean varieties were used. In all case ALS severity, 100 seed weight and seed yield were higher in treatments which received supplementary sprays at the three bean growing stages described above. In absence complete varietal resistance the use of reduced fungicide sprays at specific bean growth stage is recommended. However, for reliable and safe disease management options search of resistant varieties and alternative integrated management option should be further studied. Furthermore the spectrum of the pathogen variability should be studied properly.

### **T3. Progress in identifying sources of resistance to angular leaf Spot (*Phaeosariopsis griseola*) in Malawi**

**R. Chirwa and B. Chataika**

*International Center for Tropical Agriculture, Chitedze Agricultural Research Station, P.O. Box 158, Lilongwe, Malawi.*  
[R.Chirwa@cgiar.org](mailto:R.Chirwa@cgiar.org)

Angular leaf spot (*Phaeosariopsis griseola*) is one of the common bean diseases of importance in the regional network breeding program for southern Africa. As such, it is important to identify good sources of resistance to ALS pathogen for use in the market-led bean breeding program. Several common bean (*Phaseolus vulgaris*) genotypes introduced from various sources including Colombia and some countries in Africa were evaluated for resistance to ALS and grain yield. The process was done in two cycles – 1) 80 genotypes were screened for ALS resistance under natural infestation at Bembeke sub-research station over 5 crop seasons from 2007 to 2012 seasons to accommodate seasonal disease pressure, where 33 promising genotypes were identified. 2) The 33 genotypes were then evaluated in replicated trials for ALS resistance and grain yield at Bembeke and at Chitedze research station for grain yield only over 2 crop seasons - 2013 and 2014. Genetic gains from selection were high in yield at Bembeke. The study identified five superior genotypes: i) BM 12732-57VEF2000 121, ii) BM 12732-133VEF2000 135, iii) GCI-ZEBRA-268-RAR-3-3, iv) BM 12732-60VEF2000 122 and v) G7874, which combined high yield and ALS resistance. The superior genotypes were mostly in the brown-tan (khaki) and pinto grain market classes. Additional lines G11405 and CFN5558 were also identified to be good sources of resistance to ALS, although not competitive in grain yield. The study also found significant interaction amongst sites, years and genotypes ( $p < 0.001$ ) for grain yield, suggesting that genotypes performance were site and season specific. However, the superior genotypes were consistently high yielding across sites and seasons. All the 33 genotypes showed susceptibility to floury leaf spot (FLS) at Bembeke and differential reaction to bean common mosaic virus (BCMV) at Chitedze, suggesting that the breeding program will need other sources of resistance to these diseases in developing varieties with multiple disease resistance and improved grain yield.

#### **T4. Genetics and breeding for ALS resistance in common bean**

**E. A. Souza<sup>1</sup>**; A. F. B. Abreu<sup>2</sup>; M. A. P. Ramalho<sup>1</sup>; R. Pereira<sup>1</sup>; S. Librelon<sup>1</sup>

<sup>1</sup> Departamento de Biologia, Universidade Federal de Lavras, Campus Universitário, Caixa Postal 3037, Lavras, Minas Gerais, Brazil CEP 37200-000; <sup>2</sup> Empresa Brasileira de Pesquisa Agropecuária. [easouza@dbi.ufla.br](mailto:easouza@dbi.ufla.br)

Efforts have been made by the Common Bean Breeding Program of the Universidade Federal de Lavras, Brazil aiming to study the Genetics of *Pseudocercospora griseola* and angular leaf spot (ALS) resistance in common bean. Wide variability in *P. griseola* has been observed for several traits including virulence. A diagrammatic scale for use of inoculation in primary leaves was developed that allows for early pathogenicity testing, thus optimizing the selection of resistant genotypes and the characterization of lines from the common bean germplasm banks. The efficiency of early pathogenicity testing has been evaluated in the identification of new sources of resistance in the Germplasm Bank of UFLA and in the recurrent selection program for ALS resistance carried out by UFLA/EMBRAPA. Artificial inoculation in common bean using single isolates or mixtures of *P. griseola* isolates has been evaluated. Information about ALS resistance in common bean and virulence of *P. griseola* isolates have been obtained. These results will be presented and discussed focusing on excellent results obtained after 18 recurrent selection cycles for ALS resistance.

## T5. Co-segregation analysis of genes conferring resistance to the angular leaf spot, anthracnose and rust pathogens of common bean

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Angular leaf spot (ALS), anthracnose (ANT) and rust are devastating diseases of common bean. In previous studies, the genetic symbols *Phg-1/Co-1<sup>4</sup>* and *Phg-3/Co-3<sup>4</sup>* were assigned to the genes conferring resistance to ALS and ANT in cultivars AND 277 and Ouro Negro, respectively. The purpose of this study was to gather data from co-segregation analysis of the ALS, ANT and rust resistance genes using F<sub>2</sub> populations and/or two identical sets of F<sub>2:3</sub> populations. In the first study, we elucidated the inheritance of ALS and ANT resistance in Andean bean AND 277 using F<sub>2</sub> populations from the AND 277 × Rudá and AND 277 × Ouro Negro crosses and F<sub>2:3</sub> families from the AND 277 × Ouro Negro cross. ANT 277 was resistant and Rudá and Ouro Negro susceptible to the races of the ALS and ANT pathogens used in this study. Co-segregation analysis revealed that a single dominant gene in AND 277 conferred resistance to races 65, 73 and 2047 of the ANT and race 63-23 of the ALS pathogens. The absence of recombinants showed that *Phg-1* and *Co-1<sup>4</sup>* were tightly linked (0.0 cM) on linkage group Pv01. We also identified two new molecular markers CV542014<sup>450</sup> and TGA1.1<sup>570</sup>, linked at 0.7 and 1.3 cM, respectively, from the *Co-1<sup>4</sup>/Phg-1* locus. In the second study we performed a co-segregation analysis of the ALS and ANT resistance genes in cultivar Ouro Negro using an F<sub>2</sub> population from the Rudá × Ouro Negro and the F<sub>2:3</sub> families from the AND 277 × Ouro Negro crosses. Ouro Negro was resistant to races 7 and 73 of the ANT and to race 63-39 of the ALS pathogens. Conversely, cultivars AND 277 and Rudá were susceptible to the same races of both pathogens. Co-segregation analysis revealed that *Phg-ON* and *Co-10* were inherited together, conferring resistance to ALS and ANT ALS. The symbols *Phg-3/Co-3<sup>4</sup>* were assigned to the ALS and ANT resistance in Ouro Negro. A third study was conducted using two samples of the F<sub>2:3</sub> families from Rudá × Ouro Negro evaluated with single nucleotide polymorphism (SNP) DNA markers and specific races of the rust and anthracnose pathogens. The results from the phenotypic evaluation revealed that all of the subfamilies but one had the same phenotypic reaction to the rust and ANT pathogens, indicating that *Phg-3/Co-3<sup>4</sup>* resistance gene cluster was tightly linked to the *Ur-14* rust resistance gene in Ouro Negro. The genetic analysis also revealed the same results. In addition, many DNA markers were found tightly linked to these genes. These markers will reduce the time and cost of pyramiding important genes for resistance to three major disease of common bean.

## **T6. Resistance breeding against major diseases of common bean in Ethiopia**

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Worldwide, common bean production and productivity are adversely affected by different diseases. Varieties resistant/tolerant to major prevailing diseases are very crucial to sustain the production of the crop in the farming system. Common beans are the most important crop in Ethiopia and the current average productivity of the crop is 1.5 t/ha. This figure is by far less than the potential of the crop (4.5 t/ha) due to different constraints among which diseases are the major problems which contribute 10 to 100% yield loss under favorable condition. Common bacterial blight (*Xanthomonas axnopodis* pv. *Phaseoli* (Smith) Dowson) and Angular leaf spot (*Phaeoisariopsis griseola* (Sacc. Ferr)) are the major diseases prevailing across different growing regions. The bean research program of Ethiopian Institute of Agricultural Research has been working to develop resistant varieties to these different diseases. The purpose of the poster is to summarize the progress and achievement of the program towards resistance breeding. The field trial, consisting of 25 advanced lines introduced from CIAT, has been conducted across five hot spot locations in 2013 and 2014 cropping seasons with the objective of identifying resistant promising varieties to be recommended. A 5X5 triple lattice with three replications has been used across all locations. All agronomic and disease data has been collected and analyzed. Six promising resistant genotypes (SEC 12, SEC 20, SEC 21, SEC 22, SEC 23 and SEC 26) are identified with 8 to 17% yield advantage over the comparable resistant variety to both diseases Awash Melka.

**T7. Status resistance levels to angular leaf spot diseases for common bean (*Phaseolus vulgaris* L.) productivity in Burundi.**

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In order to evaluate the prevalence of Angular leaf spot disease of common bean (*Phaseolus vulgaris* L.) in the low, middle and high altitude of Burundi, this experiment was carried out in Gisozi, Murongwe and Moso research station. In most of the sites and both cropping seasons (2013A and 2013B), ANOVA showed significant differences at different levels of significance on ALS disease indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. Most of the genotypes showed low to moderate reaction to the disease studied. From these genotypes, source of resistance to diseases can be obtained.

## **T8. Genome resequencing for marker discovery in 16 common bean genotypes used in the African Breeding Consortium disease resistance breeding programs**

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The African Bean Consortium, funded by the Kirkhouse Trust, seeks to pyramid resistance genes for five major diseases that drive yield reduction in common beans grown in East Africa. Each of the national projects in Rwanda, Ethiopia, Uganda, Kenya and Tanzania has identified several diseases that are drivers of yield reduction throughout their region, chosen germplasm to serve as disease resistance donors and preferred varieties, and implemented a breeding program that utilizes marker assisted selection and pathological screening to identify resistant plants after crosses. In order for marker assisted breeding to be successful, markers located near the disease resistance loci to be selected must be tightly linked with the causal locus, co-dominant and polymorphic amongst the parents. In order to identify useful DNA markers amongst the 16 breeding parents used throughout the ABC programs, we performed next generation sequencing using the Illumina platform to generate an average per genome coverage of 22X. The whole genome sequences were used to identify polymorphic, co-dominant single nucleotide polymorphisms and simple sequence repeats, with an average number occurring across the 11 bean chromosomes of 2,566 and 431,000 respectively. Simple sequence repeats had an average length of 26 base pairs and occur at a frequency of ~18,000 base pairs, whereas single nucleotide polymorphisms occur every ~100 base pairs, indicating single nucleotide polymorphisms are more useful as markers because of their greater frequency. Due to the monomorphism between parents used in the Ugandan breeding program for the SNO2 marker, which is used to select the *Phg-2* Angular Leaf Spot resistance gene, using the whole genome sequences we identified three new polymorphic markers closely linked with SNO2 that can be used for marker assisted selection. One of these markers, the previously published Sequence Tagged Site, g796, has a 24 base pair insertion in the allele of the ALS resistant parent, Mexico 54, whereas none of the susceptible parents have the same sequence. This work is an example of how genome sequencing and the common bean reference genome can be leveraged to generate large numbers of new markers that can be used for breeding and genetic mapping experiments. In the future the marker data will be made available through the PhaseolusGenes marker database where polymorphism data for each accession sequenced can be viewed in a genome browser in alignment with the reference genome, facilitating easy comparison of sequences for multiple genotypes as well as identification of polymorphisms between them (<http://phaseolusgenes.bioinformatics.ucdavis.edu/>).

## T9. PhaseolusGenes database: from a marker database to a sequence database

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The Kirkhouse Trust (KT) supports a large project aimed at introducing an independent capability of marker-assisted selection for multiple disease resistance in common-bean breeding programs in Eastern Africa. This MAS supplements ongoing phenotypic selection to develop new varieties in a genetic background preferred by local farmer and consumers, e.g., Kablanketi type in Tanzania, Sugar type in Uganda, small red and red mottled type in Ethiopia, and Gasilida (large red) type in Rwanda. The five most important diseases of dry bean focused on in this project include angular leaf spot, anthracnose, bean common mosaic virus/bean common mosaic necrosis virus, common bacterial blight, and root rot (*Pythium* sp.). One project also works on rust in green beans. A significant contribution is made by the CIAT (Kawanda, Uganda) laboratory in the training of individual project members in the areas of marker analysis and plant pathology. Several principles animate the ABC project: a) promote independent research by each of the projects involved; b) favors higher education within Africa unless other opportunities arise; and c) supports training of all involved in the projects, including PIs, co-PIs, students, and staff to build a strong human infrastructure. Some of the first achievements are the development of physical infrastructure in several of the projects, the training of several students and technicians in marker and phytopathology techniques, the first field-testing of advanced lines, the first genome-wide sequencing of a bean genotype (BAT93), and the development of a marker-database (PhaseolusGenes), and the development of alternative marker tags. The PhaseolusGenes has served the community well, not only for marker development, but also in the assembly of new genome sequences (e.g., BAT93) and marker information. It is in need, however, of updating to reflect the changing marker and sequence landscape of genomics. Increasingly, lines are now being sequenced leading to large sets of several 100s of genome sequences within species, including beans. New markers are then identified based on polymorphisms among these sequences. After barely five years of existence, the PhaseolusGenes database now needs to be modified to accept this type of high-throughput and genome-wide sequence information and continue its role as a source of markers for bean breeding.

## T10. Screening Andean dry bean germplasm for root rot resistance and phenotyping *Pythium* species for pathogenicity and virulence

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In 2014, a field trial was conducted in East Lansing, Michigan to assess fifty Andean dry bean germplasm lines for resistance to common root rot pathogens. Three meter, single row plots were inoculated in furrow at planting with either *Rhizoctonia solani* (AG2-2IIIB and AG4), *Fusarium phaseoli*, or *Pythium* (*P. torulosum* and *P. dissoticum*), and compared to a non-inoculated control. The *Rhizoctonia* treatment significantly reduced plant stands in all 50 dry bean lines assessed, often killing nearly 100% of the plants. The *Pythium* and the *Fusarium* treatments significantly reduced plant stands compared to the controls for 37 and 9 of the 50 dry bean lines, respectively. The screen was very effective at identifying material with resistance to the pathogens tested. In 2015, the screening is being refined for assessment of *Rhizoctonia* resistance, by screening *Rhizoctonia solani* anastomosis groups AG2-2IIIB and AG4 individually and with less inoculum input. In addition, seed rot agar plate and seedling pathogenicity assays are being conducted to evaluate a broad range of anastomosis groups of *Rhizoctonia solani* isolated from Uganda and Michigan on Andean and Meso-American drybean germplasm lines. Initial results from the seed rot assay show a wide range of seed rotting capability across anastomosis groups, with AG 2-2IIIB and AG2-2IV being the most aggressive. *Pythium* species were assayed for pathogenicity and virulence against black bean 'Zorro' and red kidney bean 'Red Hawk' from the Meso-American and Andean gene pools, respectively. Pathogenicity experiments were conducted in a growth chamber at 20°C and evaluated for disease severity 12 days after planting. Three isolates of twenty *Pythium* species were evaluated in the study. Each isolate was replicated three times over three separate experiments, for a total of nine replicates. A replicate consisted of six dry bean seeds planted into 340 mL cups containing medium vermiculite, with *Pythium* rice inoculum layered in the root zone. To verify pathogenicity, Koch's postulates was performed by isolating the pathogen from roots, extracting DNA from mycelium, and using single strand confirmation polymorphism to confirm DNA from isolations and inoculum were identical. Emergence was significantly reduced by five *Pythium* spp. Root dry weight of 'Red Hawk' and 'Zorro' was reduced significantly by thirteen and nine *Pythium* spp. species, respectively. Suggesting Meso-American *Pythium* resistance may be higher than Andean. The following species, *Py. acanthicum*, *Py. attrantheridium*, *Py. coloratum*, *Py. aff. diclinum*, *Py. heterothallicum*, *Py. lutarium*, and *Py. ultimum* var. *sporangiferum*. tested in this study are not reported as dry bean pathogens in the USDA ARS Fungal Database. This phenotypic data will assist in the selection of *Pythium* species for screening of dry bean germplasm.

## T11. Diagnosis of fungal bean root rot pathogens using molecular and culture methods

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Over the years the cause of root/crown rot (RCR) of dry beans (*Phaseolus vulgaris*) has been attributed to various fungal or Oomycete species. The disease, previously thought to be of minor importance, has become problematic in developing countries, like Zambia and Mozambique, due to various factors such as environmental extremes, use of noncertified seed, not using crop rotation and lack of genetic resistance to target pathogen(s). Our objective is to compare molecular and culture based methods to ascertain the identity and predominance of fungal RCR pathogen(s). Bean RCR samples have been collected yearly since 2013 at the ADP nursery sites and farmer fields in bean producing zones in both countries. The interface of diseased and healthy tissue was either cut for direct plating on agar or DNA extraction and blotting of their homogenates onto FTA cards. DNA extracted from FTA cards and root tissue were subjected to 454 pyrosequencing of small subunits of the r RNA gene and PCR amplification with genus/species specific primers. Isolates from cultures were identified by morphological features and Sanger sequencing of the ITS region and tested for pathogenicity. Multivariate and phylogenetic analysis were used to compare efficacy of the methods. Higher fungal diversity was associated with RCR than previously reported. The 454 pyrosequencing revealed more diverse and higher numbers of operational taxonomic units with similar sequences that suggests clonal population within countries. PCR detections were dependent on the primers used. Species of *Fusarium* such as *F. solani*, *F. oxysporum* and *F. equiseti* were the most prevalent identified (> 90%) by molecular and cultural based methods in RCR samples from both countries. In some samples *Macrophomina phaseolina*, species of *Pythium* and *Rhizoctonia solani* were detected mostly by PCR primers not as single species but co-occurring with *Fusarium* spp within the same plant. Most isolates of *Fusarium*, *R. solani*, and few *Pythium* spp obtained from cultures were pathogenic. In spite of its limitations, only the culture method provides pathogenic isolates for RCR resistance screening.

## T12. Species identification and diversity of *Fusarium* spp. causing common bean root rot in Brazil

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This study aimed to identify *Fusarium* spp. species causing root rot in common bean; to compare the disease severity caused by 96 monosporic isolates collected in the Brazilian states of Parana, Minas Gerais, Goiás and São Paulo; and to assess the genetic diversity of this isolate pool. The endorsement of isolate pathogenicity was done with the inoculum layer method in 500 mL plastic glasses, with the planting of common bean (cv. Pérola) seeds in a vermiculite layer with PDA medium previously colonized by the pathogen. The test was carried out in a completely randomized design with five replications. After 21 days of incubation at  $20 \pm 2^\circ\text{C}$ , disease severity was assessed by means of a 1-9 scale and an estimate of the McKinney index. The results were subjected to analysis of variance (ANOVA) after normal adjustment by  $\sqrt{x} + 0.5$ , as recommended by the Shapiro-Wilk test (5%), and mean comparison by the Scott-Knott test (5%). All 96 isolates produced root rot symptoms, with disease severity distributed into two groups. The isolates identification at the species level was held in cultures grown in carnation leaf-agar medium, and their morphological traits were analyzed with a stereoscopic microscope. Molecular identification consisted of polymerase chain reaction and sequencing of the TEF-1 $\alpha$  gene. The sequences of the TEF-1 $\alpha$  gene obtained for 95 isolates were compared with GenBank references, with species identity supported by the Fusarium-ID database. The outcomes of the morphological assessment matched those found by molecular analysis, with the identification of 65 isolates of *F. solani*, 27 of *F. oxysporum* and three of *F. proliferatum*. Furthermore, a phylogenetic tree was generated from consensus sequences, with all the *F. solani* isolates arranged in a single clade, while *F. oxysporum* and *F. proliferatum* were grouped in a second cluster. According to the phylogenetic analysis, all isolates pathogenic to the common bean were clearly distinct from the outgroup formed by reference sequences of *F. tucumaniae*, *F. cuneirostrum*, *F. virguliforme* and *F. brasiliense*, which are part of the soybean *F. solani* species complex. The results of pathogenicity tests and sequence analyses of the TEF-1 $\alpha$  gene did not group the isolates according to their species or their geographical origin. This is the first report about *F. proliferatum* infecting common bean in Brazil. These results support a better overview of the *Fusarium* species complex that affects the common bean and Brazil, and they will assist field management of root diseases and breeding for resistance programs that are intended to reduce yield losses in this important crop.

## T13. Root rots in beans: Generating knowledge and resources for their control

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Root rots are an increasing limitation for bean production in many countries. In contrast with the extensive information on foliar diseases, information and control measures for root rots is very limited and this translates into an increasing constraint for bean production already affected by climate change. For instance, increased soil water potential on beans under root rot pressure in cool environments has been reported as main factor for disease severity caused by *Pythium ultimum* and *Pythium* spp. Recent observations have shown that there is a strong *Pythium*-like infection on bean plants in heat stress trials in Colombia. Although temperatures ranging between 14 and 17°C have been documented as an important factor in determining which *Pythium* species will cause disease in beans, observations suggest that this pathogen would be able to affect beans at higher temperatures if soil humidity is also high. To prove this hypothesis, we focused our research on identifying the causal agent of the disease and also identify sources of resistance. Results obtained so far have shown that *Pythium* is causing severe limitations for bean plant growth under favorable climatic conditions and that three highly pathogenic species, *P. myriotylum*, *P. aphanidermatum*, and *P. deliense*, have been identified from beans grown in environments with daily temperatures above 35°C. On the other hand, germplasm testing is being done under greenhouse conditions to identify sources of resistance for root rots caused by the three different *Pythium* species. The results obtained show that there are bean genotypes that are able to tolerate *P. myriotylum* infection and that could be used as donors of resistance. The same lines will be tested against the other two species to evaluate if the resistance in these bean lines is specific for each *Pythium* species or if it is broad spectrum resistance. Interaction between different *Pythium* species, temperature, soil moisture, and resistant bean lines are being established to develop strategies for the improvement of bean germplasm resistant to *Pythium* infection under different environmental conditions including heat stress. Bean varieties with stable resistance to *Pythium* through diverse abiotic conditions would be the best control measure for root rots caused by this pathogen.

## T14. Morphological and molecular identification of *Pythium* spp. isolated from common beans infected with root rot disease

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Common bean (*Phaseolus vulgaris* L.) is the principal legume crop grown primarily by small-scale farmers in eastern and southern Africa. It is the second most important source of human dietary plant protein after soybean. This crop is highly affected by root rot disease caused by soilborne pathogens including *Pythium* which causes yield loss of up to 70% to farmers in most commercial common bean cultivars grown in parts of East African countries. Forecasts of predictive models identified new areas in Tanzania, Kenya, Malawi, Ethiopia and Uganda where *Pythium* root rot is expected to become a serious problem including surveyed areas during this study. This study focused on: ascertaining preliminary information on bean cultivation practices within the collection area, morphological and molecular characterization and identification of *Pythium* species from infected bean plants collected from farmers' fields and determining the association of soil pH and the occurrence and distribution of *Pythium* root rot disease. A survey was conducted for gathering information regarding bean cultivation practices. Infected bean plants showing root rot symptoms were collected from farmers' fields in Mbozi and Lushoto districts in Tanzania followed with aseptic pathogenic isolation in the laboratory. Purified isolates on corn meal agar growth media were observed using a microscope and based on morphological characteristics of sporangia, oogonia, antheridia and oospores as distinctive features for *Pythium* pathogen identification. *Pythium* mycelia tissues were used for DNA extraction and the Internal Transcribed Sequence (ITS) region was amplified using universal primers (ITS1 and ITS4) followed with sequencing. Most farmers (63.0%) practiced sole bean cropping, (31.0%) mixed cropping and (6.0%) intercropping. Corn was a major crop for either mixing or intercropping (22.7%) with beans; other crops were, banana, cassava, Irish potatoes and coffee. In total, 52.4% of farmers use farmer saved seeds, 32.1% bought from local market, 3.6% got seeds from their neighbours, 6.0% from agro-dealers (certified seeds) and 6.0% from research centers. Farmers (92.9%) do not use fertilizer in their bean fields while 7.1% use fertilizer during bean cultivation. Thirty two *Pythium* isolates were sequenced using single pass sequencing technology and eleven species were identified; *Pythium aphanidermatum* (31.25%) and *Pythium splendens* (28.13%) being widely distributed in the entire collection area. Other species confirmed include: *Pythium ultimum* (6.25%), *Pythium attrantheridium* (6.25%), *Pythium graminicola* (6.25%), *Pythium oligandrum* (6.25%), *Pythium dissotocum*, (3.13%), *Pythium irregurale* (3.13%), *Pythium camurandrum* (3.13%), *Pythium paroecandrum* (3.13%), and *Pythium acanthophoron* (3.13%). Phylogenetic analysis showed diversity and homogeneity of *Pythium* spp. across the collection area. Incidence and distribution of *Pythium* species from farmers' fields were dominant in soil pHs of 5.1 – 5.6 and less incidence was found the 6.1 – 6.5 pH values, classified as strongly/moderately acidic and slightly acidic respectively.

## **T15. Identification of root rot resistant germplasm for Mozambique and Zambia**

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This research is part of a NIFA-Root Rot Project that was initiated in Zambia and Mozambique in 2013. The objective was to evaluate the reaction of dry bean lines to root pathogens and to identify the causal agents of the root rot diseases in these two countries. Initial efforts focused on evaluating under field conditions 352 and 357 lines, respectively, in Zambia and Mozambique. The evaluated beans included drought tolerant/root rot resistant lines derived from a Puerto Rico-Nebraska shuttle breeding nursery, Andean Diversity Panel (ADP), and CIAT's regional nurseries that included landraces from Zambia and Mozambique. The evaluation continued during 2014 in Zambia, Mozambique, and Nebraska. A total of 66 of these lines were selected for root rot resistance and grouped by growth habit. In addition, the trials in Mitchell, Nebraska permitted to compare the impact of drought stress with lines planted in adjacent irrigated (non-stressed, NS) and non-irrigated (drought-stressed, DS) plots. The trials in North Platte, Nebraska were also evaluated for the reaction to common bacterial blight. Based on the results from the 2014 trials, 12 lines were selected for root rot resistance. These lines are being evaluated in Zambia, Mozambique, and Nebraska during 2015. Four of the 12 entries, G 10994 (RR-142), Larga Comercial (RR-186), NE34-12-28 (RR-346), and NE34-12-50 (RR-368), are common to both Zambia and Mozambique. Four local cultivars, two with determinate and two with indeterminate growth habit, are being used as reference checks. The 2015 trials will focus on evaluating root rot and multiple disease resistance and yield and its components. The Mitchell, Nebraska trials will again evaluate the impact of Drought stress/Non-drought stress. Based on recommendations from the 2014 Mid-term review, the African trials will also evaluate the effect of fertilization/non-fertilization and fall control/non-control of armyworms using a factorial treatment design. Elite adapted East Africa/Southern Africa lines will be crossed to several sources of germplasm possessing multiple disease resistance and good agronomic traits using the 'Good x Good' approach. Single, three-way, double, and multiple crosses will be used to incorporate multiple traits such as root resistance, bean common rust, and common bacterial blight. Cyclical intercrossing of elite superior lines will be performed. During every step of the breeding process, we will screen the plants for resistance to root rot pathogens. Only the resistant plants will be advanced to the next generations. Once the protocols for various root pathogens are established, we will develop different Recombinant Inbred Line populations to identify QTLs regions associated with root rot resistance. Some of the RILs showing resistance to root rot pathogens will be released as either germplasm or cultivars.

**T16. Selection for combined resistance to bean root rots and angular leaf spot diseases and potential yield increase on beans in Western Kenya.**

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This paper summarizes the research findings of recent studies on bean root rot and angular leaf spot in Kenya, where bean production has been constrained by the two diseases. These studies have covered pyramiding of resistance genes for the two diseases into a commercial cultivar and fielding testing of the advanced lines obtained from segregating population for the two disease. On-farm field testing of the advanced lines and yield potential on farmers' fields has also been reported. Future work on the advancement of the materials towards commercialization is indicated.

## T17. Breeding for resistance to BCMV and BCMNV in common bean

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The potyviruses *Bean common mosaic virus* (BCMV) and *Bean common mosaic necrosis virus* (BCMNV) cause yield loss and reduce the quality of common bean worldwide. The viruses are seed borne and readily propagated via infected seeds which is often the primary source of inoculum. Several aphid species transmit the virus from plant-to-plant in a nonpersistent manner. Genetic resistance is critical for the control of these virus diseases. No new genes (*I*, *bc-u*, *bc-1*, *bc-1*<sup>2</sup>, *bc-2*, *bc-2*<sup>2</sup>, *bc-3*) conditioning resistance to BCMV/BCMNV have been identified since Drijfhout's dissertation was published in 1978, except for a new allele *bc-3*<sup>2</sup> at the *Bc-3* locus that was recently discovered based on differential reaction to *Clover yellow vein virus* (CIYVV). Thus, *bc-3* is still the desired allele to deploy against the threat of BCMV/BCMNV. The *I* gene and some of the *bc*-resistance genes are effective against *Peanut mottle virus* (PeMoV); *Cowpea aphid-borne mosaic virus* (CABMV), and several other potyviruses, in addition to CIYVV. Meanwhile BCMV and BCMNV strains continue to recombine within and among each other to create new pathotypes. One such pathotype, newly described, overcomes *bc-2* and *bc-3* alleles but not *bc-1* or *bc-1*<sup>2</sup>. This pathogen variability has necessitated the long standing breeding strategy to combine (protect) the *I* gene with at least one of the recessive alleles *bc-1*<sup>2</sup>, *bc-2*<sup>2</sup> (that also require *bc-u*), or *bc-3*, to obtain broad and sustained resistance to BCMV/BCMNV. Any of these protected *I* gene combinations provide resistance to all known strains of BCMV/BCMNV with some minor exceptions (*I* + *bc-1*<sup>2</sup> is overcome by the NL-5 strain). Markers linked with *I*, *bc-1*<sup>2</sup> and *bc-3* are available and can be used to facilitate breeding for protected *I* gene resistance in common bean. It is noteworthy that the *I* and *bc-1*<sup>2</sup> genes are present in many high yielding cultivars within many different market classes but that the *bc-2*<sup>2</sup> and *bc-3* alleles with or without *I* gene are present in fewer high yielding cultivars. The presence of the *I* gene can have a negative effect on seed color (creams, reds, yellows) due to its association with the *B* locus which causes problems with its deployment in certain market classes. Additional issues concerning breeding for resistance to BCMV/BCMNV will be discussed.

## T18. Major genes conditioning resistance to rust in common bean and a protocol for monitoring local races of the bean rust pathogen

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The narrow genetic base of common bean, *Phaseolus vulgaris*, and the high virulence diversity of the bean rust pathogen, *Uromyces appendiculatus*, result in continual challenges to maintain effective rust resistance in common bean cultivars. Resistance to rust in common bean to date is conditioned by 10 single, dominant, and independent genes identified with the *Ur* symbol. Some of these genes are of Mesoamerican origin (*Ur-3*, *Ur-5*, *Ur-7*, *Ur-11*, and *Ur-14*) while other are of Andean Origin (*Ur-4*, *Ur-6*, *Ur-9*, *Ur-12*). The *Ur-13* gene is present in Andean bean Redlands Pioneer but it appears to be of Mesoamerican origin. All of these 10 genes have been mapped to the comprehensive genomic map of disease resistance genes and QTL in common bean. The reported map locations of some of these rust resistance genes are gene clusters on linkage groups Pv01, Pv04, and Pv11. These clusters include other disease resistance genes. Linkage group Pv01 contains a cluster of Andean rust, anthracnose, and angular leaf spot disease resistance genes. The genes on Pv01 include *Ur-9* for rust, *Phg-1* for angular leaf spot, and the *Co-1*, with four of its alleles, for anthracnose resistance. Linkage group Pv04 contains a cluster of disease resistance genes that includes the Mesoamerican *Ur-5* and *Ur-14* for rust and the *Co-3*, and three of its alleles, for anthracnose, as well as the Andean *Co-15*, *Co-16*, *Co-y* and *Co-z* for anthracnose, and the Mesoamerican *Phg-3* for angular leaf spot resistance. Linkage group Pv11 has a cluster that includes the Mesoamerican *Ur-3*, *Ur-7*, and *Ur-11* along with the Andean *Ur-6* gene for rust, and the *Co-2* for anthracnose resistance. Angular leaf spot and other disease resistance genes not yet named have also been mapped on Pv04. No multiple alleles have been reported for any of the of the known rust resistance genes. Evidence has accumulated that generally rust resistance genes of Mesoamerican origin tend to be resistant to Andean races of *U. appendiculatus* while genes of Andean origin are resistant to many highly virulent Mesoamerican races. Additional rust resistance genes have been identified in *P. vulgaris* but they have not been named yet. In addition, in tepary bean *P. acutifolius*, rust resistance that has been found but not yet published was broader than that observed in all known common bean rust resistance genes and other sources of rust resistance. A simple method of determining what sources of rust resistance would be effective in local bean fields is available through use of a mobile nursery and inexpensive mist chamber.

## T19. Anthracnose update

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Anthracnose (*Colletotrichum lindemuthianum*), is a seed-transmitted disease of common bean (*Phaseolus vulgaris*) and is cosmopolitan in its distribution. To date, over 100 pathogenic races have been reported globally using the 12 differential cultivars and the binary naming system for race identification. Seventeen loci, Co-1 to Co-17, conditioning resistance have been mapped to the eight chromosomes Pv01, Pv02, Pv03, Pv04, Pv07, Pv08, Pv09 and Pv11 in addition to seven other genes Co-u, Co-w, Co-x, Co-y, Co-z, CoPv02c and CoPv09c, some of which have been mapped to the same chromosomes where the numbered loci are located. Anthracnose resistance is dominant at all loci except the co-8 locus, and multiple alleles have been identified at the Co-1, Co-3, Co-4, and Co-5 loci. In addition, the co-localization of the major Co-1 gene (Co-1<sup>4</sup> allele) with the Phg-1 gene conditioning resistance to angular leaf spot (ALS) was confirmed on Pv01. A major resistance cluster consisting of the Co-3 locus with five alleles, those formerly known as Co-9 (renamed Co-3<sup>3</sup>), Co-10 (renamed Co-3<sup>4</sup>), Co-7 (renamed Co-3<sup>5</sup>), along with Ur-5, and Ur-14 genes for rust, and Phg-3 gene for ALS and the Andean genes Co-15 and Co-16, are all located on Pv04. The Co-17 is the second anthracnose resistance gene (Co-13) to be mapped to Pv03, and a new resistance locus on Pv02 appears to be the Co-u gene previously mapped near the *I* gene on Pv02. A second resistance locus on Pv03 is being proposed in MDRK (Co-1), Kaboon (Co-1<sup>2</sup>) and Widusa (Co-1<sup>5</sup>) and the presence of the Co-5 gene was also confirmed in AB136, the original source of the Co-6 gene on Pv07. Quantitative resistance loci (QRL) coincided with two previously characterized major genes Co-u and Co-5 located on Pv02 and Pv07, respectively and additional QRL were recently identified on Pv01, Pv03, Pv04, Pv05, Pv07, Pv08 and Pv09. The only unique resistance locus detected resided on Pv05. Having access to the whole-genome sequence of *Phaseolus* now available in PhaseolusGenes genome database has resulted in the fine mapping of many of these resistance sources including: Co-x, Co-1, Co-1<sup>2</sup> and the Co-4<sup>2</sup> and the discovery of new genomic regions and candidate genes associated with anthracnose resistance. The Co-x gene was fine mapped to Pv01, close to the Co-1 locus, and to a syntenic region, located at one end of soybean chromosome 18 that carries Rhg1, a major gene conditioning resistance to soybean cyst nematode. Fine mapping of the Co-4 (COK-4) locus on Pv08 revealed 18 copies of the COK-4 gene in a 325kb segment of that chromosome. Recent genome wide association mapping studies (GWAS) of the Andean diversity panel (ADP) did not reveal new resistance loci but confirmed many of the existing loci. Given the formidable information on resistance sources many mapped and now tagged with SNP markers, bean breeders are poised to build more selective gene pyramids of both Andean and Middle American resistance sources to stem the rapid evolution of new races of the anthracnose pathogen.

## T20. Breeding for resistance to common and halo bacterial blights in common bean

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Common (CBB) and halo (HBB) bacterial blights are seed borne diseases that plague common bean production, primarily in warmer and cooler environments, respectively. CBB is caused by *Xanthomonas axonopodis* pv. *phaseoli* and *Xanthomonas axonopodis* var *fuscans*. HBB is caused by *Pseudomonas savastanoi* pv. *phaseolicola*. Genetic resistance is the primary means used to control these blight diseases combined with clean seed programs. Genetic resistance to CBB is conditioned primarily by QTL with large effects and HBB is conditioned by R genes. CBB host resistance x pathogen strain interactions are becoming more evident while a HBB host-pathogen differential set is well established. The major QTL for CBB resistance are defined by the SCAR markers linked to them: BC420 on chromosome Pv06, SU91 on Pv08, and SAP6 on Pv10. Combining QTL (at least two) is an effective strategy to breed for a moderate level of resistance to CBB. MAS has been widely used to develop CBB resistant lines and cultivars and there are several Andean and Middle American lines developed with various combinations of two of the three QTL, with SAP6 and SU91 the most common combination. The SAP6 QTL is the most difficult to work with because the marker is present in susceptible materials originating from the Middle American gene pool. A new major QTL named Xa11.4 and discovered in VAX 1 and 3 germplasm lines is on Pv11 but not yet tagged for MAS. There is a minor effect QTL on Pv07 which is also untagged. For HBB resistance there are major R genes *Pse-1* on Pv10, *Pse-2* on Pv10, *Pse-3* associated with I gene on Pv02, *Pse-4* tentatively assigned to Pv10, *pse-5* (which co-locates with *Pse-2*) and *Pse-6* on Pv04. The *Pse-2* gene has the broadest effect conditioning resistance to 7 of the 9 differential *Psp* races. None of the R genes condition resistance to the most prevalent race 6 but some lines like CAL 143, PI 150414, and GN #1 sel 27, have quantitative resistance to this race. The QTL for resistance to Race 6 in CAL 143 resides within a large R gene cluster toward the proximal end of Pv04. US14 pinto has resistance to race 6 conferred by two independent recessive resistance genes. Use of MAS in breeding for resistance to HBB awaits markers linked with the QTL/genes conferring resistance to race 6. A few new sources of HBB resistance await verification and inheritance studies to ascertain their uniqueness. New sources of CBB resistance are likely to arise from interspecific introgressions from secondary (*P. coccineus*) and tertiary (*P. acutifolius*) species. These and other issues concerning breeding for resistance to CBB and HBB will be discussed.

## **T21. Breeding for bruchid resistance into farmers' preferred common bean (*P. vulgaris*) varieties: Developments and challenges.**

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Common bean (*P. vulgaris*) is one of the most important legume based protein source from its dry pulse types of beans. Production and post harvest management of this crop is constrained by various environmental factors, diseases and insects. Bruchids are one of the key stored pests of dry common beans including two species *Zabrotes subfasciatus* and *Acanthoscellides obtectus*. Variable levels of bruchid resistance conditioned by accumulation of arcelin-2 and Arcelin-like (ARL - APA) proteins from wild tepary beans were introduced into farmers preferred (FPV) common bean varieties using backcrossing. A total of 12 lines from three FPVs backgrounds have been selected as resistant to *A. obtectus*, four containing arcelin 2 and ARL lines resistant to both bruchids species have been identified, 3 Calima type bean varieties with uncharacterized resistance have been identified and advanced for variety registration in Malawi and Tanzania. However, most of the developed bruchid resistant FPVs succumb to BCMV and BCMNV, CBB and anthracnose. Efforts to incorporate resistance to these foliar diseases is in progress. Performance and selection criteria for abiotic stresses is presented in this work.

## ABSTRACTS OF POSTERS

### **P1. Introgression of angular leaf spot resistance to French beans adapted to Kenyan environment using molecular markers**

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Angular leaf spot (ALS), caused by the fungus *Phaeoisariopsis griseola*, is considered a serious disease of common beans in many regions. The disease has been also been observed on French beans growing in Kenya, in addition to other major diseases including rust (*Uromyces appendiculatus*) and anthracnose (*Colletotrichum lindemuthianum*). Previous French bean breeding programs in Kenya focused mainly on bean rust but there is need to breed for multiple disease resistance including ALS, rust and anthracnose. The present study therefore aims at introgressing ALS resistance genes to French beans through marker assisted backcrossing. A total of 36 French beans accessions collected in Kenya and 12 ALS differential cultivars were grown in two disease hotspots in western Kenya: Kisii and Kakamega in the years 2013 and 2014. The results showed that none of the 36 French bean accessions were resistant to ALS in the field. The most resistant differentials were from the Mesoamerican gene pool: Mexico 54, BAT 332 and Cornell 49-242. Consequently, the project focuses on using Mexico 54 and Cornell 49-242 as donor parents to introgress genes for resistance to a locally adapted, market class French bean cultivar Amy, in a backcross breeding program. The backcross breeding program incorporates sequence characterized amplified regions (SCAR) markers linked to Mexico 54 and Cornell 49-242 to facilitate selection. The project has achieved the first backcrosses and will continue to the fourth backcross. It is expected by the end of the project that locally adapted, market class French bean cultivars with resistance to ALS will be available to Kenyan farmers.

## P2. ALS and root rot of the bean in Angola

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A list of the main crop diseases in Angola have been published by Noronha (1949, 1951, 1959) and Serafim *et al.* (1963, 1968, 1971, 1982). For bean (*Phaseolus vulgaris* L.), the first disease described was rust (*Uromyces appendiculatus*) and *Heterodera* sp. Were the first nematode (1949). Before 1956, anthracnose (*Colletorichum lindemuthianum* Br. & Cav.) had also been reported. A reference was also made to the intensity of the attacks observed, economic importance and systems of fighting them. From 1962 up to 1975, Serafim *et al.* carried out basic research for the plant disease survey, the study of phytopathological problems of major economic importance, the profit of the knowledge already acquired in other countries and its adaptation to the specific conditions of Angola. Results from these studies are summarized in an annotated list of main crop diseases, including Angular Leaf Spot (ALS) caused by *Phaeoisariopsis griseola*, wilt and root rot among other bean diseases. After 1975, Fernandes has continued with Serafim studies and described some new diseases in collaboration with Mbuata José, Dovala-Chicapa and A. Pascoal Muondo. Estévez de Jensen *et al.* (2011), CRSP-project, completed the molecular characterization of major diseases in *Phaseolus vulgaris* nurseries in Angola. She revealed that ALS and *Rhizoctonia solani* were prevalent on the local cultivar Olho de Perdiz and incidence was moderate in the nurseries. *Pythium myriotylum*, producing damping-off, was identified in a farmer's field; this is the first report of this pathogen for common beans in Angola. Now, a new team has continued with the principal crop diseases survey, in collaboration with CIAT and the Legume Innovation Lab (previously-CRSP). For the study of disease symptoms and identification and pathogenicity of causal agents, host plants or parts of host plants were collected from different ecological localities of Angola. ALS has increased its severity on some local varieties, perhaps due to the introduction of improved susceptible varieties. The most common diseases and their soil-borne pathogens are Fusarium root rot or dry rot (*Fusarium solani* f. sp. *phaseoli*), Fusarium wilt (*Fusarium oxysporum* f. sp. *phaseoli*), Rhizoctonia root and pod rots (*Rhizoctonia solani*), and Pythium damping off and wilt (*P. myriotylum*, *Pythiums* spp.). They are widespread throughout dry bean growing areas of Angola, and soon after emergence delicate bean seedlings can be attacked by one or more than one pathogen. In Angola, ALS, root rot, damping-off and wilt are diseases that usually occur only when hosts are in poor condition; are widely distributed; cause fairly light damage; while cultural practices and sanitary measures can be used to control these diseases.

### **P3. Response of different common bean lines to *Phaeoisariopsis griseola* in Puerto Rico**

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Angular leaf spot (ALS), caused by *Phaeoisariopsis griseola* (Sacc.) Ferraris sin. *Pseudocercospora griseola* (Sacc.) Crous & U. Braun., is an important disease in common bean *Phaseolus vulgaris* L. in the Caribbean and Central America. The wide pathogen variability makes it necessary to continuously monitor virulence patterns when breeding common bean for resistance. An isolate from *Phaeoisariopsis griseola* was inoculated on 63 advanced black and white lines and parental cultivars “Verano” and “Beniquez”. The lines were derived from crosses with ALS 9951-101, BMD RMR 12 and PR0443-151. The standard differential series for determination of the ALS pathotype, consisting of 12 lines were also included in the study. The experiment was arranged in a completely randomized design replicated three times and inoculated twice with isolate ALS-9029 JD2 (105 conidia ml<sup>-1</sup>) from Juana Diaz. The evaluation was carried out 21 days after inoculation (18 and 25 days after planting) using the CIAT scale where: 1 = no visible disease symptoms and 9 = 25% of the leaf area covered with sporulating lesions. Based on the reaction of the ALS differentials, the ALS-9029 JD2 isolate was classified as pathotype 61:11 and this pathotype was pathogenic to the Andean (Don Timoteo, Amendoin, Bolon Bayo and Montcalm) and Mesoamerican (Pan 72, G02858 and Mexico 54) genotypes. Parental lines Verano and Beniquez were similar in their disease reaction showing susceptibility to the pathogen by producing lesions that covered approximately 5 - 10% of the leaf area. Three lines exhibited a susceptible reaction and 14 lines an intermediate reaction to the pathotype evaluated. Fifteen lines were resistant to isolate ALS-9029 JD2 with no sporulating lesions. Additional isolates of the pathogen from Puerto Rico should be evaluated to provide more information about ALS variability on the island.

#### **P4. Variability of the angular leaf spot pathogen in Argentina**

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Angular leaf spot (ALS) caused by the fungus *Pseudocercospora griseola* (Sacc.) Crous & U. Braun, has been reported to be one of the most destructive and widespread problems of common bean production in Argentina. The importance of the disease has increased in recent years, becoming one of the main causes of yield losses and seed quality decrease. The success of breeding for resistance to ALS requires a thorough identification of the pathogen diversity. In the northwestern region of Argentina, which is the principal area of common bean production of the country, 13 races of the ALS pathogen have been identified based on a set of differential cultivars. From a total of 45 isolates analyzed 37 were Mesoamerican and eight were Andean, resulting in ten and three races, respectively. The aim of this study was to analyze the genetic variability and population structure of *P. griseola* isolates collected in several bean fields in northwestern Argentina by means of URP-PCR and ITS-rDNA sequences. Based on the ITS sequences the isolates were identified as Andean (*P. griseola* f. *griseola*) or Middle American (*P. griseola* f. *mesoamericana*) and the haplotype structure of each group was inferred. A total of 135 bands were amplified using 12 URP primers. Principal coordinate analysis (PCoA) was performed to estimate genetic similarity between isolates. The Andean isolates showed a higher dispersion suggesting lower genetic similarity than the Middle American isolates. The AMOVA based on the URP data showed that the Andean isolates significantly differed from the Middle American ones, with low levels of gene flow and 75% of the variation remaining among groups, supporting the idea of coevolution of the pathogen with its host. Some admixed genotypes evidenced in the structure analyses might be the result of parasexual reproduction. The URP approach was more efficient than other genome-wide multilocus techniques used in previous studies to characterize the *P. griseola* isolates since URP markers identified 37 unique multilocus haplotypes compared with 18 haplotypes defined with RAPD and ISSR markers. Our results demonstrate that this technique is a powerful tool to characterize intraspecific polymorphisms and detect diversity among *P. griseola* isolates. Increased knowledge of the population biology of the ALS pathogen would contribute to better management of the disease in agricultural ecosystems. Furthermore, the great variability reported herein should be considered when identifying genotypes with durable resistance to angular leaf spot.

**P5. Virulence diversity of *Pseudocercospora griseola* and its implication for breeding common bean for resistance to angular leaf spot**

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The “First International Angular Leaf Spot (ALS) Workshop” of common bean was held in 1995 at CIAT, Cali, Colombia. Angular leaf spot is caused by *Pseudocercospora griseola*. At this workshop, the use of differential varieties proposed by CIAT's Bean Pathology program was approved and a binary system for identification of ALS races was established. This binary system unified criteria and led to a better understanding of the pattern of virulence diversity of the ALS pathogen, *P. griseola*. Since 1995 a total of 589 isolates have been characterized. Of these, 184 isolates were from 13 countries in Africa; 158 from nine countries in Central American, and 247 isolates from five countries in South American. Of these, 429 isolates were classified as Mesoamerican isolates and 160 isolates as Andean. Andean isolates of *P. griseola* can only infect common bean of Andean origin, whereas Mesoamerican isolates infect both Andean and Mesoamerican bean varieties. In total, 134 *P. griseola* races were identified worldwide. Of these races, 31 were unique to Africa, and 80 unique to the Americas. The remaining 23 races were identified in the two continents. This information has been used to better target the deployment of ALS resistance genes and prolong the usefulness of these genes in the regions where ALS is an important disease. This presentation shows the pattern of *P. griseola* virulence diversity, in each country, continent and between countries. In addition, we have generated important information revealing the importance of each differential cultivar that will guide their inclusion or exclusion into a new set of differential cultivars that are needed to study the extensive virulence diversity observed in *P. griseola*.

## **P6. Angular leaf spot in the Southern Highlands of Tanzania: Occurrence and management practices**

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Angular leaf spot disease caused by the fungus *Pseudocercospora griseola* is among the principle factors limiting common bean (*Phaseolus vulgaris* L.) production in the Southern highlands of Tanzania. Estimated yield losses of up to 60% of grain yield occur when bean plants are infected early by angular leaf spot. Use of contaminated seeds are the main sources of primary inoculum through introducing pathogens into new areas, or from season to season under environment conditions favoring these diseases. The losses can be minimized with the use of management strategies, such as use of correct nutrients can help reduce of the disease intensity during crop development. Nine improved common bean varieties and a local cultivar (Kigoma) were used to determine incidence and management options for Angular leaf spot at Uyole - Mbeya; Ismani - Iringa; and Ludewa - Njombe. Seed sorting, use of fertilizer and improved varieties were the recommended management options tested in a randomized complete block design with three replications while no fertilizer and unsorted seeds were the farmers practices selected. Disease reactions show that among the three locations tested, Ismani had no angular leaf spot with all varieties scoring a severity of 1. There was incidence of angular leaf spot disease in Ludewa and Uyole with Uyole 03, Uyole 94, Uyole 84 and Roba 1 showing a resistant response in both locations, while Njano-Uyole and Kigoma were susceptible to angular leaf spot. The combination of seed sorting and use of fertilizer resulted in lower disease attack in both locations compared to zero fertilizer application and unsorted seeds which are the common farmer practices. Angular leaf spot resistant in each location can be recommended to farmers coupled with the use of fertilizer and seed sorting as options for disease management in each area while Ismani can be used as a seed production area for angular leaf spot disease. Uyole 94, Uyole 03, Roba 1 and Uyole 84 are recommended varieties against angular leaf spot at Ludewa whereas Uyole 84, Roba 1, Uyole 04 and Uyole 98 are recommended varieties against angular leaf spot at Uyole.

## **P7. Reaction of selected South African dry bean cultivars, breeding lines and differential cultivars to angular leaf spot in the field**

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Angular leaf spot is an important seed-borne disease of dry beans caused by the fungus *Phaeoisariopsis griseola*. The disease occurs globally mainly in tropical and subtropical areas including South Africa. The aim of this study was to assess the disease reaction of twelve international differential cultivars of angular leaf spot, five selected breeding lines and five South African commercial cultivars developed at the Agricultural Research Council – Grain Crops Institute of South Africa. Trials were established in the field with natural infection. Trials were conducted at Cedara Research Station (KwaZulu Natal province of South Africa) during the 2012/13, 2013/14 and 2014/15 dry bean growing seasons. Trials were arranged in complete randomization consisting of single row plots that were 4 m long, 75 cm apart with a 7.5 cm intra-row spacing. Weeding was done chemically using Bateleur Gold (active ingredient: metolachlor at 1.7 L/ha) and also manually. ALS was scored during pod filling (R8 stage) and repeated two weeks later using the International Center for Tropical Agriculture's 1 to 9 rating scale, where 1 is resistant and 9 susceptible. The majority of the differential cultivars showed resistance to the disease through all the three seasons, except for Montcalm and PAN 72. Sederberg and Teebus-RR 1 were the only two cultivars that showed resistance while all the breeding lines showed resistance.

## **P8. Occurrence and distribution of angular leaf spot of common beans in Northern Zambia**

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Angular leaf spot (ALS) caused by *phaeoisariopsis grieola* (Sacc.) Ferraris is considered the most important disease of common bean in tropical and subtropical regions. The disease has been reported in more than 70 countries worldwide. Although the disease has been found to occur in farmers' fields in Zambia, no study has been completed on its occurrence and distribution. Therefore, this study was conducted in five districts to assess the incidence and distribution of ALS in April 2014 in the Northern Province of Zambia. In all the districts, ALS was found to be widespread with a mean incidence 19.4%. Isoka district registered the highest incidence (37%), while Mwense district recorded the lowest (3.2%). In order to manage the disease and assist the smallholder farmers to obtain high yields, integrated disease management is required.

## **P9. Distribution of *Pseudocercospora griseola* Pathotypes in Uganda**

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Common bean has become a staple food in East Africa where it is the second most important source of dietary protein and the third most important source of calories after cassava and maize. Due to a myriad of pests and diseases, however, its production has been much lower than its potential. Angular leaf spot disease caused by *Pseudocercospora griseola* (Sacc) Crous & Braun is one of its most important production constraints causing yield losses as high as 281,300 MT in East Africa. Genetic resistance to the disease is difficult to attain due to the high pathogenic variability of the pathogen. This study aims at supporting the development of resistant varieties in Uganda by providing a comprehensive understanding of the pathogenic variability of the pathogen in the country. Disease sample collection has been taking place in all the 9 bean agro-ecologies in the country and so far a total of at least 600 diseased leaf samples have been collected. Out of these, a total of 170 single spore isolates have so far been cultured and refrigerated at -80 °C. DNA extraction from the stored isolates is also being done concurrently using the Mahuku (2004) extraction protocol. Following the DNA extraction, 4 universal Randomly Amplified Microsatellite (RAM) primers will be used for the initial DNA screening, and the primers that produce reproducible and consistent banding patterns will be adopted. PCR will then be carried out and the products visualised by polyacrylamide gel electrophoresis. The electrophoresis products will be documented and analysed and a dendrogram of the relationship between the isolates will be produced. Virulence characterisation will be done for each of the races that have been genetically identified. The 12 ALS differential cultivars established by CIAT will be used and the CIAT 1-9 disease scale will be employed. Plants with scores of 1-3 will be considered resistant and those with scores of 4-9 as susceptible. The total of the binary numbers of susceptible Andean and Mesoamerican cultivars of the bean differentials will be used to define pathotypes.

## **P10. Reactions of common bean genotypes to the causal agent of angular leaf spot and implications for genetic improvement**

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The fungi *Pseudocercospora griseola*, causal agent of angular leaf spot of bean, presents wide pathogenic variability that constrains the development of resistant cultivars. Knowledge of the aggressiveness of different strains, as well as of the mechanisms of genetic resistance, are important for breeding programs to successfully obtain common bean cultivars with durable resistance. The aim of this study was to study the variation within race 63.63 by evaluating the aggressiveness of different strains, to analyze the genetic resistance of common bean lines to *P. griseola*, and to discuss the implications for genetic improvement in obtaining resistance in this pathosystem. Four strains, collected from different regions, were inoculated in three groups of common bean lines in the greenhouse, and the severity of the disease was subsequently evaluated. Statistical analyses were carried out using the diallel method, which allowed obtaining information concerning the vertical and horizontal resistance of the host, and information about the pathogens' aggressiveness. The aggressiveness of *P. griseola* differed between the strains of race 63.63. The diallel method proved to be promising for the identification of horizontal and vertical resistance in the common bean-*P. griseola* pathosystem, with a predominance of horizontal resistance. Gene pyramiding, using marker-assisted selection, may not be the most effective strategy for obtaining durable resistance.

## **P11. Characterization of *Pseudocercospora griseola* isolates using differential cultivars of common bean from Parana state, Brazil**

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Angular leaf spot (ALS), caused by the fungus *Pseudocercospora griseola*, is one of the most important diseases of common bean (*Phaseolus vulgaris* L.) in tropical and subtropical bean producing areas. When infected seeds are planted under environmental conditions favoring this disease the yield losses caused by the ALS pathogen can reach 70% or more. Thus, considering the importance of the common bean for Brazil and the incidence of ALS, this study was conducted with the objective of characterizing *P. griseola* isolates from Parana state, Southern Brazil by using differential cultivars. Pods and leaves with angular leaf spot symptoms were collected from infected plants of common bean in the north region of Parana state, Brazil. The monosporic cultures of the *P. griseola* isolates were first multiplied in petri dishes containing 1-2 mL of a solution of 800 mL of sterilized water, 200 mL of commercial tomato sauce, 15 g of agar, 4.5 g of calcium carbonate (CaCO<sub>3</sub>), and 10 µg mL<sup>-1</sup> of streptomycin. Subsequent inocula of isolates were produced in Petri dishes containing the tomato medium and maintained in a BOD incubator at 24°C for 15 days. Spore suspensions were adjusted to 1.2 × 10<sup>4</sup> conidia mL<sup>-1</sup> of distilled and sterilized water to the dilutions. To distinguish the races derived from different *P. griseola* isolates, the differential cultivar set was used. The cultivars were sown in plastic trays containing a sterilized mixture of the soil and organic material. These trays were kept under greenhouse conditions until the seedlings reached the primary leaf stage. Twelve seedlings of each differential cultivar were inoculated with the spore suspension by using a De Vilbiss air compressor. The inoculations were done on 12 differential cultivars and the plants were moved to a mist chamber, where they remained for 72 h at 20°C, 12 h light / 12 h dark and a relative humidity of nearly 100%. Ten days after the inoculation, the plants were scored as resistant or susceptible, where 1 to 3 = resistant and 4 to 9 = susceptible. The characterization of *P. griseola* isolates collected in Parana state provided the identification of the race 31.61. This is the first report of the occurrence of this race in Parana, Brazil. The race 31.61 was compatible with Don Timóteo, G 11796, Bólon Bayo, Montcalm and Amendoim, PAN 72, Flor de Mayo, México 54, BAT 332 e Cornell 49-242. This isolate infected not only differential cultivars of Mesoamerican origin but also the ones of Andean origin.

## **P12. Morphological and molecular characterization of *Pythium* and *Fusarium* species on common beans in Uganda**

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Bean productivity in Africa is severely constrained by several fungal diseases including a complex of root rot species such as *Rhizoctonia* spp., *Sclerotium* spp., *Fusarium* spp., and *Pythium* spp. The objective of this study was to conduct analysis of morphological and molecular characteristics of *Pythium* and *Fusarium* spp., on common beans in major growing agroecologies in Uganda: lowlands in northern Uganda ( $\leq 1000$  masl), Lake Victoria crescent ( $\sim 1200$  masl), mid-highland (1400-1700 masl) and highlands ( $> 2000$  masl). Whereas agroecology did not appear to significantly affect the growth rate of *Pythium* isolates, on average most of the fastest growing isolates were obtained from the Mid-highland and Lake Victoria crescent with a maximum growth period of 72 h, while the slower growing isolates originated from all four agro-ecologies. The isolates showed four types of colony patterns (flat, fluffy, floral and fluffy with clear zones). The majority of the isolates had a fluffy type of colony (67%), followed by fluffy with clear zones (14%), and flat (10%). The isolates exhibited either creamy or white colony colors with the latter being the majority. Genotyping using BOX PCR revealed considerable diversity among the isolates, irrespective of geographic origin. The highest diversity was observed among isolates from northern Uganda and the least from the Lake Victoria crescent. BOX-PCR did not show any significant relationship between morphology and genogrouping. When genotyped using ISSR markers, *Fusarium* isolates formed two major clusters; one containing isolates from all agro-ecologies and second group exclusively composed of isolates from the highland agro-ecological zones. Genotypic richness predicted by expected multi-locus genotypes (eMLG) showed that Mid- and highland isolates were genotypically most diverse (eMLG=10), while lowland and Lake Victoria crescent isolates were the least diverse (eMLG=3).

### **P13. Disease resistance of locally bred and selected bean varieties for their market class**

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The recent release and commercialization of high yielding and marketable climbing bean varieties in Rwanda has enhanced productivity, internal and regional trade and farmers' incomes. Rwanda is now a net exporter of beans. In spite of the above, on farm bean productivity was still lower than the researchers' expectations of 3.0 t/ha to 6.0 t/ha. This is principally attributed to climate changes, degeneration, and limitations in numbers, access and utilization of existing improved varieties. The objective of this study was to evaluate the agronomic performance of 9 varieties, including 7 newly bred and selected bean varieties, for their market class across the country along with two checks. A completely randomized block design was used with 3 replications in 11 different environments. Trials were grown in plots of 4m x 4m. The varieties RWV 2381A and RWV 2350A-2B performed better despite drought periods across Rwandan Agroecological zones with the maximum yields of 3,438 kg/ha and 3,024 kg/ha, respectively. Variety RWV 2379-3A is adapted in specific agroecological zones of Rwerere, Muhanga Ngoma and Nyagatare, Karama with the potential yield of 2,731 kg/ha while RWV 26242B-2-3-1 is adapted in Rubona, Nyamagabe, Karama and Nyagatare with the potential yield of 2,357kg/ha. The variety RWV 2411A-2 performed better at Rubona, Muhanga and Karama with the potential yield of 2,500kg/ha. The tested plant materials were resistant to most of diseases including angular leaf spot, halo blight, common bacterial blight, bean common mosaic virus, ascochyta blight, anthracnose and rust.

**P14. Screening *Fusarium* species isolated from dry bean (*Phaseolus vulgaris*) for virulence using greenhouse and laboratory methods**

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*Fusarium* root rot (FRR) is one of the most significant root diseases of dry bean that can severely constrain bean productivity. *Fusarium* root rot resistance has been reported in some Mesoamerican bean genotypes. Crossing has been done to introduce resistance genes from Mesoamerican to Andean beans and to analyze quantitative trait loci (QTL) associated with root rot resistance. An appropriate screening strategy as well as effective *Fusarium* inoculum is necessary for the phenotyping in QTL analysis. In this research, both 14 day greenhouse and 7 day laboratory screening methods were used. Among the *Fusarium* species being tested are isolates from both Michigan and East Africa. An Andean and a Mesoamerican bean cultivar were used in the screening. The disease symptoms were observed and evaluated on the cultivars using a 1 (no disease)-9 (root completely rotted) scale in the greenhouse and a 1-5 scale in the lab screening. In addition, the plant fresh and dry shoot and root weight were measured. The virulence of the tested *Fusarium* species varied from mild to severe. One of the three tested *Fusarium brasiliense* (MIMTC-A3) caused the most severe root rot disease symptom and 70% reduction in plant dry weight. Another *Fusarium brasiliense* strain (MIMTC-A9) caused significantly different disease severity on two bean cultivars.

## P15. Root rots of common and tepary beans in Puerto Rico.

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Root rots are a disease complex affecting common bean and can be severe in bean growing areas in the tropics and subtropics. The presence of several pathogens makes it difficult to breed for resistance because of the synergistic effect of the pathogens in the host and the interaction of soil factors and environmental conditions. During 2015, isolates were collected from a root rot nursery in Isabela from common bean genotypes with symptoms of root rot. The most prevalent pathogens found were *Rhizoctonia solani* (Rs), *Fusarium solani* (Fs) and *Pythium ultimum* (Pu). Inoculation tests were carried out under greenhouse conditions using the local check 'Verano' and TARS-LFR1. Furthermore, to determine the resistance of elite tepary and common bean lines, a trial was carried out with each pathogen inoculated separately. In a complete randomized design replicated three times, tepary and common bean lines were sown in a PROMIX substrate. The inoculum consisted of an agar disk of Rs grown in an acidified potato-dextrose-agar (aPDA) placed under the seed at planting. For Fs, a suspension of 1 ml of 10<sup>5</sup> macroconidia ml<sup>-1</sup> was inoculated at the seedling stage. An un-inoculated control was included and the evaluation was carried out 15 days after inoculation. Rs was evaluated using a disease severity (DS) scale of 1-5, where 1 = healthy root and hypocotyl, 2 = 1-25% of hypocotyl infected, 3 = 25-50% of hypocotyl affected, 4 = 25-50% hypocotyl affected and 5 = 75–100% hypocotyl affected, dead plant. For Fs, the DS scale used was 1-9. In tepary beans, reddish to brown lesions in the hypocotyl and depressions at the base of the stem were consistent with the inoculation of Rs. Results showed that tepary line Tep 32 (4.5) the interspecific hybrids INB-848 (DS 4), INB-846 (DS 4.6), INB-826 (DS 4.5) and INB-829 (DS 4.6) were susceptible to Rs. Tep 1 (DS 3), Tep 23 (DS 3.3) and INB-809 (DS 3) were intermediate in reaction to Rs. Interspecific hybrids INB-835 and TARS-LFR1 were resistant. The common beans 'Verano' (DS 5), ADP-269 (DS 4), AND-469 (DS 4.5), ADP-54 (DS 4), ADP-633 (DS 4.5), ADP-115 (DS 5) were susceptible to Rs when compared with TARS-LFR1 (DS 2), ADP-518 (DS 2.7), ADP-508 (DS 2) and ADP-475 (DS 1.7). Tepary beans inoculated with Fs did not develop symptoms, in contrast, common beans showed reddish lesions in the hypocotyl and browning of the tap rot. The results indicated that Rs and Fs independently produced hypocotyl and root rot and that the combination of the pathogens should be included in future studies.

**P16. Screening bean germplasm for response to *Rhizoctonia solani* AG 2-2 and AG 4.**

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*Rhizoctonia solani* can cause damping-off of seedlings and root rot of mature plants in a number of different crops, including dry bean. *R. solani* is a species complex that is further subdivided into anastomosis groups (AG) that have been shown to vary in their host range or type of disease caused. For example, *R. solani* AG 4 is a common cause of seedling damping-off in diverse crops including angiosperms and gymnosperms worldwide while AG 3 is primarily a pathogen on the Solanaceae. In the past in survey work from the Midwestern United States, *R. solani* AG 2-2 has been found as the most common *R. solani* on dry bean while in samples from African countries, AG 4 tended to predominate. Similar to these results, we identified primarily AG 4 in *R. solani* from East Africa while AG 2-2 was common in Michigan. Isolates are being tested for effect on dry bean germplasm at both a seedling (inoculated at planting) and seedling to adult plant transition (inoculated 14 days after planting) growth stages. Material from an Andean diversity panel have shown variable response to both AG 4 and AG 2-2. The responses to the different AG appears to be independent from each other in the germplasm examined. While the AG 2-2 isolate tested showed higher severity on seedlings than adult plants for four out of five germplasm tested, the AG 4 isolates were not significantly different between seedlings and adults for four out of five germplasm. Further screening with AG 4 on the adult plants only has identified significantly reduced disease severity in 13 out of 32 ADP germplasm tested.

**P17. Occurrence of root rot disease of common bean (*Phaseolus vulgaris*) and selection of resistant genotypes in Mozambique**

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Common bean (*Phaseolus vulgaris*) is one of the priority legume crops in Africa, Latin America and the Caribbean, and it is the main source of dietary protein and minerals for millions of people in both developing and developed countries. In Africa, including Mozambique, beans are grown primarily by smallholder farmers, especially women, for home consumption, and the excess production is sold. Pests and diseases affect bean production in many producing regions in Africa. Beans are grown intensively in consecutive seasons with limited crop rotation in many regions in Africa and this practice has led to an increase in pest and disease pressure, including soil borne pathogens. More than 200 bean lines were planted in replicated nurseries in Chokwe and Gurue in 2013 and 2014 and symptoms of soil borne pathogen infection were recorded using a 1-9 scale. Significant differences in root and stem infection between genotypes in different sites were detected. The incidence of root and stem rots was higher in Gurue (central Mozambique) than in Chokwe (southern region). In addition, the incidence of root and stem rots was higher in genotypes from the Andean gene pool than in Mesoamerican genotypes. Bean genotypes were identified that had high stand count, low foliar diseases and yield potential. Early fungal root pathogen identification at UNL found *Fusarium* spp most frequently.

**P18. Analysis of defense genes in response to soil borne pathogen white mold infection in different common bean (*P. vulgaris*) cultivars**

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White mold, caused by *Sclerotinia sclerotiorum* (Lib.) De Bary, is a serious yield reducing fungal pathogen of common bean (*Phaseolus vulgaris* L.). It is a soil borne pathogen that persists in the soil for up to five years. Due to increase in bean production and variable weather patterns the incidence and severity of white mold is also increasing in tropical countries like Malawi. Understanding the function of quantitative resistance genes and their mode of expression is necessary to enable breeders to select which genomic regions to deploy in marker assisted selection. We investigated the role of three genes; PGIP, Glucanase, and PAL in the defense response of different bean genotypes (AN-37, P02630, Beryl and G122) following infection with *Sclerotina sclerotiorum*. Analysis of defense genes in response to white mold infection showed variable temporal transcription. These results suggest that the resistance reported in different cultivars of beans to white mold is due to different defense pathways. The induction of defense genes at wounding may have a confounding role in the interpretation of results from the greenhouse straw test which usually does not correlate with field tests. There is need to investigate the role of other genes from the genomic regions containing these defense genes to gain a better understanding of the variation in reaction to white mold in different cultivars of common bean.

## **P19. Identification and morphological characterization of soil borne pathogens collected from field sites in Rwanda**

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*Rwanda Agriculture Board*

The fungi that can cause root rots and seedling disease often occur together and are difficult to distinguish visually. Some diseases develop under different conditions where some are worse when the soil is wet while others prefer a dry environment. The objective of this study was to identify and characterize the soil borne diseases of common bean (*Phaseolus vulgaris*) in Rwanda. Infected plant samples were collected across the country in all Districts. Isolation of the pathogen was done on Potato Dextrose Agar (PDA) medium. Cultures were purified by picking a single hyphal tip. Four root rot diseases were identified and characterized including *Rhizoctonia spp*, *Fusarium spp*, *Sclerotium spp* and several *Pythium spp*. Morphological characterization showed that *Fusarium*, *Rhizoctonia* and *Sclerotium* isolates were more predominant than *Pythium species*. The four diseased were observed mainly in the Northern and Southern parts of Rwanda as compared to the Eastern and Western parts of Rwanda. We concluded that a total bean root rot disease control program is necessary to reduce losses associated with these diseases especially the use of resistant varieties since the fungi are widespread and survive in soils for a long time.

## **P20. Carbon assimilation profile of *Fusarium* species from different Brazilian regions associated to common bean root rot**

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The carbon assimilation profile of *Fusarium* spp. was assessed in 92 isolates obtained from traditionally common bean-cropping regions in the Brazilian states of Paraná, Minas Gerais, São Paulo and Goiás, known as the country's four main producers of this crop. The set of genotypes, consisting of 65 *F. solani* and 27 *F. oxysporum* isolates, was previously tested for pathogenicity in common bean. This group was evaluated for its physiological diversity and the assimilation profile of 95 carbon sources using Biolog FF microplates. The tests were carried out with a 100 µl suspension of  $2 \times 10^5$  conidia ml<sup>-1</sup> adjusted in a phytigel sterile solution added to each microplate well. After 72 hours of incubation in the dark at 25°C, mycelial growth on carbon sources was spectrophotometrically estimated, with absorbance read at 750 nm. Each isolate was assessed in two replications in a completely randomized experimental design, with a  $2 \times 4 \times 95$  factorial arrangement for comparisons between species, geographical origin and carbon sources and interactions between the three factors. The results were evaluated by means of box-plot descriptive statistics and by ANOVA, with averages compared by the Scott-Knott test (5%). Principal component analysis (PCA) was used to identify the major sources of variation and the correlation between carbon sources and the main components (significant to 5%). ANOVA showed interactions between all factors, with differences in the isolates' metabolic profile within each species. On average, *F. solani* had higher mycelial growth than *F. oxysporum*. Results also demonstrated different carbon assimilation profiles among the two *Fusarium* species, and diversity of isolates according to the different geographical origins. The PCA's first component explained 93.23% of the variance in the carbon metabolism of *F. solani* and *F. oxysporum*. There were also differences between the isolates from the four states, with the Goiás population arranged in a distinct metabolic profile that had lower average mycelial growth than the samples from Minas Gerais, Paraná and São Paulo. Such differences were confirmed by PCA, with 84.07% and 8.50% of the variance explained by these two components, respectively. Such results indicate that the two *Fusarium* species may occupy different niches in the soil and that physiological differences between isolates of different states are probably influenced by adaptations to environment and cultural practices in different agroecosystems. These achievements indicate broad facility to colonize different carbon sources and potential differences in the saprophytic survival of *F. solani* and *F. oxysporum*, which can support root disease management strategies in common bean crops.

## **P21. Screening field resistance to the root rot complex within the Andean Diversity Panel (ADP)**

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Dry bean root rot is caused by a fungal complex mostly including *Fusarium solani* f. sp. *phaseoli*, in association with *Rhizoctonia solani*, *F. oxysporum*, *Phythium* spp., among others. Root rots are an increasing problem in Minnesota, the largest producer of kidney beans in the U.S. Root rot can reduce seed yield up to 100% under severe disease pressure (Schwartz, 2014). Large seeded-cultivars planted in the area are especially susceptible to the Fusarium root rot complex when conditions are favorable. *F. solani* is the primary pathogen involved in bean root rot in Minnesota (Estévez de Jensen, 1998), and few sources of resistance exist, especially within the Andean Gene Pool. The objective of this study was to evaluate the reaction of a set of Andean genotypes to the root rot complex in the field. A total of 310 genotypes from the Andean Diversity Panel (ADP) (Cichy et al., 2015) were screened at Perham, MN in 2013. From those, 45 genotypes were photoperiod-sensitive or did not complete the production cycle. Remnant 265 genotypes were screened again in 2014 in two trials separated by days to maturity. The early maturity trial consisted of 144 genotypes, and the late maturity trial of 121 genotypes. Six common checks, one resistant, two intermediate, and three susceptible were used. The early and late maturity trials were planted in a 12 x 12 and 11 x 11 alpha-lattice design with two replications per trial. Root rot disease severity was determined on a scale 1-9 (1= healthy, 9= dead plant) at flowering stage (R6) using four plants per plot, evaluating individually and computing the average. In addition to root rot, seed size and seed yield were also measured. Resistant genotypes were considered those ranging from 1 to 3, intermediate from 4 to 6, and susceptible from 7 to 9. Plant samples collected in the field allowed to confirm that the most abundant pathogen was *F. solani*. In the early trial there were significant differences ( $P<0.05$ ) among genotypes for Fusarium root rot. Using Least Square Means, 23 genotypes are in the range 1 to 3, 102 in the range 4 to 6, and 19 in the range 7 to 9. Among the checks VAX 3 was resistant, Talon and Dynasty were intermediate, Montcalm, Cabernet, GTS-104 were susceptible as expected. The average 5 and the reaction of the checks suggest high disease pressure in the field. In the late trial there were also significant differences ( $P<0.1$ ) among genotypes for Fusarium root rot. Using Least Square Means, 21 genotypes are in the range 1 to 3, 62 in the range 4 to 6, and 38 in the range 7 to 9. The average 5 and similar reaction of the checks (compared to early trial) suggest high disease pressure in the field. A subset of contrasting genotypes will be evaluated again in the field in order to confirm results.

## **P22. Sclerotium root rot of common beans: A novel disease that requires novel management approaches**

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Common bean (*Phaseolus vulgaris* L.) root rots cause an estimated yield loss of 221,000 metric tons per year in sub-Saharan Africa. *Pythium* spp. and *Fusarium solani* f.sp. *phaseoli* (FSP) are known to cause severe root rots in high altitude areas characterized by cool temperatures and high relative humidity. However, high incidences of bean root rots are now observed in low and medium altitude bean agro-ecologies characterized by dry and warm conditions. Our studies have identified *Sclerotium rolfsii* Sacc. as the most important cause of bean roots in Uganda, except in the Southern highlands where *Pythium* spp. and *Fusarium solani* f.sp. *phaseoli* still cause severe root rots. Results of a survey in 51 districts in 7 bean agroecologies revealed that the incidence of *S. rolfsii* in 32 districts was above 80%. The agroecology that showed the highest Sclerotium root rot disease incidence (90%) and severity (41%) was West Nile Mixed Farming zone. Screenhouse pathogenicity tests have shown that the effect of *S. rolfsii* infection starts prior to germination, with 4 isolates consistently inhibiting germination by 100% in lines MLB-49-89A, NABE15, RWR719 and CAL96. Lines MLB-49-89A and RWR719 are resistant to *Pythium* and *Fusarium* root rots. However *S. rolfsii* isolates SIR400, HOI356-G, ARU511, SRK67 and ARU525 resulted in 5-88% germination, 100% root rot incidence, 4-5 severity scores (maximum score being 5) and 79-100% root rot severities in both MLB-49-89A and RWR719. Given the current significance of this disease, and the observed reaction of the known bean root rot resistance sources, there is urgent need to validate known root rot management practices for the control of Sclerotium root rots; and to identify resistance sources for use in variety improvement.

## **P23. Effect of drought on cooking time of root rot resistant germplasm**

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Drought is the most limiting abiotic stress affecting dry bean production worldwide. Cooking time may also be affected by drought. Cooking time is a major concern in Africa because longer cooking time requires use of more energy resources. This is particularly an issue in countries where firewood is scarce as rural households depend on firewood for cooking and must spend time searching for it. This study explored the effect of drought on cooking time by comparing the cooking time of selected root rot resistant lines grown under irrigated and terminal drought conditions in western Nebraska. Based on the combined analysis of the 2013 Zambia and Mozambique trials, 66 root rot resistant lines were identified. Of these, 55 were evaluated in replicated trials in adjacent irrigated (non-stressed, NS) and non-irrigated (drought-stressed, DS) plots at Mitchell, Nebraska (41°56.6' N, 103°41.9' W, 1240 m elevation) during 2014. Within each block, the 55 lines were assigned to experimental units using an 11 x 5 incomplete block design with 2 replicates. Each plot consisted of two 7.6-m rows spaced 0.6 m apart. Targeted plant density was 200,000 plants ha<sup>-1</sup>. 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. Data recorded included daily rainfall during the growing season (mm), seed yield (kg ha<sup>-1</sup>), 100-seed weight (g), and number of days to flowering and maturity. After bean plots were harvested, a Matson Bean Cooker was used to evaluate the effect of drought stress on cooking time. This cooker had 24 weighted plungers (metal rods) that pierced the seed when fully cooked. Seed from each plot was processed separately as follows. A 60-seed sample was soaked in distilled water overnight (16 hours). 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. An observer recorded the time when the beans were placed in the cooker and when 80% were cooked (indicated by the plungers dropping). The NS and DS plots received 453.0 and 248.2 mm, of total water, respectively. A total of 63.2 mm of precipitation occurred after flowering, resulting in moderate drought stress. In general, dry beans grown under DS took 10 minutes longer to cook. INIAP 480 (RR297), MBULAMTWE (RR21) and NE14-12-49 (RR367) cooked more rapidly when grown under NS than under DS conditions. Under NS conditions NE34-12-49 (RR-367), Kablanketi (RR-75), and Kasukanywele (RR-83) had the shortest cooking times (35, 39, and 41 minutes, respectively), but with less than 100% water absorption. Larga Comercial (RR-186) and G 10994 (RR-142) had the longest cooking time under both DS and NS conditions.

## **P24. Differentiation and quantification of pathogens from roots using PCR-GBS**

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In the Midwestern United States, root rots are arguably the most important diseases of pulse crops. A diverse group of pathogens cause root rots of pulse crops including *Rhizoctonia solani*, numerous *Fusarium* species and Oomycete pathogens, and many more opportunistic colonizing organisms are often present in diseased root tissue. As a result, differentiation and quantification of pathogens from roots can be a very elusive task, particularly when conducting large-scale surveys. Traditional plating techniques are extremely labor intensive, require a very skilled eye for pathogen identification and are not useful in pathogen quantification. Quantitative PCR (qPCR) has become the standard for quantifying pathogens within a sample and its use has resulted in substantial advances in our understanding of the host:pathogen interaction. While qPCR is very effective in pathogen quantification of low-to-moderate throughput of up to four pathogens within a reaction, it becomes less efficient when more organisms are targeted, or when several hundred samples are evaluated. Genotyping by sequencing (GBS) is primarily used for association studies and marker assisted breeding. However, by manipulating existing GBS technology, multiple organisms can be identified and quantified within a single sample. To differentiate diverse organisms, conserved genes or gene regions are targeted for amplification such as the nuclear ribosomal genes, transcription genes or translation genes. Closely related organisms are differentiated by targeting less conserved genes or gene regions for amplification such as membrane receptor genes, pathway enzyme genes, structural genes and noncoding regions. Organism identification is determined based on resulting sequences. Determining the frequency of distinct sequence reads, which represent distinct organisms, results in the relative quantification of each organism present in individual samples. Therefore, the objective of this research was to demonstrate the utility of PCR-GBS to identify and quantify organisms within samples and compare the PCR-GBS with qPCR results. PCR-GBS primers were designed in conserved sequence regions which span single nucleotide polymorphisms or small indels to allow the differentiation and quantification of seven highly similar *Fusarium* species using this method. This PCR-GBS application will be invaluable, particularly in population research, since it can simultaneously quantify multiple organisms from hundreds of samples in less than two weeks. The number of organisms identified is limited only by the availability of reliable sequence data

## **P25. Response of the Andean diversity panel to root rot in a root rot nursery in Puerto Rico**

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The Andean Diversity Panel (ADP) was evaluated under low-fertility and root rot conditions in two trials conducted in 2013 and 2015 in Isabela, Puerto Rico. About 246 ADP lines were evaluated in the root rot nursery with root rot and stem diseases caused predominantly by *Fusarium solani*, which causes root rot; *Macrophomina phaseolina*, which causes charcoal rot; *Sclerotium rolfsii* which causes southern blight; and *Pythium* spp. that cause damping off. The nursery is also not fertilized, thus poor soil fertility conditions were prevalent. A small number of lines were identified with moderate tolerance to these multiple stress conditions. Association mapping was conducted after genotyping the panel using genotyping-by-sequencing. Subsequent evaluation of ADP lines with resistance to specific soil borne pathogens can be used to identify specific disease resistance.

## **P26. Marker Assisted Selection (MAS) to deploy disease resistance in common bean (*Phaseolus vulgaris* L.) varieties for Ethiopia**

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Common bean (*Phaseolus vulgaris* L.) is one of the most important grain legumes in Ethiopia, and produced in all the regional states with varying intensity. Although traditionally a food and nutritional security crop in Ethiopia, its importance as a source of foreign currency and cash income for smallholder farmers is increasing. The productivity of this important crop under farmers' condition is below 0.6 tons/ha, which still is low as compared to the crop's potential yield (up to 4.5 tons/ha). Among a number of factors that could attribute to the low achieved yield, diseases especially common bacterial blight (*Xanthomonas campestris* pv *phaseoli*) (CBB) and angular leaf spot (*Pseudocercospora griseola*) (ALS) pose a significant harvest loss in common bean in farmers' fields. Therefore, developing bean varieties with improved and durable resistance to biotic stresses is the primary goal of the bean breeding program. To facilitate selection of resistance bean lines the application of molecular markers in the breeding program is fundamental. Molecular markers have been implemented in a marker assisted backcrossing (MABC) breeding program to deploy CBB and ALS resistance genes in farmer preferred but susceptible bean varieties. The use of molecular markers (SU 91, SAP6 and g796) allowed early selection of bean lines resistant to one or more pathogens currently part of the breeding program. Therefore, the bean breeding program at SARI, Ethiopia is implementing MAS/ MABC in deploying multiple disease resistance genes in popular farmer preferred red and mottled but susceptible common bean varieties to develop common bean varieties with durable resistance for the important pathogens so as to increase the productivity of this important crop.

## P27. Fungal pathogens and their implications for bean production in Uganda

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Because of its geographical location, Uganda is among the countries with the highest incidence and severity levels for crop pests and diseases in the world. As disease causing organisms, fungal pathogens are a major constraint to common dry bean (*Phaseolus vulgaris* L.) production. The dry bean is the most important legume grown and consumed in Uganda where it plays a major role as a source of human dietary protein, food security and an income generating crop for most resource poor families, but its production is mainly hindered by various fungal diseases. In a bid to develop an effective fungal diseases management strategy and improve production, a series of surveillance studies were conducted to determine the prevalence of fungal pathogens in farmers' bean fields within the five (5) different agro-ecological regions of Uganda. Disease incidence was measured as either the presence or absence of a particular disease with a given field and severity was determined as the average percentage of bean plants infected with a particular disease in five (5) randomly placed one metre square (1m<sup>2</sup>) quadrants within farmers' fields. The surveillance data obtained showed that the majority of farmers' fields surveyed (78.4%) were affected by more than two fungal diseases concurrently. Disease incidence results obtained from farmers' fields showed angular leaf spot (ALS) (94.6%), root rots (Pythium, Fusarium, and Sclerotium) (80.4%), anthracnose (58%) and rust (46.7%) as the most prevalent fungal pathogens, while aschoyta (7.5%) and white mold (5.2%) were less common and restricted to mostly to two agro-ecologies. The severity of the different pathogens was observed to be highest for root rots followed by ALS and anthracnose at 68.7%, 65.3% and 38.2%, respectively. Significant differences ( $P \leq 0.05$ ) were noted in the levels of pathogen incidence and severity within and among agro-ecologies, with the South Western and the Northern agro-ecologies being the most and least affected respectively. The magnitude of the fungal diseases observed in farmers' fields, impact negatively on smallholder bean production in Uganda. These findings suggests the need for an holistic breeding strategy that takes into consideration the need to introgress resistance for more than one pathogen in the same background at the same time.

**P28. Performance of parental genotypes and inheritance of angular leaf spot (*Phaeosariopsis griseola*) resistance in the common bean (*Phaseolus vulgaris*)**

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Two studies, one on performance of six common bean parental genotypes and another on inheritance of resistance to *Phaeosariopsis griseola* (*Pg*) in common bean were carried out in Malawi. Common bean entries, namely: Chimbamba, Nasaka, RC 15, CAL 143 and Mexico 54 were evaluated on station in the 2004/2005 growing season at Bunda, Dedza, Ng'onga and Ntchenachena sites. The second study started by generating F1s and then F2 and F3 seeds in a greenhouse at Bunda College. CAL 143 and Mexico 54 were sources of *Pg* resistance genes while Chimbamba, Nasaka and RC 15 were susceptible recipient parents. Following green house trials, *Pg* resistance was evaluated on station in the same sites. CAL 143 was the highest yielding genotype but unstable across sites. RC 15 was stable and gave the highest yield at the dry-spell-stricken Ng'onga whereas Mexico 54 was superior at Ntchenachena but highly unstable across sites. Yield was strongly correlated to number of effective pods per plant in all genotypes. The inheritance study showed that resistance to *Pg* in the common bean is controlled by one gene using both CAL 143 and Mexico 54 as resistant parents.

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62	Tedla	Yayis Rezene	<a href="mailto:rezene77@gmail.com">rezene77@gmail.com</a>	Southern Agricultural Research Institute (SARI)	Ethiopia
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65	Wendland	Adriane	<a href="mailto:adriane.wendland@embrapa.br">adriane.wendland@embrapa.br</a>	EMBRAPA, Rice and Beans	Brazil
66	Williams	Magdalena	<a href="mailto:mmagere@yahoo.com">mmagere@yahoo.com</a>	Maruku Agricultural Research Institute	Tanzania

### **Websites of Organizers:**

Feed the Future Grain Legumes Project, Common Bean Research Website:

<http://arsftfbean.uprm.edu/bean/>

USDA-ARS Website:

<http://www.ars.usda.gov/main/main.htm>

Agricultural Research Council, South Africa:

<http://www.arc.agric.za/Pages/Home.aspx>

### **Upcoming common bean meetings:**

**2015 BIC Biennial Meeting** - November 2-4, 2015

Location: Niagara Falls, Canada

Venue: Marriott Gateway on the Falls

<http://bic.css.msu.edu/>

<http://www.uoquelph.ca/hosted/bic2015/>