ANNUAL REPORT OF THE

BEAN IMPROVEMENT COOPERATIVE

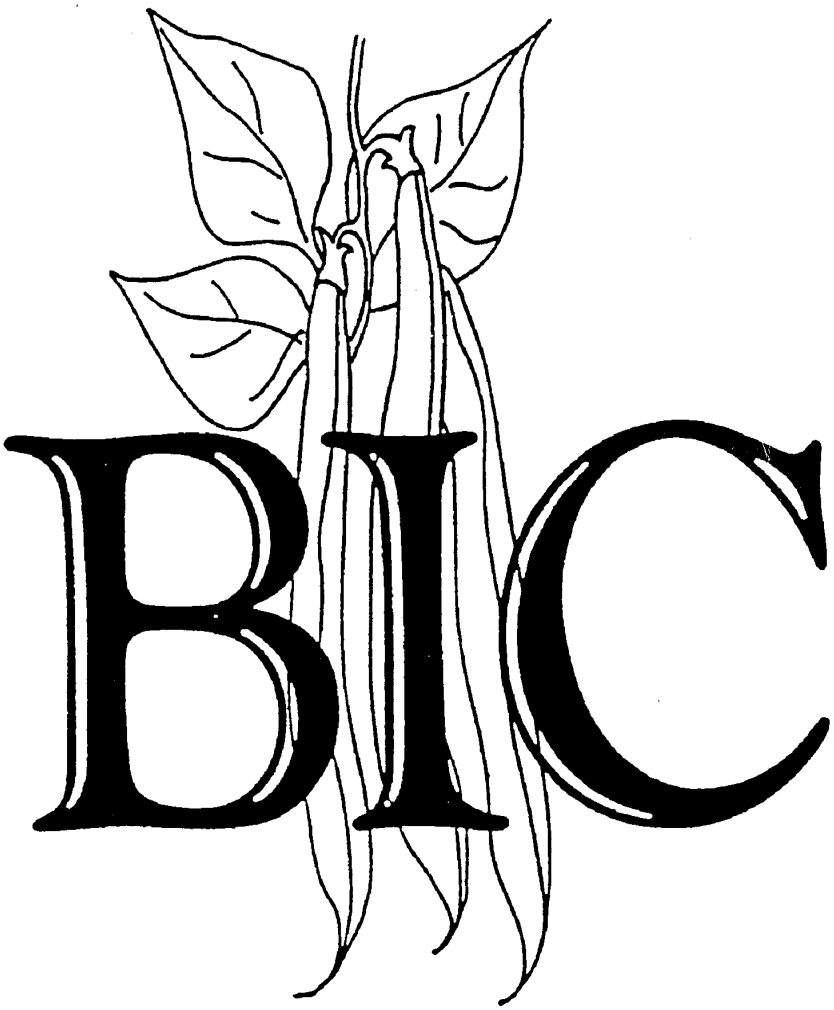
BIC

A VOLUNTARY AND INFORMAL ORGANIZATION
TO EFFECT THE EXCHANGE OF INFORMATION AND MATERIALS

VOLUME 66
2023

ANNUAL REPORT OF THE

BEAN IMPROVEMENT COOPERATIVE



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THE LXVI

Report of The

BEAN IMPROVEMENT COOPERATIVE

No. May 2023

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Coordinating Committee

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SITE REGULARLY UPDATED

Note: It will be assumed that interested individuals may freely cite (including author credit) any report or note in this BIC report, unless the author indicates to the contrary. As a professional courtesy, individuals citing BIC notes should notify the authors of his or her intentions. The BIC Coordinating Committee approved this statement on November 5, 1975.

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Cover: Photo by Juan Osorn

THE 66th ANNUAL REPORT OF THE BEAN IMPROVEMENT COOPERATIVE

The Bean Improvement Cooperative (BIC) will celebrate its 32nd Biennial Meeting from the 6-8 of November 2023. This will be a concurrent meeting with our colleagues in the North American Pulse Improvement Association, with NAPIA as the principal organizer of this meeting. The local meeting organizers are: Dr. Dil Thavarajah (NAPIA Past President; dthavar@clemson.edu); Tristan Lawrence (NAPIA Treasurer/Secretary; tjlawre@clemson.edu) and Summer Chandler (Clemson Event Planner; spriddy@clemson.edu). The Phaseolus Crop Germplasm Committee, BIC Genetics Committee and the Regional W-4150 Committee are scheduled to meet on November 8. A field trip is also planned for November 8th to Clemson University. Please refer to the information provided by the local organizing committee in this report. Registration, abstract submission information, and updates from the organizers are available on the Meeting website https://www.clemson.edu/cafls/bic-napia/.

Please review the call for nominations for the BIC Meritorious Service Award, BIC Achievement Award, and new BIC Technical Merit Award, and forward your nominations to the Awards Committee Chairperson, Carlos Urrea (currea2@unl.edu) by July 15, 2023. The Frazier-Zaumeyer Distinguished Lectureship will also be awarded and will honor our founding members. Nominations for this Lectureship should be sent to Carlos Urrea. A current membership list of BIC Committees and those who have received awards throughout the history of the BIC is provided in the current issue and on the BIC website to assist you in nominating colleagues for these awards.

Please share information about the BIC with interested colleagues who might like to attend the 2023 meeting or who would like to join the BIC as members. Also, feel free to contact us with any new ideas, contributions, or updates for the BIC website or this Annual Report. We are especially interested in receiving new or updated methods that can be shared with the general community for the Research Techniques page of the BIC website.

The BIC Coordinating Committee welcomes Simon Chang as a new member and thanks Drs. Dan Wahlquist and Thiago Souza for their valuable and extended service on the Coordinating Committee. The BIC continues to conduct business by email, postings on the webpage, and through the online publication of this Annual Report. We are always open to new ideas to make the BIC a more effective organization and any suggestions can be shared with members of the Coordinating Committee.

We wish you a fulfilling and successful year. Warm regards,
Tim Porch, BIC President

BIC COMMITTEE MEMBERSHIP - 1957 to 2023

Coordinating Committee (approximate year of appointment):

1957 Dean, Enzie, Frazier* (BIC Coordinator/President), McCabe, Zaumeyer
1960 Anderson, Atkin, Dean, Enzie, **Frazier**, McCabe, Zaumeyer
1962 Anderson, Atkin, Dean, **Frazier**, Pierce, Polzak, Zaumeyer
1968 Anderson, **Coyne**, Dean, Jorgensen, Polzak, Zaumeyer
1971 Briggs, **Coyne**, Dean, Jorgensen, Polzak, Zaumeyer
1972 Burke, **Coyne**, Dean, Jorgensen, Kiely, Polzak, Zaumeyer
1974 Ballantyne, Bravo, Burke, **Coyne**, Dickson, Emery, Evans, Kiely, Saettler, Zaumeyer
1977 Ballantyne, Bliss, Coyne, **Dickson**, Emery, Evans, Graham, Meiners, Morris, Saettler, Zaumeyer
1978 Atkin, Ballantyne, Bliss, Coyne, **Dickson**, Graham, Meiners, Morris, Saettler, Sprague
1979 Atkin, Bliss, **Dickson**, Graham, Hagedorn, Meiners, Morris, Sprague, Wallace
1980 Atkin, Bliss, **Dickson**, Hagedorn, Morris, Sprague, Steadman, Temple, Wallace
1982 Atkin, Coyne, **Dickson**, Hagedorn, Sprague, Steadman, Temple, Wallace, Wyatt
1983 Coyne, **Dickson**, Hagedorn, Saettler, Silbernagel, Steadman, Temple, Wallace, Wyatt
1985 Coyne, **Dickson**, Mok, Saettler, Silbernagel, Steadman, Temple, Wallace, Wyatt
1986 Coyne, **Dickson**, Mok, Saettler, Schoonhoven, Schwartz, Silbernagel, Steadman, Wallace
1988 Brick, Dickson, Emery, Magnuson, Roos, **Schwartz**, Singh, Steadman, Uebersax
1992 Dickson, Emery, Grafton, Magnuson, **Schwartz**, Singh, Stavely, Steadman, Uebersax
1994 Antonius, Dickson, Grafton, Magnuson, Park, **Schwartz**, Singh, Stavely, Uebersax
1996 Antonius, Grafton, Park, **Schwartz**, Singh, Stavely, Myers, Kotch, Miklas, Riley
1998 Antonius, Park, Schwartz(ex officio), Singh, Myers, Kotch, Miklas, Riley, Beaver,Vandenberg,**Kelly**
2000 Antonius, Beaver, **Kelly**, Kotch, Miklas, Myers, Park, Riley, Schwartz, Singh, Vandenberg
2001 Antonius, Beaver, **Kelly**, Kotch, Miklas, Myers, Park, Riley, de Ron, Schwartz, Vandenberg
2003 Beaver, **Kelly**, Kmiecik, Kurowski, Miklas, Myers, Park, Riley, de Ron, Schwartz, Vandenberg
2007 Beaver, **Kelly**, Kmiecik, Miklas, Myers, Park, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2008 Beaver, **Kelly**, Kmiecik, Miklas, Myers, Pauls, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2010 Beaver, Kelly, Kmiecik, **Miklas**, Myers, Pauls, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2011 Bett, Kelly, Kmiecik, **Miklas**, Myers, Osorno, Pastor-Corrales, Pauls, Riley, de Ron, Wahlquist
2015 Bett, Cichy, Kelly (ex officio), Kmiecik, **Miklas**, Myers, Osorno, Pauls, Souza, Trapp, Wahlquist
2020 Bett, Cichy, Kmiecik, Miklas (ex officio), Myers, Osorno, Pauls, **Porch**, Souza, Trapp, Wahlquist
2021 Bett, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Osorno, Pauls, **Porch**, Souza, Wahlquist
2023 Bett, Chang, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Osorno, Pauls, **Porch**

Awards Committee:

1971 Baggett, Briggs, Burke, Dean, Wallace
1973 Burke, Dean, Mauth, Zaumeyer
1975 Ballantyne, Frazier, Mauth
1977 Ballantyne, Curme, Frazier, Schuster
1979 Ballantyne, Schuster, Silbernagel, Temple
1981 Abawi, Bliss, Monis, Silbernagel
1983 Adams, Bliss, Burke, Dean, Morris
1985 Emery, Hagedorn, Sandsted, Schwartz
1987 Emery, Hagedorn, Sandsted
1989 **Coyne**, Silbernagel, Wallace
1995 **Coyne**, Dickson, Stavely
1997 **Coyne**, Schwartz, Stavely
2001 **Hosfield**, Magnuson, Schwartz
2004 Hosfield, **Schwartz**, Singh
2012 Noffsinger, **Schwartz**, Singh
2014 **Beaver**, Noffsinger, Urrea
2015 **Beaver**, Myers, Urrea

Genetics Committee

2004 **Bassett** (Chair), Beaver, Blair, Gepts, McClean, Miklas, Welsh (ex officio)
2005 **Beaver** (Acting Chair), Blair, Gepts, McClean, Miklas, Porch, Welsh (ex officio)
2007 Beaver, Blair, Gepts, McClean, Miklas, **Porch** (Chair), Welsh (ex officio)
2008 Bett, Blair, Gepts, McClean, Miklas, **Porch** (Chair), Urrea, Welsh (ex officio)
2014 **Bett** (Chair), Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, Kelly, Kisha (ex officio), McClean, Osorno, Porch, Urrea
2018 Bett**,** Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, **Kelly** (Chair), Kisha (ex officio), McClean, Osorno, Porch, Urrea
2020 Bett**,** Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, Kelly, McClean, **Miklas** (Chair), Osorno, Porch, Urrea
2021 Bett**,** Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, Kelly, McClean, **Miklas** (Chair), Osorno, Parker, Porch, Urrea
2022 Brown, Dohle, Ferreira, Gepts, Gomez, Goncalves-Vidigal, Kelly, McClean, **Miklas** (Chair), Osorno, Parker, Porch, Urrea

RECIPIENTS of BIC AWARDS for MERITORIOUS SERVICE, ACHIEVEMENT, TECHNICAL MERIT & FRAZIER-ZAUMEYER DISTINGUISHED LECTURESHIP

Year	Recipients
1970	Melvin E. Anderson- Rogers Bros. Seed Co., Plant Pathologist William A. Frazier- Oregon State Univ., Horticulturist (**BIC Founder** & **Coordinator**, 1957-67) Walter H. Pierce- Asgrow Seed Co., Plant Pathologist William J. Zaumeyer- USDA, Plant Pathologist
1971	Walter H. Burkholder- Cornell Univ., Plant Pathologist James R. Douglass- USDA, Entomologist Howard S. Gentry- USDA, Plant Explorer Charles W. Hungerford- Univ. of Idaho, Plant Pathologist Herbert A. K. Lamprecht- Pl. Breeding Inst. of Sweden, Geneticist John J. Natti- Cornell Univ., Plant Pathologist Melbourne C. Parker- Gallatin Valley Seed Co., Plant Breeder Francis L. Smith- Univ. of California, Agronomist Robert E. Wester- USDA, Plant Breeder
1973	Leslie L. Dean- Univ. of Idaho, Plant Pathologist Nicolaas Hubbeling- Inst. of Phyto. Res.- Netherlands, Plant Pathologist
1975	M. Wayne Adams- Michigan State Univ., Plant Breeder Dermot P. Coyne- Univ. of Nebraska, Plant Breeder (BIC **Coordinator**, 1968-76) Shigemi Honma- Michigan State Univ., Plant Breeder Max. L. Schuster- Univ. of Nebraska, Plant Pathologist
1977	Douglas W. Burke- USDA, Plant Pathologist Roelof Prakken- Utrecht Univ. of the Netherlands, Geneticist Clibas Vieira- Univ. Federal de Vicosa of Brazil, Agronomist
1979	Barbara J. Ballantyne- New South Wales, Plant Pathologist Donald J. Hagedorn- Univ. of Wisconsin, Plant Pathologist Marshall LeBaron- Univ. of Idaho, Agronomist
1982	Eelco Drijfhout- Agr. Inst. of the Netherlands, Plant Breeder Donald H. Wallace- Cornell Univ., Plant Breeder Donald R. Wood- Colorado State Univ., Plant Breeder
1983	Leland W. Hudson- USDA, Horticulturist Roger F. Sandsted- Cornell Univ., Horticulturist
1987	Michael H. Dickson- Cornell Univ., Plant Breeder (BIC **Coordinator**, 1976-87) Aart van Schoonhoven- CIAT, Entomologist Frederick A. Bliss- Univ. of Wisconsin, Plant Breeder Matt J. Silbernagel- USDA, Plant Pathologist
1989	Axel L. Andersen- Michigan State Univ., Plant Breeder/Pathology John D. Aktin- Asgrow Seed Co., Plant Breeder Colin L.A. Leakey- England, Geneticist Alfred W. Saettler- USDA/ARS, Plant Pathologist Arthur P. Sprague- Del Monte, Plant Breeder James R. Steadman- Univ. of Nebraska, Plant Pathologist J. C. "Mike" Tu- Agriculture Canada, Plant Pathologist

1991	Iver L. Jorgensen- Northrup King & Co., Plant Breeder John L. Morris- Rogers/NK Seed Co., Plant Breeder Rosario Provvidenti- Cornell University, Plant Pathologist Shree P. Singh- CIAT, Plant Breeder J. Rennie Stavely- ARS/USDA-Beltsville, Plant Pathologist Daniel Debouck- IBPGR, Rome, Plant Geneticist [Achievement Award] Paul L. Gepts- Univ. of Calif.-Davis, Plant Geneticist [Achievement Award] Pat Barnes-McConnell- Bean/Cowpea CRSP, Director [Achievement Award]
1993	Hubert L. Bannerot- INRA, Versailles, Plant Breeder Cesar Cardona- CIAT, Entomologist Robert B. Colville- Del Monte Foods, Variety Development George L. Hosfield- ARS/USDA, East Lansing, Genetics/Nutrition Oswaldo V. Voysest- CIAT, Agronomy/Germplasm Evaluation James S. Beaver- Univ. of Puerto Rico, Plant Breeder [Achievement Award]
1995	Howard F. Schwartz- Colorado State University, Plant Pathologist (BIC **President**, 1988-97) Kenneth F. Grafton- North Dakota State University, Plant Breeder [Achievement Award]
1997	George Emery- Ferry Morse, Plant Breeder James D. Kelly- Michigan State University, Plant Breeder (BIC **President**, 1998-2009) Steve Magnuson- Harris Moran, Plant Breeder David Nuland- University of Nebraska, Bean Extensionist Phillip Miklas-USDA-ARS, Prosser, WA, Plant Geneticist [Achievement Award]
1999	James R. Baggett - Oregon State University, Plant Breeder James S. Beaver - University of Puerto Rico, Plant Breeder Phillip McClean - North Dakota State University, Geneticist [Achievement Award] James Myers - Oregon State University, Plant Breeder [Achievement Award]
2001	Dermot P. Coyne - University of Nebraska, Plant Breeder [Frazier-Zaumeyer Distinguished Lectureship] Mark J. Bassett – University of Florida, Plant Geneticist Soon J. Park – Agriculture and Agri-Food Canada, Plant Breeder Mark A. Brick – Colorado State University, Plant Breeder [Achievement Award] Ron Riley – Syngenta, Plant Breeder [Achievement Award] Juan Carlos Rosas – Escuela Agricola Panamericana, Honduras, Plant Breeder
2003	Fredrick A. Bliss – Seminis Seeds, Plant Breeder [Frazier - Zaumeyer Distinguished Lectureship] Steve Beebe – CIAT, Colombia, Plant Geneticist Paul Gepts – University of California, Plant Geneticist Marcial A. 'Talo' Pastor-Corrales – USDA-ARS, Beltsville, Plant Pathologist
2005	Perry B. Cregan – USDA-ARS, Beltsville, Geneticist, Soybean Genomics [Frazier - Zaumeyer Distinguished Lectureship] Jorge A. Acosta Gallegos, INIFAP, Mexico, Plant Breeder Phillip N. Miklas, USDA-ARS, Prosser, Plant Geneticist (BIC **President**, 2010-2019) David M. Webster, Seminis Seeds, Plant Breeder A. 'Bert' Vandenberg, University of Saskatchewan, Plant Breeder [Achievement Award]
2007	Molly Jahn – University of Wisconsin, Plant Geneticist and Dean CALS [Frazier - Zaumeyer Distinguished Lectureship] Robert L. Gilbertson, University of California-Davis, Plant Pathologist Walter Edwin (Ed) Kee Jr. University of Delaware, Vegetable Specialist Hans Henning Muendel, Agriculture and Agri-Food Canada, Lethbridge, Plant Breeder Matthew W. Blair, CIAT, Colombia, Plant Breeder [Achievement Award]

2009	Maurice Bennink, Michigan State University, Nutritionist [Frazier - Zaumeyer Distinguished Lectureship] Henry Thompson, Colorado State University, Nutritionist [Frazier - Zaumeyer Distinguished Lectureship] Mark Brick, Colorado State University, Plant Breeder
2011	Phillip McClean, North Dakota State University, Geneticist [Frazier - Zaumeyer Distinguished Lectureship] Kenneth F. Grafton, North Dakota State University, Plant Breeder and Dean, Director, & Vice President of Agriculture Juan Jose Ferreira Fernández , SERIDA Spain, Plant Breeder [Achievement Award] Timothy G. Porch, USDA-ARS, Mayaguez, Plant Geneticist [Achievement Award] Carlos A. Urrea Florez, University of Nebraska, Plant Breeder [Achievement Award]
2013	James D. Kelly, Michigan State University, Plant Breeder [Frazier - Zaumeyer Distinguished Lectureship] James Nienhuis, University of Wisconsin, Plant Breeder K. Peter Pauls, University of Guelph, Plant Geneticist Kirstin E. Bett, University of Saskatchewan, Plant Geneticist [Achievement Award] Thomas Smith, University of Guelph, Research Technician [Technical Merit]
2015	Paul Gepts, University of California-Davis, Plant Geneticist [Frazier - Zaumeyer Distinguished Lectureship] Karen A. Cichy, USDA-ARS, East Lansing, Plant Geneticist [Achievement Award] Juan M. Osorno, North Dakota State University, Plant Breeder [Achievement Award]
2017	David M. Kramer, Michigan State University, Photosynthesis and Bioenergetics [Frazier - Zaumeyer Distinguished Lectureship] Maria Celeste Gonçalves-Vidigal, Plant Geneticist [Meritorious Service Award] Gregory V. Varner, Research Director [Meritorious Service Award] Irvin E. Widders, Director of the Legume Innovation Lab [Meritorious Service Award] Deidré Fourie, ARC Grain Crops Institute, Plant Pathologist [Achievement Award] Clare Mukankusi Mugisha, CIAT Uganda, Plant Breeder [Achievement Award] Rian Lee, Research Technician [Technical Merit Award] Evan M. Wright, Research Technician [Technical Merit Award]
2019	James Beaver, University of Puerto Rico, Plant Breeder [Frazier - Zaumeyer Distinguished Lectureship] Juan Carlos Rosas, Zamorano University, Plant Breeder [Frazier - Zaumeyer Distinguished Lectureship] James R. Myers, Plant Breeder and Geneticist [Meritorious Service Award] Sara F. Rose, Vice President at Bush Brothers and Company [Meritorious Service Award] Frédéric Marsolais, Research Scientist [Achievement Award] Albert Jody Vander Wal, Research Technician [Technical Merit Award]

Please consider nominating your colleagues for the 2023 BIC Awards. Details on nominating colleagues are provided below

2023 BIC AWARDS – NOMINATION REQUEST

The Bean Improvement Cooperative has proudly acknowledged outstanding contributions made by many of its members to bean research and education. The **Meritorious Service Award** has been presented to over 75 of our colleagues during the 66-year history of the BIC. These recipients have devoted many years of their illustrious careers to bean research and education, and have consistently provided outstanding service to our organization.

The **BIC Achievement Award** acknowledges a scientist with fewer than 15 years of post-graduate service who has demonstrated outstanding contributions to bean research and/or education. This special award recognizes BIC members who have devoted less time to their "bean careers" than our Meritorious Service Award recipients.

The BIC Coordinating Committee and Awards Committee proudly also present the **Frazier-Zaumeyer Distinguished Lectureship**. The purpose of this lectureship is to honor an individual who has contributed significantly to bean research over the past 5-10 years or longer. The recipient will provide the keynote address and a short publication (maximum of 6 pages) for the BIC report. The recipient is not excluded from receiving the BIC Achievement Award or the Meritorious Service Award. Further details can be acquired from the BIC Awards Committee Chair.

The Technical Merit Award recognizes outstanding and long-standing contributions made to bean research, extension and education by bean program support personnel. Criteria used in selection by the BIC Awards Committee, with approval by the BIC Coordinating Committee, are as follows:

- minimum of 10 years of service as a Bean Program Technician, Associate, Assistant
- membership for 5 years in the BIC is desirable
- 1-page typewritten summary giving place of birth, date and name of institution granting each degree, career history
- summary of accomplishments, innovations, and impacts made by the nominee to the Bean Program and stakeholders locally, nationally and/or internationally
- evidence of participation in development and release of at least one improved germplasm line and/or cultivar; or contribution to the development and application of a technique or process to further knowledge related to pulse crops, pathogens or pests, nutritional uses
- evidence of participation in publication of at least one refereed research and/or extension article

Nomination for these awards should be sent to the BIC Awards Committee Chair (see below). The awards will be presented at the next BIC Biennial Meeting to deserving candidates nominated by their peers and selected by the BIC Awards Committee. Award recipients will be acknowledged at the thirty-second Anniversary of the BIC/NAPIA Biennial Meeting in Greenville, South Carolina, on the 7th of November 2023.

BIC AWARD NOMINATION
Return by July 15, 2023 to:

Carlos Urrea
Panhandle Research & Extension Center
University of Nebraska- Lincoln
4502 Avenue I
Scottsbluff, NE 69361
currea2@unl.edu

The other Awards Committee member is Dr. James Myers

Nominee: Name: _____

Address: _____

_____

_____

_____

Discipline: _____

Nominated for: _____ Meritorious Service Award

_____ Achievement Award

_____ Frazier-Zaumeyer Distinguished Lectureship

_____ Technical Merit Award Nomination

Submitted by: _____

Date of Submission:_____

[Please include a 1-page typewritten summary statement giving place of birth, date and name of institution granting each degree, career history and accomplishments of the nominee]

FIRST ANNOUNCEMENT FOR THE BIENNIAL BIC/NAPIA 2023 MEETING

The 32nd BIC Meeting will be hosted by Clemson University
Nov 6-8, 2023

The BIC and NAPIA Meetings will be held during concurrent sessions on Nov 6 and Nov 7, 2023 and hosted by Clemson University in Greenville, South Carolina. We look forward to seeing you and are expecting a large attendance since our last in-person meeting was in 2019!

Venue
The Westin Poinsett Greenville in downtown Greenville, SC. The hotel offers complimentary shuttle service to and from the Greenville-Spartanburg International Airport (GSP). Please make hotel reservations by calling 1-800-WESTIN1 by October 15, 2023 and identifying yourself as part of the BIC/NAPIA group. A block of rooms has been reserved for $199/night + taxes.

Registration
Details on Registration have been posted on a Clemson University website: https://www.clemson.edu/cafls/bic-napia/. We would like to encourage the participation of students and researchers internationally. Student travel award will be awarded. The pricing of the registration is $300 for students and $450 for the rest of the community.

Abstracts
Abstracts for talks and posters can be submitted through the same webpage: https://www.clemson.edu/cafls/bic-napia/. The site is open for abstracts and the deadline for both talk and poster abstracts is August 30, 2023. Individuals will be notified on Oct. 1, 2023 regarding their selection for oral or poster presentations.

Schedule
A preliminary meeting schedule will be presented on the webpage.

Business meetings
Business meetings, including the W-4150, the Phaseolus Crop Germplasm Committee, and the BIC Genetics Committee Meetings, will be held on Wednesday, Nov. 8.

Awards
Please consider your colleagues for the Frazier-Zaumeyer Distinguished Lectureship and for the Distinguished Achievement, Meritorious Service, or Technical Merit Awards.

Contacts
Our local NAPIA host are organizing the meeting:
Dr. Dil Thavarajah (NAPIA Past President; dthavar@clemson.edu); Tristan Lawrence (NAPIA Treasurer/Secretary; tjlawre@clemson.edu) and Summer Chandler (Event Planner; spriddy@clemson.edu)
BIC business contacts: Tim Porch (President; timothy.porch@usda.gov); Juan Osorno (Treasurer; juan.osorno@ndsu.edu)

BIC GENETICS COMMITTEE MEETING MINUTES

Location: Hybrid (in-person and zoom) meeting hosted by Carlos Urrea (U. of Nebraska, Scottsbluff)
Date: Monday, August 22, 2022, 2:45 – 3:15pm MST
Committee Members: Bett, Ferreira, Gepts, Goncalves-Vidigal, Hoyos-Villegas, Kalavacharla, McClean, Miklas (Chair), Osorno, Porch, and Urrea.

Present:
In person: Gomez, Osorno, Porch (Acting Secretary), Urrea
Zoom: Ferreira, Gepts, Goncalves-Vidigal, Hoyos-Villegas, Miklas (Chair), Pastor-Corrales, Parker

A. Old Business:

1. The Genetics Committee 2021 meeting minutes were approved by email and published in the 2022 BIC v65.
2. The new table of SNPs and INDELS (converted to Tm-shift assays) published on the BIC website (11/03/21) replaces the old SCAR Table (reviewed by Alvaro Soler-Garzón et al., BIC 2022 v65:95-96).
    a. There are a total of 42 SNP/KASP markers in the table. This is a collaborative and interactive effort so any input regarding experience with these markers would be useful and can be sent to Phil Miklas or Tim Porch. The research community is encouraged to submit additional markers.
    b. Phil Miklas presented the list of markers. For some loci there is more than one marker listed when there is not enough evidence to indicate which is most tightly linked or which works across gene pools/races. Others have been extensively tested. For example, the *bgm-1* marker tracks the causal mutation within the candidate PvNAC1 gene. Additional markers or testing are needed for ANT, bean rust (need to include *Ur-4*, *Ur-5* KASP markers), ALS, and white mold, among others.
3. The Gene List was published in the 2022 BIC v65 with a modified preface and gene symbol updates (http://www.bic.uprm.edu/?page_id=91).
    a. Candidate gene (PvNAC1) information was added to the description for ***bgm*** (syn *bgm-1*) Soler-Garzon (2021a).
    b. The KTR2/3 (truncated CRINKLY4 kinase) candidate gene information was not added to the description for ***Co-1*** cluster alleles (Richard et al. 2021) given additional investigation of this locus is pending.
    c. Candidate gene information for ***bc-4***, a new recessive gene locus that interacts with ***bc-2*** to condition resistance to BCMV [*bc-4* was found in host groups 4, 5, and 7], was added to the Gene List. Candidates for *bc-2* and *bc-4* include genes encoding Vps4 AAA^+ ATPase ESCRT proteins on Pv11 and Pv05 (Soler-Garzon, 2021b).
    d. As genetic information is found for other genes, the gene list can be updated with a short description of candidate gene information.
4. The Committee decided to include information for different mutations within the same gene in the Bean Genes List. In these cases, use superscripts in brackets to denote different mutations for the same gene (i.e. the different mutations are not different alleles in the genetic sense). For example, **bc-2$^{[UI\ 111]}$** denotes a 10 kb deletion of Durango origin

and **bc-2$^{[Robust]}$** a single SNP deletion found in navy bean landrace selection (Robust) for the gene encoding Vps4 AAA+ ATPase ESCRT on Pv11. Both mutations (frameshift) result in truncated proteins.

B. New business

1. The following membership changes were approved by the committee:
    a. Kirstin Bett and Kal Kalavacharla will rotate off the committee.
    b. New members include Francisco Gomez, Sarah Dohle, and Judy Brown.
2. Travis Parker will send Phil Miklas updates to the Bean Gene list on genes involved in the domestication syndrome. Candidate gene information for *fin*, *ppd*, and stringless, etc. (Gepts BIC 2022 v65:1-10) can be added.
3. Published articles are often not following the Genetics Committee naming protocols or having gene symbols reviewed by the Committee. This is occurring partly because researchers who are not participating in the BIC are publishing on common bean and not reviewing the literature.
    a. At the next BIC meeting, participants will be encouraged to participate in the Germplasm and Genetics Committee Meetings and reminded about the naming protocols.

Finish: 3:14pm

IN MEMORY OF JULIO CÉSAR NIN SÁNCHEZ

Julio César Nin passed away unexpectedly in December 2022. Julio studied at the Universidad Autónomo de Santo Domingo in the Dominican Republic where he earned an 'Ingeniero Agrónomo' degree. He began his professional career at the Arroyo Loro Experiment Station in the Dominican Republic in 1984 as a technical research assistant for the Bean/Cowpea CRSP projects.

Julio spent his entire career as an agronomist and bean breeder for the Ministry of Agriculture and the Instituto Dominicano de Investigaciones Agropecuarias y Forestales (IDIAF) promoting the crop, especially in his beloved San Juan de la Maguana Valley. He was also a farmer and had a unique perspective of the challenges facing bean producers in the Dominican Republic. His opinion was highly regarded among fellow farmers and the bean cultivars released by IDIAF bean program were widely adopted in the Dominican Republic and, in some cases such as the black bean 'Arroyo Loro Negro,' in Haiti. During almost four decades of research, Julio participated in the release of numerous bean cultivars including the red mottled beans 'PC-50', 'JB-178', 'CIAS-95', 'Saladin 97', 'Buena Vista' and 'Maravilla', the cranberry bean 'Yaconin', the white beans 'Anacaona' and 'Blanca San Juan' and the black beans 'Charlona Negra', 'Arroyo Loro Negro', 'Perla Negra' and 'Sequia 1'.

Julio served as a valuable collaborator for several different international bean research and training programs. From 1993 to 2002, he served as the national coordinator in the Dominican Republic for the PROFRIJOL regional project. He collaborated with CIAT, Zamorano University, the University of Nebraska and the University of Puerto Rico by conducting performance trials at the Arroyo Loro Research Station.

In the last three years of his life, Julio represented the Dominican Republic as the principal investigator on a project funded by the South Korean government to improve drought tolerance in beans. He showed initiative in adapting the evaluation system at his research station for drought evaluation by working with irrigation experts to determine the proper level of stress. In the first two years communication was limited by the pandemic to virtual interactions, but in August of 2022 Julio participated in the first face-to-face project meeting, interacting with colleagues throughout the region for the last time.

His sudden departure evoked expressions of sympathy from colleagues in several countries, both old friends and new acquaintances. He is survived by his four children: Elvis, Lisbeth, Marjorie and Lisannia.

REACTION TO *BEET CURLY TOP VIRUS* IN A DRY BEAN POPULATION UNDER NATURAL FIELD INFECTION

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INTRODUCTION

BCTV is a member of the Geminiviridae family and causes severe yield loss in susceptible dry bean cultivars, with symptoms including leaf curling, chlorosis, stunting, and plant death. The most effective way to control the virus is through natural genetic resistance, but screening for such resistance is cumbersome and unreliable. Thus, marker-assisted selection (MAS) provides a useful tool for developing resistant cultivars. Herein we used a dry bean population (DBP) of assorted accessions to gain deeper insight into the genetic basis of the *Bct* resistance allele that was previously fine-mapped in a snap bean diversity panel (Soler-Garzón et al., 2018).

MATERIALS AND METHODS

A dry bean population (DBP) of 88 accessions was field-tested for CTV resistance. The experiment used a randomized complete block design with two replications. Disease severity was rated on a 1-9 scale (Larsen and Miklas, 2004). Trait data were corrected for spatial effects and analyzed using BLUPs calculated with a P-spline mixed model in the Mr.Bean web application (Aparicio-Arce, 2018). Leaf tissue samples from infected plants were analyzed for specific CTV strains using a PCR protocol (Chiginsky et al., 2021).

Genomic DNA was extracted from 20 mg of leaf tissue from individual plants of the DBP using a Qiagen DNeasy 96 Plant Kit and genotyped using the 11,292 SNPs BARC Illumina chip assay at the USDA-ARS Soybean Genetics and Improvement Laboratory in Beltsville, MD. The SNPs were updated by alignment to the v2.1 reference genome assembly of G19833 and filtered based on a MAF of 0.01 and a missing data rate of less than 20%.

GWAS analysis was conducted by mixed linear model (MLM) using genome association and prediction integrated tool (GAPIT) (Lipka et al., 2012). In addition, one SNP marker developed by Soler-Garzón et al. (2018) for *Bct* gene segregating in a snap bean diversity panel was included. Lastly, an analysis of variance between resistant and susceptible groups was conducted.

RESULTS AND DISCUSSION

A total of 88 DBP accessions were field-tested for reaction to CTV based on a 1-9 scale. The PCR assay of infected leaf samples detected the Worland strain. Of 88 accessions tested, 43 exhibited resistance to the CTV-Worland strain (disease score 1-4), 33 showed tolerance (4.1-6.9), and 14 were susceptible (7-9) based on BLUP values for CTV reaction.

GWAS was performed in the DBP using 7,983 SNP markers after filtering, but no associated peak was detected for resistance to the CTV-Worland strain. A SNP marker for resistance to CTV from a snap bean GWAS (Soler-Garzón et al., 2018) was included in a second DBP GWAS. The added SNP S07_2970381 (G19833v2.1 reference genome) on Pv07 was identified in the '*Bct* region' with a high p-value (p = 1.84E-07) (Fig. 1). Furthermore, a high significance p_{Holm}-adjusted value (p = 2.19E-12) was detected between resistant and susceptible DBP accessions that were genotyped with the S07_2970381 SNP marker.

According to Soler-Garzon et al. (2018), fine mapping in the snap bean diversity panel narrowed the genomic interval for the *Bct* region, which led to identification of Exonuclease V gene (Phvul.007G036300) as a candidate gene for *Bct*. Exonuclease V has an unclear viral resistance function in plants, but its Arabidopsis homolog, AT5G60370, which encodes an Exonuclease V-Like (EXOVL), plays critical roles in biological processes related to morphology (Huang et al., 2022). Initially, Exonuclease V was identified and purified from *Saccharomyces cerevisiae*, encoded by the YBR163w gene (subsequently renamed EXO5). This protein is capable of degrading single-stranded DNA (ssDNA) from the 5′-end and plays a critical role in mitochondrial maintenance (Burgers et al., 1988).

Overall, these results indicate the S07_2970381 SNP marker is a reliable indicator of resistance to CTV in snap and dry bean lines, providing a rapid and breeder-friendly molecular marker assay for *Bct* in common beans.

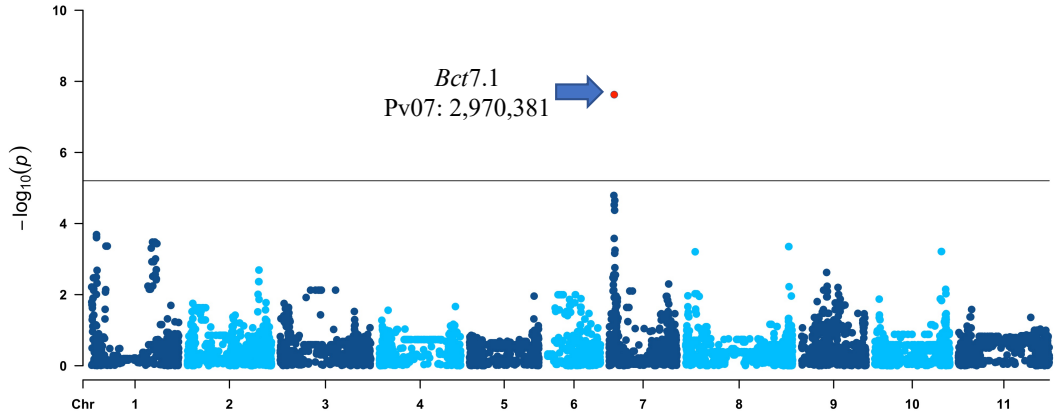

Figure 1. GWAS for 88 dry bean genotypes evaluated under field conditions with CTV-Worland strain identifies an association of the added SNP S07_2970381 (red dot) in the *Bct* region.

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GENETIC PROGRESS AFTER 18 CYCLES OF RECURRENT SELECTION FOR COMMON BEAN ANGULAR LEAF SPOT RESISTANCE IN BRAZIL

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INTRODUCTION: The angular leaf spot (ALS) disease, caused by *Pseudocercospora griseola* is one of the main diseases that occurs in common bean in Brazil. Control strategies include crop management, fungicides and genetic resistance. Some factors have increased the occurrence of the disease, such as the use of fungicides, contaminated seeds, susceptible cultivars and the high variability of pathogen. Therefore, the most feasible alternative for ALS control is by resistant cultivars. Thus, in 1998 a recurrent selection (RS) program was started in Minas Gerais State, Brazil, aiming at resistance to ALS. The aim of this work was estimating the genetic progress (GP) obtained for pathogen resistance in 18 recurrent selection cycles, and improvements in grain yield.

MATERIALS AND METHODS: Initially, a partial diallel with seven carioca-type lines and ten sources of resistance to *P. griseola* was carried out, resulting in 29 segregating populations that constituted the cycle 0 (C-0) of the RS program. In the F_2 (S_0) generation of C-0, the plants with the lowest ALS symptoms were phenotypically selected and derived the $S_{0:1}$ progenies. To obtain the cycle I population (C-I, sown in 2001) the 29 best $S_{0:1}$ plants from the C-0 population were intercrossed, one per population, selected phenotypically for resistance to *P. griseola* and including those plants presenting carioca type grains as close as possible to the market standard of beige grains with pale brown stripes, as related by Amaro et al. (2007) and Nay et al. (2019). The process was repeated until cycle XVIII (C-XVIII), obtained in 2018 (Figure 1). We assessed the ALS severity under conditions of natural occurrence of ALS in progenies $S_{0:1}$ of each RS cycle in the field using the scale from 1 to 9, where 1=resistance and 9=susceptibility. In all cycles, the cultivars Pérola (resistant) and Carioca MG (susceptible) were used as checks. The genetic progress (GP) of RS cycles was estimated for the reaction to ALS and grain yield using the $S_{0:1}$ progenies performance in the 18 selection cycles. Because the $S_{0:1}$ progenies from each cycle were assessed in different years for ALS severity, and to attenuate the environment effect, the genetic deviation was obtained from the difference between the mean of the resistant Pérola check cultivar and the mean of the $S_{0:1}$ progenies for each cycle. The linear regression equation was obtained for the number of cycles, independent variable (x) and the genetic deviation, dependent variable (y). The GP (%) per RS cycle in relation to the mean of the $S_{0:1}$ progenies of C-I was calculated as: $GP(\%) = (b_1 / \bar{X}_{CI})$ x 100, b_1=linear regression coefficient and $\bar{X}_{CI}$= mean of the $S_{0:1}$ progenies for cycle 1 (C-I). The same procedure was used to estimate the response to selection for grain yield, but the genetic deviation of the $S_{0:1}$ progenies was compared to the mean of the two checks.

RESULTS AND DISCUSSION: In almost all RS cycles, the average of the $S_{0:1}$ progenies was lower than that of cultivar Pérola (Figure 2), i.e., the progenies have presented greater resistance than this check. These results show that, despite the great variability in the fungus, the progeny resistance has been maintained over the years. The GP for ALS resistance was 1.35% and the grain yield response was 0.88% per cycle under conditions of natural occurrence of ALS. Thus, even after 18 cycles of recurrent selection for resistance to ALS, the selection has been efficient.

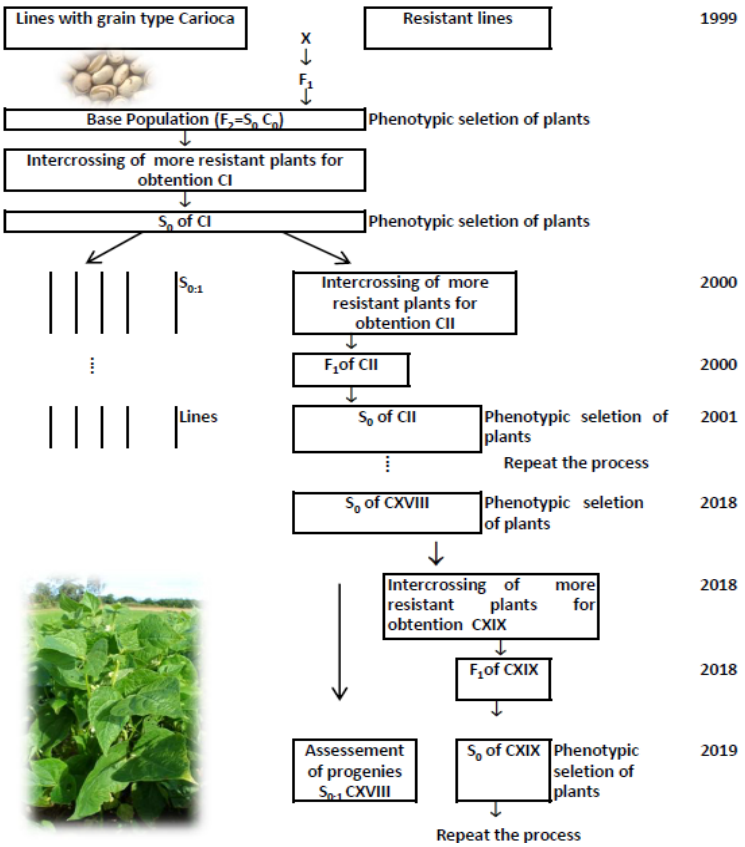

Figure 1. Scheme of recurrent selection program aiming at resistance to ALS in the common bean.

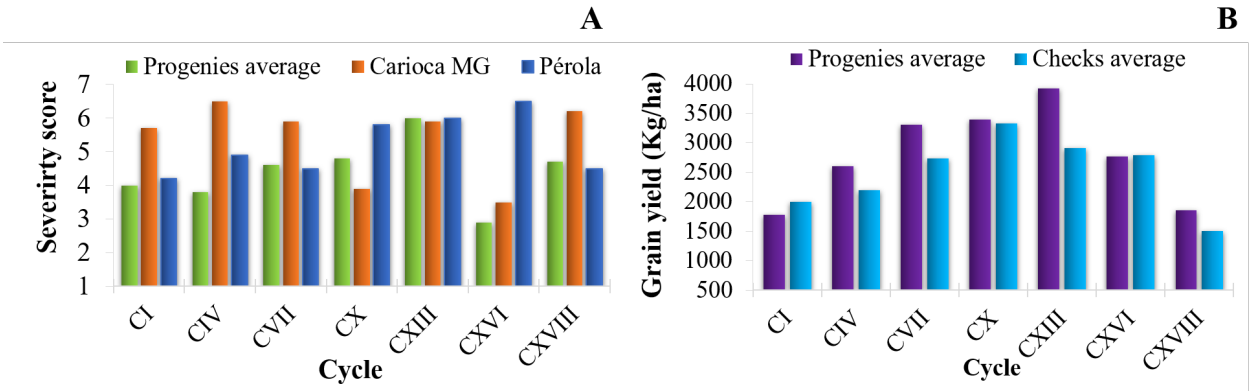

Figure 2. Averages of ALS severity scores (A) and grain yield (kg / ha) (B) of $S_{0:1}$ progenies of 18 cycles of recurrent selection and checks.

ACKNOWLEDGEMENTS: CNPQ, CAPES and FAPEMIG for financial support.

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FINE MAPPING OF THE ANTHRACNOSE RESISTANCE GENE *Co-12* IN THE ANDEAN COMMON BEAN CULTIVAR JALO VERMELHO

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INTRODUCTION

The development of cultivars that are resistant to multiple races of *Colletotrichum lindemuthianum*, (CL) the fungus that causes anthracnose in common beans (*Phaseolus vulgaris* L.), is one of the most effective strategies for controlling the disease. Among Andean genotypes, the common bean cultivar Jalo Vermelho stands out for its broad-spectrum resistance to both Andean and Mesoamerican races of the anthracnose pathogen, thanks to the *Co-12* gene it contains (Vidigal Filho et al., 2007; Gonçalves-Vidigal et al., 2008; de Lima Castro et al., 2017). The aim of this study was to precisely map the *Co-12* gene in Jalo Vermelho using SNP and SSR molecular markers and to examine the candidate genes related to disease resistance in the genomic region that encompasses *Co-12*.

MATERIAL AND METHODS

A total of 1,651 F_3 plants derived from 172 F_2 plants of the Jalo Vermelho (R) × Crioulo 159 (S) cross were inoculated with race 1545 of CL. DNA was extracted from each one of the 172 F_2 plants. Based on the phenotyping of the F_3 plants, DNA from F_2 resistant and susceptible genotypes, and DNA samples from the parents, were genotyped with the BARCBean6k_3 beacdchip using the Infinium HD Assay Ultra protocol (Song et al., 2015). In order to saturate the genomic region that contains the *Co-12* gene, SSR molecular markers were included in the analysis. The physical position of the gene was obtained using the sequence of molecular markers in blast analysis on the reference genome of *P. vulgaris* v. 1.3, available in Phytozome (https://phytozome-next.jgi.doe.gov/blast-search). Genes annotated in the reference genome with a function related to disease resistance and located within the range of the molecular markers found linked to *Co-12* were assigned as candidate genes.

RESULTS AND DISCUSSION

The segregation observed in the $F_{2:3}$ families fitted the segregation 1RR:2RS:1SS with a chi-square equal to 0.221, indicating the presence of a dominant gene for resistance to race 1545 of *C. lindemuthianum*. Through genotyping with the SNP markers, we located the *Co-12* gene in the Pv04 chromossome, flanked by the markers ss715649768 (11,168 bp) and ss715646644 (9,259,094 bp) (Fig 1a). This region was refined using SSR markers locating the *Co-12* gene between the markers BARCPVSSR04557 and BARCPVSSR04570, which flank a 41 kb region (Fig. 1b). Three candidate genes (Fig. 1c) were identified within this region, two of which are of the same class and express antifungal activity. The identification of these SSR markers will enable marker-assisted selection and will be of utmost importance for the introgression of the *Co-12* gene into elite cultivars.

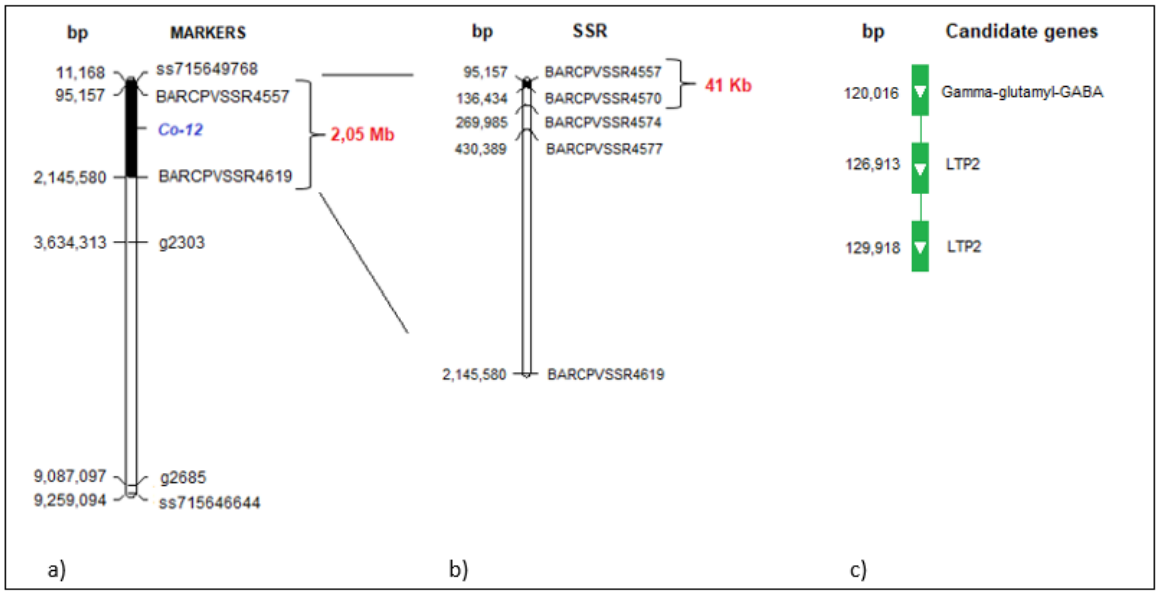

Figure 1. Mapping of the *Co-12* gene present in the Andean common bean cultivar Jalo Vermelho, located in the Pv04 chromosome through the Jalo Vermelho × Crioulo 159 cross. a) Physical map of the *Co-12* gene constructed with 172 F_2 plants and delimited by SNP markers. b) Fine-mapping using molecular SSR markers using recombinant plants. c) *Co-12* genomic region of 41 kb containing three candidate genes using the reference genome G19833.

ACKNOWLEDGMENTS

This research was financially supported by CNPq and Capes (Brazil).

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FUSARIUM ROOT ROT DISEASE SCORES OF WILD BEAN PI417775 AND SEVERAL CHECKS

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INTRODUCTION: Fusarium root rot (FRR) disease resistance is an important target trait for *Phaseolus vulgaris* breeding programs due to the ubiquitous and potentially devastating nature of root rot caused by *Fusarium* spp. Unfortunately, FRR resistance is scarce among developed common bean cultivars and often insufficient to prevent crop losses in environments favorable to the pathogen. Wild *Phaseolus vulgaris* germplasm may contain FRR resistance and could provide valuable resources for improving elite common bean breeding germplasm if resistance were identified. Haus et al.[1] screened 248 wild bean accessions for resistance to Fusarium wilt (*F. oxysporum*) & FRR (*F. cuneirostrum*). Several wild accessions with consistently low FRR severity were selected for further testing to confirm resistance to *F. cuneirostrum* and analyze response to other FRR-associated species found in Michigan common bean cultivation areas[2]. Here we report the root rot disease scores of accessions of interest (PI 417775, a Middle American wild bean collected from Jalisco, Mexico) and several developed common bean cultivars.

MATERIALS AND METHODS

Plant Material. Six cultivars (Red Hawk, VAX 3, Sanilac, Zorro, Domino, Maverick, & CDC-Expresso) and one wild accession (PI 417775) of *P. vulgaris* were grown from seed obtained from the MSU Dry Bean Breeding Program and USDA-GRIN, respectively. These accessions were chosen based on their common usage as check varieties in FRR experiments (Red Hawk: susceptible; VAX 3: resistant) and/or the stratification of their FRR severity ranking in published data[3] (low: Sanilac, CDC-Expresso; moderate: Zorro; high: Domino, Maverick).

Fungal Cultures. *F. oxysporum* (F_14-37), *F. cuneirostrum* (F_14-40), & *F. brasiliense* (F_16-137) cultures were grown on potato dextrose agar at 20°C for spore production and *F. acuminatum* (F_15-78) was only found to sporulate sufficiently on oatmeal agar. An aqueous spore suspension was prepared on the day of inoculation as described previously[1]. All cultures yielded macroconidia except *F. oxysporum* which produced primarily microconidia.

Experimental Design. On three occasions for each *Fusarium* sp., two seeds of each *P. vulgaris* genotype were planted in separate 355ml paper cups filled with pre-wetted vermiculite and grown to apical hook stage (5 days) before inoculation with 5mL of 10^6 conidia/mL aqueous spore suspension. The experiment was conducted in two BioChambers growth chambers (model: FXC-10), both of which were configured in 2-tier mode with temperature set-points of 21.1°C, relative humidity of 50%, and an approximate canopy PPFD of 750 $\mu mol/m^2/s$.

Disease Scoring. All plants were scored 14 days after inoculation for root rot severity based on the established 1-9 scale[1,3] where 1 indicates healthy roots; 3 - mild root discoloration; 5 - moderate discoloration and cortical lesions; 7 - severe discoloration and degradation of the root cortex; and 9 - extensive root necrosis and loss. All roots were washed in 0.1% Liquinox solution to remove vermiculite, then rinsed in tap water. Averages of two independent researcher scores were used for statistical analyses and data presentation.

Statistical Analysis. The R software environment was used for all analyses. The package 'ordinal' was used to fit a cumulative link model on the ordinal data; ANOVA of the model was conducted with 'stats'; main and interaction effects were analyzed with 'emmeans'.

RESULTS

Mean Disease Scores (MDS) for each *P. vulgaris* genotype and *Fusarium* isolate were analyzed for variance using a cumulative link model method of fitting ordinal data. Two-way ANOVA indicated that disease scores were primarily influenced by *Fusarium* sp. ($p < 0.0001$) rather than genotype ($p = 0.463$) but found a significant interaction effect ($p=0.038$). Across all genotypes, *F. acuminatum* was not significantly different from the water control while *F. oxysporum*, *F. cuneirostrum*, & *F. brasiliense* differed significantly from the control ($p = 0.001$, <0.0001, & <0.0001). PI 417775 differed significantly ($p = 0.041$) from VAX 3 when inoculated with *F. cuneirostrum*, while all other observed differences from VAX 3 were insignificant ($p > 0.05$) within each *Fusarium* sp. treatment. Sanilac had a significantly higher MDS in the control treatment compared to VAX 3, however, this is most likely due to experimental error.

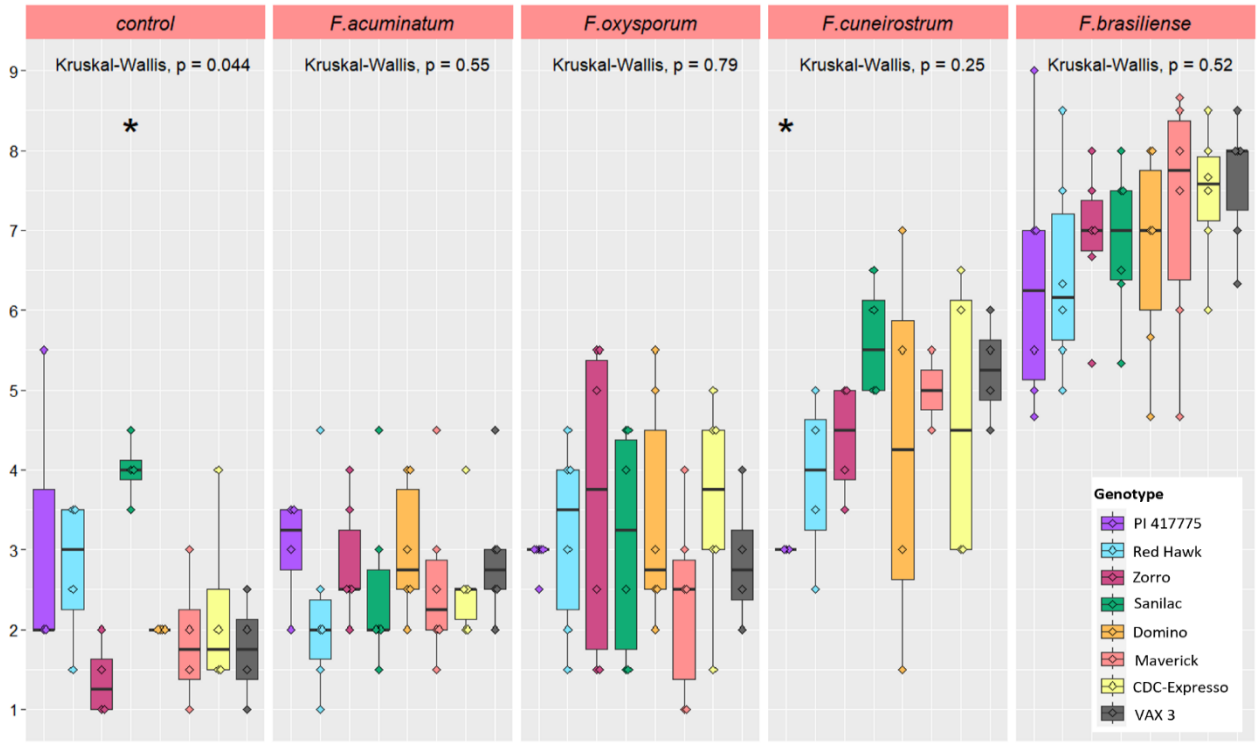

Figure 1. Boxplots of *Phaseolus vulgaris* root rot severity scores 14 days after inoculation with *Fusarium* or water control. Asterisks indicate accessions whose means differ significantly ($p<0.05$) from VAX 3. Points represent the disease scores of individual plants after averaging between two scorers.

CONCLUSION: Despite being preliminary in nature, our data support the previous observation of PI 417775's relative FRR resistance and highlight the high variability in disease scores among individual plants of the same accession under controlled conditions.

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SCREENING 105 COMMON BEANS FROM THE USDA GRIN CORE COLLECTION TO SELECT GENOTYPES WITH HIGHER ASHY STEM BLIGHT RESISTANCE

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INTRODUCTION: Ashy stem blight caused by the seed-transmitted fungus *Macrophomina phaseolina* (Tassi) Goidanich is an important disease of common bean (*Phaseolus vulgaris* L.) worldwide (Singh and Schwartz, 2010). Partial-resistance has been reported in Andean common bean genotypes and breeding lines with pyramided resistance to this pathogen (Viteri and Linares, 2017, 2022; Viteri et al., 2019). However, it is important to identify other common bean genotypes with higher levels of resistance as sources of resistant genes/QTL for breeding against ashy stem blight. Our objectives were to (1) assess the levels of resistance of 105 common beans from the USDA GRIN core collection, and (2) select common bean genotypes with scores < 4.5 and higher percentages of resistant plants.

MATERIALS AND METHODS: The susceptible pinto 'Othello' and the Andean PRA154, with partial-resistance to *M. phaseolina*, and 105 common bean genotypes from diverse origins were evaluated in a greenhouse at the Lajas Research Substation at the University of Puerto Rico in October, 2022. A randomized complete block design with three replications was used. One inoculation with the PRI21 *M. phaseolina* isolate was carried out at the fourth internode by the cut-stem method (Viteri and Linares, 2017). The percentage of resistant plants, and the disease range and severity, were noted at 42 d after inoculation. Also, the area under the disease progress curve (AUDPC) was calculated from 14, 28, and 42 d post-inoculation. A 1-9 scale was used to score the disease severity where 1= no sign of *M. phaseolina* infection, 4= the fungus infection passed the first node above or below the point of inoculation, but did not infect more than 50% of the internode, and 9= the fungus infection passed the third node above or below the point of inoculation (Viteri and Linares, 2017). Data were analyzed using SAS 9.4 PROC GLM (SAS Institute, 2012).

RESULTS AND DISCUSSION: There were significant differences *($P \leq 0.001$)* between genotypes for the disease severity and AUDPC. 'Othello' was highly susceptible (mean score of 9) while PRA154 had an intermediate response (3.6), as expected. Forty-three genotypes were susceptible (scores ≥ 6.5) to PRI21 *M. phaseolina* isolate. Within this group, PI 171783, PI 175821, PI 218106, and PI 219702 had mean scores of 8.0-8.8 and AUDPC values between 193.7 and 208.8. Sixty-one genotypes had an intermediate response (3.5-6.4) to ashy stem blight and 15 accessions had mean scores and AUDPC values below 4.5 and 115, respectively (Table 1). In contrast, PI 264786 was the only resistant (3.3) genotype identified in this study although that its AUDPC value did not differ significantly from the common bean accessions with intermediate resistance (Table 1). Furthermore, PI 163116, PI 264142, and PI 264186 had the higher percentages of resistant plants (> 65%). These three accessions may be crossed with the recently developed UPR-Mp breeding lines (Viteri and Linares, 2022), Andean common beans (e.g., A 195, 'Badillo', PRA154, PRA155, VA 19) (Viteri and Linares, 2017, 2022; Viteri et al., 2019) or common bean cultivars to increase the levels of ashy stem blight resistance. Furthermore, a genome wide association study between these 105 genotypes and other 200 common bean

accessions from the USDA-GRIN, and the identification of single nucleotide polymorphism markers for ashy stem resistance would be useful for molecular breeding.

Table 1. Disease range, mean ashy stem blight disease scores, area under the disease progress curve values and percentage of resistant plants of common bean (*Phaseolus vulgaris* L.) genotypes to PRI21 *Macrophomina phaseolina* (Tassi) isolate evaluated at 42 d after inoculation in the greenhouse at the Lajas Research Substation, University of Puerto Rico in 2022.

Genotype	Range	Mean	AUDPC[a]	Resistant plants (%)
'Othello' (susceptible check)	9	9.0[b]	224.0	0.0
PRA154 (partial-resistant check)	3-5	3.7	101.5	50.0
Common bean accessions from the USDA GRIN core collection				
PI 150405	3-6	4.2	110.8	33.3
PI 161952	3-4	3.7	106.2	33.3
PI 163116	3-6	3.7	98.0	66.7
PI 169790	3-5	4.3	102.7	16.7
PI 169880	3-6	4.2	105.0	33.3
PI 173208	3-4	3.5	91.0	50.0
PI 209473	3-8	4.3	103.8	33.3
PI 226523	3-5	4.0	103.8	33.3
PI 262163	3-5	3.7	95.7	50.0
PI 264142	3-7	4.2	102.7	66.7
PI 264786	3-4	3.3	93.3	66.7
PI 293355	3-6	3.8	100.3	50.0
PI 309702	3-6	3.8	100.3	50.0
PI 309834	3-7	4.2	110.8	33.3
PI 310692	3-5	4.2	116.7	33.3
PI 313749	3-6	4.3	110.8	16.7
Mean (107 genotypes)	…	6.0	143.1	…
LSD ($P \leq 0.05$)	…	1.8	37.9	…

[a] AUDPC, area under the disease progress curve; [b] ashy stem blight disease severity was scored on a 1 to 9 scale, where 1 to 3.4= resistant, 3.5 to 6.4= intermediate, and 6.5 to 9= susceptible.

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NEW SOURCES OF WHITE MOLD RESISTANCE DERIVED FROM WIDE CROSSES IN COMMON BEAN AND EVALUATED IN THE GREENHOUSE AND FIELD USING MULTI-SITE SCREENING NURSERIES

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INTRODUCTION: In 2022, field and/or greenhouse evaluations were used to screen 12 candidate dry bean lines for putative sources of white mold disease tolerance in adapted backgrounds. Evaluations were conducted at multiple sites located in five states (MI, NE, ND, OR, WA) and in one province in Canada (Quebec). Collectively, these locations represent the major bean-production areas of the North American continent. Multi-site testing is essential for robust evaluation under different environmental conditions and with white mold pathogen populations that previous research has shown are significantly different in both genetic variation and aggressiveness.

MATERIALS AND METHODS: Greenhouse evaluations were conducted using a straw test that consistently identifies sources of physiological resistance in adapted and unadapted bean germplasm and requires only a small number of seeds to confirm resistance. Twelve bean lines were evaluated, plus G122 (with partial resistance), Bunsi (mostly field avoidance) and Beryl (susceptible) that were included as the control lines. Field tests were conducted in all locations and greenhouse evaluations were only conducted in NE, WA, and OR. Unfortunately, field data was collected from only three of the locations while greenhouse evaluations were only conducted in four locations. This was due to multiple field and greenhouse issues that impeded collection of the data. As in years past, this illustrates the necessity of multiple sites for generating data despite weather or other natural complications in field trials. Data from the past 15 years of the NSI multi-state trials have been analyzed to determine the rate of genetic gain of dry bean cultivars.

RESULTS AND DISCUSSION: Results of the greenhouse trials identified three promising candidate lines ('Ex2141-P', 'Ex2143-P', 'WMM-820-1',) that performed like the tolerant / resistant 'G122' line (Figure 1). This material represents useful sources of resistance with potential for improving pinto bean and the other Durango market classes. Results from the field trial were similar to the greenhouse trials where no lines outperformed the resistant check (Figure 2). However, we identified three dry bean cultivars with good tolerance to white mold like the tolerant/resistant 'G122' line which include 'ND122454', 'ND151660', and 'Ex 2143-P'. Some environments were excluded from the final analysis. Michigan continued to score higher for white mold rating across all tested locations followed by Oregon (data not shown). Data collected since 2015 across multiple locations was organized and will be evaluated using mixed models and a common check to evaluate genetic gains for white mold across 15 years and multiple locations (Figure 3).

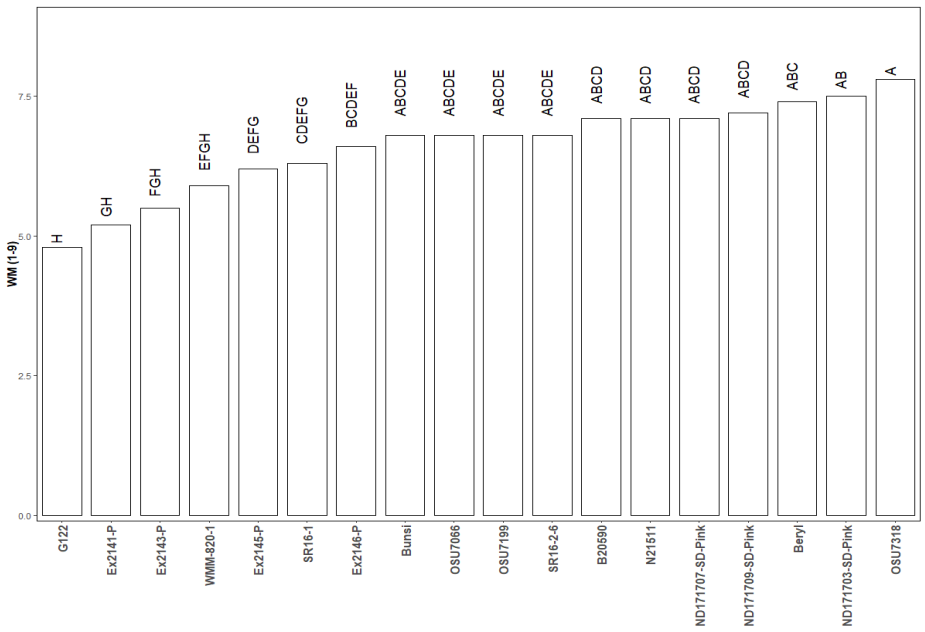

Figure 1. * Petzoldt & Dickson scale: 1-3= resistant, 4-6= intermediate, 7-9= susceptible **Levels not connected by the same letter are significantly different at $\alpha = 0.5$.

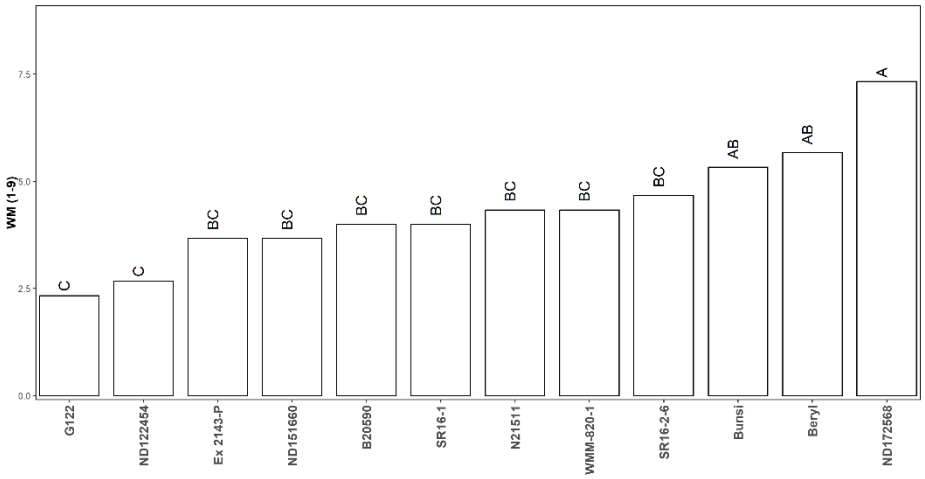

Figure 2. *CIAT scale-1-9; 1= no disease, 9 = dead plant.; **Levels not connected by the same letter are significantly different at $\alpha = 0.5$.

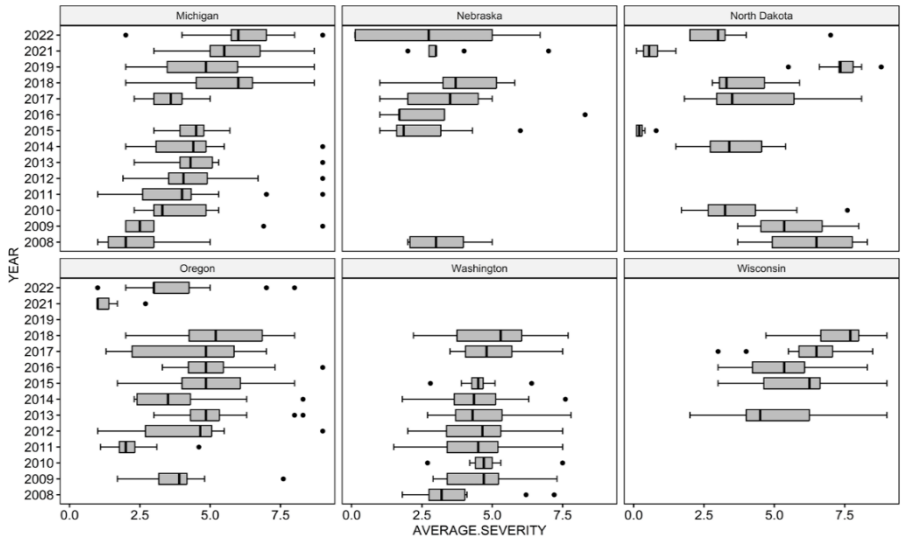

Figure 3. Average disease severity for white mold across years and locations (2008-2022) for US sites only.

PHENOTYPIC DIVERSITY OF *SCLEROTINIA SCLEROTIORUM* L. DE BARY IN CANADA

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INTRODUCTION

Sclerotinia sclerotiorum L. de Bary is one of the most destructive pathogens in Canada and all around the world affecting over 500 species of plants including common bean (Gerard et al., 2011; McDonald & Boland, 2004). The deployment of resistant cultivars is one of the most effective methods to fight against this pathogen, however, existing studies on its genetic diversity lack a complete overview of the genetic composition of the pathogen population within a production area, which is limiting the breeding efforts. The goal of our project was to perform mycelial compatibility group's assays (MCG) and whole genome sequencing (WGS) on a collection of 38 *Sclerotinia sclerotiorum* (*Ss*) samples collected in different commercial fields primarily from Quebec, Ontario, and Alberta along with an additional set of 30 samples collected in a single farm from Quebec to assess the genetic diversity of the region of study.

MATERIALS AND METHODS

Isolate collection. A total of 68 *S. sclerotiorum* samples were collected from three provinces between 2021 and 2022. From the total set of samples, two subsets were established: 1) the main set of samples comprised of 38 samples (17 samples from Alberta, 16 from Quebec and 5 from Ontario), collected mainly on common bean and soybean, and 2) a group of 30 samples from a single farm in Quebec collected from different infected crops. All samples were assigned a number by the order in which they were collected along with specific IDs composed by a number and 2 letters depending on province provenance. For visual purposes, the former was preferred to display the results (Table1).

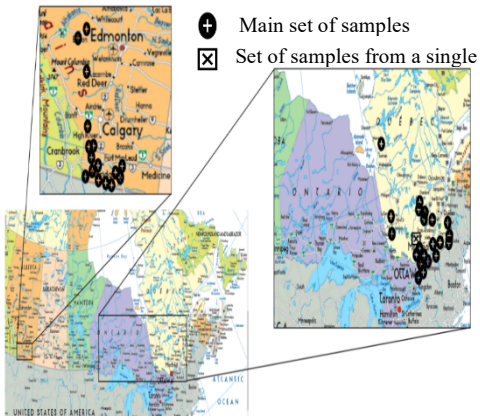

Figure 4. Geographic distribution of isolates of S. sclerotiorum from AB, QC, ON. Map was built with GPS coordinates and displays approximate geographical locations of both set of samples.

Mycelia Compatibility Group testing. Small mycelia plugs were taken from the edge of 3 to 4-day old colonies growing on Potato Dextrose Agar (PDA) amended with 100 µl/L of McCormick's red food coloring. All collected *Ss* samples were challenged against themselves as a control for compatibility as well as against each other in non-self-combinations and then incubated at 23°C for a week. After a week, samples were rated for incompatibility or compatibility, with a rating system to report the presence of a red barrier between colonies for (I) incompatibility, while no reaction line for the ability of samples to fuse and grow together as single colony for (C) compatibility (anastomosis). The red food coloring was added as suggested by (Schafer & Kohn, 2006) to facilitate rating.

RESULTS AND DISCUSSION

Preliminary results suggest the presence of seventeen different mycelia compatibility groups across the three provinces studied. More than half of these MCGs (n=9) included at least three or

more isolates, the rest (n=8) included only one isolate. Interestingly, five MCGs (MCG 1, 2, 5, 6, 7) predominated across provinces**, other MCGs (MCG 3, 4, 8, 9) are also believed to be highly distributed across*. However, the small number of samples collected from Ontario limits the possibility of making such assumptions. MCG testing is a quick phenotypic marker widely used for classifying *Ss* populations (Schafer & Kohn, 2006). It is argued that a relationship exists between different MCG and genotypically different strains as demonstrated by (Kohn et al., 1991), and most recently by (Liu et al., 2018). It is believed that increasing the number of samples in the study would further understanding about the presence of a genetically different group of isolates originated through predominantly clones that are contributing to the spread of *Ss* isolates and contributing to the diversity through other non-clonal modes of reproduction across the country. This hypothesis might be supported by the observation of 2 samples from Alberta (25,29) which displayed compatibility with most of the MCGs in ON and QC. This agrees with similar findings recently reported by Buchwaldt et al. (2022). Although MCG testing has been widely used as a preliminary marker to determine the extent of genetic diversity in *S. sclerotiorum* isolates, there are still some limitations especially due to inconsistencies regarding mycelial relationships displayed, which is one of the main reasons why MCGs results are often complemented with genotyping techniques (Kamyar and Everhart, 2018). To confirm these findings, whole genome sequencing is expected to be performed in the coming steps of this research. The second set of samples is being tested for comparison (data not included).

Table 1. Identified MCGs found and its corresponding isolates.

MCG number	Isolate designation
1**	1,5,11,12,13,14,24,25,29,31
2**	2,8,29
3*	3,15,18,30,25,29
4*	4,31,32,25,29,31
5**	6,9,14,23,32,25,29
6**	7,18,25,29
7**	10,15,16,33,23,25,29,32
8*	17,25,29
9*	19,25,29
10	26
11	27
12	28
13	34
14	35
15	36
16	37

** At least one isolate of each province was found in this group
* The group didn't have isolates from all provinces

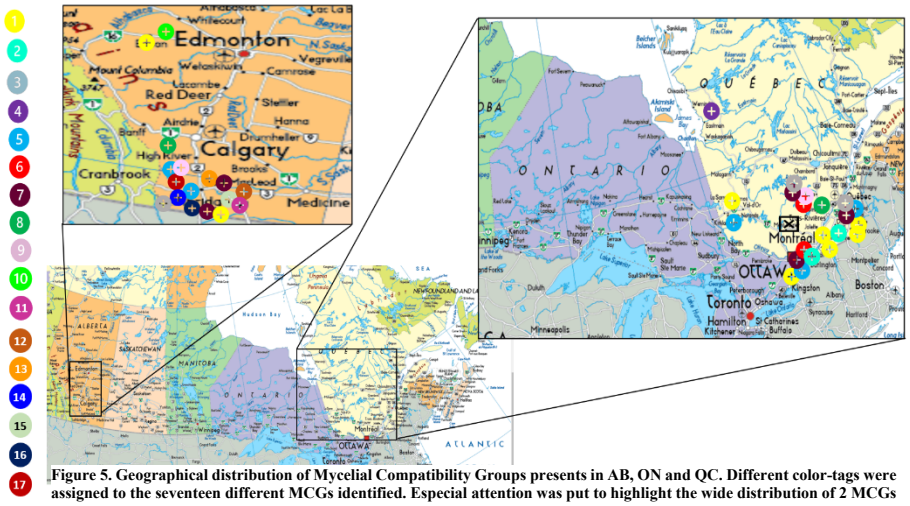

Figure 5. Geographical distribution of Mycelial Compatibility Groups presents in AB, ON and QC. Different color-tags were assigned to the seventeen different MCGs identified. Especial attention was put to highlight the wide distribution of 2 MCGs (MCG 1 -yellow tag- and 7 – violet tag-). Although some of the isolates from Alberta showed recurrent compatibility with most of the MCG from ON and QC it was decided to visually display those that contained highest number of isolates when compared MCGs individually. For more reference see Table 1.

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EFFICIENCY OF CARPOGENIC GERMINATION OF *SCLEROTINIA SCLEROTIORUM* IN DIFFERENT CULTURE MEDIA

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INTRODUCTION

White mold, caused by the necrotrophic fungus *Sclerotinia sclerotiorum*, is a disease that infects a wide range of plant species. This disease is the main challenge of common bean crop in the autumn-winter season in Brazil, when there are favorable climate condition for the pathogen. The white mold symptoms are intensified in humid and cold environments, favoring the production of sclerotia, which makes it difficult to manage the disease (Silva et al., 2021). Germination through sclerotia can occur in two ways: asexual (myceliogenic) or sexual (carpogenic). Carpogenic germination results in the production of apothecia that release millions of ascospores responsible for infection in the field (Rather et al., 2022). Therefore, it is important to carry out artificial inoculation with ascospores to select for resistant plants. The efficiency of carpogenic germination is essential to ensure the phenotyping of many plants contributing to obtaining resistant cultivars. This work evaluated the efficiency of different culture media for carpogenic germination of *S. sclerotiorum* isolates in controlled conditions.

MATERIALS AND METHODS

Three culture media were evaluated: A) commercial substrate (Tropstrato HA® Hortaliças), B) soil and C) mixture of the soil, fine sand, and substrate. The culture media were sterilized, placed in polypropylene gerbox containers, and incubated under controlled conditions. The sclerotia were deposited at a depth of 0.5 cm in the gerbox containers and kept humid with periodic additions of distilled water. Four traits were evaluated: number of days to germination (DG), number of apothecia (NA), percentage of germinated sclerotia (GS), and apothecia per sclerotia ratio (Ap/Sc). The experiment was conducted in a completely randomized design (CRD) with three replications and 15 treatments arranged in a 3x5 factorial, three culture medias and five Brazilian isolates of *S. sclerotiorum*: UFVss318, UFVss381, UFVss478, UFVss510 and UFVss605. Data were submitted to analysis of variance, and treatments means were compared by the Scott-Knott test (1974), with a significance level of $P \leq 0.05$. The statistical analysis was performed using the Genes software (Cruz, 2013).

RESULTS AND DISCUSSION

The effects of media were not significant for all traits except to days to germination (DG) (Table 1). In this case, the means for commercial substrate and soil media (40.6 and 39.5 days) were classified in same group by the Scott-Knott test. The mixture media mean was arranged in other group and presented the lowest value to DG (24.9 days). Therefore, the mixture media can be considered the best one because of the reduced 14 days for the time of germination of sclerotia. There was significant difference among the pathogen isolates for all evaluated traits and the averages were grouped in different groups by the Scott-Knott test. The UFVss478 isolate had the lowest number of days for germination of apothecia and the highest number of apothecia and percentage of germinated sclerotia (Table2).

Table 1. Summary of the analysis of variance for the number of days to germination (DG, days), number of apothecia (NA), percentage of germinated sclerotia (GS, %), and apothecia per sclerotia ratio (Ap/Sc) of five isolates of *S. sclerotiorum* evaluated in three culture media.

Sources of variance	df	Mean Squares							
		DG		NA		GS		Ap/Sc	
Isolate (I)	4	932.19	**	279.02	**	7900.85	**	0.79	ns
Media (M)	2	1149.36	**	12.57	ns	1163.25	ns	0.16	ns
I x M	8	43.69	ns	34.91	**	435.99	*	0.60	**
Residuals	30	38.27		5.64		185.07		0.18	
Mean		35.02		9.19		70.79		1.63	
CV(%)		17.67		25.84		19.20		26.27	

**, *: Significant at 1% and 5% probability by F-test, respectively; ns = Not significant.

Table 2. Means for number of days to germination (DG, days), number of apothecia (NA), percentage of germinated sclerotia (GS, %), and apothecia per sclerotia ratio (Ap/Sc) of five isolates on the three culture media mean.

Isolates	Means[1]			
	DG	NA	GS	Ap/Sc
UFVss318	34.2 b	14.0 a	88.4 a	1.8 a
UFVss381	46.8 a	4.7 c	52.0 b	1.6 b
UFVss478	24.7 c	15.8 a	96.3 a	2.0 a
UFVss510	25.6 c	8.3 b	89.5 a	1.3 b
UFVss605	43.8 a	3.2 c	27.8 c	1.4 b

[1]Means followed by the same letter belong same group by Scott- Knott test at 5% probability.

ACKNOWLEDGEMENTS
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GENOMIC PREDICTIONS: WHITE MOLD RESISTANCE IN DRY BEANS USING A MAGIC POPULATION

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INTRODUCTION: Genomic prediction (GP) is the estimation of the genetic value using molecular markers and phenotypic data (Meuwissen et al., 2001). Combined with other techniques, GP can improve the selection efficiency of the genotypes in a plant breeding program, especially for quantitative traits such as resistance to White Mold (WM) caused by the fungal pathogen *Sclerotinia sclerotiorum* Lib. de Bary in dry beans. Northarvest Bean Growers Association reported that dry bean growers from North Dakota and Minnesota ranked WM as the worst disease problem in dry bean production during the 2021 growing season (Knodel et al., 2022). Screening new genotypes for this disease under field conditions is complex. The presence of the pathogen in the soil, climate conditions, plant density, and avoidance and physiological mechanisms interact together to hinder the selection of resistant genotypes. In this study, the accuracy of six GP models was measured using a previously developed Multiparent Advanced Generation Inter-Cross (MAGIC) population (Escobar et al., 2022).

MATERIALS AND METHODS

Phenotypic data were obtained from the study by Escobar et al. (2022), using the seedling straw method in the greenhouse (Arkwazee and Myers, 2017). A subset of the MAGIC population (Fig. 1), with a total of 500 genotypes was used in this study. Twenty-one genotypes scored from 1 to 3 (resistant), 126 genotypes scored with a value of 4 (tolerant), and 355 genotypes scored from 5 to 9 (susceptible). Genotypic data was obtained from the same subset of 500 genotypes from the MAGIC population as described by Escobar et al. (2022). A second SNP dataset was generated using UI111 (Middle American) as a reference genome following the methods of Escobar et al. (2022). GP models, Ridge Regression Best Linear Unbiased Prediction (rrBLUP), Bayes A, Bayes B, Bayes Cπ, Bayesian LASSO, and Bayesian ridge regression, were evaluated using the phenotypic and genotypic data previously described. All models were evaluated in the R language using the packages "rrBLUP" version 4.6.2 (Endelman, 2011) and "BGLR" version 1.1.0 (Pérez & de los Campos, 2014). To identify the best predictive model, the predictive ability was calculated as the Pearson correlation between the average of the predicted phenotypes and the observed phenotypes.

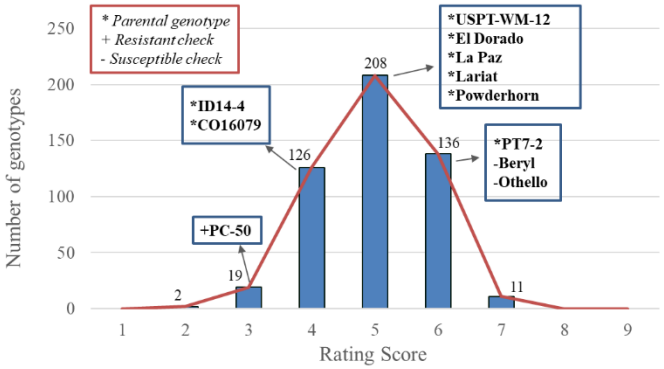

Figure 1. Phenotypic distribution in 1st subset of the MAGIC population.

RESULTS AND DISCUSSION: The total amount of genotypic data used in the models differ depending on the reference genome used. For the G19833 v2.1 genome reference (Andean), a total of 52,201 SNPs were identified (Escobar et al., 2022), while a total of 76,286 SNPs were obtained here using the UI111 v1.1 reference genome (Middle American). The prediction accuracy depended on the genotypic data set used in the models. When using 76,286 SNPs, the accuracy

ranged from 63 to 79%, whereas using 52,201 SNPs, the accuracy ranged from 77 to 92% (Fig. 2). In general, the Bayes A model had the best predictable ability for both sets of genotypic data. A low prediction ability was detected in the models for resistant genotypes and very susceptible genotypes (scores from 7 to 9), which is caused by the absence and low number of genotypes with scores in these categories.

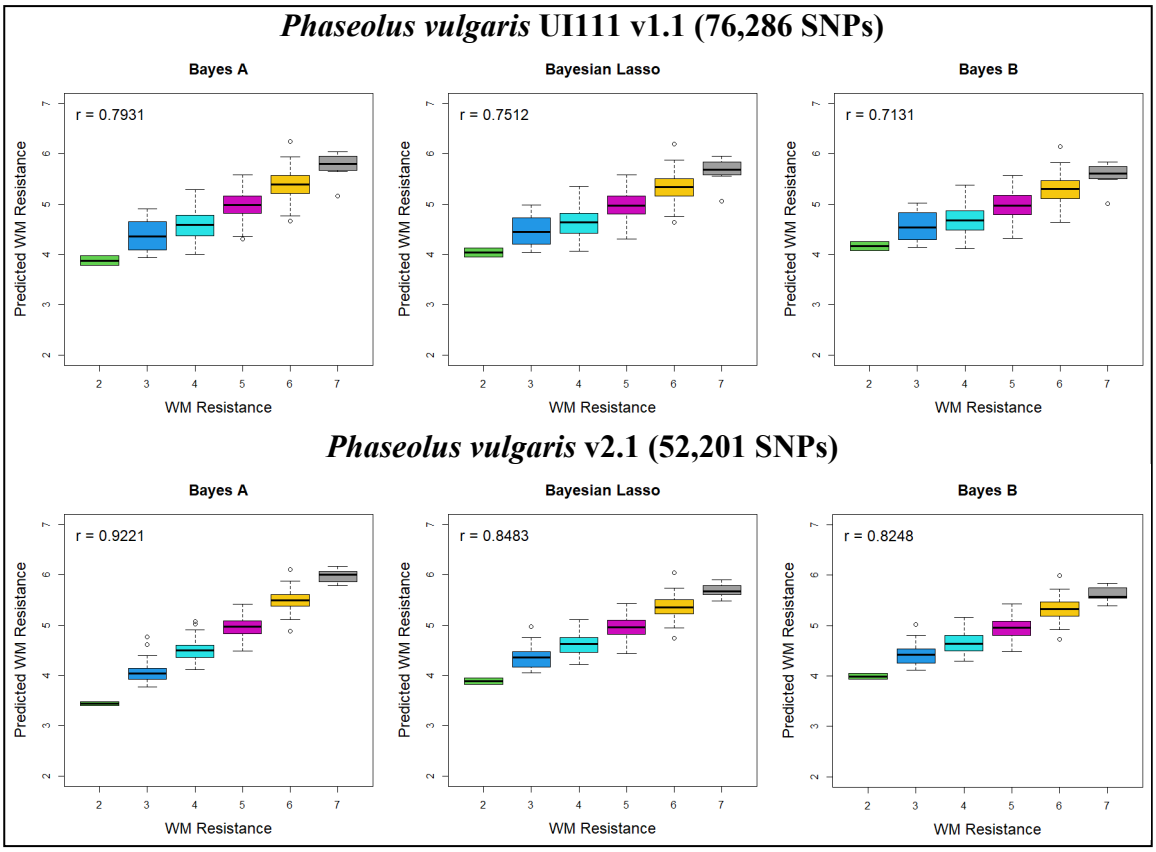

Figure 2. The best three predictable model for each genotype data set.

As future work, the Bayes A model will be validated as a genomic selection tool for a second subset of the MAGIC population, as well as for the advanced breeding lines in the dry bean breeding program at North Dakota State University. This research has been funded by the USDA-ARS National Sclerotinia Initiative.

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POTENTIAL OF GENOMIC PREDICTION FOR WHITE MOLD IN DRY BEAN (*PHASEOLUS VULGARIS* L.)

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INTRODUCTION

Michigan is the second largest producer of dry beans in the U.S. However, white mold caused by the fungus *Sclerotinia sclerotiorum* (Lib.) de Bary is ranked the top yield limiting disease of dry bean production in the U.S. To date there exist no cultivars with high levels of resistance and progress in breeding new cultivars has been hindered due to the quantitative inheritance of this trait and screening dependence on the presence of the pathogen under suitable environmental conditions. Due to the quantitative inheritance of this trait, methods such as marker-assisted selection (MAS), that aim to pyramid only a few target genes, take time. A new alternative breeding strategy is using genomic prediction and selection, which utilizes genome-wide marker coverage to predict genotypic values for quantitative traits. Therefore, the purpose of this study is to evaluate a training population for genomic prediction to increase the accuracy of selection for white mold resistance in dry bean.

MATERIALS AND METHODS

A total of 272 advanced breeding lines from the three major market classes (black, navy, and red) were used to evaluate the potential of genomic prediction models to screen for white mold resistance. All lines were grown under natural white mold infestation using overhead pivot irrigation in a disease nursery at Montcalm County, MI during the 2021-2022 growing season. The visual rating consisted of plotwise disease severity on a scale of 1 to 9, as described in Miklas et al., 2001. Lines were genotyped using the Illumina Infinium BARCBean12k Bead chip in collaboration with the USDA-ARS, in Beltsville, Maryland. SNP quality filtering in TASSEL resulted in a total of 3,929 markers. A principal component analysis (PCA) to evaluate population structure was also performed in TASSEL (Bradbury et al., 2007). Two genomic prediction models (rrBLUP and GBLUP) were implemented in the rrBLUP package in R and trained using phenotypic and genotypic data from the training sets using a 8 fold cross-validation scheme (Endelman, 2011). Best linear unbiased predictors (BLUPs) were predicted for individuals in the validation set and prediction accuracy was evaluated as the ratio between the observed and predicted genotypic values.

RESULTS AND CONCLUSION

The PCA analysis of the training population revealed a population structure with three distinct clusters (Figure 1). There is a significant overlap among black and navy beans which reflects the crossing scheme of the breeding program. Average prediction accuracy was moderate for every subset and model with a mean prediction accuracy ranging from 0.25 to 0.40 percent (Figure 2). For most subsets rrBLUP and GBLUP were not significantly different in prediction accuracy. These preliminary results indicate that genomic prediction has potential as a tool to assist screening efforts for white mold. Moving forward we will continue to increase/update the training population to further increase genomic prediction accuracy.

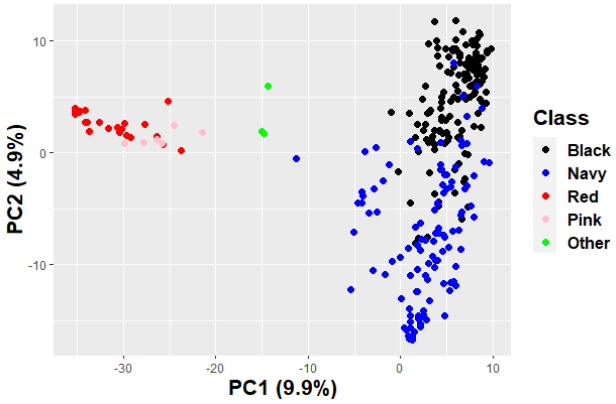

Figure 1. Principal component analysis for the entire population used as the training set for genomic prediction.

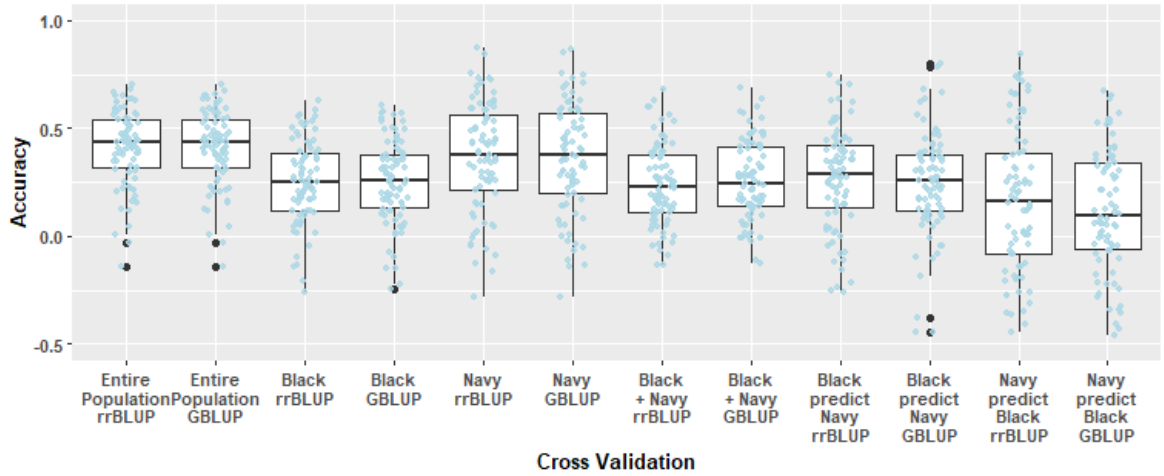

Figure 2. Comparison of genomic prediction accuracy for two models, rrBLUP and GBLUP, over training population cross validation subsets

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AUTOMATING HIGH-THROUGHPUT SCREENING OF COMMON BEANS FOR ANTHRACNOSE RESISTANCE GENES USING ALLELE SPECIFIC PCR

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INTRODUCTION: The Kompetitive Allele Specific PCR (KASP) assay is a genetic screening tool that can provide useful information to breeding programs, however, DNA extraction and PCR plate preparation is time consuming which limits the scale of KASP's application. Several KASP markers linked to loci involved in bean anthracnose (*Colletotrichum lindemuthianum* (Sacc. & Magnus) Briosi & Cavara, 1889) resistance have been developed but their application is hindered by the labor required for each sample. The objective of this research was to develop publicly available protocols for DNA extraction and KASP assaying using a liquid handling robot (LHR) to facilitate faster, high-throughput genetic screening. Manual and automated results were compared for four anthracnose resistance markers.

MATERIALS AND METHODS: The aim of this work was to create an automated system for KASP assaying from raw samples to fluorescence results and to validate its efficacy. The LHR used was the Opentrons OT-2. The twelve bean anthracnose differential cultivars were screened for four anthracnose resistance KASP markers linked to the genes *Co-1*, *Co- 3* and *Co-4*[2] (Intertek ID: snpPV00177, snpPV00050, snpPV00070 and snpPV00183) both by hand and with the use of the LHR. To implement the LHR, a protocol was written for DNA extraction and KASP assay thermocycling using the Opentrons web protocol designer (https://opentrons.com/).

DNA was extracted manually and with the LHR, using either a silica-based DNA extraction kit (DNeasy® Plant Pro Kit) or a magnetic bead based extraction kit (MagMAX™ Plant DNA Isolation Kit). During the automated procedure, lysis steps were carried out manually before samples were placed into the LHR along with an Opentrons temperature block and magnetic module.

Three KASP assays were done for each marker: a manual temperature optimization test with positive and no template controls, a manual assay of the anthracnose differential cultivars then an automated assay of the anthracnose differential cultivars. KASP primers were ordered from IDT and PACE 2.0 mastermix, functionally identical to KASP, was ordered from 3cr Bioscience. The manual assays took place in a BioRad CFX connect PCR machine while the automated assays took place in the Opentrons thermocycler attachment in the LHR. The allele calling function of CFX Maestro software was used to visualize the results. Protocols developed in this research for extraction and KASP assaying in the LHR are available at https://github.com/McGillHaricots/peas-andlove/tree/master/protocols

RESULTS AND DISCUSSION: The concentration of DNA extracted manually or with the LHR was always high enough to perform a KASP assay, although it was consistently higher

when extracted manually. Using the MagMAX™ extraction kit, manual extractions had a mean concentration of 1038 ng/µL while automated extractions had a mean of 291ng/µL.

Presence or absence of the resistance gene markers was determined for the anthracnose differential cultivars and several check lines. Their results were consistent but not entirely as expected according to present knowledge of anthracnose resistance loci. This suggests a need for more tightly linked markers and continued efforts to elucidate the anthracnose resistance loci present in important cultivars.

Automated KASP assays made the same calls as manual assays in 94% of the tests. All the errors made were for KASP assays linked to the *Co-3* marker (snpPV00050). For the *Co-1* and *Co-4*[2] markers (snpPV00177, snpPV00070 and snpPV00183), automated and manual results matched 100% of the time.

The total cost of the LHR and all required attachments was $26,470 USD when purchased in 2020. It is easily programmable and has many publicly available programs which facilitates its quick application in labs.

CONCLUSIONS: Using a LHR, active time required to conduct KASP assays dropped significantly without changing results. KASP assays with the selected anthracnose resistance markers were highly repeatable but did not always adequately reflect what is known about resistance loci in the anthracnose differential cultivars. The low cost of the LHR and public availability of protocols to run on it could facilitate the use of high throughput KASP assays in many labs. This research suggests that with a LHR, KASP can be applied as an effective genetic screening tool to many samples with little active time or additional cost required.

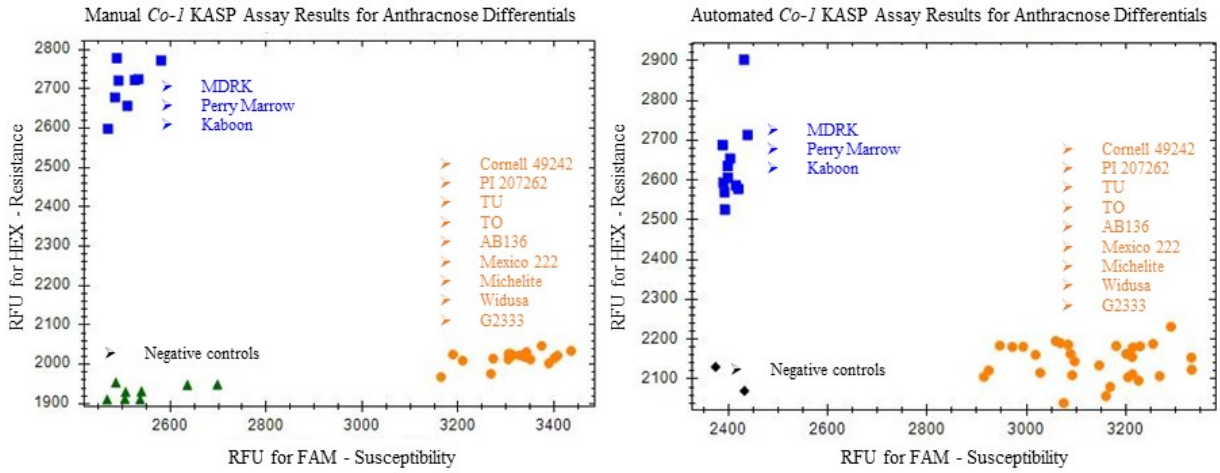

Figure 1. Comparison of KASP results for the *Co-1* marker when done manually (left) or by the LHR (right). Cultivars that are homozygous for resistance at the *Co-1* marker appear blue while homozygous susceptible cultivars appear orange. Negative controls are green or black.

INVESTIGATING GENOMIC SELECTION PREDICTION MODELS IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)

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INTRODUCTION: Genomic selection (GS) has been proposed as a promising technology for revolutionizing plant breeding and increasing the rate of genetic gain in a breeding program. Simulations will assist in decision-making for the ultimate development of an applied genomic selection pipeline. The success of GS depends heavily on the performance of the prediction model used to estimate the breeding value of selection candidates (Rutkoski, 2021, Crossa, 2017). This study investigated the impact of different prediction models on genetic gain.

MATERIALS AND METHODS: A series of simulations were carried out to investigate the application of genomic selection to a breeding population of common beans. Three different prediction models (ridge regression BLUP: rrBLUP, random forest: RF, and support vector machine: SVM) were used to predict genomic estimated breeding values for 2 traits (seed yield and days to flowering) on 3 differently structured simulated common bean populations undergoing different systematic effects (population 1: no systematic effects - population 2: natural selection - population 3: natural selection and migration between subpopulations). To train the prediction models, 2 different training population configurations (a random sample, and a sample selected through a stratified clustering method) were tested (Isidro, 2015). The three different populations were simulated using the python package SimuPop (Peng 2005). The common bean consensus map (Galeano, 2011) was used as a framework for simulating genotypes which were then loaded into the AlphaSimR framework for simulation (Gaynor 2021). Varieties were developed from each of the three populations, with selections being chosen based on GEBVs for seed yield and days to flowering, following the pedigree method. Genetic gain and model performance were assessed across all scenarios.

RESULTS: Results of the simulations indicated that the standard linear rrBLUP model performs best and results in strong gains when compared against nonparametric models (Figure 1). The SVM performed poorly, however the RF performed competitively with rrBLUP when the model was re-trained within the breeding cycle (Figure 2). Because RF showed peak performance during the F5 retrain, an ensemble scenario was tested where rrBLUP was used at the start of the cycle and RF was used at the end of the cycle after the model retrain. This ensemble model yielded the highest gains (8.74%).

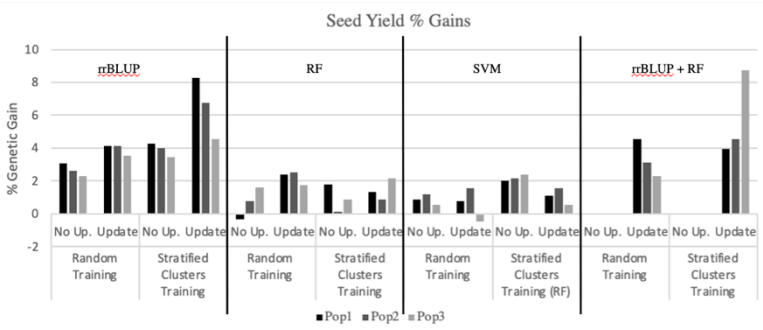
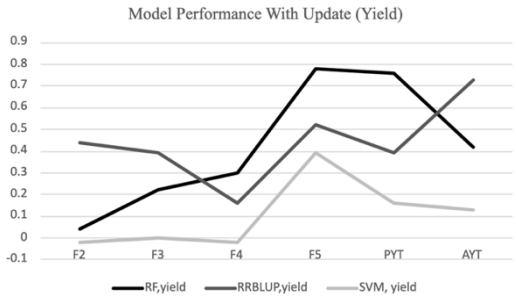


Figure 1. Percent gain (seed yield) for each model, population, and training population with and without a model update. Population 1 underwent no systematic effects. Population 2 underwent natural selection. Population 3 underwent natural selection and migration between subpopulations. rrBLUP = ridge regression best linear unbiased prediction, RF = random forest, SVM = support vector machine.

Implementing a stratified clustering training population showed an increase in model performance, and in turn genetic gain for the rrBLUP model and the SVM (Figure 1). However, RF did not benefit from a stratified clusters training population. This is likely because each decision tree in the RF takes a separate subset of samples and variables so it is best to feed the model a snapshot of the entire dataset, as opposed to a specific grouping of samples.



Across the board, updating the model resulted in increased prediction performance and increased gains. This suggests that a breeding program wishing to increase genetic gain by implementing genomic selection should use one model for parent selection and early cycle selections, and a re-trained version of the same model (and possibly a different model entirely) for later-cycle selections. If rrBLUP is implemented, it is worthwhile to carefully select those individuals used to train the model, but this may or may not be necessary when nonparametric ML models are utilized.

Figure 2. Model performance when predicting GEBVs for yield. The model was updated at F5.

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MAPPING OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH YIELD COMPONENTS IN THE AWAUNA UEM×IPR88 UIRAPURU POPULATION OF COMMON BEAN (*PHASEOLUS VULGARIS* L.)

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INTRODUCTION

The ongoing identification of genomic regions through molecular markers in mapping studies continues to advance our understanding of Quantitative Trait Loci (QTL; Kromdijk et al. 2014). By mapping QTLs in plants, we can uncover the genetic basis for the inheritance of quantitative traits and develop functional markers for the selection of complex traits (Bernardo 2008). This leads to a deeper understanding of the genetic architecture and interplay between genotype and phenotype, which is crucial for crop improvement efforts. Therefore, this study aimed to map quantitative trait loci (QTLs) associated with yield components in the Awauna UEM×IPR88 Uirapuru population of recombinant inbred lines (RILs) of common bean.

MATERIALS AND METHODS

A total of 208 RILs, the two parents, and six control cultivars were analysed in field at Universidade Estadual de Maringá over three agricultural years (2017, 2018, and 2019). Important agronomic traits, such as plant height (PH), number of pods per plant (NPP), first pod height (FPH), seed weight (SW), and seed yield per plant (GYP) were evaluated in each treatment. The experiment was conducted in a triple Lattice 15x15 design with 2.0m rows spaced 0.5m apart and 24 plants per row. Mixed models and Harmonic Mean of the Relative Performance of the Genotypic Values were used to analyze the phenotypic data and evaluate the G×E interaction for QTL mapping purposes. Total genomic DNA was extracted from the 208 RILs and parents using the DNeasy plant mini kit from Qiagen, and screened with 5,398 SNP DNA markers on the BARCBean6K_3 Illumina BeadChip. The QTL analysis was conducted using IciMapping® Version 4.2, with the Inclusive Composite Interval (ICIM), BIP, and MET analysis modules to map QTL with genes of additive effect and environmental interaction. The markers associated with these QTLs were named according to the guidelines for QTL naming in common bean, proposed by Miklas and Porch (2018). Additionally, the QTLs were graphically represented in the genetic linkage maps using MapChart 2.3 (Voorrips, 2002) to provide a visual representation of their location in the genome of the common bean.

RESULTS AND DISCUSSION

A total of five QTLs associated with these traits were identified on chromosomes Pv01, Pv04, Pv08, and Pv10 (Figure 1). Of particular interest, the ss715646884 (46,961,454 bp) marker on chromosome Pv01 was identified as being linked to PH, NPP, and GYP. The marker ss715649973 (1,575,721 bp) on chromosome Pv04 was found to be close to the peak of the QTL for PH and FPH. On Pv08, the markers ss715646109 (58,231,277 bp) and ss715646101 (58,006,525 bp) were linked to the NPP and SW QTLs, respectively. On Pv10, two QTLs for SW were identified and linked to markers ss715650584 (40,255,828 bp) and ss715641827 (16,330,477 bp). The coincidence of QTLs found for different traits suggests the presence of pleiotropy or closely linked genes (Haggard et al. 2015). The QTL mapping results for PH, FPH, NPP, and SW showed consistent performance across the experimental years, indicating their stability.

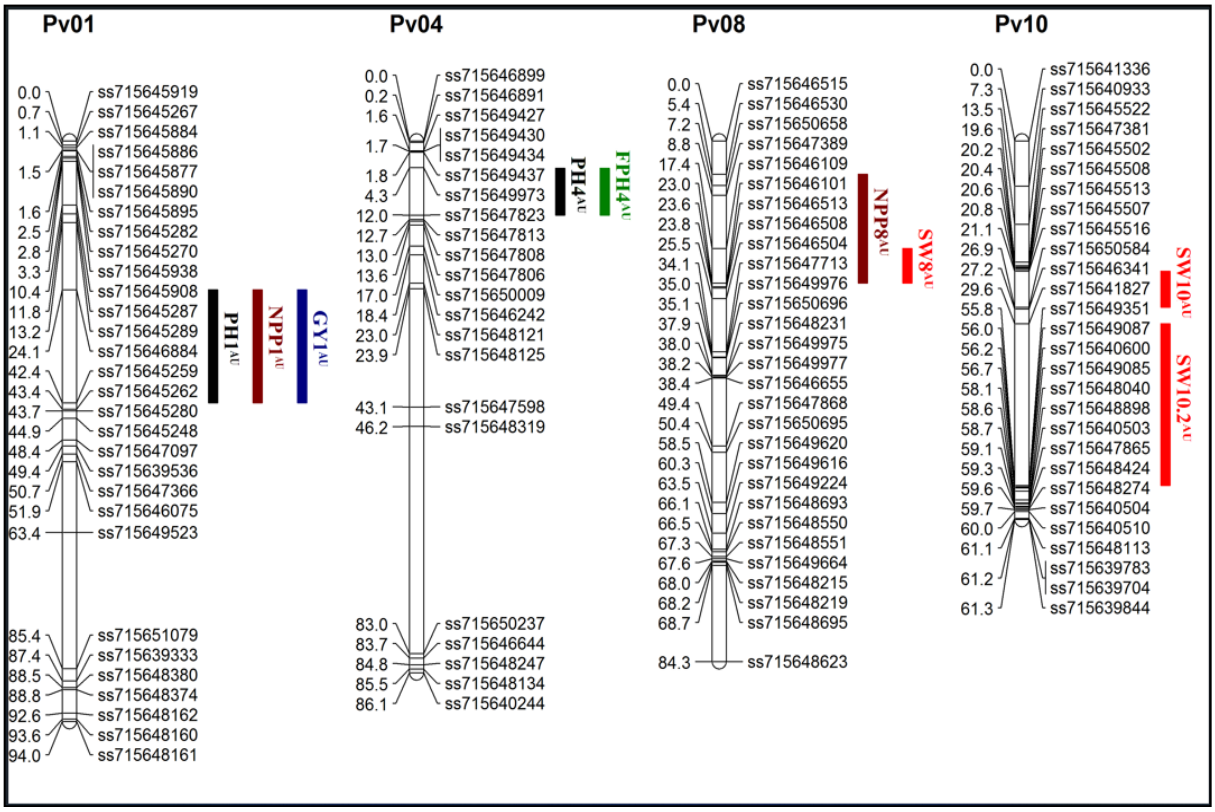

Figure 1. Genetic linkage map showing the QTLs for plant height (PH), number of pods per plant (NPP), first pod height (FPH), seed weight (SW), and seed yield per plant (GYP) mapped on the chromosomes of common bean using the Awauna UEM×IPR88 Uirapuru population. Distances between markers are indicated in centimorgans.

ACKNOWLEDGEMENTS

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QUICK AND INEXPENSIVE MAS FOR COMMON BEAN AT USASK

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INTRODUCTION: Over the past decade we have worked to make MAS in our common bean breeding program as efficient as possible. We have been asked to share this protocol several times so we decided to put it out to the BIC community. We are always looking for improvements and welcome any suggestions.

MATERIALS AND METHODS

1. Isolation of DNA for Genotyping

We typically isolate DNA from seeds before we plant them. Seeds are arrayed in 96-well microfuge tube racks for tracking purposes. A small chip in the seed coat is made and a tiny bit of cotyledon is sampled. Here is a link for our DNA Isolation protocol in our KnowPulse web portal:
https://knowpulse-knowledgebase.github.io/Laboratory-Protocols/01-Crude-DNA-Isolation-from-Seeds/index.html

This is strictly a DNA isolation protocol; the DNA is not purified. It produces a product that works well for standard PCR and fluorescence-based PCR; however, the quality will not be sufficient for any type of sequencing. We use it routinely with bean and lentil, and it also works for other pulse and cereal crops. We use it mostly on seed tissue, but it can also be used on leaf or other tissues. Once trained it takes a technician about an hour to do a plate of 96 isolations. It costs us ~C$6 to do 96 isolations (or about C$0.06 / sample), not including labour. These isolations can then be loaded directly into a PCR reaction (with maybe a dilution step in between). The isolations provide enough DNA to screen dozens of markers and can be stored in a fridge for a week, or in a freezer for about a month.

2. Genotyping with Fluorescence-based PCR

We started using KASP (LGC Technologies) technology ten years ago. There are informational videos on YouTube and the LGC Technologies website that describe how the technology works. About two years ago we switched to PACE (3cr Biosciences) MasterMix. PACE MasterMix is the same as KASP MasterMix, meaning we can use either with our current assays. We use these technologies for several reasons:

a) assays can be designed to detect SNPs and indels in a co-dominant fashion. SNPs and indels are ubiquitous, usually providing us with more options when looking at specific genomic regions. The co-dominant nature of the assays means we can score heterozygotes, which is important for us when we screen early generation material.

b) the assays are easy to design once you know how to do it. The oligos can be ordered from anywhere and don't require any special modifications. The universal nature of the KASP/PACE MasterMix means we can design and test potential new markers cheaply. Ordering the primers for a KASP/PACE assay costs us around C$26 and can be used to screen several thousand samples.

c) using fluorescent-based markers has allowed us to eliminate the need to run any agarose or polyacrylamide gels; saving time, space, and the need to deal with potentially hazardous materials.

d) we switched to PACE MasterMixes because they introduced a multi-plexing MasterMix that allows us to run two markers in the same reaction. This doubles the number of datapoints, saving both money, time, and plastic consumables.

Here is a link for the PCR program we use:
https://knowpulse-knowledgebase.github.io/Laboratory-Protocols/03-KASP-PCR-Protocol/index.html

We run our PCRs on a QuantStudio 5 (ThermoFisher Scientific) in 384-well plates. However, there are many options for rtPCR machines that will range in quality and price. An important note is that while all rtPCR machines will handle KASP and PACE fluorescences, multiplexing using PACE MP requires a machine with specific capabilities.
Running PACE 2.0 (single-plex) in 384-well format - it is currently costing us ~C$0.23/well.
Running PACE MP (multiplex) in 384-well format - it is ~C$0.30/well or ~C$0.15/data point.
Running in a 96-well format will be more expensive per well. These costs do not include labour.
It takes a trained technician about 30-40 minutes to set up a 384-well PCR. The PCR itself takes ~3.5 hours. Analyzing the data afterward, on a clean run, only takes ~15-20 minutes.

Overall, a trained technician can easily extract and genotype 400 samples/day. With multiplexing that is 800 datapoints/day. We could run our PCR program three times per workday (maybe a 4th run overnight) meaning, if needed, and with more manpower, we could ramp up to >3000 datapoints per day on the one PCR machine.

3. Our Current MAS Primers

While we have designed and used hundreds of common bean markers, our routine MAS consists of the following markers:

a) SU-91 for CBB Tolerance

This assay detects a SNP (Pv2.1Chr08p62837508) that falls within the amplicon produced by the SU91 SCAR described by Pedraza et al. (1997 – see citation below). Primers:

A1 - GAAGGTGACCAAGTTCATGCTGGAAGCAAGTCAAGATACGTAAAAGAT
A2 - GAAGGTCGGAGTCAACGGATTGGAAGCAAGTCAAGATACGTAAAAGAA
C – TTACTTTTTGAATTTGATTACTTCTTCTGC

b) Bean Common Mosaic Virus (BCMV) Resistance (*I*)

We use the KASP assay reported by Bello et al. (BMC Genomics, 2014, 15:903) for BCMV resistance assaying a SNP at Pv2.1Chr02p48918075:

A1 - GAAGGTGACCAAGTTCATGCTTGAAAATGGGTCGGGTCGGAC
A2 – GAAGGTCGGAGTCAACGGATTCTTGAAAATGGGTCGGGTCGGAT
C – CCCTAATTCACTTTCCGAGTAAGAGAAGC

c) Slow Darkening seed coat (P^{sd})

We use the KASP assay we described in Alvares et al. (Euphytica, 2019, 215:141) assaying a SNP at Pv2.1Chr07p28765330:

A1 – GAAGGTGACCAAGTTCATGCTCCACGTGCTCGCGGAGCG
A2 – GAAGGTCGGAGTCAACGGATTACCACGTGCTCGCGGAGCA
C – GCGGGGTGGGTGGGTGTTAAAA

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DRY BEAN MATURITY ESTIMATION BASED ON UAS-RGB IMAGERY

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INTRODUCTION

Plant breeding programs aim to develop improved crop varieties combining many desirable traits of economic importance. As part of that process, thousands of field measurements are taken to support plant breeding decisions. Among them, crop maturity estimation is a necessary trait to be measured since it is an important factor for harvest management. Most commonly, crop maturity is determined by visually rating the fields several times at the end of the growing season (Volpato et al., 2021). That task can be time-consuming, labor-intensive, and expensive. The incorporation of new technologies, such as unmanned aerial systems (UAS), into plant breeding, can help to improve efficiencies by allowing the implementation of high-throughput phenotyping (HTP) approaches, which in turn can accelerate crop improvement (Sankaran et al., 2018). Therefore, the overall goal of this study was to estimate crop maturity dates of dry bean lines using RGB cameras mounted on a UAS platform and to validate UAS-based data with ground-truth data.

MATERIALS AND METHODS

The study was carried out on field trials belonging to the dry bean breeding program at North Dakota State University, located at Hatton and Prosper, North Dakota during the 2022 growing season. The dry bean advanced yield trials (AYT) consisted of six market classes including pinto bean (PAYT), slow darkening pinto (SDPAYT), great northern (GNAYT), navy (NAYT), black (BAYT), and red and pink (RPAYT) beans, totalizing 139 plots with three replications. Images were collected using an Autel Evo II 6K aircraft, which was outfitted with a 20-megapixel (MP) camera. Flights were conducted once a week at an altitude of 50 meters above ground level (AGL), starting from when the earlier lines began to mature until the last plots matured. After each flight, images were processed using Pix4DMapper software from Pix4D (v4.7.5; Pix4D SA, Switzerland). The resulting orthomosaic was brought into ArcGIS Pro (ESRI, United States) for further analysis, where Excess Green Index (ExGI) was calculated, and statistics (mean, median, max, min, and range) were generated for each individual plot. These metrics were then compared to the ground truth data taken visually, and correlations were established to validate the UAS collected data.

RESULTS AND DISCUSSION

Preliminary results from the 2022 season showed similar trends in plant maturity for data manually collected in the field vs. UAS-based data in certain market classes. For instance, in NAYT figures 1A and 1B, Blizzard, ND172087, and ND172173 genotypes fell into the early maturity group, while, ND131944, NDPolar, and T9905 were considered late. In the simple linear regression analysis (Figure 1C) a strong relationship between the variables excess green index (UAS data) and days to maturity can be observed, with a correlation coefficient (r) of 0.7960. In the other market classes, the correlation coefficient values ranged from 0.46 to 0.66 (data not shown).

A previous study on temporal UAS-based imagery analysis to estimate plant maturity date in soybeans achieved high correlations between ground and UAS-based estimates (r = 0.84-0.97) when using the mean greenness leaf index in combination with LOESS regression (Volpato et al.,

2021). The NDSU dry bean breeding program will continue further studies with other agronomic traits such as canopy cover, plant disease, and plant height to test whether or not UAS-based data generates values of similar magnitude to what is observed in the field. This work has been supported by the ND Agricultural Experiment Station Precision Ag grants program and by the Northarvest Bean Growers Association.

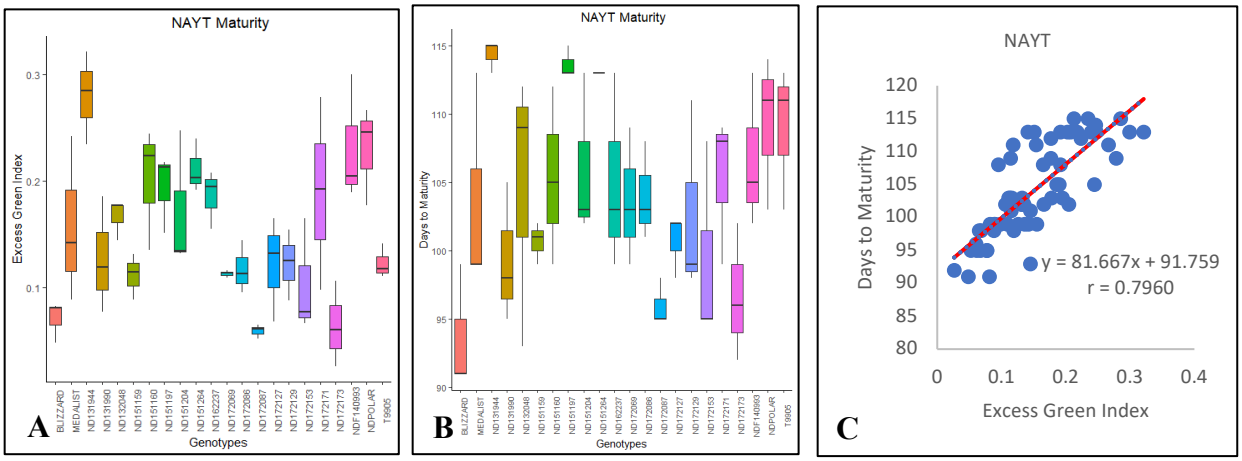

Figure 1. A) Identification of early maturity genotypes within the NDSU Dry Bean breeding program using the Excess Green Index extracted from an RGB camera, B) using Days to Maturity manually collected, and C) Linear Regression between Excess Green Index and Days to Maturity. Preliminary results from Hatton, ND in 2022.

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DRONE-IMAGERY PHENOTYPING USING DEEP LEARNING APPROACHES TO ESTIMATE PLANT MATURITY IN DRY BEANS

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INTRODUCTION: Days to maturity (DM) is one of the most important physiological components affecting yield and seed quality outcomes in dry beans (*Phaseolus vulgaris* L.). Days to maturity play a key role in determining the yield potential and commercial success of dry bean cultivars, and it is determined by the duration of the growth cycle from planting to physiological maturity. On average, DM varies from 85 to 115 days, which is affected by environmental factors such as temperature and rainfall (Karavidas et al., 2022). To ensure the successful cultivation and production of dry beans, it is essential to select the appropriate DM cultivar for the desired growing location (Kazai et al., 2019). Visual inspections to determine accurate DM are labor-intensive, time-consuming, and tedious, contributing to inaccurate ratings. Therefore, alternative approaches to estimating DM in a high-throughput phenotyping mode (HTP) are warranted. The aim of this study was to develop a Deep Learning (DL) HTP pipeline to capture the sequential behavior of time series data for estimating DM using aerial RGB images at the field plot level.

MATERIAL AND METHODS: Ground-truth and aerial imagery data were measured during the 2020-2022 growing season at two locations in Michigan (Saginaw and Huron counties) using black and navy market classes from standard yield (SYT) and preliminary yield (PYT) trials conducted by the Michigan State University (MSU) dry bean breeding program. Entries were planted in four-row field plots of 4.5 m in length and 0.5 m between rows in which the two-center rows represent the breeding line and the outside rows the border. All experimental trials were laid out in an alpha lattice block design with 4 replications, except one trial in 2020 which was an augmented block design with only one replication. Trials received industry-standard seed treatments, fertilization, and weed control applications at recommended rates. The UAS imageries were collected using a DJI Phantom 4 Pro v2 (DJI Technology Co., Ltd.) equipped with a digital red-green-blue (RGB) camera (5472x3648) and sensor dimensions of 12.833x 8.556 (mm). Flights were conducted at the beginning of maturation, and during the DM ground-truth data measurements until all plots reached physiological maturity. In 2020, flights were conducted once per week, while in 2021 and 2022, we aimed to fly two times per week. The flight frequency in 2021 and 2022 allowed the simulation of the DM data analysis using 6 and 9 flight missions in total for each location. A state-of-the-art hybrid model combining Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM) was used to extract DM features and capture the sequential behavior of time series data using two image sizes (256x64 and 512x128).

RESULTS AND DISCUSSION: Results suggest the effectiveness of the CNN-LSTM model employed produced similar outcomes compared to traditional methods. The correlations and errors across the environments between ground truth and aerial predictions showed reliable results to estimate DM (Figure 1). The results were not influenced by the image size. However, the performance of the model was negatively influenced by flight frequency, indicating lower performance when flight frequency increased beyond two flights per week. The traditional method previously published in the literature (Volpato et al., 2021) using LOESS (non-parametric local polynomial regression) and SEG (segmented linear regression) demonstrated similar correlations performance, but the errors were increased significantly in both flight frequencies (Table 1). The

adjusted CNN-LSTM model utilized in this study provided similar performance to the proposed method in soybeans (Moeinizade et al., 2022), which also demonstrated reliable performance with less frequent flights. In soybeans, the proposed DL model was able to estimate DM with less than 2 days of error, while for dry beans the error was less than 3 days. Due to the shorter growth cycle compared to soybeans, the results presented in this study of dry beans showed a reliable approach for estimating DM to assist in aiding dry bean breeding decisions. Furthermore, this study highlighted the technical parameters that can influence the DL model results in breeding program decision-making, such as light conditions and image resolution, which proved the CNN-LSTM model's robustness to data quality issues. Therefore, the phenotyping method used in this study to estimate DM can be generalized to data in new environmental conditions.

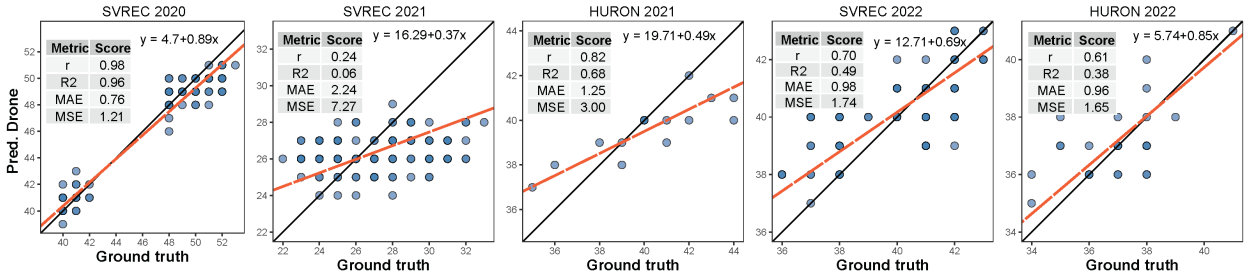

Figure 1. Results by environment between ground-truth and predicted by the DL drone phenotype method using 256x64 image size and a set of 6 flights.

Table 1. Days to Maturity (DM) correlations and errors between ground-truth and estimated by drone imagery phenotyping using two sets of flights to compare the CNN-LSTM model with two image sizes and the benchmark results using the traditional LOESS and SEG methods. The results were obtained by averaging across all five environments in this three year study.

	6 Flights				9 Flights			
Metric	**CNN-LSTM (256x64)**	**CNN-LSTM (512x128)**	**LOESS**	**SEG**	**CNN-LSTM (256x64)**	**CNN-LSTM (512x128)**	**LOESS**	**SEG**
r	0.67	0.70	0.71	0.69	0.49	0.49	0.60	0.57
r^2	0.51	0.54	0.59	0.56	0.29	0.30	0.45	0.37
MAE	1.24	1.25	6.07	4.29	1.35	1.39	4.63	4.78
MSE	2.97	3.14	43.44	26.58	3.40	3.45	25.33	27.76

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PHASEOLUS IMPROVEMENT COOPERATIVE (PIC) POPULATIONS DEVELOPED VIA INTERCROSSING OF STRESS-TOLERANT GERMPLASM AND THEIR PERFORMANCE UNDER DROUGHT CONDITIONS

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INTRODUCTION

Continued germplasm exchange and introduction of exotic useful alleles are essential in sustaining long-term genetic gain for common bean improvement. The objective of developing the *Phaseolus* Improvement Cooperative (PIC) plant breeding populations was to create a collection of progenies derived from parents with desirable complementing characteristics such as combinations of disease resistance with tolerance to abiotic stresses like heat, drought, and low soil fertility, that are important in multiple countries [1]. This study aimed to characterize the PIC and the parental lines for their genotypic diversity and phenotypic traits in Puerto Rico (PR).

MATERIALS AND METHODS

Sixty-five Andean Diversity Panel (ADP) accessions and other parental lines from available sources were selected for disease resistance, heat and/or drought tolerance, and crosses were made to generate about 140 F_4 bulk PIC populations. The F_4 bulk populations were grown in PR, Tanzania (TZ), South Africa (SA), and Washington, USA (WA), and single F_4 plants and subsequent $F_{4:5}$ lines were selected from them based on their performance in each environment. After progeny row trials in each environment, 71 F_4-derived lines were selected in PR, 80 lines in SA, 152 lines in TZ, and 81 in WA. The number of F_4-derived selections (PIC lines) from any one population varied from 0 to 22. The 384 selected PIC lines and 58 parental lines were genotyped using the 12K common bean SNP chip [2]. The raw genotype calls were filtered for missing data <20%, heterozygosity rate <25%, MAF >3% using PLINK v1.9, resulting in 6,741 SNPs with 442 individuals. Furthermore, SNPs in high LD (r^2>0.9) with neighboring SNPs were removed with a sliding window size of 50 bp and a shift size of 5 bp using PLINK ver. 1.9. The LD-pruned 2,334 SNPs were used for Principal Component Analysis (PCA) using TASSEL. Forty-five parental and 242 PIC lines (69 selected in PR, 99 selected in TZ, and 76 selected in WA) were grown for a yield trial in RCBD with 2 replications with drip irrigation and severe drought in the dry winter season of 2019 in Juana Diaz, PR. Best Linear Unbiased Predictions (BLUP) were calculated based on the raw yield data, and the mean BLUP of the PIC lines from various selection environments (PR, TZ, WA) were compared by the HSD.test function of the agricolae package in R [3].

RESULTS AND DISCUSSION

The Andean parents and the PIC lines were scattered in the PCA biplot, whereas five MA parents formed a tight cluster (Fig. 1). The new 12K SNP chip enabled finer characterization of the diversity of the Andean parents, compared to the original 6K chip, as was expected.

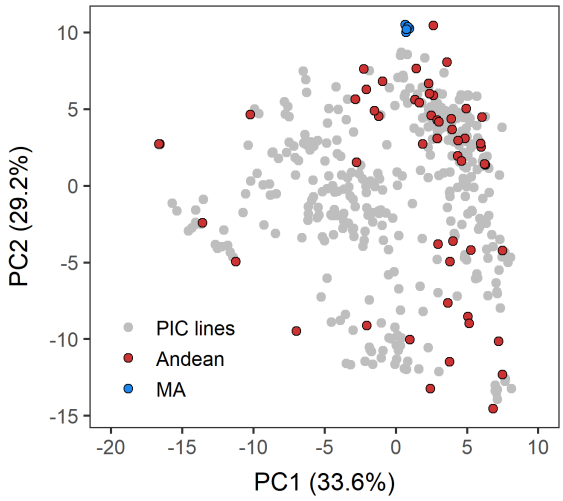

Figure 1. PCA biplot of 58 parental lines (red or blue) and 384 PIC lines (grey).

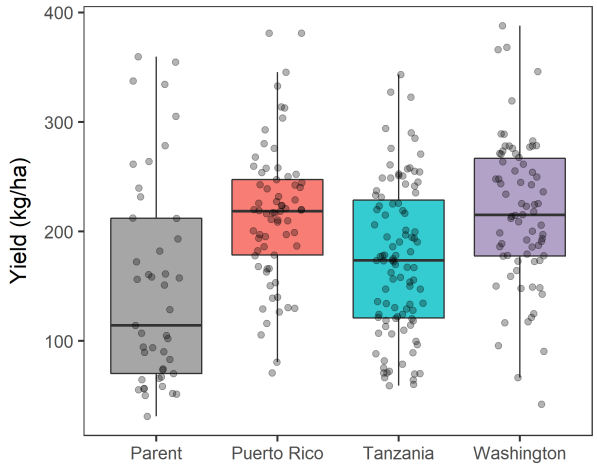

Figure 2. Yield distribution in PR drought trial for the 45 parents (grey) and 242 PIC lines grouped by which environment they were originally selected.

Table 1. The BLUP for seed yield of the parental lines and PIC lines selected in three environments, and the composition of the top 10% yielding lines (n=28) under severe drought in PR 2019.

Selection environment	n[1]	Mean yield (kg ha^{-1})	SD[2]	Number of top 10% yielding lines	% of lines included in top 10%
Parent	45	149.4 [b]	94.2	5	11
Puerto Rico	69	215.7 [a]	63.3	9	13
Tanzania	99	174.6 [b]	68.7	6	6
Washington	74	216.7 [a]	67.8	8	11

[1]Number of lines tested in PR, 2019; [2]Standard deviation. Means with the same letters are not significantly different (α=0.05).

The PIC lines selected in PR and WA had higher seed yield means than the parents and the PIC lines selected in TZ (Table 1, Fig. 2). The PIC lines from all three selection environments outperformed the parents, indicating yield improvement through recombination of favorable alleles from the parents. TZ PIC lines were selected under high disease pressure (rust, angular leaf spot, etc.) which may have contributed to their lower yield in the PR trial. The top yielding lines were of various origin as 11% of the tested parents, 13% of PR lines, and 11% of WA lines were included in the top 10% highest yielding lines. Conversely, only 6% of the TZ lines were in the highest 10% of yielding lines. Overall, the PIC lines showed general yield improvement in PR 2019. The yield trial data collected for these lines in PR in 2020 will be analyzed to examine performance across environments. It is expected that PIC lines with stable and high yields across environments will be released as germplasm lines or cultivars.

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ELITE BLACK DRY BEAN LINES ASSESSED IN ACID-PRONE SOILS OF TROPICAL SOUTHEASTERN MEXICO

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INTRODUCTION: In the humid tropics of southeastern Mexico, mainly in the states of Chiapas and Veracruz, low fertility acid soils with a pH below 5.5 limits the development and productivity of crops such as dry beans. In this type of soil, the plants present nutritional deficiencies caused by the constant leaching of calcium, magnesium, and potassium, as well as due to the low availability of phosphorus and, in some cases, the high concentration of exchangeable aluminum, which causes toxicity to the plants and root growth reduction (Zetina et al., 2002). Seed bean yields obtained in these strongly acid soils can be very low (<300 kg ha^{-1}), especially if there is a combined effect with drought (Tosquy et al., 2020). This work aimed to evaluate a group of recombinant black bean breeding lines to identify those that produce better grain yields under conditions of high edaphic acidity.

MATERIALS AND METHODS: Eleven dry bean breeding lines derived from three different crosses were evaluated in comparison to three control varieties (Negro Medellín, Negro Jamapa, and Verdín). The field trial was conducted in 2019-20 during the fall-winter growing season (September-January) under residual moisture conditions in four locations with high acidity soils: three in central Chiapas (Villa Corzo with a pH of 4.79, CECECH with a pH of 5.74 and El Gavilán with a pH of 4.26) and one in Veracruz (CEIXTA, Tlapacoyan with a pH of 5.18). The experimental design used was a RCBD with three replications and experimental plots that consisted of three rows 5 m long and 0.80 m between rows. The grain harvested from the central row of each experimental unit was cleaned and dried until it reached 14% humidity, then seed yield (kg ha^{-1}) was obtained. Analysis of variance by location and combined analysis of the four crop environments were performed; the least significant difference test (LSD, $\alpha = 0.05$) was used for the separation of means.

RESULTS AND DISCUSSION: Seed yield varied significantly between genotypes in all test locations (Table 1). In the combined analysis of variance, seed yield differed between environments ($P \leq 0.05$), genotypes ($P \leq 0.01$), and the interaction of both factors ($P \leq 0.01$). In the localities of El Gavilán (L3) and Villa Corzo (L1) in Chiapas and CEIXTA (L4) in Veracruz, average seed yields were statistically similar to each other but lower than that of CECECH (L2) (Table 1). This was mainly because of the strongly acidic soil conditions found in these locations, which limits the development and productivity of the crop due to the low availability of interchangeable bases (K+, Ca++, and Mg++), and in some cases, due to a high aluminum saturation (Zetina et al., 2002). In the genotype factor, the average seed yield obtained from eight elite lines and cultivar Verdín was similar among them but higher than check cultivars Negro Medellín and Negro Jamapa (Table 1). Of this group, the most productive breeding lines were Jamapa Plus/XRAV-187-3-4-4 and Negro Papaloapan/SEN 46-7-7, with average seed yields greater than 1,000 kg ha^{-1}. In contrast, cultivars Negro Medellín and Negro Jamapa and the elite line Negro Citlali/XRAV-187-3-1-5 were the most affected genotypes by soil acidity, with average seed yields of less than 800 kg ha^{-1} (Table 1). The highly significant effect of the G x A interaction

indicated that the seed yield response of some genotypes (G) varied with the environment (A). For instance, Negro Papaloapan/SEN 46-3-2 was the highest seed-yielding breeding line in El Gavilán (L3) under severe soil acidity (pH of 4.26), while in CECECH (L2), with moderate edaphic acidity (pH=5.74), the same breeding line was the least productive of all lines (Table 1).

Table 1. Average grain yield (kg ha^{-1}) of 14 black dry bean genotypes assessed in acid soils of four locations in Chiapas and Veracruz, tropical southeastern Mexico. Fall-winter, 2019-20.

T	Genotype	L1†	L2	L3	L4	Average seed yield
1	Negro Papaloapan/SEN 46-2-6	802.7	724.0	813.7	904.7	811.2
2	Negro Papaloapan/SEN 46-3-2	851.7	792.7	987.3*	1080.7*	928.1*
3	Negro Papaloapan/SEN 46-7-7	1079.3*	1268.7*	862.0*	947.0*	1039.5*
4	Negro Papaloapan/SEN 46-7-10	924.0*	1048.0	802.7	788.3	890.7*
5	Negro Papaloapan/SEN 46-7-12	756.7	1033.3	873.7*	928.0*	897.9*
6	Negro Citlali/XRAV-187-3-1-5	739.0	957.3	898.3*	537.3	783.0
7	Negro Citlali/XRAV-187-3-1-6	837.3	1154.7*	879.7*	896.3	942.0*
8	Negro Citlali/XRAV-187-3-1-8	887.3	1056.0	828.7	797.7	892.4*
9	Jamapa Plus/XRAV-187-3-1-2	810.0	1310.0*	848.7*	800.0	942.2*
10	Jamapa Plus/XRAV-187-3-4-1	681.3	860.0	747.3	882.0	792.7
11	Jamapa Plus/XRAV-187-3-4-4	1125.7*	1244.7*	897.0*	978.0*	1061.3*
12	Negro Medellín	737.0	754.0	680.7	877.0	762.2
13	Negro Jamapa	719.3	734.7	760.3	884.7	774.7
14	Verdín	903.3*	1042.7	858.0*	939.7*	935.9*
	Location average seed yield	846.8	998.6*	838.4	874.4	
	ANOVA	*	**	*	**	**
	CV (%)	15.9	14.9	10.2	11.8	13.6
	LSD (0.05)	226.4	250.4	143.7	173.9	171.3

†L1= Villa Corzo, Chiapas (pH=4.79). L2 = CECECH, Ocozocoautla, Chiapas (pH=5.74). L3 = El Gavilán, Ocozocoautla, Chiapas (pH=4.26). L4 = CEIXTA, Tlapacoyan, Veracruz (pH=5.18). *($P \leq 0.05$), **($P \leq 0.01$). *Seed yield values statistically higher than the other genotypes according to the LSD test (0.05).

CONCLUSIONS: Under the edaphic acidity conditions in Chiapas and Veracruz, Mexico the Jamapa Plus/XRAV-187-3-4-4 and Negro Papaloapan/SEN 46-7-7 elite lines were the most productive, with a significantly higher seed yield than the control cultivars Negro Jamapa and Negro Medellin.

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STUDY OF WATER USE TRAITS IN COMMON BEAN (*PHASEOLUS VULGARIS* L.) REVEALS CANDIDATE GENES IN RESPONSE TO DRYING SOIL

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INTRODUCTION

Common bean yields are affected by multiple environmental factors such as drought (Beebe et al., 2014). Plants exhibit diverse physiological responses to overcome water deficits. Stomatal closure and the subsequent reduction of transpiration rates are one of the main mechanisms to avoid excessive water loss. Variation in those stomatal dynamics has been observed in multiple crops which may lead to the development of new cultivars with improved water use. Thus, this study was aimed at studying the transpiration rate in common bean in response to drying soil under greenhouse conditions.

MATERIALS AND METHODS

A subset of 82 common bean accessions was selected from the Mesoamerican Diversity Panel (MDP) and evaluated in three independent experiments between 2013 and 2014 at Michigan State University following the methodology previously reported by Ray and Sinclair (1997) and Egan et al. (2021). At the beginning of each experiment, pots were saturated, and weight was measured. Pots were sealed at the bottom and top to avoid any water loss from runoff and evaporation. Daily pot weight was recorded and plants under control conditions were replenished up to saturation. Plants under drought treatment underwent a progressive dry-down with no water replenishment. Data from the three experiments (replicates) were jointly analyzed. Transpiration rate was calculated as the ratio between the weight of well-watered and non-watered plants and normalized (NTR) as previously described (Ray and Sinclair 1997). The fraction of transpirable soil water (FTSW) was determined as:

$$FTSW = \frac{(Daily\ pot\ weight - Final\ pot\ weight)}{(Pot\ weight\ on\ 1\ DAT - Final\ pot\ weight)}$$

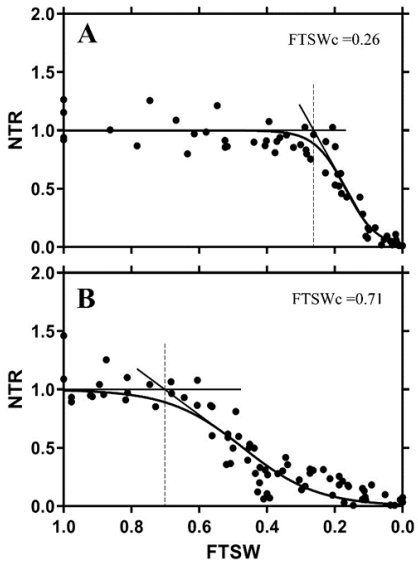
The relationship between NTR and FTSW was established for each genotype (Muchow and Sinclair, 1991). A linear-plateau regression was used to determine the critical FTSW (FTSWc) in each replicate, which is when the NTR starts decreasing linearly and indicates that stomata start to close in stressed plants.

As part of the MDP, the subset of evaluated accessions was previously genotyped (Moghaddam et al., 2016). A genome-wide association (GWA) analysis was performed using 182,243 SNPs with a MAF > 0.02 and the BLUP-adjusted means for the FTSWc, and the average NTR under water deficit for each genotype using the Fixed and random model Circulating Probability Unification (FarmCPU), and Bayesian-information and LD Iteratively Nested Keyway (BLINK). Haplotype blocks were analyzed and candidate genes were selected within a ± 100-Kb window centered on each associated SNP and based on previous reports.

RESULTS

The average NTR per genotype during the evaluation period ranged from 0.33 for Yolano to 0.96 in ABCP-8, with a global mean of 0.52 and a H^2 of 0.53. The FTSWc had a H^2 of 0.38 and varied

from 0.23 in the pink bean genotype Harold to 0.99 in the black bean T-39 with significant differences (p<0.05). Figure 1 shows the average response of NTR to drying soil for the top and the bottom five genotypes.



After FDR correction, two significant SNPs were found for FTSWc on Chr01 (ss33516386) and Chr07 (ss9224979). For NTR, two significant SNPs were found on Chr01 (ss28451384 and ss35489136). Previous studies on drought tolerance in common bean have identified QTLs on Chr01 and 07 (Dramadri et al., 2019). A total of 23 genes were identified for the four haplotypes, and 14 were selected based on their potential role in drought resistance. Interestingly, four genes are annotated as transcription factors. Our results provide novel information on the genetic architecture of drought tolerance in common bean and provide the bases for further studies of the physiological responses involved. Moreover, after validation, markers for assisted selection may be designed. Extended results and analysis can be found in pre-print (Cordoba-Novoa et al., 2022).

Figure 1. Average normalized transpiration rate (NTR) in response to the fraction of transpirable soil water (FTSW) in the five genotypes with the lowest FTSWc (A) and the highest FTSWc (B).

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STEM DIAMETER AND ITS RELATIONSHIP TO OTHER AGRONOMIC TRAITS IN DRY BEAN (*PHASEOLUS VULGARIS* L.)

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INTRODUCTION

Dry bean (*Phaseolus vulgaris* L.) has great importance in human nutrition, as it is considered an economical source of protein, especially in developing countries. Domestication has played an important role in changing different traits from the wild relative to its domesticated form, and one of the most important changes has been growth habit. Cultivated beans show more growth habit diversity compared to wild forms, which has led to classifying genotypes into four types (Singh, 1982). In the U.S., dry beans with Types I, II, and III are mainly cultivated, but in most cases, there is a preference for Type II indeterminate upright varieties. The U.S. is the third-leading dry bean producer in the world, and genetic improvement for upright plant architecture has helped farmers to easily switch from historic two-pass harvest to one-pass direct harvest (Eckert et al., 2011). Previous studies by Soltani et al. (2016) showed that stem diameter and plant height are highly correlated and could play an important role in selecting upright plants. They suggested a stem diameter value of 5.6 mm could be a threshold to select plants with less lodging and therefore, better Type II architecture for direct combining. However, this study was made with a diverse panel of genotypes. The objective of this study was to validate the correlation between stem diameter and other agronomic traits using breeding lines from a commercial program and further investigate stem diameter as a selection criterion to select genotypes that combine high seed yield and upright architecture.

MATERIALS AND METHODS

A total of 262 black, navy, great northern, red and pink, pinto, and slow-darkening (SD) pinto beans breeding lines and cultivars were tested in replicated advanced yield trials (AYT) at different locations of North Dakota, during 2020, 2021 and 2022. A randomized complete block design with 3 replications was used. Two rows per plot were harvested with a total effective plot size of 3 m^2. Plant height (cm), stem diameter (mm) were measured right above the soil surface at maturity, maturity, determined as days after planting, 100-seed weight (g), and seed yield (kg ha^{-1}) were measured. Combined analysis of variance across and within market classes was performed, with genotype, environment, genotype x environment (GxE), and block nested in each environment as sources of variation. Environment was considered as the combination of location and year. A mixed linear model was used where genotype was considered as a fixed effect while the other sources of variation were considered as random. Variance components were obtained using genotype, environment, and genotype x environment as random effects. Broad-sense heritability based on the entry mean was calculated. Pearson's correlations between agronomic traits were obtained. Single and multiple linear regressions were calculated using R to estimate seed yield variation due to plant height and stem diameter.

RESULTS

Genotype and environment showed highly significant differences ($P \leq 0.001$) across all market classes for all traits. Stem diameter showed two market classes with no significant GxE interactions, pinto and SD pinto. For stem diameter, mean values ranged between 7.6 and 8.0 mm, with the highest value for pinto (8.0) (Table 1). Overall, these values were higher than that

suggested by Soltani et al., (2016), which suggest that selection for upright architecture and low plant lodging within the breeding program may have indirectly increased stem diameter.

Table 1. Means for agronomic traits across environments (2020-2022).

Market Class	Stem Diameter	Plant Height	Maturity	100-Seed weight	Seed Yield
			Mean		
	mm	cm	d	g	kg ha^{-1}
Pinto	8.0 a	54 a	101 bc	35.0 b	1,754 ab
SD Pinto	7.7 b	50 cd	102 ab	35.7 a	1,664 bc
Red and Pink	7.6 b	52 ab	103 a	31.3 d	1,827 a
Black	7.6 b	50 cd	103 a	19.0 e	1,694 b
Navy	7.6 b	51 bc	101 c	17.9 f	1,582 cd
Great Northern	7.6 b	49 d	101 c	34.0 c	1,539 d

Broad-sense heritability estimates for stem diameter ranged between 0.43 for great northern and 0.87 for pinto. Pinto (0.87) and SD Pinto (0.84) were the two highest, which suggest that this trait is highly heritable and stable across environments for these market classes. Moderate correlations were found between plant height and stem diameter, ranging from 0.28 for great northern and 0.45 for navy, therefore, separate measurements are still necessary for these traits. Highest correlations in the study were found between plant height and seed yield in black (0.54), great northern (0.50), and navy (0.60). For these market classes, regression analysis found that plant height explained at least 24% of the variability in seed yield, while stem diameter was either non-significant or had no effect on seed yield. For pinto, red/pink and SD-pinto, plant height explained between 15% and 21% of seed yield variation, while stem diameter around 11%. Regressions confirm that both plant height and stem diameter are required to explain between 20 and 24% of seed yield variation for red/pink and both pintos. Then, even though stem diameter has high heritability and stability for pinto and SD-pinto, selection in these market classes should not rely only on this trait and therefore, plant height should be taken also into account. Results of this study suggest that plant height could be a better indicator for seed yield than stem diameter in black, great northern and navy. For pinto, red/pink and SD-pinto, both, plant height and stem diameter are required to continue selecting upright and high yielding plants. This study was supported by USDA-ARS Pulse Crop Health Initiative and Northarvest Bean Growers Association.

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SEED SIZE EFFECT ON SEEDLING ESTABLISHMENT IN WILD *PHASEOLUS VULGARIS* L.

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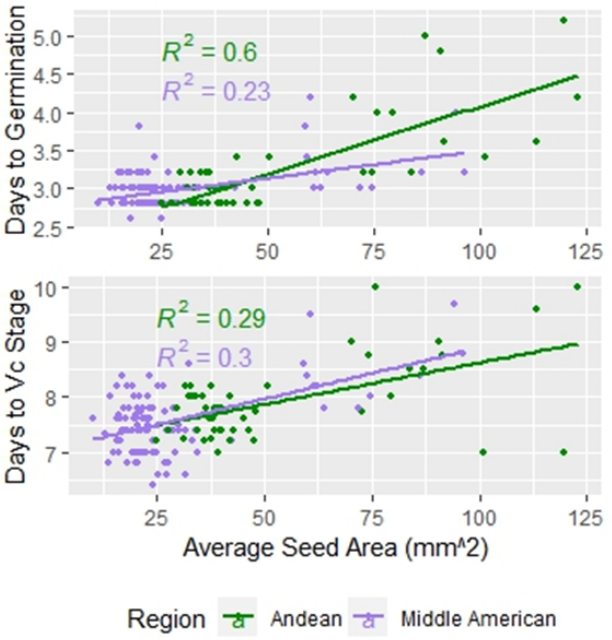
INTRODUCTION: Seedling establishment describes the developmental transition from heterotrophy to autotrophy. It has vital implications for uniformity in the field, onset of yield and harvest, advantages against pest or pathogen pressures, mitigation of drought, and overall resiliency. The relationship between seed size and seedling performance has been examined across many species, however, this relationship remains somewhat unclear. Some studies suggest that seed size impacts initial germination, growth rate, or overall plant fate and performance[1,2,3] while others show that the probability and timing of germination are not affected by seed size[4] or remains inconclusive[5]. For *Phaseolus vulgaris*, it is thought that seed size does impact early development and vigor, but this relationship remains somewhat difficult to elucidate.

While seed size has been attributed to favorable seedling characteristics, studies seem to diverge on the influence. The proposed mechanisms for understanding this relationship vary widely between species, but it is generally understood that seedling establishment is related to both the specific genotype present as well as the current environmental factors rather than a single determinant[6,7]. Amongst the many factors that influence seedling establishment, soil characteristics, individual plant genotype, environmental conditions, pest or pathogen pressures, and even possibly parental factors remain persistent drivers and determinants of this process[6]. While not necessarily contradictory, a lack of consensus between studies provides the basis for this work and the ongoing discussion regarding this relationship. In general, seedling growth rate is faster in small-seeded species while percent germination is higher in large-seeded species, but this relationship is species specific[8].

Phaseolus vulgaris has two domesticated events resulting in two major gene pools, Andean and Middle American[9]. Domestication bottlenecks have caused a decrease in genetic diversity[10], which can reduce adaptability to climate change. Cultivars from the Middle American gene pool tend to have smaller seeds than Andean cultivars, a trend which precedes domestication. When comparing growth rate and seed size of the two gene pools, it was expected that the Middle American seedlings established faster because of their smaller seed size. By analyzing the rate of seedling establishment within the different gene pools and seed size, context on the adaptability of wild beans can be collected.

MATERIALS AND METHODS: To study the relationship between seed size and establishment rate, 154 georeferenced accessions were provided by USDA Germplasm Resources Information Network. Of these 154 accessions, 105 were collected from regions within the Middle American native range, 47 were collected from regions within the Andean native range, and 2 were the cultivars Red Hawk and Stampede. Sixteen accessions in this data set had signs of domestication (e.g. increased seed size or white seed coat color). Twenty seeds were scanned and measured for area using ImageJ. Seeds from each accession were planted in individual rhizoboxes to monitor germination and root growth. The plants were scored daily as they reached five developmental stages: germination (radical emerged from seed), basal root emergence (basal roots emerged from the root crown), V_e stage (apical hook emerging from soil), apical hook straightening, and V_c stage

(unifoliate leaves unfurling). This experiment was repeated 5 times and scores were averaged for growth rates of each accession.



RESULTS AND DISCUSSION: Middle American seeds were smaller than Andean, but did not take notably longer to germinate or reach the V_c stage (Figure 1). Middle American seeds averaged 29.84 mm^2 with a range of 15 mm^2 to 25 mm^2. They germinated between 2.6-4.2 days and reached V_c in about 7.6 days. Andean seeds were larger averaging 53.6 mm^2 with a wider range, from 25 mm^2 to 75 mm^2, and took 2.8-5.2 days to germinate. Andean seeds reached the V_c stage at 7.9 days, on average. Interestingly, of the nine accessions that took over 4 days to germinate, all but one had evidence of domestication.

To test if the relationship between seed size and seedling growth differed between gene pools, Pearson correlations were determined at each developmental stage (Table 1, Figure 1). Overall, larger seeds took longer to germinate and reach the V_c stage; the smaller seeds reached autotrophy before the larger seeds. Andean seeds had a stronger positive correlation between seed size and all days to reach growth stage, until the V_c stage. At this stage, the relationship between seed size and growth rate no longer differed between gene pools. This could be explained by less seed size range in the Middle American seed set or by potential selection during domestication in the Andean seed set.

Table 1. Pearson correlation R^2 values between days to developmental stages and seed size separated by gene pool.

R^2 Values	Germination	Basal Root Emergence	V_e Stage	Hook Straightened	V_c Stage
Andean	0.60	0.43	0.46	0.46	0.29
Middle American	0.23	0.00045	0.00038	0.15	0.30

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ASIAN BEAN THRIPS OF FABACEAE IN ISABELA, PUERTO RICO

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INTRODUCTION

Megalurothrips usitatus is considered a recently introduced pest in the neotropical region, and particularly in the Caribbean, where its distribution began, to the extent that it is currently present in various countries. It has been documented in the literature that its preferred species are within the Fabaceae. Khan et al. (2022) mentioned the existence of 28 species of host plants that are among the Fabaceae. This thrip has been detected in Cuba in 2020, where it has been affecting various crops such as beans, soybeans and chickpeas (Ruiz, 2020). This pest is very aggressive, where it can cause production losses of 30% to 60% in some countries (Campos et al., 2023) (Khan et al., 2022). Therefore, it is important to be aware of the abundance and dispersion of the pest in different hosts. In areas infected by this pest in Isabela, Puerto Rico, high populations were found in common beans.

MATERIALS AND METHODS

The evaluation of the number of larvae and adults in a sample of Andean beans was carried out in a common bean nursery at the Experimental Station in Isabela, Puerto Rico. A preliminary evaluation of the populations of larvae and adults present in the organs of infested plants was carried out and a stereoscopic microscope was used. In this evaluation, the insect-plant relationship was classified according to the organs evaluated, including leaves, pods and meristems.

RESULTS AND DISCUSSIONS

In the evaluated common bean plants, the larvae and the adults developed to high numbers in the leaves, in the pods and meristems. The injured surfaces of these organs showed scars, tanned spots, as well as deformations in the affected organs (Fig. 1). The larvae were significantly more abundant ($p<0.0001$) than the adults in the leaves, pods and meristems (Fig. 2). The adults were found scattered and in low numbers in the three areas of the plant. Therefore, it is necessary to continue sampling dry and snap beans and other legume hosts in all areas of Puerto Rico to determine the abundance and dispersal pattern of this thrip species.

ACKNOWLEDGEMENTS

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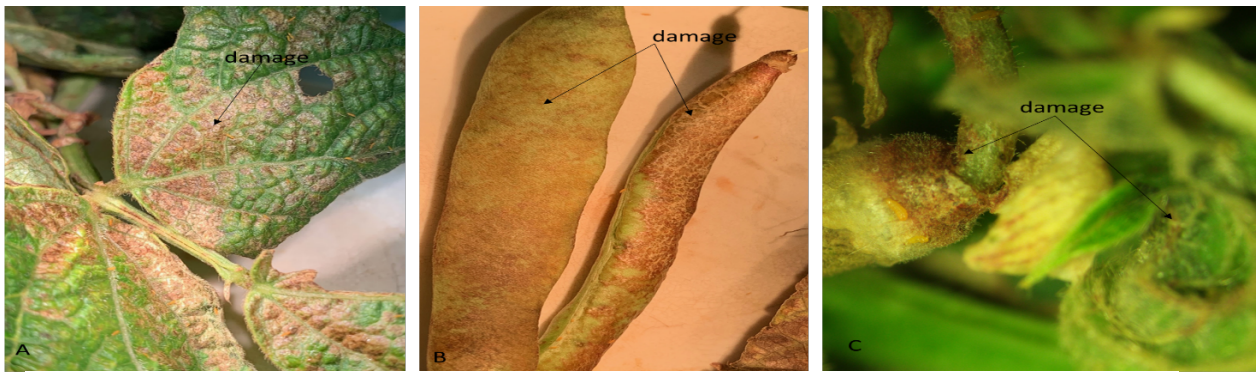

Figure 1. Damage of *Megalurothrips usitatus.* A) leaves, B) pods and C) meristems in Andean beans in Isabela, PR

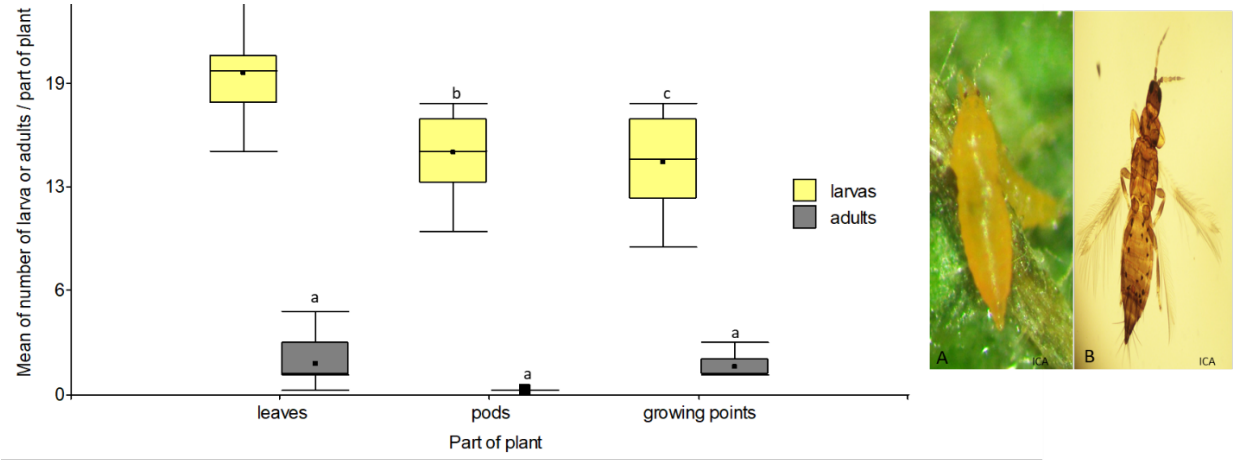

Figure 2. Numbers of larva and adults of *Megalurothrips usitatus* per leaf, pod and meristems. Results of the Anova for: Stage (larva and adults) F= 391.01, P<0.0001; Part of plant F= 63.21, P <0.0001; Stage*Part of plant F=40.33, P<0.0001. Bars represent means ± SD, bars with different letters indicate significant differences at, p<.05, (Di Rienzo et al. 2018). A) larva of *M. usitatus*, B) adult of *M. usitatus.*

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AGRONOMIC AND COOKING CHARACTERISTICS OF COMMON BEAN GENOTYPES WITH BRUCHID RESISTANCE AND MOLECULAR MARKER VALIDATION

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INTRODUCTION

For common bean (*Phaseolus vulgaris* L.) seed, the bean weevil/bruchid (*Acanthoscelides obtectus* Say) and the Mexican bean weevil/bruchid (*Zabrotes subfasciatus* Boheman) are the most important storage pests worldwide, resulting in a 48-100% loss in seed quality and quantity. This leads to market value loss, reduced germination rates and seedling vigor, and a threatened seed and food supply. Effective resistance to these bruchids was discovered in a tepary (*P. acutifolius* A. Gray) germplasm accession G40199 (Goossens et al., 2000). This resistance is hypothesized to be controlled by the APA locus on chromosome Pv04 and it is associated with related seed storage lectin proteins such as arcelin (ARC), phytohaemagglutinin (PHA), and alpha-amylase inhibitor (α-AI) (Kami et al., 2006; Kamfwa et al., 2018). The resistance has been successfully introgressed into common bean germplasm such as AO-1012-29-3-3A (Kusolwa et al., 2016). Screening for resistance is cumbersome and time-consuming (up to 60 days), so it is necessary to identify accurate diagnostic molecular markers to speed up variety development. A primary ongoing breeding objective has been to introduce bruchid resistance into commercial market classes of importance in Africa, such as reds, yellow, cranberry (sugar types), red-mottled, and purple-mottled (kabulangeti types), among others. At least three bruchid-resistant varieties have been released in Tanzania (Myers et al., 2021). However, is not clear if farmers have broadly adopted them. This study aimed to evaluate the agronomic and cooking characteristics of newly developed common bean genotypes with bruchid resistance and to validate an existing molecular marker (Mazaheri, 2018).

MATERIALS AND METHODS

Agronomic field evaluations were conducted in 2022 on 30 bruchid breeding lines (17 resistant and 5 susceptible, 6 resistant and susceptible parents, and 2 resistant checks) using a randomized complete block design with two replications at Hatton in North Dakota, USA. Because of low seed availability, the trial was planted using a one-row plot 4 m long and 0.76-m row spacing. Traits such as days to flowering and maturity were recorded at R2 and R6, respectively. Canopy height was measured at the R2 to R3 mid-pod-fill growth stage. Then, 100-seed weight and seed yield were obtained from the harvested rows. The lines were then evaluated for cooking time using a Mattson cooker. For validation of the molecular marker, an INDEL marker (α-AI) (Mazaheri, 2018) was run on the breeding lines to assess its effectiveness by comparing genotypic and phenotypic data.

RESULTS AND DISCUSSION

The ANOVA indicated significant differences for all agronomic traits ($P<0.05$, Table 1). The lines showed considerable genetic variation for days to flowering (42-65 days), maturity (104–129 days), and canopy height (30.0–50 cm). For all agronomic traits, some lines are potential

candidates either as new cultivars or improved germplasm. Preliminary results suggest that the APA introgression does not appear to affect cooking time. Finally, the α-AI marker amplified a DNA fragment with a 45 base pair insertion/deletion at the locus and was 100% accurate. This marker may be used to track APA introgression into susceptible lines (Figure 1). This work was supported by USAID Feed the Future Innovation Lab for Legume Systems Research.

Table 1. Grain yield and bruchid score at 60 days after infestation (DAI) of promising breeding lines evaluated in the field trial at Hatton, ND.

Genotype	Market Class	Score at 60 DAI	Grain Yield (Kg ha^{-1})	Cooking Time (Min)
AO-3A-ADP1-13	Purple Mottled	1.0	1523	35
AO-3A-LSK-11	Yellow (Njano)	1.7	1509	48
AO-3A-ADP725-27	Red speckled	1.2	1424	50
AO-3A-ADP1-2	Red Mottled	1.5	1240	45
AO-3A-ADP763-86	Red speckled	1.0	1217	56
AO-3A-ADP1-51	Brown	1.2	1205	47
AO-1012-29-3-3A	Red (Check)	1.5	980	43
			LSD P<0.05=719	LSD P<0.05=17

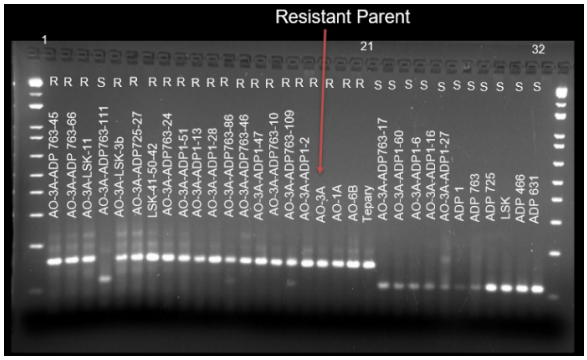

Figure 1. Differences in PCR products generated using the α-AI-1 marker with resistant parent AO-3A (AO-1012-29-3-3A), susceptible parents, ADP763, ADP725, and ADP1, $F_{5:6}$ Resistant (1-21) and susceptible (22-32) breeding lines progeny on 3% Agarose gel. A 1kbp ladder was used.

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EVALUATION OF COMMOM BEAN GENOTYPES FOR ORGANIC CULTIVATION IN RIO GRANDE DO SUL, BRAZIL

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INTRODUCTION

Ecologically and organically based systems represent an evolution to conventional agriculture in view of the need to use renewable inputs that do not negatively impact agroecosystems. The readjustment of bean production systems involves the use of management practices that are friendly to the environment and the replacement of inputs. However, there is a need to define and adopt a set of management practices to obtain adequate productivity (Bevilaqua, et al., 2021). The identification of genotypes adapted to the organic system is of great importance in the scenario of conventional agriculture, whose varieties were developed to respond to high solubility fertilizers and the wide use of pesticides. Common bean (*Phaseolus vulgaris*) cultivars from Embrapa Clima Temperado were developed with several characteristics that make them adapted to these types of production systems (Antunes et al., 2017). On the other hand, farmers have used a wide range of ecologically-based inputs whose characteristics and use in organic agriculture have been sought in research, such as biofertilizers (Goncalves et al., 2008). The objective of this work is to verify the adaptability of common bean genotypes to ecologically based systems used in Rio Grande do Sul.

MATERIAL AND METHODS

An evaluation trial was carried out with 26 genotypes, at the Cascata Experimental Station, of Embrapa Clima Temperado, using a Federer augmented block design. The Cascata area is traditionally dedicated to the organic cultivation of various crops of interest to family farming. The controls used were the cultivars BRS Intrépido and BRS Paisano. In the management of the area, black oat and vetch cover crops were used, conducted in winter, with semi-mechanized cultivation. For base fertilization, 500 $kg.ha^{-1}$ of turkey manure was used. Previously, the area had been corrected with limestone, natural phosphate and basalt powder, within a rotation program with other annual crops, mainly maize and cassava. The row spacing was 0.5m and the sowing density was 250,000 plants ha^{-1} (Araujo et al., 1996).

RESULTS AND DISCUSSION

In Figure 1 the grain yields of the evaluated genotypes are presented and it is verified that Guapo Brilhante, PGR II and Agudo 0220 genotypes presented results above the controls and the other evaluated genotypes. The cultivar Guapo Brilhante, recommended for conventional cultivation in the 1990s, stood out, reaching a grain yield of 4,200 kg ha^{-1}, while the best control, cultivar BRS Paisano, yielded approximately 3,000 kg ha^{-1}. The genotype PGR II also stood out in terms of grain yield, demonstrating the effectiveness of using populations with a broad genetic base to obtain high yields in organic systems, and such populations may also have better tolerance to pests and diseases (Antunes et al., 2017). The Agudo 0220 genotype, selected from landrace germplasm, showed higher yield than the controls too. The genotypes Bico de Ouro, Chocolate, Preto Ibérico, Vermelho Escuro, Manoel João, Rosinha 415, Pérola, Guardião TB 0223 and BRS Campeiro showed lower grain yield than the controls. Those genotypes with color grain or high thousand-seed weight such as Vermelho Escuro, Manoel João, Rosinha 415 and Bico de Ouro, must be compared and should be also evaluated as varieties with qualifications in terms of consumption

preference and nutritional quality. Under organic cultivation, a fundamental point is the choice of the area that presents a low occurrence of weeds that are difficult to control, avoiding humid areas or with strong wind, preferably with east-north exposure and one of the main necessary practices is the use of cover crops preceding cultivation, such as black oat (*Avena strigosa*), vetch (*Vicia sativa*), rye (*Secale cereale*) and fodder radish (*Raphanus sativus*) (Bevilaqua et al., 2021). No visible symptoms of anthracnose and occurrence of pests were observed in the experimental plots, not requiring corrective measures.

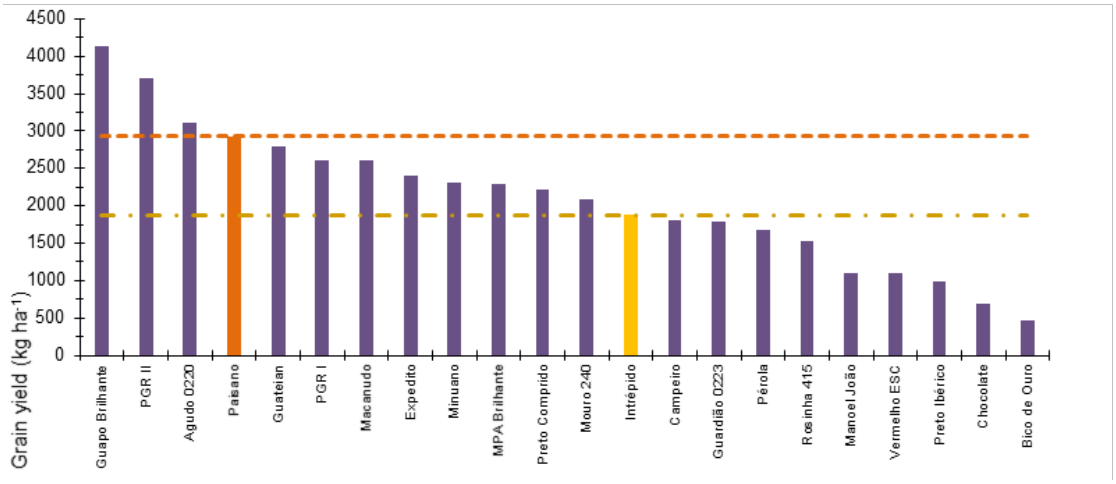

Figure 1. Adjusted means of grain yield of common bean genotypes under organic cultivation. Cascata Experimental Station. Embrapa Clima Temperado, Pelotas, RS, 2023.

CONCLUSIONS

The commom bean genotypes Guapo Brilhante, PGR II and Agudo 0220 showed higher grain yield than the controls and other evaluated genotypes and can be indicated for cultivation in organic systems, with the cultivar Guapo Brilhante reaching approximately 4,200 kg ha^{-1}. The cultural practices adopted are essential to achieve an adequate grain yield, with a low incidence of diseases and pests, which allow the organic certification of production.

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COMMON BEAN AS A COMPONENT IN RAINFED AGROFORESTRY SYSTEMS IMPLEMENTED IN THE SEMIARID HIGHLANDS OF MÉXICO

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INTRODUCTION: Artisanal and industrial production of maguey (*Agave* spp.) spirits have acquired productive, ecological, and economic importance in Durango, Zacatecas, and other states of the Semiarid Highlands of México. Under intensive cropping systems, the maguey growth period between plantation and flowering (vegetative phase) requires eight to twelve years until the harvest (jima) is performed before the stalk (quiote) development. In commercial and intensive maguey plantations established in Durango spaces between maguey plants and between rows are underutilized during several years, thus productive options are required by producers to obtain food and fodder for human and cattle feeding. Common bean (*Phaseolus vulgaris* L.) is an important food crop due to its multiple benefits for soil fertility, economic income for farmers, and nutritive traits for humans, mainly related to the seed protein content (Yadav and Raverkar, 2021). Corn (*Zea mays*) and oat (*Avena sativa*) are among the most important crops for grain (mainly corn) and fodder production in the Highlands of México (Montemayor et al., 2012; Sánchez et al., 2014). For all these crops improved cultivars were released to increment adaptation under rainfed conditions, also showing disease resistance for plant pathogens present in agricultural systems. The objective was to evaluate fodder (maize and oat) and seed (common beans and maize) yield in plant species adapted in maguey agroforestry systems implemented at the Semiarid Highlands of Northern México.

MATERIALS AND METHODS: During 2022, an agroforestry commercial plot was established in the state of Durango, México. Maguey cenizo (*Agave durangensis*) intensive plantations were used as the main crop, to evaluate adaptation and yield of three annual plant species such as: common bean cv. Pinto Centauro, maize cv. CAFIME and oat cv. Turquesa. Maguey plantation was established 15th July, 2022, using rectangular system with 4 m between lines and 3 m between plants. Agricultural crops were established on August 3rd in the spaces between maguey plant lines. Crop plants were sown in two row strips (common beans and maize), 150 m in length and 0.81 m apart, while oat was planted in 2.6 m wide beds and 0.15 m among plant rows. Three fertilizer treatments were applied once during vegetative phase: organic, chemical granulated and foliar with four replications. Chemical granulated fertilizer was applied at the dose 35-50-00 (for N-P_2O_5-K_2O) in common beans, 120-60-00 for oat and 200-90-00 for maize. Organic treatment consisted in 6 t ha^{-1} of compost mechanically incorporated into the soil. Foliar fertilizer mix (6 L/ha UAN 32® + 5 L/ha FertigroP®) was also sprayed at vegetative phase. Herbicide [fomesafen (common bean) and 2,4-D amine (maize and oat)] was sprayed once for the control of weeds and insecticide (dimethoate) was also applied for pod weevil (*Apion* sp.) control in common beans. Data were taken for fodder (seed filling period) and seed yield estimations (maturity), using four plant samples harvested in maize and oat for forage and common bean and maize for grain yield. For oat, forage samples consisted in a bed 2.0 m in width and 3 m in length (6.0 m^2). In maize and common bean, samples consisted of two rows, 5 m in length by 0.81 m in width (8.1 m^2). The analysis of variance was obtained by plant species under a completely randomized design with four replications and mean comparisons were performed using the Tukey's test ($p \leq 0.05$), in both cases using the computer program SAS ver. 9.4®.

RESULTS AND DISCUSSION: In each crop species, significant differences ($p \leq 0.05$) were detected among treatments only for forage yield in maize and oat (Table 1). The mean forage yield in maize was higher in the organic (12.6 t/ha) and chemical (12.2 t/ha) treatments compared to foliar applications (9.2 t/ha). Similar results were obtained in oat therefore higher fodder yields were registered in the chemical (3.7 t/ha) and organic (3.5 t/ha) treatments, overpassing foliar spraying (2.7 t/ha). No significant differences were observed for the mean seed yield obtained in common beans (2.1 t/ha), since greater variation was observed in maize from 1.4 t/ha under foliar spraying to 1.7 t/ha in the chemical (granulated) treatment. Common bean represent an important productive option during maguey vegetative growth period, obtaining additional feeding, nutritional and economic benefits, as well as for soil fertility maintenance.

Table 1. Fodder and seed yield in annual crops sown in an intensive maguey cropping system established in Semiarid Highlands, México. 2022.

Plant species	Chemical Fertilizer		Organic Amendment		Foliar Spraying	
	[1]FY (kg/ha)	SY (kg/ha)	FY (kg/ha)	SY (kg/ha)	FY (kg/ha)	SY (kg/ha)
Common Bean	--	2.1	--	2.1	--	2.1
Maize	12.2[a]	1.7	12.6[a]	1.6	9.2[b]	1.4
Oat	3.7[a]	--	3.5[a]	--	2.7[b]	--
Average	**8.0**	**1.9**	**8.1**	**1.9**	**6.0**	**1.8**

[1]FY = forage yield, SY = seed yield. [a-b]Different letters in rows indicate statistically significant differences (Tukey; $p \leq 0.05$) between treatments.

Due to the short period of evaluation, all the treatments resulted statistically similar for maguey plant height and rosette diameter, in spite of variations observed between evaluation dates from 20.9 cm to 25.9 cm in plant height. In each treatment, rosette diameter also showed increments between evaluation dates: 1st (19.9-21.6 cm) and 2nd (24.3-26.4 cm). Results showed that after maguey plantation under field conditions rosette diameter registered growth priority to broaden the plant photosynthetic apparatus and produce photoassimilates that sustain root and apical growth.

CONCLUSIONS: Common beans represent the best productive option in maguey agroforestry systems implemented at the Semiarid Highlands of México.

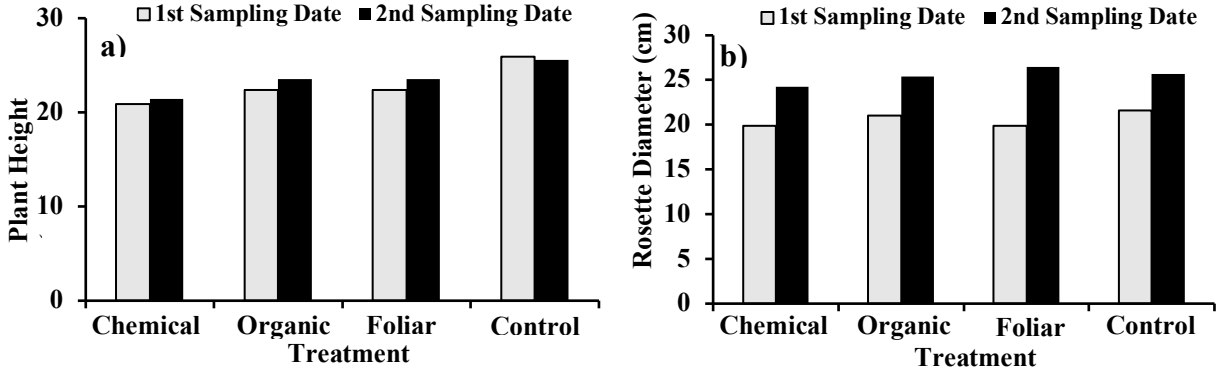

Figure 1. Plant height (a) and rosette diameter (b) at two evaluation dates in maguey (*Agave durangensis*) plants grown in an intensive commercial plantation established in Durango, México.

IMPROVED SEED YIELD IN COMMON BEANS BY BIOMASS INCORPORATION INTO DEGRADED SOILS IN THE MEXICAN HIGHLANDS

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INTRODUCTION: Degraded soil is a common condition observed in common bean producing areas in the Semiarid Highlands of Northern México (Reyes et al., 2019). Degradation includes low organic matter content and low nutrient availability related to increased pH values (>7.9). Degraded soils are combined with low input agriculture performed in the Mexican Highlands resulting in low seed yield in common beans. Farmers apply chemical fertilizers (granular or liquid) only when an acceptable amount of rain (> 200 mm) is registered between the planting and flowering period of common bean. Under these conditions, organic matter incorporation is recommended to obtain constant and long-lasting increments in common bean seed yield, also reducing problems caused by drought and low soil fertility. The organic matter incorporation must be combined with crop breeding and other low-cost, efficient, and agroecological strategies to perform sustainable production of common beans in Northern México. The objective was to evaluate common bean seed yield improvement related to organic matter incorporation into degraded soils at the Semiarid Highlands of Northern México.

MATERIALS AND METHODS: During the years from 2019 to 2022, six experimental plots were established at different locations in the common bean production area of the state of Durango, México. Two common bean cultivars (Pinto Saltillo and Negro San Luis) were sown at experimental and commercial plots in the municipalities of Durango, Canatlán, Cuencamé and Poanas. Biomass or compost (organic matter) was incorporated into the soil to be compared to the chemical fertilizer in granular and liquid forms. Organic treatment consisted in 6 t/ha of maralfalfa (*Pennisetum* sp.) dry biomass or commercial compost products mechanically incorporated into the soil. Chemical granular fertilizer was applied at the rate of 35-50-00 (for N-P_2O_5-K_2O). Liquid fertilizer (6 L/ha UAN 32® + 5 L/ha FertigroP®) was sprayed during the pre-flowering and pod set stages. In Durango and Canatlán, supplementary irrigation was applied once, and insecticide (dimethoate or spinetoram) was sprayed (up to four times) to control the common bean beetle (*Epilachna varivestis*) and pod weevil (*Apion* sp.). Seed yield was obtained from an area 5 m long and 0.81 m wide (8.1 m^2) replicated five times. The seed yield data were used for the analysis of variance (ANOVA) obtained under a completely randomized design using a factorial design and five replications. Analyses of adaptability and stability were also performed, in both cases using the SAS ver. 9.4® computer program.

RESULTS AND DISCUSSION: Similar results were registered for seed yield between complementary nutrition systems and common bean cultivars (Figure 1). Only slight (non significant) differences were observed between common bean cultivars for seed yield among plant nutrition systems, and higher values (1,929 to 2,156 kg/ha) were registered in Negro San Luis, mainly due to biomass incorporation into the soil combined with the full-length life cycle (115 days after planting; DAP). Pinto Saltillo showed lower seed yields with values between 1,853 kg/ha to 1,917 kg/ha related to intermediate maturity (96 DAP). For each increase in Environmental Index (EI), higher but not significant seed yield increments were registered in soils treated with biomass incorporation, mainly in the full-season cultivar (Negro San Luis) (Figure 2). Higher values for seed yield in Negro San Luis were observed for the organic system with values from 915 kg/ha in the less productive environment to 3,498 kg/ha in the most productive site.

Liquid fertilizer application caused low yields in Negro San Luis (687 kg/ha to 2,695 kg/ha), however, it was statistically similar to those obtained using of chemical fertilizer 766 kg/ha to 2,700 kg/ha. Organic matter incorporation into the soil must be considered as a low cost and sustainable system related to yield increases in the Semiarid Highlands of México. Early biomass application date (before planting) needs to be evaluated for the efficient use of organic matter by the common bean plants showing different number of days to physiological maturity.

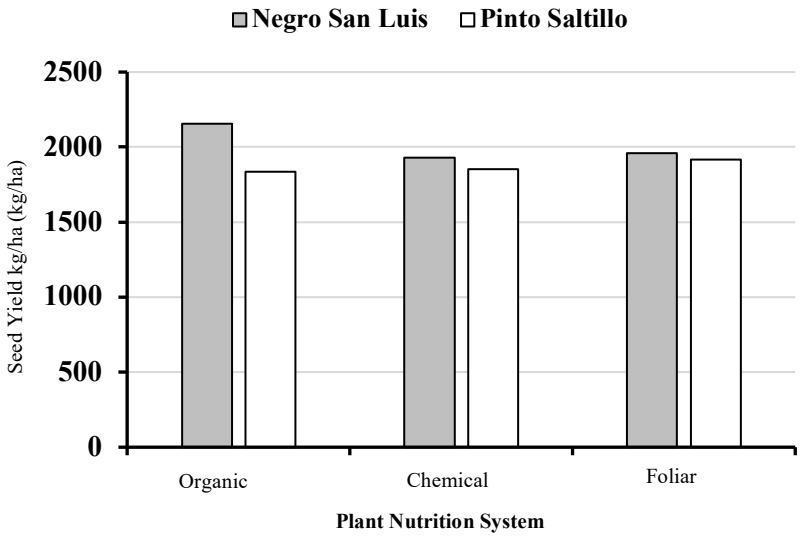

Figure 1. Effects on yield in two common bean cultivars of organic matter incorporation into the soil compared to traditional methods of plant nutrition.

CONCLUSIONS: Although the observed a trend, it was not statistically significant, with post-emergence incorporation of organic matter having a positive effect on seed yield of common beans, mainly in the late maturity cultivar (Negro San Luis). Liquid fertilizer favored the intermediate maturity cultivar (Pinto Saltillo). It is necessary to adjust the application date (pre-planting) of organic matter to optimize seed yield and promote sustainable agriculture in common beans.

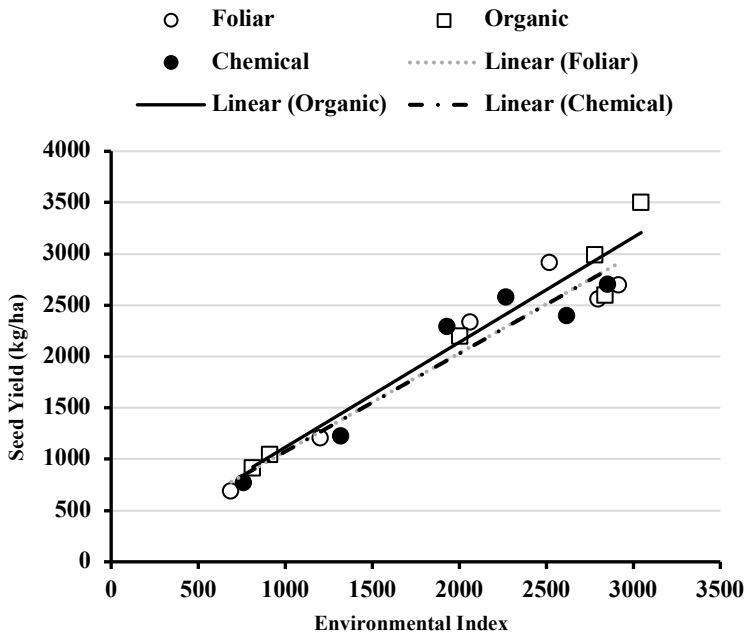

Figure 2. Effects on yield of Negro San Luis common bean cultivar of organic matter incorporation into the soil compared to traditional methods of plant nutrition.

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YIELD RESPONSE OF DRY BEANS TO ORGANIC AND INORGANIC FERTILIZERS AND BIOFERTILIZER

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INTRODUCTION: Common bean is widely adapted to a wide range of environments, grown in latitudes between 52°N to 32°S in the humid tropics, in the semi-arid tropics and even in the cold climatic regions (Beebe, 2012). By 2050, an increase in cereal food supply is required to feed the predicted world population of 9.8 billion people. Common bean, like other crops, is affected by many external and internal factors (soil fertility degradation, less fertilizer use, soil properties, drought, weeds and pests, lack of genetic improvements etc.), that decrease yield potential (Rurangwa et Bernard, 2020). The objective of this study undertaken by the Vegetable and Protein Research Program (VPRP) of the National Center for Agronomic Research (CNRA) and PABRA was to assess the response of dry bean to different levels of organic, inorganic fertilizers and biofertilizer.

MATERIALS AND METHODS: Seven treatments were used on 3 bean varieties [SMR53 (Hari25/GHA19), Roba1 (Hari35/GHA19) and Zabra (Hari36/GUI20)] as follow: Dose 0 (Control), Dose 1 (100 kg of NPK/ha before sowing), Dose 2 (50 kg/ha Urea 2 weeks after sowing), Dose 3 (reference dose,100 kg/ha of NPK before sowing + 50 kg Urea 2 weeks after sowing), Dose 4 (5 t of organic manure/ha before sowing), Dose 5 (10 t organic manure/ha before sowing), Dose 6 (Green Humico 500 ml in 16 l of water ; this corresponds to 12 l of Green Humico/ha).

SMR53 (HARI25/GHA19) Roba1 (HARI35/GHA19) Zabra (HARI36/GHA19)

Figure 1. Seeds of three (3) dry bean varieties proposed for the fertilizer tests.

RESULTS AND DISCUSSION: For the variety SMR53, yields varied from 0.44 to 1.13 t/ha. The best performance were found with Dose 4 (5 t organic manure/ha before sowing) and Dose 6 (Green Humico 500 ml for 16 l of water; 12 l/ha) which produced, respectively, 1.07 t/ha and 1.13 t/ha (Table 1). Concerning the variety Roba, yields ranged from 0.46 to 1.22 t/ha. The highest yields were obtained with Dose 2 (50 kg/ha of Urea for 2 weeks after sowing) which generated 1.22 t/ha (Table 2). As for variety Zabra, the yields have evolved from 0.5 to 1.25 t/ha. The optimal doses were Dose 3 (100 kg/ha of NPK before sowing + 50 kg Urea 2 weeks after sowing) and Dose 4 (5 t organic manure/ha before sowing) with yield, respectively, of 1,25 t/ha and 1,11 t/ha (Table 3).

Table 1. Flowering time, number of nodules per plant, 100-seed weight and yield for SMR53

Variety	Treatment	Flowering time (JAS)	Nodules number/plant	100 seed weight (g)	Yield (t/ha)
SMR53	DO	36±0,00	4,66±2,60	24,33±2,88	0,61±0,33
SMR53	D1	36±0,00	9,66±7,75	25,33±1,15	0,44±0,07
SMR53	D2	36±0,00	10,33±7,35	28±3,46	0,72±0,75
SMR53	D3	36±0,00	07,00±1,73	25,66±0,57	0,56±0,39
SMR53	D4	36±0,00	09,66±4,63	24,66±3,21	1,07±0,42
SMR53	D5	36±0,00	09,00±2,08	26,33±1,52	0,72±0,32
SMR53	D6	36±0,00	10,66±0,33	25,66±1,52	1,13±0,15
	Means	36±0,00	7,56±1,25	27,11±6,62	0,83±0,51
	Probabilities	-	0,987365	0,000000	0,900816
	CV (%)	-	16,52	24,42	60,71

Table 2. Flowering time, number of nodules per plant, 100-seed weight and yield for Roba1

Variety	Treatment	Flowering time (JAS)	Nodules number/plant	100 seed weight (g)	Yield (t/ha)
ROBA 1	DO	32±0,00	3,66±3,66	25,00±9,64	0,79±0,31
ROBA 1	D1	32±0,00	1,00±0,93	18,66±2,08	0,69±0,24
ROBA 1	D2	32±0,00	1,66±1,66	20,00±2,00	1,22±0,15
ROBA 1	D3	32±0,00	14,33±13,83	21,66±3,21	0,96±0,20
ROBA 1	D4	32±0,00	9,33±6,98	21,00±2,64	0,95±0,58
ROBA 1	D5	32±0,00	14,66±14,16	20,66±0,57	0,96±0,33
ROBA 1	D6	32±0,00	3,66±3,17	20,00±2,64	0,46±0,17
	Means	32±0,00	7,56±1,25	27,11±6,62	0,84±0,06
	Probabilities	-	0,987365	0,000000	0,900816
	CV (%)	-	16,53	24,42	7,14

Table 3. Flowering time, number of nodules per plant, 100-seed weight and yield for Zabra

Variety	Treatment	Flowering time (JAS)	Nodules number/plant	100 seed weight (g)	Yield (t/ha)
ZABRA	DO	32±00	10±10,00	34,33±4,04	0,763±0,22
ZABRA	D1	32±00	4,33±2,03	33,33±5,53	0,92±0,13
ZABRA	D2	32±00	5,00±,100	34,66±4,16	0,87±0,72
ZABRA	D3	32±00	2,00±0,95	37,33±2,52	1,25±1,23
ZABRA	D4	32±00	9,00±4,04	34,66±2,52	1,11±0,66
ZABRA	D5	32±00	11,33±7,33	37,66±3,06	0,75±0,46
ZABRA	D6	32±00	8,00±6,00	32,00±00,0	0,50±0,46
	Means	32±00	7,56±1,25	27,11±6,62	0,83±0,51
	Probabilities	-	0,987365	0,000000	0,900816
	CV (%)	-	16,53	24,42	61,45

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DICAMBA HERBICIDE DRIFT TOLERANCE ACROSS DRY BEAN MARKET CLASSES UNDER GREENHOUSE CONDITIONS

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INTRODUCTION

Dicamba (3,6-dichloro-2-methoxybenzoic acid), is a benzoic acid herbicide for post-emergence control of broadleaf weed species in monocot grain crops (Cao et al., 2011). In the plant, dicamba mimics the action of the natural auxin indole-3-acetic acid, and causes abnormal cell division and growth. Aside from crops with engineered resistance, such as dicamba-resistant (DR) soybean (*Glycine max* L. Merr.), most broadleaf crops are sensitive to dicamba, including dry beans. The introduction of DR crops and concomitant increase in the use of dicamba due to the prevalence of glyphosate-resistant weed species have increased the risk for injury to sensitive crops in nearby fields from off-target movement of dicamba (Soltani et al. 2020). In dry bean, seed yield losses of 5, 10 and 15% have been reported with dicamba application rates of 3.7, 9.8 and 17.9 g ae ha^{-1}, while seed weight has been reduced by 10% when 56 g ae ha^{-1} of dicamba was applied in navy and black beans (Bales and Sprague, 2020). Despite the development of new lower volatility formulations such as N,N-bis(3-aminopropyl)methylamine (BAPMA) dicamba, off-target movement of dicamba due to particle drift, tank contamination, and post-application volatilization remains a challenge (Riter et al., 2021). This study aims to evaluate the effect of dicamba off-target injury across different market classes of dry beans under greenhouse conditions.

MATERIALS AND METHODS

The current study was conducted at the Agricultural Experiment Station Research Greenhouse Complex at North Dakota State University in 2022 and 2023. A set of 81 dry bean cultivars from different market classes, including pinto, navy, black, great northern, white kidney, light red kidney, and dark red kidney beans were grown in 1-L plastic pots and were sprayed with a one-time application of herbicide when they reached the first fully expanded trifoliate stage (V1). All the genotypes were replicated thrice using a complete randomized block design. Plants were sprayed using a track spray booth equipped with a TeeJet 8002E flat-fan nozzle delivering 140 L ha^{-1} pressurized to 206.84 kPa (deVries Manufacturing). To simulate off-target herbicide concentrations, plants were sprayed with 1% of the average recommended label rate for DR soybeans (5.6 g acid equivalent (a.e.) per ha). The effect of dicamba exposure on the plants was scored based on the level of injury using a visual scale of 1-5 (Figure 1) after 2, 3 and 4 weeks of the herbicide application.

RESULTS AND CONCLUSION

Preliminary results have shown that dicamba injury symptoms were observed across all market classes one week after herbicide application. The most noticeable injury symptom was downward cupping of both unifoliate and trifoliate leaves. Initiation of newly developed leaves and lateral shoots were observed for the majority of pinto, navy, black and great northern beans two weeks after herbicide application. Averaged results from 2nd, 3rd and 4th weeks after herbicide application showed that pinto beans were slightly more tolerant to dicamba followed by navy and black beans with the average score between 2 to 3 (Figure 1). Contrastingly, kidney beans exhibited severe plant deformation, leaf cupping, leaf chlorosis and necrosis with an average score between 3 and

4 (Figure 1). Furthermore, breeding lines and cultivars developed at North Dakota State University will be tested under both greenhouse and field conditions, while a genome wide association study will be conducted to identify candidate genes for dicamba tolerance.

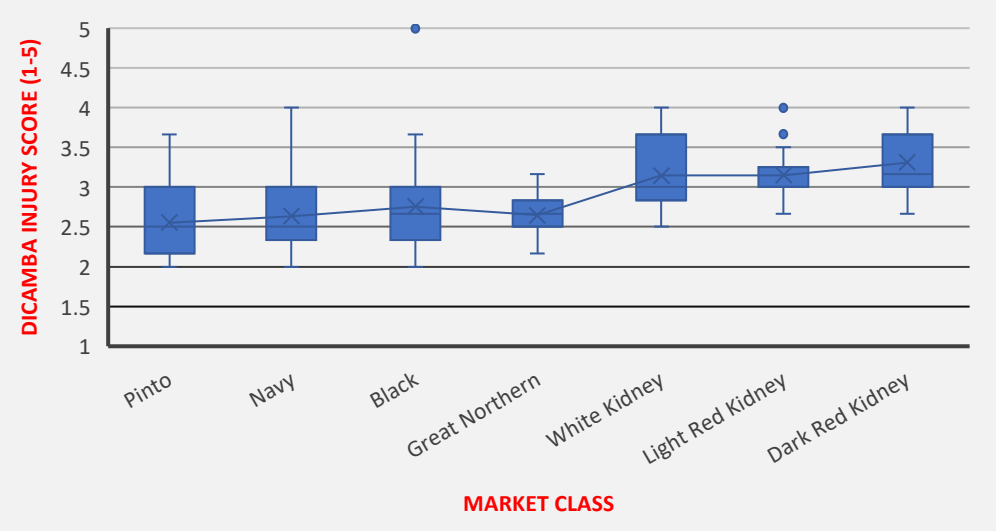

Figure 1. Visual ratings of commercial dry bean cultivars to dicamba herbicide injury based on a 1–5 visual scale*.

***Dicamba injury score: 1-5:*1**= No effect, growth normal **2**= Slight cupping of terminal leaflets, terminal bud death while the re-initiated buds have normal growth **3**= Leaflets of two terminal leaves cupped, terminal bud death, re-initiated buds have slow growth with cupped leaves **4**= Strongly malformed shoot development, leaves mostly chlorotic and necrotic **5**= Complete plant death.

ACKNOWLEDGEMENTS

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GENETIC FACTORS INFLUENCING SNAP BEAN TOLERANCE TO SEVERAL SOIL-ACTIVE HERBICIDES

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INTRODUCTION: Weeds in snap bean (*Phaseolus vulgaris*) compete for limited resources, interfere with machine harvest, and can contaminate consumer products. Weeds of the genus *Amaranthus* are particularly troublesome because most herbicides registered on snap bean are ineffective and, at harvest, stems of waterhemp (*Amaranthus tuberculatus*) break into bean-sized fragments which can be difficult to remove from consumer products. Certain soil-active herbicides suppress emergence of many *Amaranthus* species for several days or more, including inhibitors of protoporphyrinogen oxidase (PPO), photosystem II (PSII), and very long chain fatty acid synthase (VLCFA). However, registration of herbicides from these sites of action on snap bean is limited in large part due to concern of crop injury. A greater understanding of crop tolerance to such herbicides would be essential to future registrations. The objectives of this research were to 1) quantify snap bean tolerance to PPO-, PSII-, and VLCFA-inhibiting herbicides, and 2) determine genomic regions associated with crop tolerance.

MATERIALS AND METHODS: The SNap Bean Association Panel (SNAP) representing up to 377 snap bean genotypes, and genotyped with 20,619 single nucleotide polymorphisms (SNPs), was used in field trials. The panel represents germplasm from two centers of diversity: Mesoamerican and Andean populations. Field experiments were conducted in Urbana, IL from 2019 to 2022. Herbicides that were tested included PPO-inhibitors (flumioxazin, lactofen, saflufenacil, and sulfentrazone), a PS-II inhibitor (metribuzin), and a VLCFA-inhibitor (pyroxasulfone). The experimental design was a strip plot with three replications. Each block consisted of vertical strips of a cultivar and horizontal strips of an herbicide. A nontreated control was included. Herbicides were applied at a 2X field use rate for soybean within one day of planting, except for saflufenacil rate (0.5X). Snap bean seedlings were counted three weeks after planting (WAP) to determine plant density (PD). Also at three WAP, three plants were randomly selected, cut at the soil surface, and dried until constant weight to determine biomass per plant (BP). Herbicide tolerance was calculated as a percent of the nontreated control. All herbicides were tested in trials across two years.

Genome Wide Association (GWAS) analysis was used to identify genomic regions associated with tolerance to each herbicide. Analyses were conducted using seed weight as a covariate.

RESULTS AND DISCUSSION: *PPO-inhibitors*: Snap bean is inherently tolerant to lactofen, as evidenced by minimal or no crop response to the herbicide across 377 cultivars in two environments. Lactofen is registered for use in Oregon and Tennessee. Given the high margin of crop safety, this work supports the effort to develop a federal label for snap bean lactofen use. The other PPO-inhibiting herbicides were injurious to certain cultivars. Tolerance to flumioxazin

showed a single significant association on chromosome 2. The region does not represent target site tolerance because the protoporphyrinogen oxidase genes are located elsewhere in the genome.

Tolerance to sulfentrazone is multigenic. Several SNPs were detected in both years for PD and BP. Several genes associated with these SNPs could be involved in metabolism of sulfentrazone, including cytochrome P450s and genes involved in reactive oxygen stress. Such mechanisms are comparable to non-target site resistance (NTSR) in weeds. Weed species with NTSR often exhibit cross resistance to other herbicides. We found many of the genomic regions associated with tolerance to sulfentrazone also were associated with tolerance to saflufenacil. However, colinear regions for tolerance were limited primarily to sulfentrazone and saflufenacil.

PSII-inhibitor: Metribuzin was highly injurious to snap bean. While there may be some genetic component to tolerance, identified SNPs accounted for a small amount of variation. One cultivar, McCaslan, had a high level of tolerance (>90%) across environments.

VLCFA-inhibitor: No genetic tolerance to pyroxasulfone was observed. There was a large effect of environment on snap bean response to pyroxasulfone. For instance, mean pyroxasulfone tolerance was 90% and 40% in years 1 and 2, respectively. Discrepancy in crop response across years may have been driven by pyroxasulfone bioavailability in the soil profile, as evidenced by greater water supply in year 2.

Seed weight was used as a covariate in GWAS analyses because of significant correlations between seed weight and crop tolerance to most herbicides. One potential conclusion from this research is that breeders could improve soil-active herbicide tolerance by selecting for larger seed. However, this approach conflicts with commercial objectives, where the consumer desires a small seed in fresh snap bean pods. Perhaps breeders can select for plants that 1) have small seed at commercial harvest, and 2) maximize seed mass by the time of physiological maturity. Such an approach may improve seedling resilience to other stresses, too.

We observed a positive relationship between seedling vigor (as measured by PD and BP in control plots) and tolerance to soil-active herbicides. The SNAP cultivars did not evolve under repeated herbicide exposures; therefore, genes associated with herbicide tolerance likely have other functions. Response to herbicide exposure shares common elements with other kinds of stress, particularly through reactive oxygen species pathways. In fact, a meta-analysis of promoter sequences of herbicide tolerance genes found *cis* regulatory elements annotated as stress responsive elements. It is possible that genes associated with higher herbicide tolerance may be involved in higher resilience to other stresses. Although the direct effect in herbicide tolerance in some of those associations may be small, identification and use of such genes may contribute to the overall goal of increasing stress tolerance in snap bean.

ACKNOWLEDGEMENTS: We thank Seneca Foods, F. Navarro, and T. Trump for increasing SNAP seed for use in these experiments. We also thank the following individuals for helping with data collection: L. Connor, D. Dhaliwal, N. Hausman, D. Kerr, N. Korres, C. Landau, P. Pavlovic, Y. Takenaka.

THE ENERGY-SAVING POTENTIAL OF FAST-COOKING BEAN VARIETIES

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INTRODUCTION: The long cooking times of dry beans are more than an inconvenience for consumers. Long cooking times combined with the need to soak beans before cooking contributes heavily to their environmental footprint (Corrado et al., 2019). Stovetop and electric pressure cookers require fewer fossil fuel resources to cook beans to completion than traditional stovetop cooking, due largely to their lower electricity consumption (Bandekar et al., 2022). It was previously demonstrated that dry bean varieties with fast cooking times require less processing time during canning to achieve an optimum texture (Bassett et al., 2020). Canning resembles pressure cooking in that both methods raise the pressure and temperature of the local environment around the beans for a short period of time to break the seeds down more quickly. Based on the observation that fast-cooking beans break down more quickly during canning, the hypothesis of this study was that dry beans with faster cooking times would also break down more quickly than slow-cooking beans in a pressure cooker and thereby could help consumers save energy while cooking at home.

MATERIALS AND METHODS: Four dry bean genotypes from two market classes (brown and yellow) with contrasting cooking times were selected for this study (Table 1). The genotypes were grown at the Michigan State University Saginaw Valley Research Farm and Extension Center in Richville, MI in 2020. The seeds were stored for 2.5 years in cold storage prior to use. Thirty seeds were soaked in duplicate for 12 hours in distilled and cooked with a Mattson pin-drop cooker to determine the baseline cooking times of the genotypes. For the pressure cooker experiment, 200 g of seeds were first soaked for 12 hours in distilled water. The samples were then split into 100 g subsamples and mixed with 1000 mL of distilled water in a 6-qt InstantPot Duo. The subsamples were cooked at high pressure for 5 or 10 minutes. Pressure was naturally released for 20 minutes, followed by a quick manual release. The cooked samples were immediately drained of liquid, allowed to cool to room temperature, and subjected to texture analysis with a 10-blade Kramer shear cell (Lloyd Instruments, UK). A high peak force (>75000 g) indicates that the beans are undercooked. A peak positive force between 50000 and 75000 g is considered an ideal texture (Hosfield and Uebersax, 1980). Statistical significance was determined using ANOVA. Multiple comparisons were conducted with LSD (α=0.05).

RESULTS: TZ-37 had a significantly shorter cooking time than the slow-cooking brown bean, TZ-27. Likewise, Ervilha had a significantly shorter cooking time than the slow-cooking yellow bean, PI527538. The cooking time of PI527538 was intermediate to that of TZ-27 and TZ-37 (Table 1). The Mattson cooking times of the genotypes were significantly positively associated with the peak pressure force required to pierce the genotypes after 10 minutes of cooking in the pressure cooker ($R=0.97$, $p=0.026$), but not peak positive force after 5 minutes of cooking, likely because Ervilha did not become significantly softer than PI527538 until minute 10 of cooking ($R=0.83$, $p=0.17$). The fast-cooking beans became softer more quickly than the slow-cooking beans did in the pressure cooker. In the case of TZ-27, it required 50% more time than TZ-37 to

achieve an optimal texture (50-70 kg). Ervilha had the softest texture after 10 minutes of cooking (Figure 1).

Table 1. Market class and cooking time characteristics of four dry bean genotypes cooked using a Mattson cooker after 12 hr soaking in DI water (n=2). Cooking times with the same letter are not significantly different from each other.

	TZ-27	TZ-37	PI527538	Ervilha
Market class	Brown	Brown	Yellow	Yellow
Cooking speed	Slow	Fast	Slow	Fast
Cooking time (mins)	49a	41b	43ab	32c

CONCLUSIONS: Four dry bean genotypes with contrasting cooking times were tested to determine if the faster cooking bean varieties soften more quickly in a pressure cooker. The Mattson cooking times of these four varieties were significantly correlated with bean texture after 10 minutes of cooking in a pressure cooker. Beans with faster cooking times may generally require less time to process in a pressure cooker. Hence, fast-cooking dry bean varieties could help decrease the carbon footprint of dry beans no matter how consumers choose to prepare them.

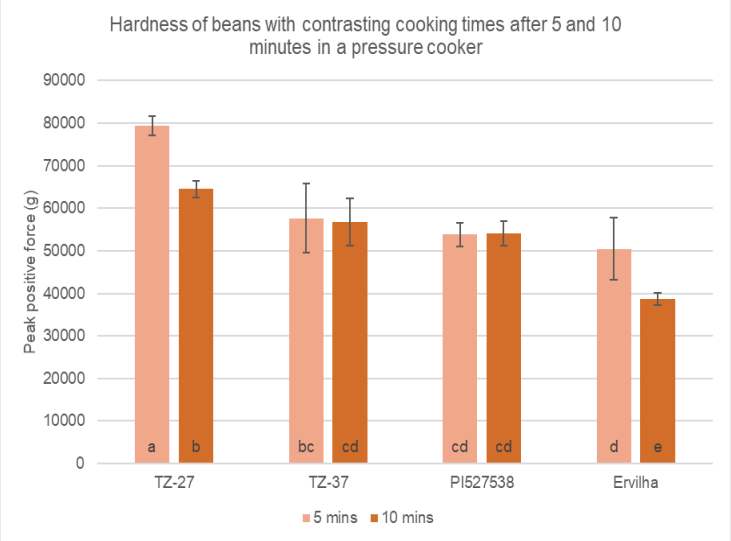

Figure 1. Texture measurements (g) of dry beans cooked for 5 and 10 minutes in a pressure cooker (n=2). Error bars are the standard deviation of the means. Texture measurements with the same letter are not significantly

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TB 02-20: A COMMON BEAN (*PHASEOLUS VULGARIS* L.) GENOTYPE WITH FAVORABLE ZINC (ZN) AND IRON (FE) CONTENT

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INTRODUCTION

The richness represented by the agrobiodiversity found in the different species that make up the food universe, has been recognized at the global level. The United Nations (UN), according to the understanding that there is a need to eradicate poverty and hunger in the world, promoting a dignified life for all, formulated the Objectives of Sustainable Development – OSDs, composing the "2030 Agenda for Sustainable Development". In its second objective, the Agenda has as one of its goals the access of all people to safe and nutritious food. As a reflection of this recognition, the search for food that have favorable nutritional profiles has become a priority. From a nutritional point of view, common bean (*P. vulgaris* L.) has adequate levels of several essential nutrients for humans and, due to this characteristic, can be a substitute for other sources, such as meat, when considering the protein content, for example, which implies in a favorable condition for low-income populations. In addition to a high protein content, common beans are also a source of other nutrients, such as calcium and iron, B complex vitamins, dietary fiber, carbohydrates and several essential amino acids. In order to contribute to the reduction of existing malnutrition in many countries, in 2002 the Consortium of International Agricultural Research Centers - CGIAR, an international organization that coordinates international agricultural research programs, approved the project entitled Biofortification Challenge Program, later renamed Harvest Plus. Among its goals, it proposed the biofortification of food species, making them higher in certain nutrients. Common bean was one of these species, and the goals included increasing the levels of Zinc (Zn) and Iron (Fe). This article reveals the strategy developed to identify the line TB 02-20, a genotype with high Zn and Fe content and high seed yield.

MATERIALS AND METHODS

TB 02-20 is a selection that was performed from a landrace population of common bean that was added to the germplasm bank of Embrapa Clima Temperado in 1999 from a donation by an extension agent. The "TB" letters corresponds to the identification for selections of common bean conducted at Embrapa Clima Temperado; "02", corresponds to the year of selection, and 20, to the order of the selection. **Nutritional characterization** – Nutritional analyzes related to seed content of Zn and Fe of TB 02-20, have been conducted at Embrapa Agroindústria de Alimentos, in 2014, and at Embrapa Clima Temperado, in 2018, Brazil. Besides TB 02-20, an additional 25 genotypes, part of the common bean research program of Embrapa Clima Temperado, were evaluated for the analyzes at Embrapa Agroindústria de Alimentos, with the seeds derived from a field experiment carried out at Pelotas, State of Rio Grande do Sul, in 2013. The analyzes made at Embrapa Clima Temperado, comprised, besides TB 02-20, additional 13 genotypes, and the seeds wer obtained from experiments conducted in the municipalities of Sobradinho and São Luiz Gonzaga, both in Rio Grande do Sul in 2011/12. **Yield performance** - The submission of TB 02-20 for evaluation in field experiments to determine the Cultivation and Use Value – VCU in Rio Grande do Sul, one of the requirements for registration at the Ministry of Agriculture, included years 2006/07 – 2010/11, that is, five agricultural years. In this period, they were planted in the two common bean

sowing seasons in the State, namely, 19 in the spring season, corresponding to spring sowings, and seven in the summer season, corresponding to summer sowings, thus summing up to 26 experiments. Experiments were carried out in 10 different municipalities located at Rio Grande do Sul State. VCU experiments were composed under a Complete Block Design, with four replications, four 4m-row plots and a seed density corresponding to 240.00 plants/ha. A by-local analize of variance was conducted and a Scott-Knott mean comparison followed.

RESULTS AND DISCUSSION

Fe and Zn content - Results on the performance of TB 02-20 reveal that, compared to the results obtained for the additional genotypes subjected to the trial, this genotype posseses a quite favorable content both for Zn and Fe. TB 02-20 showed the highest Fe content (85.997 mg/kg – under a spectrum that ranged from 55.517 to 85.997 mg/kg), and the second highest content of Zn (37.373 mg/kg - under a spectrum from 25.631 to 39.963 mg/kg), among the 26 genotypes, from the analyses carried out at Embrapa Agroindústria de Alimentos. From the evaluation conducted at Embrapa Clima Temperado, with seeds of 14 genotypes from experiments carried out in the municipalities of Sobradinho and São Luiz Gonzaga, both in Rio Grande do Sul, in 2011/12, TB 02-20 also had the highest Zinc content in Sobradinho (31.67 mg/kg, under a spectrum of 26.00 to 31.67 mg/kg), and a medium response in São Luis Gonzaga (26.44 mg/kg - under a spectrum of 22.57 to 32.58 mg/kg). For Iron content, in Sobradinho, TB 02-20 reached the highest value (120 mg/kg, for a spectrum of 80 to 120 mg/kg) and), and a below-average in São Luiz Gonzaga (70 mg/kg, under a spectrum of 60 to 100 mg/kg). Its important to observe the higher Iron content found in Sobradinho and São Luis Gonzaga as compared to that found in Pelotas, and a similar content for Zinc at these locations. The results point out to the high performance of TB 02-20 for Zn and Fe content in seeds from distinct environemnts, what implies in a favorable condition for this genotype in achieving the goals proposed by the CGIAR, considering being a selection from a landrace. **Yield performance –** TB 02-20, from the 26 experiments carried out, in 14 of them was statistically identical in seed yield to the best genotypes in the average comparison tests, such results in 10 of the 19 spring season experiments and in four of the seven summer season experiments. Likewise, it showed productivity, in absolute terms, superior to that of the best control in 13 of the 26 experiments, this results being observed in seven of the 19 in the spring season and in six of the seven, in the summer season.This last result reveals a trend that can be translated as a greater adaptation to summer crops, in Rio Grande do Sul that are established in the months of January and February. In terms of yield potential, in a Sobradinho experiment, in the 2010/11 season, presented 3,617 $kg.ha^{-1}$, the highest yield observed in all experiments, attesting to its high potential. In the summer season, its highest observed productivity was 2,760 kg^{-1}, also the highest observed in this growing season in all experiments. So, TB 02-20, from the behavior observed, has a great potential as an outstanding genotype for cultivation in Rio Grande do Sul State and, probably, in other environments.

CONCLUSIONS

TB 02-20, due to its high Fe and Zn performance, as well as seed yield, has a great potential for adoption by common bean farmers in South Brazil.

MANTECA YELLOW BEAN PASTA IS A NATURALLY RICH SOURCE OF BIOAVAILABLE IRON

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INTRODUCTION: Dry bean consumption is low in the United States and development of new bean products offer an opportunity to increase demand. Milling whole beans into flours can expand their uses into products such as pastas, snacks and baked goods. Ideal beans for flours were found to have light seed coat colors and low off flavors. Manteca yellow beans are a market class of dry beans with a pale-yellow seed coat and many favorable end-use quality characteristics, which makes them an ideal flour ingredient for food production. Manteca beans tend to have short cooking times, subtle flavor and high nutritional value. In addition, Manteca yellow beans have more bioavailable iron when compared to other market classes of dry beans, which makes them an ideal target for improved iron nutrition. USDA-ARS has an active Manteca breeding program, adapting them to commercial production with improved seed yield, maturity, harvest quality, cooking time, canning quality and iron bioavailability. There is currently no information on the nutritional properties of Manteca beans after being processed into flour, therefore, the goal of this research was to evaluate the nutritional attributes of Manteca bean pasta made from advanced breeding lines as compared to commercially available chickpea, wheat and gluten free pastas.

MATERIALES AND METHODS: A composite flour was formulated with advanced breeding lines of Manteca yellow beans (Y1608-14, RRY1803-1-1 and Y1610-01) produced in Montcalm Township and Saginaw Valley, Michigan (field season 2022). To produce flour, Manteca yellow beans were first oven treated before milling into an ultra-fine powder using a commercially available compression-decompression mill (Enagon LLC, Saugatuck, Michigan). Bean flour was mixed with small amounts of cassava flour and xanthan gum before being extruded into rotini pasta and dried at West Michigan Pasta & Provisions LLC located near Kalamazoo, Michigan (Table 1). Chickpea, wheat and gluten free rotini was purchased at local grocery stores located in Ithaca, New York. Pasta was cooked in distilled water according to package instructions (Table 1); drained, cooled to room temperature and then stored at -80^{o}C for 16 hours. Cooked pasta samples were freeze-dried and milled into powder (Kinematica Polymix® analytical hammer mill, Bohemia, NY) for ICP-AES mineral analysis and iron bioavailability according to the methods described in Glahn, 2022 (Glahn, 2022 *JoVE*, 182:e63859).

RESULTS AND DISCUSSION: Cooking in only 5 minutes, Manteca yellow bean pasta had similar calories, total fat, total carbohydrates and potassium when compared to commercially available chickpea, wheat and gluten free pasta (Table 2). However, one serving of Manteca rotini provides more fiber, calcium and iron compared to rotini purchased at the supermarket (Table 2). The results in Figure 1 show that Manteca yellow bean pasta has more than twice the iron content and 3x the iron bioavailability as chickpea, wheat and gluten free pasta. This research demonstrates that the unique iron nutrition of the Manteca yellow bean can be translated into a convenient food product, beating out the other supermarket brands for the delivery of iron, even fortified wheat pasta. This research reveals that the use of other dry bean market classes, which demonstrate high iron bioavailability (i.e., slow-darkening Pinto) should also be considered for

bean flour development; possibly creating a specialty market for convenient plant based foods, which can be gluten free and targets consumers interested in their dietary fiber or iron needs.

Table 1. Description of Manteca, chickpea, wheat and gluten free pastas.[1]

Pasta Type	Cooking Time, Ingredients and Attributes
Manteca	5 min – bean flour (90%), cassava (5%) & xanthan gum (< 5%)
Chickpea	9 min – chickpea flour (100%); gluten free, high fiber
Enriched Wheat	8 min – fortified wheat (folate, thiamin, niacin, riboflavin and iron)
Whole Wheat	10 min – durum wheat (100%); rich texture, high fiber
Gluten Free	9 min – corn & rice flour, monoglycerides; gluten free

[1]Descriptions based on packaging labels of dry rotini pasta.

Table 2. Food label comparisons of Manteca, chickpea, wheat and gluten free rotini pastas.[1]

Pasta Type	Calories	Total Fat (g)	Total Carb. (g)	Fiber (g)	Protein (g)	Calcium (mg)	Potassium (mg)	Iron (mg)
Manteca[2]	180	1.5	34	11*	7	80	380	5.7*
Chickpea	190	3.5	34	8	11	29	622	3.0
Enriched Wheat	200	1.0	42	3	7	12	118	2.0
Whole Wheat	180	1.5	39	7	8	17	274	2.0
Gluten Free[3]	190	1.0	44	2	4	2	77	0

[1]Serving size: 2 oz. (56 g of dry pasta). [2]Food label generated by Great Lakes Scientific, Inc. (Stevensville, MI) [3]Gluten free rotini is formulated with corn and rice flour. *Considered an excellent source (>30% Daily Value) of dietary fiber and iron with each serving.

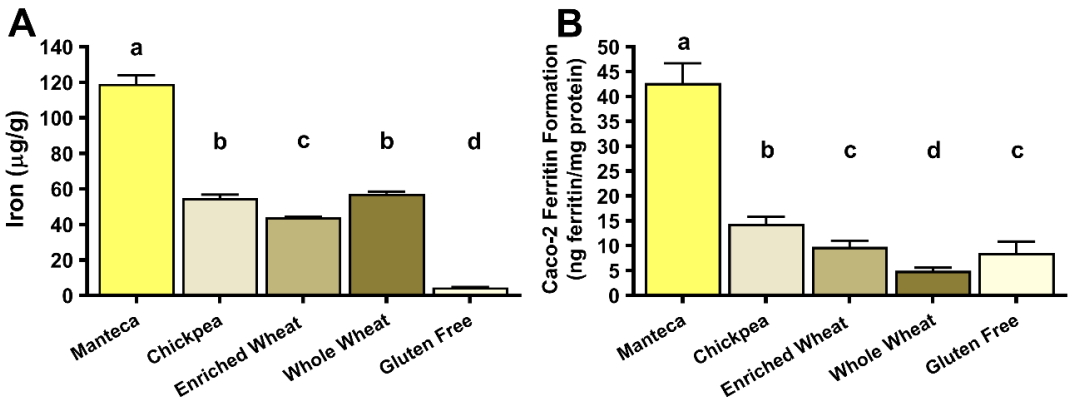

Figure 1. Iron concentrations (**A**) and iron bioavailability (**B**) of Manteca yellow bean rotini pasta compared to commercially available chickpea, wheat and gluten free rotini pasta. Values are means ± standard deviations of six replicates from each pasta sample. Iron concentrations are measured as micrograms per gram of cooked, drained, lyophilized and milled pasta sample (dry weight). Iron bioavailability is measured as Caco-2 cell ferritin formation (ng ferritin / mg total cell protein) after exposure to an *in vitro* digestion of cooked, drained, lyophilized and milled pasta sample. Means sharing the same superscript are not significantly different at $P \leq 0.005$.

SEED DAMAGE COMPARISON BETWEEN SLOW DARKENING AND REGULAR DARKENING PINTO BEANS

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INTRODUCTION: Common bean (*Phaseolus vulgaris* L.) seed quality is negatively affected during harvest and post-harvest activities (Shahbazi et al., 2011). Light-colored legume seeds have been reported to have lower levels of proanthocyanidines and thinner seed coat thickness compared to darker seeds (Mirali et al., 2016). Slow-darkening (SD) pinto beans tend to have more splitting and cracking issues (Miklas et al., 2020) which could be related to thinner seed coats. Similar anecdotal observations at commercial operations have also been reported. However, this has not been well quantified. In addition, thicker seed coats usually have longer cooking times (Bassett et al., 2021). Interestingly, SD beans have been identified to have shorter cooking times than regular-darkening (RD) (Wiesinger et al., 2021), which could be also associated with thinner seed coats. The purpose of this research is to quantify split and cracked seeds in SD and RD pinto beans and its relationship with some agronomic traits.

MATERIALS AND METHODS: Seed samples were collected from field trials at Johnstown and Prosper in North Dakota during the 2022 growing season using a Wintersteiger classic plot combine for direct harvest. A total of 14 RD and 19 SD pinto bean cultivars and advanced breeding lines developed at the North Dakota State University (NDSU) Dry Bean breeding program were sampled. The field design was a RCBD with 3 replications. Agronomic traits (days to maturity, days to flowering, plant height (cm), seed yield (kg ha^{-1}), and stem diameter (mm)) were measured during the 2022 growing season. Each sample consisted of 100 g of seed from each plot in which split and cracked seeds were visually identified and weighted separately and expressed as split/cracked g per 100 g of seed. Principal component analysis (PCA) was conducted to visualize cultivar and breeding line distribution related to split and cracked seed data. A t-test ($P \leq 0.05$) analysis was implemented to detect differences between RD and SD groups. Pearson correlation analysis was performed for split and cracked seed traits against agronomic traits.

RESULTS AND DISCUSSION: PCA shows that RD cultivars La Paz, Monterrey and Windbreaker tend to have less split and cracked seeds than SD cultivars ND Palomino and Vibrant (Figure 1). However, nine SD breeding lines showed similar values as RD for split and cracked seed, suggesting that there is potential to genetically improve and reduce the amount of seed splits and cracks. Preliminary results from t-test showed significant differences between SD and RD pinto beans. SD showed an increment of 111% for split seed and 36% for cracked seed compare to RD (Figure 2). Cracked seed values were

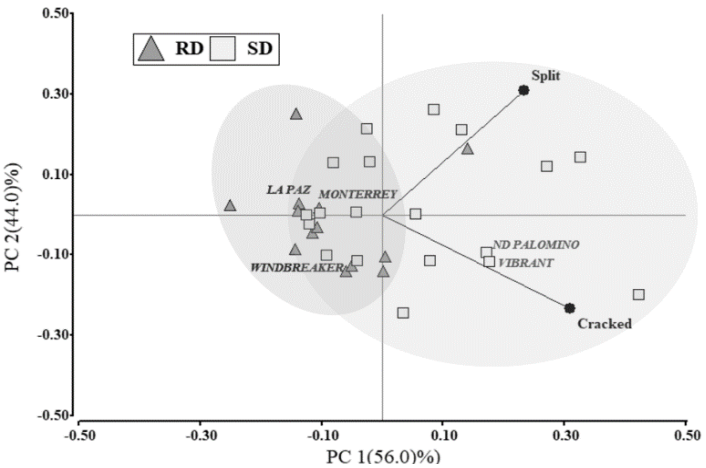

Figure 1. PCA and grouping of SD and RD genotypes

significantly higher than splits because the weight of a cracked seed was higher than a split seed in most of the recorded measurements. There were no significant correlations between the split/cracked seeds and the other agronomic traits measured.

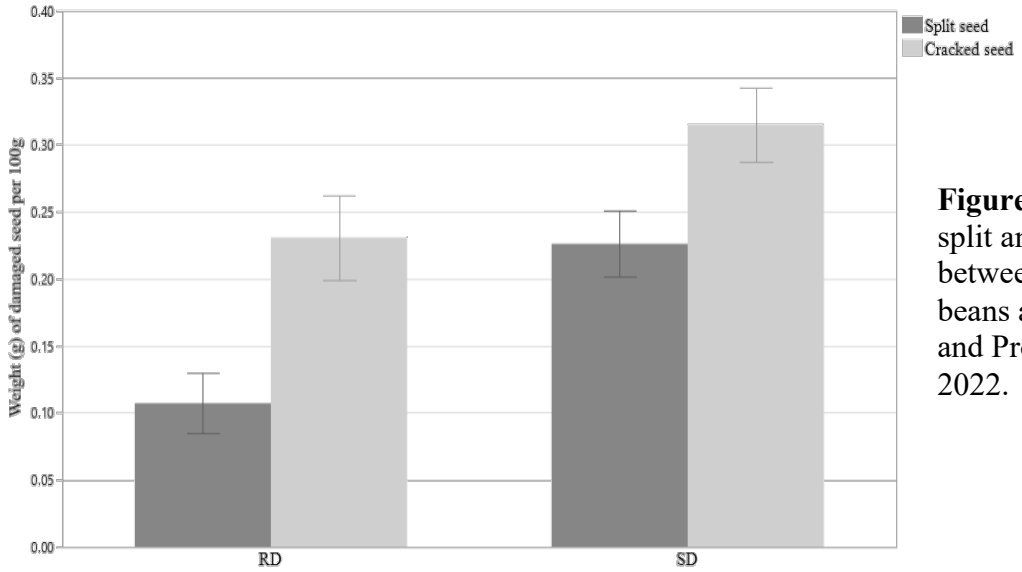

Figure 2. Comparison of split and cracked seeds between RD and SD pinto beans across Johnstown and Prosper locations in 2022.

Differences observed for split and cracked seed traits could be explained in part by the flavonoid content, since Windbreaker and La Paz pinto beans have almost two times more than Vibrant and ND Palomino pinto beans (Wiesinger et al., 2021). Polymers in the seed coat use flavonoids as precursor molecules (Ganesan and Xu, 2017; Wiesinger et al., 2021). Thus, lower levels of flavonoids in SD can be one of the factors affecting the seed coat.

This research has been supported by Northarvest Bean Growers Association and USDA Pulse Crop Health Initiative.

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OBSERVATIONS OF PRODUCT QUALITY VARIABILITY IN COMMERCIALLY CANNED AND POUCH PROCESSED BLACK AND KIDNEY BEANS: A MARKET 'SNAPSHOT'

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INTRODUCTION: Quality has been defined as "conformance to specifications" (i.e., the designated range of specific product attributes). Dry beans are prepared and thermally processed in a wide range of packaging types for consumer convenience. "Canned beans" may be packaged in hermetically sealed metal cans, foil pouches, or aseptically filled cartons. These products require heating to levels sufficient to inactivate the spores of *C. botulinum* and are shelf stable. Canned beans are particularly noted for their overall character, flavor, and convenience. Bean quality encompasses sensory attributes including *appearance* (seed size & shape, and integrity or wholeness); *color* (seedcoat and sauce), *texture or viscoelastic properties* (firmness/tenderness, viscosity, and mouthfeel) and *flavor* (distinctive taste and aroma). Visual appearance is perhaps the most readily apparent attribute that connotes quality. Causes for quality variability in canned beans have been studied extensively and are well documented (White et al., 2022). Clearly, there is broad genetic variability within *P. vulgaris*, and thus different cultivars possess distinctive characteristics (Miklas et al., 2022). Numerous biotic and abiotic stresses, post-harvest handling, and thermal processing conditions impact quality. Further, processors strive to develop "*robust processes*" that are relatively stable to inherent dry bean variability. The purpose of this paper is to demonstrate the variability of quality appearance of two specialized canned bean types (black and kidney) that are readily available in the commercial marketplace.

MATERIALS AND METHODS: Commercially available canned and pouch-processed dark red kidney (DRK) and black (BLK) beans were purchased from retail markets in the East Lansing, MI region. Samples were assigned "blind codes" and used as experimental samples in the laboratory for processing quality sensory evaluation. The samples included multiple brands of conventional and organic products.

All samples were rated by a group of 11 trained panelists using a hedonic scale ranging from 1 to 5 (1= worst quality, 5= best quality). Statistical analyses were conducted using 'among panelist' variance. Tukey's test was used to conduct the pairwise comparison for rating scores.

RESULTS AND DISCUSSION: Product descriptors and sensory results are provided in Table 1. Quality variations were identified among the experimental samples. The conventionally canned products had the highest sensory scores for processing quality appearance among all samples in both DRK and BLK beans. In DRK bean samples, the conventional canned product had superior quality scores compared to the organic canned product, and the organic canned product had higher quality scores than the organic pouch-processed product. However, in BLK bean samples, one organic canned product (BLK-2) had the same quality as the conventional canned product, while all the other organic products had lower quality scores.

Organic products tended to have simpler ingredients and fewer (or no) additives, compared to conventional products. The ingredients of most organic products were only beans, water, and salt, while in DRK-1 conventional beans calcium chloride is used as a firming agent and EDTA for color retention.

Table 1. Quality evaluation of conventional or organic market samples of dark red kidney beans and black beans processed in cans or pouches.

	Code	Processed format and ingredients	Score	Quality Description
Dark Red Kidney Beans	DRK-1	Conventional (Can): Prepared kidney beans, water, salt, sugar, dextrose, calcium chloride (firming agent), and disodium EDTA (promotes color retention).	4.2a*	Good to excellent appearance, with about 10% of seeds having breakage.
	DRK-2	Organic (Can): Prepared organic kidney beans, water, sea salt.	3.3b	Above-average appearance, with ~30% seed breakage.
	DRK-3	Organic (Can): Prepared organic kidney beans, water, sea salt, calcium chloride (firming agent).	3.3b	Above-average appearance, with about ~30% seed breakage.
	DRK-4	Organic (Pouch): Filtered water, organic kidney beans.	2.2c	Poor appearance with over 50% split seeds.
	DRK-5	Organic (Pouch): Water, organic dark red kidney beans.	1.3d	Very poor appearance with mushed-up seeds.
Black Beans	BLK-1	Conventional (Can): Prepared black beans, water, salt.	3.3a	Above-average appearance, dark black color.
	BLK-2	Organic (Can): Prepared organic black beans, water, sea salt.	3.2a	Average appearance, dark black color.
	BLK-3	Organic (Can): Organic black turtle beans, water, kombu seaweed.	1.4b	Poor appearance with seeds severely split, black color.
	BLK-4	Organic (Pouch): Water, organic black beans, water, kombu seaweed.	1.5b	Poor appearance with mushed-up seeds, black color.
	BLK-5	Organic (Pouch): Filtered water, organic black beans.	1.3b	Poor appearance with seeds severely split, brown color.

*Quality ratings followed by different letters within each bean type are significantly different at $p \leq 0.05$ based on Tukey's test.

CONCLUSIONS: The bean processing quality appearance is an indication of how beans withstand thermal processing. Appearance is dependent on multiple factors in addition to genetics, including hydration, seed integrity, starch leaching, and brine color. From this limited snapshot, a wide range of quality appearance is evident, with inferior quality observed in organic beans. In addition to the fewer additives used with organic beans during processing, the inferior quality can likely also be traced to poorer starting dry bean quality. While conventional dry beans are treated with desiccants to aid timely and uniform dry down at harvest, the use of these is restricted in organic production.

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COMPARATIVE STUDY OF THE NUTRITIONAL COMPOSITION OF *PHASEOLUS VULGARIS* (COMMON BEAN), *VIGNA UNGUCULATA* (COWPEA) AND *VIGNA RADIATA* (MUNG BEAN)

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INTRODUCTION: Malnutrition is a condition that occurs when the human diet is unbalanced, as with under-nutrition, over-nutrition, or both, all of which could coexist and result in adverse health effects (WHO, 2021). In 2020, the World Health Organization (WHO) reported that 149.2 million children under five years of age were stunted, 45.4 million were wasted, and 38.9 million children were overweight (McClements & Grossmann, 2021). To combat malnutrition and ensure food sovereignty, the Ivorian government has encouraged crop diversification adoption. Thus, the Vegetable and Protein Crops Program of the University of Abomey Calavi and CIAT have undertaken the selection of high-yielding bean varieties with good agro-morphology and nutritional attributes. Results of this study will be useful in promoting bean consumption as part of a healthy diet and support new breeding initiatives towards nutritional and health benefits.

MATERIALS AND METHODS: Laboratory based nutritional analysis on 4 dry common bean varieties HARI02/KEN18 (Kenya), HARI04/BKE18 (Central Ivory Coast), HARI03/FER18 (Northern Ivory Coast and HARI08/GHA18 (Ghana); 2 cowpea varieties KN1 and Touba local (Ivory Coast); and a *Vigna radiata* variety (Ivory Coast). Nutritional parameters studied were total and reducing sugars, lipids, proteins, calcium, potassium, magnesium, iron, and zinc.

Figure 1. Seeds of 4 dry bean, 2 cowpea and 1 Vigna varieties used for nutrition analysis in this study.

RESULTS AND DISCUSSION: The nutrient analysis showed that the protein content was the same for both bean and cowpea varieties. The same results were observed for iron and zinc content in dry beans, but slightly higher for zinc values. For lipid content, the highest value was found in one common bean variety (HARI08/GHA18) and the lowest in Vigna.

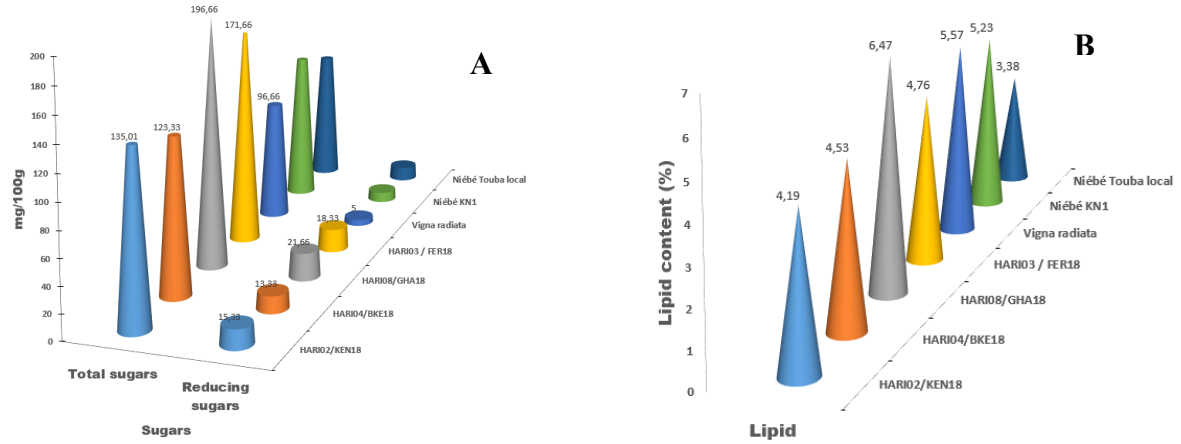

Figure 2. Sugar (A) and lipid (B) content in 4 dry bean varieties, 2 cowpea varieties and 1 *Vigna radiata* variety

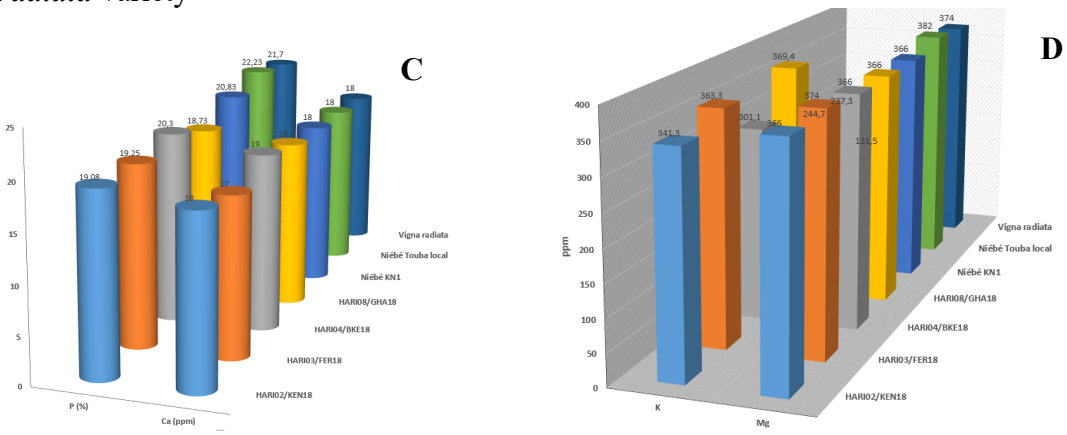

Figure 3. Protein and Calcium (C) and Potassium and Magnesium (D) content in 4 dry bean varieties, 2 cowpea varieties and 1 *Vigna radiata* variety

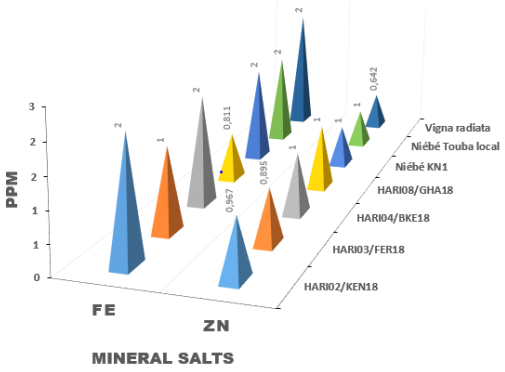

Figure 4. Iron and Zinc content in 4 dry bean varieties, 2 cowpea varieties and 1 *Vigna radiata* variety

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PROSPECTS FOR INTRODUCING DRY COMMON BEAN *(PHASEOLUS VULGARIS L.)* PRODUCTION IN BENIN (WEST AFRICA)

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INTRODUCTION: In the Papilionaceae family, common bean (*Phaseolus vulgaris* L.) is the most consumed bean in the world (Gupta et al.,2019). Regular consumption of this legume is thus widely recommended by the WHO (Schmutz et al., 2014), known to reduce cardiovascular diseases and diabetes, and improve physical strength and cognitive benefits (Nchanji et al., 2002). In Benin, cowpea is the largest produced grain legume; thus, dry beans are still little known despite their great nutritional quality. As part of contributing to crop and food diversification, this study analyzed prospects for the production of dry beans in Benin.

MATERIALS AND METHODS: Study areas and sampling strategy. A mixed-method approach was used to collect data from potential growers and researchers involved in field experiments. Surveys were conducted in 18 villages across six main legume-producing communes in Benin (Covè, Djidja, Dogbo, Glazoué, Kétou, Savalou). The panel of interviewees comprised 463 people (114 women and 349 men), in six communes. Enumerators carried pictures of dry bean seeds with various colours (Fig.1), shown to informants to reduce confusion where different names can be attributed to different varieties.

SEF 29 *BFS 55* *AWASH* *SEMANHYIA*

Fig. 1. Dry bean seeds of different colors

Experiments. 15 dry bean genotypes were evaluated across two sites. Experiments were laid out in a Randomized Complete Block Design (RCBD) with three replications over two seasons. Plots consisted of four 5 m long rows, with a spacing of 50 cm between rows and 20 cm between plants. Two seeds were sown per hole and thinned to one. Data on flowering, maturity and yield were recorded. All data were analyzed in R.

RESULT AND DISCUSSION: Common bean cropping systems in Benin. In Benin, survey results indicated that common beans were unknown to many producers. However, a comparison was made between *Phaseolus vulgaris* and *Phaseolus lunatus* L., a climbing type, with larger seeds, well known and grown in Benin.

Fig 2. Seeds of *Phaseolus lunatus* L. collected in Benin

Producers have fully expressed their desire to adopt dry common beans (*Phaseolus vulgaris*) after being made aware of their nutritional importance. Besides, they preferred varieties that resist pests

and diseases, are drought tolerant and have a higher yield. These results indicate that the crop has the potential to get promoted in Benin, and this raises the need to undertake actions to introduce dry beans production in Benin.

Adaptation and agronomic performance of common bean varieties evaluated in Benin. The multi-location trials showed that the common bean varieties deployed had very good emergence and growth. However, average yields at both sites ranged from 123.9 kg/ha (Adoye) to 360.8 kg/ha (SEF 62), with an average yield of 241.4 kg/ha across lines (Table 1). The overall yield obtained was very low, which confirms the findings of Gepts et al. (2008) that the average productivity of developed countries (1,944 kg/ha) far exceeds that of developing countries (1,035 kg/ha), making the situation more dramatic in less developed regions that depend mainly on beans as a primary food source. This could be the result of lack of or limited use of appropriate agronomical practices. In addition, all varieties matured earlier in Djidja (56 days) than in Glazoué (67 days), indicating the presence of GxE effect in the crop (Table 1), which needs to be investigated.

Table 1. Average seed yield, days to flowering, days to maturity, and 100-seed weight across locations.

Variety	Yield			100 seed weight	Days to 50% of flowering	Days to maturity		
	Mean of locations	Glazoué	Djidja			Mean of locations	Glazoué	Djidja
	kg/ha	kg/ha	kg/ha	g	days	days	days	days
SEF 62	360.8	379.4	342.2	19	38	63	67	58
SEF 44	346.1	442.2	250	21.8	31	64	73	50
BFS 55	342.2	404.4	280	20.8	35	59	60	57
SEF 64	316.9	329.4	304.4	19.9	32	65	75	55
SEF 55	298.1	318.9	277.2	19.8	33	63	70	57
SEF 49	285.8	410.6	161.1	21.8	30	60	67	53
Nsroma	281.5	325.1	237.8	20.2	25	54	62	45
BFS 60	230.6	228.9	232.2	19.1	33	55	52	57
BFS 35	203.9	185	222.8	20.1	33	63	70	56
SEF 52	193.3	117.8	268.9	19.7	33	66	75	57
SEMANHYIA	171.9	201.7	142.2	15.8	39	67	73	58
ENNEPA	166.2	98.5	233.9	17	39	67	75	59
SEF 29	161.9	168.3	155.6	18.1	34	69	77	57
AWASH 1	138.9	114.4	163.3	13.2	33	66	75	57
Adoye	123.9	106.5	141.3	15.2	38	66	75	58
Mean	**241.4**	**250.1**	**232.6**	**19.1**	**33**	**62**	**67**	**56**
LSD	**136.3**	**243.8**	**134.9**	**2.1**	**4.5**	**10.6**	**11.7**	**5.7**
CV (%)	**49.4**	**59.2**	**35.2**	**9.6**	**11.7**	**15**	**10.7**	**6.2**
Variety signif.	**	**NS**	**NS**	***	***	**	**	**

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SEED YIELD STABILITY IN LANDRACE AND IMPROVED COMMON BEAN CULTIVARS GROWN IN CONTRASTING ENVIRONMENTS

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INTRODUCTION: Common bean (*Phaseolus vulgaris*) is the most important food legume cultivated in the Semiarid Highlands of Northern México. The state of Durango is considered one of the most important centers of common bean genetic diversity, including several market classes such as: pinto (brown spotted), bayo (cream), ojo de cabra (brown stripped) and others. Several landrace cultivars have been displaced by the common bean improved cultivars developed for this region, however some seed classes show persistence across locations and years due to farmers´ preference. Landrace cultivars are considered as widely adapted germplasm, showing high yield under favorable conditions, and reaching at least some yield even under severe environmental conditions. The objective was to evaluate seed yield stability in common bean landrace cultivars sown under contrasting environments in Durango, México.

MATERIALS AND METHODS: Four landrace and four improved common bean cultivars were sown in four locations across rainfed and irrigated producing areas in Durango. Common bean landrace seed was obtained during collection trips performed during 2022 in several towns and local markets across Los Llanos de Durango (Santana *et al*., 2022). Semi-commercial plots (1 ha) were established in four municipalities: Canatlán (La Soledad), Durango, Guadalupe Victoria (Santa Catalina de Siena) and Vicente Guerrero. Experimental plot consisted in 16 rows, 100 m long and 0.81 m wide. Agronomic practices were applied according to farmers´ criteria complemented with INIFAP´s technical recommendations. For seed yield determination, five plant samples consisting of two rows 5 m long and 0.81 m wide (6.48 m^2) were taken in each cultivar. The analysis of variance (ANOVA) was obtained by using a Completely Randomized Design with Factorial Treatment Structure (Environment and Cultivar). AMMI model was used to evaluate genetic (G) by Environment interaction (G x E) to identify cultivars that are adapted to specific environment or stable across environments (Kahn *et al*., 2021).

RESULTS AND DISCUSSION: Highly significant ($p \leq 0.01$) differences were observed between environments and cultivars for seed yield (Table 1). Significance was also observed for G x E interaction due to genetic effects related to seed yield and its dependence upon variability in the environment. Durango and Santa Catalina showed lower effect for G x E interaction ensuring the better performance of all the cultivars evaluated, specially the improved line PT14053 (Figure 1). Both sites could be considered for the selection of high yielding cultivars under favorable growing conditions. La Soledad registered high level for G x E interaction related to delayed planting, low temperature, and modifications of the yield response in some cultivars compared to other varieties and other environments. The most stable cultivar across environments was Pinto Nacional (Landrace) followed by Pinto Saltillo (Improved), which were less influenced by the environment and showed adaptation in all the environments, especially in La Soledad and Santa Catalina de Siena. Other cultivars showing intermediate yield stability were Querétaro and Canario with better response at the same planting sites. Lower yield stability was obtained for recent released cultivars, such as: PID 1, NOD 1 due to its adaptation under a specific environment (Durango). Negro San Luis also registered low values for yield stability and positive PC1 score indicating stability with intermediate and favorable adaptation to all environments, showing

positive response in La Soledad and Vicente Guerrero. Seed yield average by planting site was Durango= 2,378 kg/ha, La Soledad = 1,469 kg/ha, Santa Catalina = 1,038 kg/ha and V. Gro =531 kg/ha. Cultivars showing higher yield average across environments were Pinto Nacional (1,621 kg/ha) and PID 1 (1,497 kg/ha).

Table 1. Mean square of the ANOVA for seed yield determinations in landrace cultivars grown in four environments. Durango, 2022.

Sources of variation	Degrees of Freedom	Yield t/ha
Environments (E)	3	24.5**
Cultivars (C)	7	0.5**
E * C	21	0.6**
Error	128	0.04
Average		1.4
Coefficient of Variación (%)		15.2

**highly significant ($p \leq 0.01$).

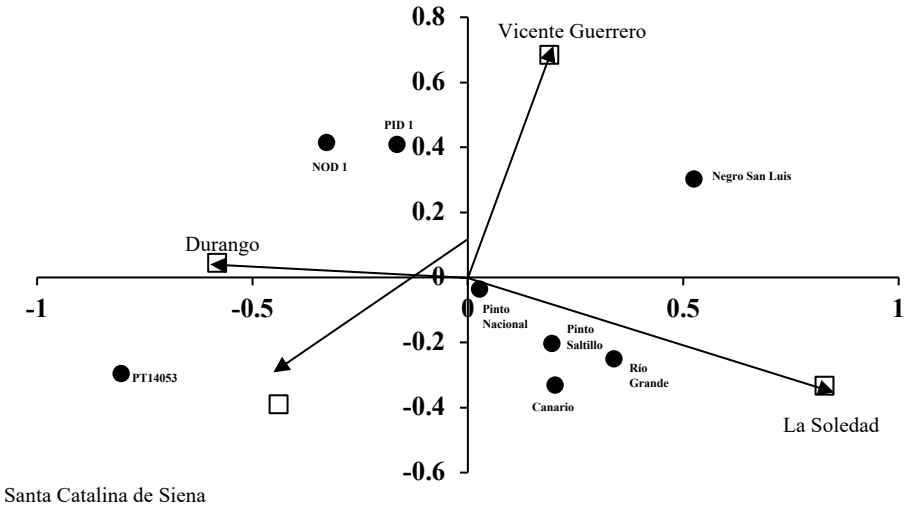

Figure 1. Contribution of environment and cultivar to interaction represented by using two principal components of the AMMI yield model of landrace and improved common bean cultivars grown in four contrasting environments.

CONCLUSIONS: Seed yield performance in landrace and improved common bean cultivars were highly influenced by environment, varieties, and G x E interaction. Common bean varieties showing yield stability were detected in both landrace (Pinto Nacional) and improved cultivars (Pinto Saltillo), but not always obtained the highest yield. The improved common bean cultivar PID 1 registered low yield stability but also showed high seed yield and quality.

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YIELD COMPONENTS OF BEANS IN REPONSE TO PHOSPHORUS AND NITROGEN

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INTRODUCTION

Beans (*Phaseolus vulgaris* L.) are a basic crop for Mexico and Latin American countries. Its consumption for its nutritional and medicinal properties helps reduce the risk of some diseases (Bennink, 2005). In order to satisfy the demand for beans in Mexico, the aim is to increase grain yield, for which the supply of nitrogen and phosphorus is decisive. Several studies have shown that increased application of nitrogen (N) increases the number of pods, grains and yield (Escalante et al., 2015). Regarding phosphorus (P), some studies indicate that the P deficit reduces the growth of the aerial parts of the plant, the leaves are smaller and more intense in color (Marschner, 1995). Apaez et al. (2013) pointed out that the supply of P stimulated the response to N that was reflected in a higher yield of *Vigna*. The objective of this study was to determine if nitrogen and phosphorus affect yield and their components in beans.

MATERIALS AND METHODS

The study was carried out under a rain and irrigation regime in Montecillo México, México, with a temperate climate, loamy-clay soil, 0.50 ppm of NO_3, moderately low in P (14 ppm), pH of 7.0 and without salinity problems. The treatments consisted of the application of 100 kg ha^{-1} of N (Urea, 46%; N, 50% before sowing and 50% 30 days after) and 100 kg of P (P_2 0_5, simple superphosphate, 19.5% P). The control treatment was the natural fertility of the soil (0 fertilizer). The bean cultivar Cacahuate 72 (Cacahuate) with a determinate type I growth habit, pink flowers and elongated cream grain with red stripes, was sown on June 16, 2018 in a density of 40 cm*20 cm that generated 12.5 plants m^{-2}. The experimental design was a randomized block with four repetitions. The grain yield (GY), number of normal grains (GN), grain size (SG, mean grain weight), number of pods (PN) and number of grains per pod (GP) were recorded. The criteria to characterize the variables was the one presented in Escalante and Kohashi (2022). In addition, the phenology and climatic conditions during crop development were recorded.

RESULTS AND DISCUSSION

The emergence occurred 10 days after sowing (d), the flowering at 42d; and physiological maturity (PM) at 95 d. The average maximum and minimum temperature was 29 ºC and 8 ºC, the pluvial precipitation and evaporation were 482 and 768 mm, respectively. In the GY, GN and PN, increases were observed with the N * P interaction (Table 1), but not in SG and GP, which on average were 0.456 and 4.4, respectively. The highest increase was with N and P combined, while the lowest when these were not applied. Similar trends were observed in GN and PN. This shows that with N supply there is a greater response to P, as also reported by Apáez *et al.* (2013).

Table 1. Yield and components of beans (*Phaseolus vulgaris* L.) cv.Cacahuate 72 depending on N and P. Montecillo México, México. Summer 2018.

N	P	YG gm^{-2}	GN m^{-2}	SG (g)	PN m^{-2}	GP
00	00	177 c	389 c	0.455	99 c	3.9 ab
00	100	229 c	472 c	0.485	126 c	3.8 b
100	00	320 b	700 b	0.457	183 b	5.0 ab
100	100	390 a	913 a	0.427	218 a	5.4 a
	N*P	** (65)	*(210)	NS	*(32)	NS

***,*,*,* P>0.001,0.01 and 0.05, respectively.; Tukey 0.05. GY = grain yield; GN= number of grains; SG= grain size; PG= pods with grain; GP= grains per pod.

CONCLUSIONS

In Cacahuate beans, the supply of nitrogen and phosphorus increases the yield, number of grains and pods. Grain size and grains per pod are not affected. The response to phosphorus is a function of the nitrogen supply.

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YIELD AND GENETIC DIVERSITY OF COMMON BEAN LANDRACE CULTIVARS GROWN IN NORTHERN MÉXICO

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INTRODUCTION: The state of Durango, is considered one of the most important centers of common bean genetic diversity and domestication. Researchers consider that several landrace cultivars have been displaced by the improved cultivars (mainly Pinto Saltillo and Pinto Centauro), thus persistence and diversity need to be evaluated. The objective was to evaluate seed yield and genetic diversity landrace cultivars collected in the state of Durango, México.

MATERIALS AND METHODS: Collection trips were performed during 2022 in several towns and local markets in Durango (Santana *et al*., 2022). Twenty-six accessions were collected, and along with four cultivar checks were planted under a Rectangular Lattice (6 x 5) experimental design. Cultivars were sown on July 1st, 2022, in experimental plots consisting of two rows 5 m in length and 0.81 m apart. Liquid fertilizer, irrigation and herbicide (fomesafen) were applied. Insecticide (dimethoate or spinetoram) was also applied four times to control the bean beetle (*Epilachna varivestis*) and the bean pod weevil (*Apion* sp.). Days to first flower and physiological maturity (CIAT, 1987), disease response, seed yield and 100 seeds weight were collected. Fifty-five phenological, morphological, and agronomic traits, included those in the characterization guide (SNICS, 2017) were also evaluated. Plant samples were taken consisting of two 4 m rows and 0.81 m wide (6.48 m^2) for seed yield determination. The data were analyzed with descriptive statistics, analysis of variance, and principal component analysis (PCA).

RESULTS AND DISCUSSION: Significant differences ($p \leq 0.05$) were detected among cultivars for most of the evaluated traits (Table 1). Higher days to flowering (53 days after planting; DAP) and physiological maturity (105 DAP) were registered in common bean landrace cultivars. Higher values for anthracnose incidence were also observed in landraces due to the absence of genes conferring resistance to plant pathogens. The absence of symptoms was detected for rust, but CBB showed intermediate to generalized symptoms among cultivars. Most of the cultivars showed statistically similar seed yield (1,526 kg ha^{-1} to 2,902 kg ha^{-1}), and only two cultivars registered significant seed yield reduction (flor de mayo 1,334 kg ha^{-1} and bayo 1,445 kg ha^{-1}). High yield potential was observed in most of the landraces due to advances in adaptation under variable climate conditions at individual and populational levels.

The PCA required 24 components to reach a higher level (>99%) in the explanation of the observed variance. Seed traits showed high diversity values among landrace and improved common bean cultivars. Cultivar groups showed separation between the germplasm of the Durango and Jalisco genetic races (Figure 1), especially for shiny black cultivars (group I). The pinto cultivars were included in the second group II, mainly in IIa_1 included pinto, borroso and ojo de cabra and a high-level separation was observed for cultivars known as Pinto Nacional and ojo de pato (duck eye) (IIa_2), all of them showing a primary color (white, cream, or gray) and one or two (brown or gray) secondary colors. Another sub-group (IIb_1) was subdivided into three subgroups including Pinto Saltillo (derived from a multiparent population) and flor de mayo (pink) ($IIb_{1\text{-}1}$), as well as blanco, bayo and garbancillo (cream) groups ($IIb_{1\text{-}2}$). The sub-group IIb2 showed and separation at high level for the Querétaro cultivar ($IIb_{2\text{-}1}$) and other bayo (cream) and sangre de toro (purple) landrace cultivars. A high level of diversity was observed due to a gradual and

prolonged selection process under highly variable environmental conditions, performed in heterogenous and heterozygotic populations represented by landraces cultivated in Durango and those introduced from the Jalisco Race.

Table 1. Average values for traits evaluated in common bean landraces grown in Durango, 2022.

Variedad	[1]DF	A	R	B	DPM	Yield kg/ha	100 Seeds Weight (g)
Querétaro	53^{ab}	3	1	5	104^{abc}	2,902^{a}	24.4
Bayo Blanco	51^{abcd}	3	1	6	105^{abc}	2,637^{ab}	45.9
Pinto Nacional	45^{cd}	4	1	6	104^{abc}	2,605^{ab}	30.7
Bayo	49^{abcd}	2	1	6	100^{bcdef}	2,120^{ab}	41.0
Sangre de Toro	53^{ab}	5	1	6	101^{abcde}	1,970^{ab}	34.6
Negro San Luis	53^{ab}	2	1	5	105^{ab}	1,888^{ab}	34.0
Pinto Saltillo	50^{abcd}	1	1	6	99^{cdefg}	1,870^{ab}	31.6
Ojo de Pato	53^{ab}	2	1	6	105^{abc}	1,744^{ab}	48.7
Borroso	49^{abcd}	1	1	6	100^{bcdef}	1,619^{ab}	40.9
Flor de Mayo	51^{abcd}	3	1	6	106^{ab}	1,334^{b}	29.4
Average	50				101	1,896	34.9
[2]C. V. (%)	3.5				1.4	18.3	4.1

[1]DF= days to flowering, A= anthracnose, R= rust, B= bacterial blight, DPM= days to physiological maturity [2]C. V.= Variation coefficient. [a-b]Significant differences Tukey ($p \leq 0.05$).

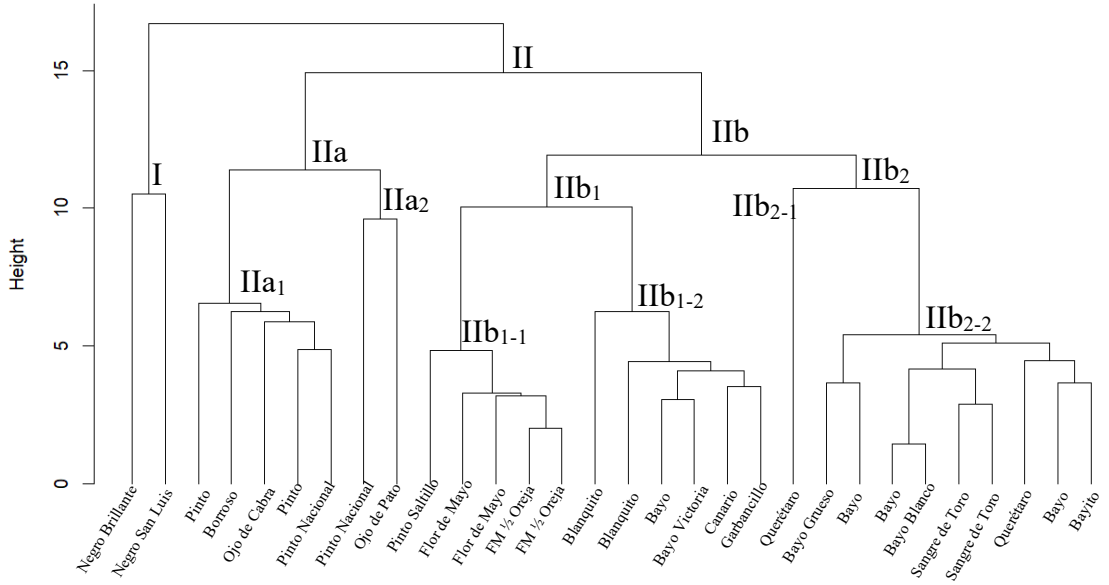

Figure 1. Dendrogram based on morpho-agronomic traits evaluated in common bean landraces and improved cultivars grown in Durango.

CONCLUSIONS: Most of the landraces and improved cultivars showed similar yield levels under irrigation and early planting dates. High levels of common bean diversity were observed in Durango where several commercial classes were collected.

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YIELD COMPONENTS OF BEANS OF INDETERMINATE HABIT AND VARIABLE POPULATION DENSITY IN A WARM CLIMATE

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INTRODUCTION

Due to its nutritional and medicinal properties, beans (*Phaseolus vulgaris* L.) are an important crop for the population (Bennink, 2005). 87% of the planted area is rainfed. Therefore, it is dependent on weather conditions. The average yield of the Iguala Gro region is 0.91 g m^{-2} (SIAP, 2021), which is insufficient to cover internal consumption, so imports are used. To increase yield, the study of population density is used (Escalante *et al*., 2015). The objective of the research was to evaluate in warm weather, the effect of population density on grain yield and its components in common bean cultivar Jamapa with indeterminate growth habit type II.

MATERIALS AND METHOD

The cultivar (cv) Jamapa of indeterminate growth habit type II was sown on July 17, 2018, under a rainy season in Iguala Gro with a warm climate (Aw0, García, 2005). In the first 30 cm, the soil is loamy-clay, pH 8.4, MO 3.5 % and assimilable N of 45 kg ha^{-1}. The treatments consisted of four topological arrangements: 80 cm *30 cm; 40cm*30cm; 40 cm*20 cm and 40 cm*10 cm, which generated population densities (PD) of 4.16; 8.3; 12.5 and 25 plants m^{-2}. The experimental design was randomized blocks with four repetitions. The variables under study were the days to emergence, to flowering (F) and to physiological maturity (PM). At PM, the number of pods with grain (PN), normal grains per pod (GP), normal grains (GN), grain size (SG) and grain yield (GY) were recorded. The criteria to characterize the variables are presented in Escalante and Kohashi (2022). An analysis of variance was applied to the variables under study and the mean comparison test was applied to the treatments with significant differences (Tukey $\alpha = 0.05$) using the statistical package SAS version 9.2 (SAS, 2011).

RESULTS AND DISCUSSION

The emergence was 8 days after sowing (d), the F and MF was at 41 and 80 d, respectively. The average minimum and maximum temperature during the cycle was 23 °C and 38°C. During the crop cycle, rainfall was 750 mm. With the exception of the number of GP and SG, the remaining variables showed significant differences to changes in PD (Table 1). The PN, GN and GY presented a response that was adjusted to a second degree polynomial, where the highest values were at the PD of 12.5 plants m^{-2} (40 cm*20cm). At higher PD, the canopy of cv Jamapa could have had greater interference between plants due to inputs, which limited a greater response in yield. Similar trends in Cacahuste 72 beans in temperate climates were reported by Escalante *et al*. (2015).

Table 1. Grain yield and its components in bean of indeterminate growth habit type II cultivar Jamapa, Iquala Gro. Summer 2018. Data presented in m^{-2}.

DP (plantas m^{-2}).	PN	GP	GN	SG (g)	GY
4.16	165bc	6	990c	0.129	1161c
8.3	177b	6.5	1150b	0.126	1449b
12.5	197a	6.4	1261a	0.128	1614a
25	155c	6.2	96.1c	0.119	1143c
Tukey(0.05)	15	2	70	0.1	159
Prob. F	**	NS	**	NS	**

PD= population density; PN= pods with normal grain; GP= normal grains per pod; GN= grain number; SG= grain size; GY= grain yield.

CONCLUSIONS

The days to the beginning of flowering and to physiological maturity did not show changes due to the population density. Changes in population density did not affect the number of grains per pod and the grain size of the Jamapa cultivar. In contrast, the number of pods, grains and yield were affected. The response to population density in the number of pods, grains, and yield showed a quadratic trend. The highest values were with the density of 12.5 plants m^{-2}.

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NOTICE OF NAMING AND RELEASE OF RINCÓN GRANDE, A NEW HIGH YIELDING OPAQUE BLACK COMMON BEAN CULTIVAR FOR TROPICAL AREAS OF VERACRUZ AND CHIAPAS, MEXICO

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INTRODUCTION: The Cotaxtla Field Station (CECOT) of the National Institute of Forestry, Agriculture and Livestock Research (INIFAP) announces the denomination and release of 'Rincón Grande', a new high-yield black bean variety. This new variety has an indeterminate bushy and erect type II growth habit (Singh, 1982), with an average plant height of 45.9 cm, purple flowers and yellow pods at physiological maturity, a stage that occurs around 76 days after planting in the tropics of southeastern Mexico. The grain of this variety is opaque black and small, light in weight (19.8 g/100 seeds), which meets the characteristics of the type of bean that consumers demand in that region. 'Rincón Grande' is resistant to bean rust (caused by *Uromyces appendiculatus* var. *appendiculatus*), anthracnose (caused by *Colletotrichum lindemuthianum*) and common mosaic virus (BCMV), and tolerant to the golden yellow mosaic virus (BGYMV), while most landraces and cultivar Negro Jamapa, commonly used in the states of Veracruz and Chiapas, are susceptible to these diseases. 'Rincón Grande' is widely adapted to the tropical and subtropical areas of both states, Chiapas and Veracruz, with a high yield potential (>2.2 t ha^{-1}), much higher than the aforementioned bean varieties.

MATERIALS AND METHODS: 'Rincón Grande' originated from the simple cross Jamapa Plus/XRAV-187-3 carried out in 2007 at the INIFAP Bajío Field Sation (CEBAJ), located in Celaya, Guanajuato, Mexico. The Jamapa Plus line was used as a parent that possesses wide adaptation to the tropics and its grain is highly accepted by consumers. The elite line XRAV-187-3 was used as a source of resistance to bean common mosaic and bean golden yellow mosaic viruses since it has the *I* and *bgm-1* genes that confer resistance to BCMV and BGYMV, respectively (Anaya-López *et al*., 2018). The process to obtain 'Rincón Grande' included mass selection in F_2 and F_3 at CEBAJ in 2009 and in 2010 in F_4 and F_5 at CECOT, located in Medellín de Bravo, Veracruz. During the 2011 growing season, the individual selection was made to derive the F_{5-6} breeding lines selected in CECOT. In the 2012 and 2013 growing seasons, the mass selection was carried out in F_7 and F_8 in Rincón Grande, Orizaba, Veracruz. From this process, the F_8 improved line Jamapa Plus/XRAV-187-3-1-2 was derived, which gave rise to 'Rincón Grande'. During the 2015 and 2016 growing seasons, this line was included along with 49 other improved lines in the Bean Adaptation Nursery (BAN) and evaluated in seven environments in Veracruz and Chiapas that encompassed rainfed, residual moisture, acid soils, and terminal drought conditions. From this nursery, a group of 12 breeding lines was selected, including the Jamapa Plus/XRAV-187-3-1-2 breeding line, which was included in the regional yield trial (RYT), and evaluated across eight different environments in Veracruz and Chiapas during the 2016 and 2017 growing seasons. In 2019, evaluation for reaction to bean rust and anthracnose isolates (a composite collected from Veracruz and Chiapas bean fields) was made in the Central Chiapas Field Station (CECECH) greenhouse. In the 2019 and 2020 growing seasons, 'Rincón Grande' was assessed as part of the Elite Regional Yield Trial (ERYT) in seven environments in Veracruz and Chiapas. Validation

plots were established in farmers' fields during the 2020 and 2021 growing seasons in the central and northern production regions of Veracruz. Subsequently, registration of 'Rincón Grande' was proposed to the National Catalog of Plant Varieties (CNVV) before the National Inspection and Certification Service (SNICS). In late 2022, 'Rincón Grande' received Provisional Registration Number 4502-FRI-113-091222/C.

RESULTS AND DISCUSSION: In the bean adaptation nursery (BAN), 'Rincón Grande' (Jamapa Plus/XRAV-187-3-1-2 breeding line) outperformed the control varieties Negro Comapa and Negro Grijalva in conditions of residual soil moisture, acid soil, and terminal drought. Its overall average yield was 19.2 and 30.7% higher than that obtained by the control varieties, respectively. Results from the RUYT indicated that the new variety obtained an average yield of 6.4 and 2.6% higher than that obtained by the same control varieties. Under greenhouse conditions, 'Rincón Grande' showed resistance to bean rust and anthracnose, whereas Negro Jamapa and Verdín cultivars were moderately susceptible to bean rust and Negro Medellín, the other control variety, was highly susceptible to anthracnose. Results from the ERYT showed that 'Rincón Grande' produced an average seed yield (1,379 kg ha^{-1}) statistically similar to that of the most productive breeding line (Jamapa Plus/XRAV-187-3-4-4), but higher than check cultivars Negro Medellín, Negro Jamapa and Verdin. However, 'Rincón Grande' showed the highest yield stability across the seven test environments. In the validation plots with the presence of drought, the average seed yield of 'Rincón Grande' was slightly higher than that of the breeding line Jamapa Plus/XRAV-187-3-4-4 and 20.5% higher than that of the commercial control Negro Jamapa (Table 1).

Table 1. Grain yield (kg ha^{-1}) of Rincón Grande in validation plots in comparison to Jamapa Plus/XRAV-187-3-4-4 breeding line and Negro Jamapa cultivar.

Location / growing season	Rincón Grande	Jamapa Plus/XRAV-187-3-4-4	Negro Jamapa
Ejido Providencia, Medellín/F-W† 2020-21	1,182.0	1,138.0	743.0
Ejido Providencia, Medellín/F-W 2021-22	1,015.0	1,083.0	818.0
CEIXTA‡, Tlapacoyan /F-W 2021-22	952.0	794.0	1,052.0
Average	1,049.7	1.005.0	871.0
% increase§	--	4.4	20.5

†F-W= Fall-Winter cropping season (October-January). ‡Ixtacuaco Field Station. §With respect to Jamapa Plus/XRAV-187-3-4-4 and Negro Jamapa.

CONCLUSIONS: The results indicated that the newly registered bean cultivar 'Rincón Grande' has a high yield potential (higher than that of the varieties commonly used in the region). It is resistant to bean rust, anthracnose and the bean common mosaic virus (BCMV). 'Rincón Grande' has a wide adaptation in the tropical and subtropical areas of Veracruz and Chiapas, and regions with similar environmental conditions in southeastern Mexico.

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AGRONOMIC PERFORMANCE OF THREE SNAP BEAN *(PHASEOLUS VULGARIS L.)* VARIETIES IN SOUTHERN BENIN (WEST AFRICA)

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INTRODUCTION

Leguminous vegetables are highly valued, having numerous nutritional and human health benefits that makes them an important crop (Kader et al., 2021) for food and nutritional security. Snap bean is often consumed in combination with several meals around the world. In Benin, snap bean production has drastically declined in recent years. The production constraints include pests, diseases, and low diversity of improved varieties (Agoyi et al., 2019). This study evaluated the adaptation and agronomic performance of snap bean varieties in diverse vegetable production sites of Benin, identified pests and diseases, characterized the most severe pathogens, and proposed solutions to boost the production of snap bean in Benin.

MATERIALS AND METHODS

Genetic material

As shown in Figure 1, a total of 3 snap bean varieties were used in this study, two varieties (PV-T002, PV-T004) introduced from Togo, and Cora, the commercial variety currently grown by most producers in Benin was used as a control.

Fig. 1 Seeds of the three snap bean varieties used in the experiment

Experiments were organized in a Randomized Complete Block Design (RCBD) with three replications at each site over two seasons. Plots consisted of four 5 m long rows, 50 cm between rows and 20 cm between plants. Two seeds were planted per hole, and thinned to one plant after emergence.

Data collection

The days to 50% flowering and days to 85% maturity were recorded. Response to the most prevalent diseases and pests was scored to determine the disease severity index (DSI) on a percentage basis, where DSI (%) = [sum (class frequency × evaluation class score)]/[(total number of plants) × (maximum disease index)] × 100.

RESULTS

In Table 1, the days to 50% flowering (DF) for the varieties evaluated ranged from 35 to 37, with a mean of 36 across genotypes and sites. PV-T002 was the earliest variety for flowering (31 DF at Grand Popo, 35 at Sèmè and 36 at Sèmè and Xêvié). Days to maturity (DM) ranged from 69 to 71, with a mean of 71 across genotypes and sites. PV-T002 was the earliest variety across sites, and PV-T004 was the latest. For mean fresh pod yield across sites showed that PV-T002 and PV-T004

were above the average (11 t ha^{-1}) and the highest yield was recorded for PV-T002 (14 t ha^{-1}), followed by PV-T004 (12 t ha^{-1}). The lowest fresh pod yield was recorded on Cora (8 t ha^{-1}).

Table 1. Means for phenological and yield of 3 snap bean genotypes across three sites

Varieties	DF (Days)					DM (Days)					Yield (t/ha)				
	Grd popo	Houé	Sèmè	Xêvié	Mean	Grd popo	Houé	Sèmè	Xêvié	Mean	Grd popo	Houé	Sèmè	Xêvié	Mean
Cora	33	36	36	36	36	68	70	71	71	71	8	7	9	7	8
PV-T002	31	36	35	36	35	66	71	71	70	69	13	14	13	14	14
PV-T004	35	35	36	35	37	70	71	70	71	72	12	12	13	12	12
Mean	**33**	**36**	**36**	**36**	**36**	**68**	**71**	**71**	**71**	**71**	**11**	**11**	**12**	**11**	**11**
LSD (0.05)	**4**	3	5	3	2	7	4	3	5	2	2	2	2	2	1
CV(%)	**13**	5	9	5	9	7	3	2	4	4	11	10	12	12	11

Snap bean tolerance assessment showed that the most prevalent disease was root rot which had the highest severity index for the three varieties. Furthermore, Cora was more susceptible than the other varieties (PV-T002 and PV-T004). The PV-T002 was the most resistant variety (Figure 2).

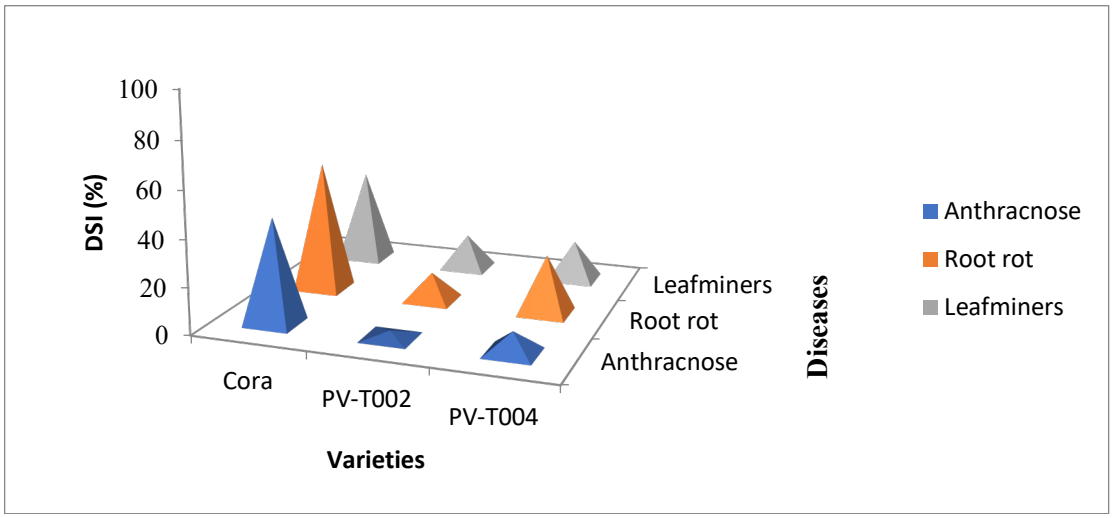

Figure 2. Anthracnose, root rot and leaf miners DSI on three snap bean varieties grown in Benin.

DISCUSSION

The snap bean varieties introduced to Benin had good adaptation abilities and performed better than the popular commercial variety. Their short cropping cycle could allow 5 production cycles a year. Their tolerance to the most prevalent pests and diseases indicates their potential to overcome some of the challenges leading to the decline of snap bean production in Benin.

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GENETIC ANALYSIS OF POD QUALITY AND YIELD COMPONENTS IN CLIMBING SNAP BEAN POPULATIONS

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INTRODUCTION

Pod quality and pod yield are important traits in snap bean production and marketing. High pod quality increases competitiveness of the product in domestic and international markets. Pod yield influences the farmers' adoption of the variety and the profitability of his enterprise. However, breeding for these traits in eastern Africa is constrained by lack of information on their heritability. Heritability influences response to selection and optimal stage in the breeding cycle when it is most effective and efficient to conduct selection for target traits. Very little is known about heritability of maturity, pod quality and pod yield in snap bean germplasm used by improvement programs in eastern Africa. Therefore, it is important to identify and characterize modes of heritability of growth habit, duration to flowering, pod quality and pod yield with the aim of designing breeding schemes for introducing superior genes to elite snap bean germplasm. Little has been done to develop improved snap bean varieties combining early maturity, good pod quality, pod yield and climbing growth habit for smallholder farmers and informal seed producers in the Eastern Africa region. The objective of this study was to estimate heritability of duration to flowering, pod quality (pod length and pod diameter) and pod yield traits using the parent-offspring regression method.

MATERIALS AND METHODS

Eleven F_2 populations were developed from crosses among six climbing and eight bush snap bean lines at the Kabete Field Station between 2012 and 2014 using the backcross breeding method. The climbing parental lines were HAV 130, HAV 131, HAV 132, HAV133, HAV 134 and HAV 135 and were obtained from the regional breeding program based at the University of Nairobi. Bush varieties were Star 2053, Morgan, Teresa, Paulista, Morelli, Serengeti, Vernadon and Samantha, which are commercial varieties of snap bean. About 100 plants in each F_2 population were evaluated for duration to flowering, pod length, pod diameter, pods per plant and pod yield. Thirty superior and 20 inferior individuals for the above traits were selected and self-pollinated to generate F_3 progeny. In 2014, the F_3, F_2, BC_1P_1, BC_1P_2 and their parents were grown in an irrigated trial at Mwea Research Station and data collected on maturity, pod length, pod diameter, pod per plant and pod yield. F_2/F_3 regression was used to estimate heritability. Heritability was calculated by the parent-offspring correlation method (Mather and Jinks, 1971; Falconer, 1989).

RESULTS AND DISCUSSION

Results showed significant differences ($P< 0.05$) for duration to flowering, pod length, pod diameter, pods per plant and pod yield across the six generations (P_1, P_2, BC_1P_1, BC_1P_2, F_2 and F_3). Duration to 50% flowering varied from 28 to 42 days in the 11 populations. Pod length varied from 6.5 to 20.9 cm. Pod diameter varied from 5.4 to 8.0 mm. Pods per plant varied from 3.6 to 27.3. Pod yield varied from 700 to 12,509 kg ha^{-1}. All the traits showed moderate to high heritability but this varied between populations. Heritability for duration to flowering varied from 0.52 to 0.91, pod length varied from 0.42 to 0.91, pod diameter varied from 0.51 to 0.91, pods per plant varied from 0.75 to 0.94, and pod yield varied from 0.68 to 0.92. Population 2, 4 and 5 were not variable for pod length and pod diameter traits. Populations 7, 8, 9 and 10 were most variable

for these traits. The results indicated that duration to flowering, pod length, pod diameter, pods per plant and pod yield are highly heritable and could be transferred to the commercial snap bean varieties via phenotypic selection with good genetic gain (Table 1).

Table 1. Narrow sense heritability of duration to flowering, pod length, pod diameter, pods per plant and pod yield of 11 snap bean populations grown at Mwea short rain season, Kenya.

Trait	h^2 (F_2: F_3)											
	Pop1[§]	**Pop2**	**Pop3**	**Pop 4**	**Pop 5**	**Pop 6**	**Pop 7**	**Pop 8**	**Pop 9**	**Pop10**	**Pop11**	**Mean**
Days to flowering	0.67	0.79	0.52	0.77	0.91	0.70	0.67	0.90	0.79	0.91	0.88	0.77
Pod length (cm)	0.42	0.58	0.64	0.64	0.58	0.84	0.83	0.91	0.87	0.90	0.88	0.74
Pod diameter (mm)	0.74	0.83	0.86	0.93	0.91	0.51	0.89	0.86	0.88	0.87	0.89	0.83
Pods plant-^{1}	0.90	0.91	0.88	0.86	0.89	0.75	0.88	0.94	0.88	0.92	0.91	0.88
Pod yield (kg ha-^{1})	0.90	0.68	0.79	0.90	0.92	0.79	0.87	0.90	0.87	0.91	0.88	0.86

[§]Pop1 – Population 1

Duration to 50% flowering trait was highly heritable. However, its heritability varied among the populations. Heritability was highest in population 5 and 10 (h^2=0.91) and lowest in Population 3 (Table 1). The mean heritability for days to flower was 0.77. Narrow-sense heritability for pod length ranged from 0.42 in Population 1, to 0.91 in Population 8 (Table 1). The mean heritability for pod length was 0.74. Heritability of pod diameter was high. It varied from 0.51 (Population 6) to 0.93 (Population 4). Heritability of pods per plant in all the populations was above 0.75 suggesting that the trait was highly heritable in all populations (Table 1). Heritability ranged from 0.75 (Population 5) to 0.94 (Population 8). Heritability for pod yield ranged from 0.68 (Population 1) to 0.92 (Population 5). The mean heritability for pod diameter was 0.83, pods per plant was 0.88, and pod yield was 0.86.

High narrow-sense heritability of the traits suggest that they are controlled by a few genes. Heritability influences response to selection and optimal stage in the breeding cycle when it is most effective and efficient to conduct selection for target traits. Traits with high heritability are not much influenced by environment and therefore, they can be phenotypically selected. Such traits can be selected during early generations (F_3 and F_4) compared to traits with low heritability which can only be selected during later generations (F_6 and F_7) increasing cost of carrying out an experiment.

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POD YIELD, POD QUALITY AND DISEASE RESISTANCE OF NEW SNAP BEAN LINES

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INTRODUCTION: Snap bean (*Phaseolus vulgaris* L.) also commonly known as 'French bean' is probably the most important high value bean grown in East and Central Africa. They are mostly grown for export markets but the domestic markets especially in urban areas are growing rapidly. However, most of the available varieties for the snap bean are low yielding and susceptible to diseases such as rust, angular leaf spot, anthracnose and common bacterial blight. Due to demand for high quality, smallholder farmers use toxic chemicals to reduce production cost and post-harvest losses associated with pests and diseases. Use of fungicides increases cost of production, reduces profitability and competitiveness of snap bean in domestic and export markets, and increases the risk of rejection of the produce due to stringent maximum residual levels in export markets. In 2001, a regional snap bean improvement programme was started at the University of Nairobi. This program was initially supported by CIAT and ECABREN, and from 2006 by ASARECA. The goal of this program was to develop improved snap bean varieties with high yield potential, resistance to biotic stresses, and high pod quality for smallholder producers (Kimani, 2006). Populations with combined resistance to rust, angular leaf spot and anthracnose were developed at the University of Nairobi (Wahome at al., 2011). Four nurseries of advanced lines were developed from these populations. These were KSB 13, KSB 14, KSB 15 and KSV 14 (Table 1). The objective of this study was to evaluate and validate the new, locally bred snap bean lines for yield potential, pod quality and disease resistance.

MATERIALS AND METHODS: One hundred and seven lines were grown at Kabete Field Station (1,737masl) for two seasons, and for one season at Kirogo Research Station, Mwea (1,159masl). The lines were evaluated for pod length, pod shape, pod curvature, pod yield, disease reaction and market class grade distribution. Three commercial varieties (Serengeti, Samantha and Julia) were used as checks. Disease resistance and vigour were scored on a 1 to 9 scale , where 1 to 3 is resistant, 4 to 6 intermediate, and 7 to 9 is susceptible. Pod length and pod diameter were determined using a Royal Sluis grading ruler. Pod yield was the cumulative weight of all harvests. The data was subjected to analysis of variance using Genstat software. Fisher's protected least significance difference (LSD) at $P<0.05$ was used for mean separation.

Table 1. Nursery code, growth habit and description of of advanced snap bean lines used in the study

Nursery and Line code	Growth habit	Number of entries	Description
KSB13	Bush	46	A nursery constituted in 2013 and evaluated at Kabete Field Station and Mwea
KSB14	Bush	28	A nursery constituted in 2014 and evaluated at Embu and Kabete Field Station
KSB15	Bush	23	A nursery constituted in 2015 and evaluated at Embu and Mwea
KSV14	Climbing	10	A climbing snap bean nursery constituted in 2014 and evaluated at Kabete Field Station and Mwea
Total		107	

RESULTS AND DISCUSSION: Results showed that there are significant differences between snap bean lines for pod yield, pod length, pod diameter, pods per plant and disease resistance. Fifty-eight new lines were higher yielding than the checks. For example, KSB15-02 (10,835.4 kg ha^{-1}), KSB15-01 (12,847.2 kg ha^{-1}), KSB13-11 (12,968 kg ha^{-1}), compared to Serengeti (6,853 kg ha^{-1}), and Samantha (4,409 kg ha^{-1}) (Table 2). Seventy-six lines had round, straight pods with required standards for pod quality and more than 80% were of premium grades. For example, KSB15-01 and KSB15-07 produced 100% extra fine and fine pods and zero bobby. The new lines showed resistant reactions to angular leaf spot, common bacterial blight and rust diseases. The highest disease reaction was intermediate susceptibility. Only two lines showed intermediate reaction to rust while the rest were resistant. All the lines were resistant to angular leaf spot and common bacterial blight. Fifty-one bush and seven climbing lines showed a combination of high yield potential, pod quality and disease resistance. Climbing types were generally better yielding compared with bush types (Table 2). Utilisation of these lines as commercial varieties will not only increase productivity, reduce cost of production, increase profitability, but also increase competitiveness in regional and international markets.

Table 2. Pod yield, pods per plant and grade distribution of KSB and KSV snap bean lines grown at the Kabete Field Station and Kirogo Research Station, Mwea, Kenya.

Genotype	Pod yield (kg ha^{-1})			Pods $plant^{-1}$			% Grade distribution					
							Extra fine		Fine		Bobby	
	Kabete	Mwea	Mean	Kabete	Mwea	Mean	Kabete	Mwea	Kabete	Mwea	Kabete	Mwea
KSB13-11	7511.3	8199.2	12968.7	40.7	18	29	37.3	23.8	61	69.3	1.7	6.9
KSB13-12	9450.8	4474.3	14338.9	56.4	12	34	55.3	40.3	44.7	59.7	0	0
KSB14-01	12922	4242.9	8582.4	14	9.6	12	61.9	57.3	37.2	42.7	0.9	0
KSB14-02	10624.5	5944.5	8284.5	19	12.1	16	48.8	33.6	51.2	66.4	0	0
KSB15-01	19981.5	5712.8	12847.2	27	12	20	43.0	64.7	57.0	35.3	0.0	0.0
KSB15-02	6446.6	15224.3	10835.4	11	30	20	44.9	37.6	51.5	62.4	3.5	0.0
KSB15-03	13390.5	5419.2	9404.9	21	9	15	53.1	44.2	46.3	55.8	0.5	0.0
KSV14-01	37170.1	4220.0	20695.1	48	8	28	24.5	45.7	54.8	40.0	20.7	14.2
KSV14-02	36739.4	4608.4	20673.9	40	11	25	24.9	35.8	51.9	49.0	23.2	15.2
KSV14-03	25680.3	5352.5	15516.4	37	14	25	11.9	39.1	45.4	53.3	42.7	7.6
KSV14-04	21476.1	6550.0	14013.1	26	13	19	26.4	32.8	41.9	67.2	31.7	0.0
Checks												
Julia	3834.5	1400	2617.2	11	2.8	7	87	40.7	13	59.3	0	0
Samantha	5180.2	3638.6	4409.4	12	13.2	13	63.1	97.8	36.9	2.2	0	0
Serengeti	7961.7	5744.4	6853.1	16	13.8	15	67	70.6	31.5	29.4	1.4	0
Trial Mean	6163.9	4643.6	5403.6	11.7	12.7	11.7						
$LSD_{0.05}$ (G) §			0.5			0.47						
$LSD_{0.05}$ Site (S)			1.8			0.83						
$LSD_{0.05}$ (G x S) §			0.8			0.66						
CV (%)	3.1	15.2		7	13.1							

LSD-least significant difference, CV-coefficient variation, §G= Genotype, G x S= Genotype x Site interaction

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CHARACTERIZATION OF LIMA BEAN ACCESSIONS FOR TOLERANCE UNDER HIGH TEMPERATURES

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INTRODUCTION

Phaseolus lunatus L. is a legume that can grow in a wide range of conditions, although it develops in hot and humid environments (CIAT, 1980). This species has a high genetic diversity (Maquet; Vekemans; Baudoin, 1999) and greater tolerance for drought, excessive humidity and heat than *P. vulgaris* (CIAT, 1980), which are characteristic conditions of the Brazilian semi-arid region. Pod set is favored by air humidity, cool nights and adequate water availability in the soil, while high temperatures cause floral abscission, which contributes to low yields. Fertilization failure results from desiccation of the stigmatic surface. According to Baudoin (1988), the varieties of the sieva cultigroup are more resistant to heat and arid conditions than those of the big-lima cultigroup. The lima bean has a high yield potential and is an excellent source of food for the population due to its protein content. However, studies with the crop are incipient, mainly in relation to abiotic stresses. In this sense, the objective was to characterize lima bean accessions under high temperature conditions.

MATERIAL AND METHODS

The experiment was conducted in an area in the Department of Plant Science at Universidade Federal do Piauí (UFPI) in Teresina, PI, at 05°05'21″ S, 42°48'07″ W, and 72 m altitude in 2021. The climate in the region is of the Aw type according to the Köppen classification. Temperature averages in that period generally range from 20.8 ºC to 22.8 ºC minimum, from 26.3 °C to 26.6 °C mean, and 31.8 ºC to 33.6 ºC maximum.

Twenty-nine lima bean accessions from the Nuclear Collection of the *Phaseolus* Germplasm Bank (UFPI), from different origins (Mesoamerican, Andean, among others), were evaluated in a completely randomized experimental design with four replications. The evaluated traits were number of emitted flowers, number of aborted flowers, number of formed pods and number of aborted pods. Data were submitted to analysis of variance and comparison of means by the Scott & Knott test ($p > 0.05$) using the statistical program R.

RESULTS AND DISCUSSION

The lima bean accessions differed significantly in terms of evaluated characteristics, except for the number of aborted pods. Accessions BGP-UFPI 922 and BGP-UFPI 1206 stood out in terms of the number of flowers emitted and the number of aborted flowers. According to Monterroso and Wien (1990), the abscission of flowers is a phenomenon that occurs naturally in most species; however, this phenomenon is intensified at the end of the reproductive period. Flower abortion is influenced by the genetic profile of the plants as well as by environmental conditions. For Terán and Singh (2002), the main limiting factors for the development of bean crops in general are high temperatures and drought, which allows inferring that such environmental variables can be determinant in floral abortion. Oliveira et al. (2014) observed intense abortion of flowers and pods

in lima beans during the flowering and pod maturation period, when cultivated under water stress conditions, which negatively affects the grain production of the crop.

The accessions BGP-UFPI 849, BGP-UFPI 1036 and BGP-UFPI 1037 were among the most productive for the number of pods produced. As observed by Guimarães et al. (2007), the variability presented in the number of pods per plant is an important genetic attribute in the identification of potentially productive accessions. Accession BGP-UFPI 1037, which also presented a high average for the number of flowers emitted, has a determinate growth habit, which favors mechanized harvesting and makes it a potential parent in future breeding programs whose objective is to increase productivity in stress conditions.

In view of the results, it appears that there is the possibility of selecting lima bean accessions that are tolerant of inappropriate conditions, such as high temperatures, which harm the development of the crop.

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USE OF MIXED MODELS IN THE SELECTION OF LIMA BEAN LANDRACE VARIETIES IN TERESINA - PI

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INTRODUCTION

The lima bean (*Phaseolus lunatus* L.), in terms of socioeconomic importance, is the second most important species of the *Phaseolus* genus (Maquet et al., 1999). The use of mixed models is fundamental for the prediction of additive and genotypic genetic values, because even in conditions of unbalanced experiments, this approach allows the accurate and unbiased prediction of genetic values (Resende, 2002; Resende, 2007). The objective was to measure genetic parameters and the behavior of morphological traits related to grain yield, in different populational arrangements, and identify superior lima bean genotypes using the mixed model methodology.

MATERIAL AND METHODS

The work was carried out in the experimental area of the Crop Science Department of the Center for Agricultural Sciences of the Federal University of Piauí (UFPI), in Teresina - PI, in the agricultural year of 2022. The experimental design used was randomized blocks, in a 6 x 2 factorial, including six landraces varieties of lima bean and two planting densities (25,000 plants/hectare and 12,500 plants/hectare), in four replications.

The landraces varieties cultivated by small farmers in the states of Maranhão, Piauí and Ceará are conserved in the *Phaseolus* Germplasm Bank (UFPI) (Table 1). The charactistics evaluated were: length, width and thickness of pods and seeds, weight of one hundred grains and grain yield. Statistical-genetic analyzes were carried out using the SELEGEN Statistical Genetic Environment, according to the mixed model 012.

Table 1. List of the landrace varieties evaluated at densities of 25,000 and 12,500 plants/hectare, in Teresina, PI, Brazil.

***Phaseolus* Germplasm Bank Code**	**Common Name**	**Origin**
BGP - UFPI 1299	Marrom	Bom Jesus - PI
BGP - UFPI 1297	Boca de Moça	Varjota Assaré - CE
BGP - UFPI 1246	Rajada	Balsas - MA
BGP - UFPI 1235	Fava Branca	Buriti Bravo - MA
BGP - UFPI 1266	Fava Branca	Araripi - CE
BGP - UFPI 1365	Boca de Moça	Várzea Grande - PI

RESULTS AND DISCUSSION

The genetic variability of a trait as well as the environmental influence on the expression of that trait in an experimental population, can be measured by the ratio between the genetic and environmental coefficients of variation. The genotypic variance was higher than the environmental variance for the evaluated traits. Estimates of heritability were low for pod thickness (11%), seed thickness (0.224%) and grain yield (10.7%), and were medium for pod length (21%), pod width (37%), seed length

(16%), seed width (20%), and hundred-grain weight (43%). For Resende (2015), individual heritabilities can be classified according to their magnitude as low ($0.01 \leq h^2 \leq 0.15$), medium ($0.15 < h^2 < 0.50$) and high ($h^2 \geq 0.50$).

The interaction between landrace varieties and planting densities was not significant for all traits. Assuming that the residuals' normality premise was met, the deviation values for the assessed traits were estimated. The model is more suitable the smaller the deviance and the smaller the residuals. The means of the pod characteristics ranged from 69.06 mm to 81.57 mm for length; from 15.18 mm to 18.66 mm for width; and from 8.67 mm to 9.85 mm for thickness. For seed characteristics, the means ranged from 13.10 mm to 14.81 mm for length; from 9.46 mm to 10.61 mm for width; and from 5.47 mm to 5.48 mm for seed thickness. For weight of one hundred grains, the range was from 52.79 g to 68.65 g; and for grain productivity from 287.33 kg to 596.95 kg.

Large pods are desirable because they facilitate manual harvesting (Silva; Neves, 2011), in addition to being positively correlated with grain yield (Silva, 2015). As observed by Assunção Neto et al. (2020), grain yield results from yield components, such as seed size, number of seeds per pod, number of pods per plant, among others.

CONCLUSION

The REML/BLUP methodology proved to be efficient in estimating the genetic parameters in lima bean landrace varieties, with the presence of genetic variability being perceptible, although no differences were observed between plant densities.

The landrace variety Boca-de-Moça (UFPI 1297) showed good agronomic performance for important traits. It has larger and wider pods and seeds, in addition to high grain yield compared to the other varieties.

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FLOWERING TIME OF *PHASEOLUS COCCINEUS* L. IN THE CENTRAL PLATEAU OF MEXICO

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INTRODUCTION: Before plant domestication, species with food potential must have experienced a long natural selection process to reach, in harmony with the photoperiod and temperature, the flowering phase and develop fruits that ripened at the appropriate time at a given location (Aitken 1974). In addition, photoperiod not only modulates time to flowering, but also the development of branches and nodes as well as the balance between vegetative and reproductive growth throughout the partitioning of assimilates as indicated by Wallace (1985) in the common bean, *P. vulgaris*. The aim of this study was to register the flowering time of several sets of ayocote landraces grown in different years to explore the onset of flowering and its duration in *P. coccineus* at Central Mexico.

MATERIALS AND METHODS: In Texcoco, México (19°29' NL, 98°53WL, 2250 masl), as part of a project for germplasm conservation, 737 landraces of the 'Ayocote' bean (*P. coccineus* L) were sown and increased in yearly sets. These landraces were collected in the early 60's in a N latitude range from 15°87' in the southern state of Chiapas to 23°13' in the central-northern state of San Luis Potosí, Mexico. Each year, the experimental plot per landrace was a row of 5 m in length, with a row separation of 0.80 m. After plant establishment, seven plants per plot were tagged for data recording. Daily climatic data were taken from a nearby weather station.

RESULTS AND DISCUSSION: In Texcoco, the natural photoperiod on Jan. 1st is 10:59 h, and increases gradually to 13:19 h on June 19 to 22nd, and then decreases to 10:59 h on Dec. 31th. The flowering data shown in Table 1 and Figure 1 correspond to averages from a mixture of landraces that include a large diversity, as such the observed response can't be ascribed to a particular landrace or provenance. In the first two year/dates, the early landraces began flowering with a 12:47 h photoperiod (April 26) and 13:07 h photoperiod (May 20) respectively, when the photoperiod was gradually increasing through time (Fig. 1), most probably influenced by the increasing temperature (data no shown). As for the dates from May onwards, the beginning of flowering (green color) was delayed and the duration of the flowering period (red color) enhanced. The date at the end of May shows the larger average vegetative and reproductive periods, which was probably the optimum planting date for this species in a rainfed environment above 2,200 m.a.s.l. in central Mexico. However, recently the onset of the rainfall period is being delayed, and there is a need for faster and earlier Ayocote beans for those environments. Results suggest a large variation in the onset of flowering and the duration of the flowering period at the test location, variation due to genetic differences among the landraces, as well as differences in the environmental niches where the landraces were collected.

Table 1. Average flowering time of different sets of Ayocote bean grown in central Mexico at several year/planting dates.

Year/planting date	Number of landraces	Flowering time (das)		Photoperiod*	
		Min	Max	Min	Max
March 26, 2012	100	31	118	12.78	13.32
April 22, 2013	69	28	93	13.10	13.32
May 17, 2011	60	38	91	12.85	13.32
May 27, 2009	100	37	117	12.15	13.27
June 21,2010	151	42	92	12.38	13.00
July 1, 2010	144	36	88	12.03	12.93
July 7, 2008	113	40	105	11.62	12.98

Das=days after planting date, *=decimals

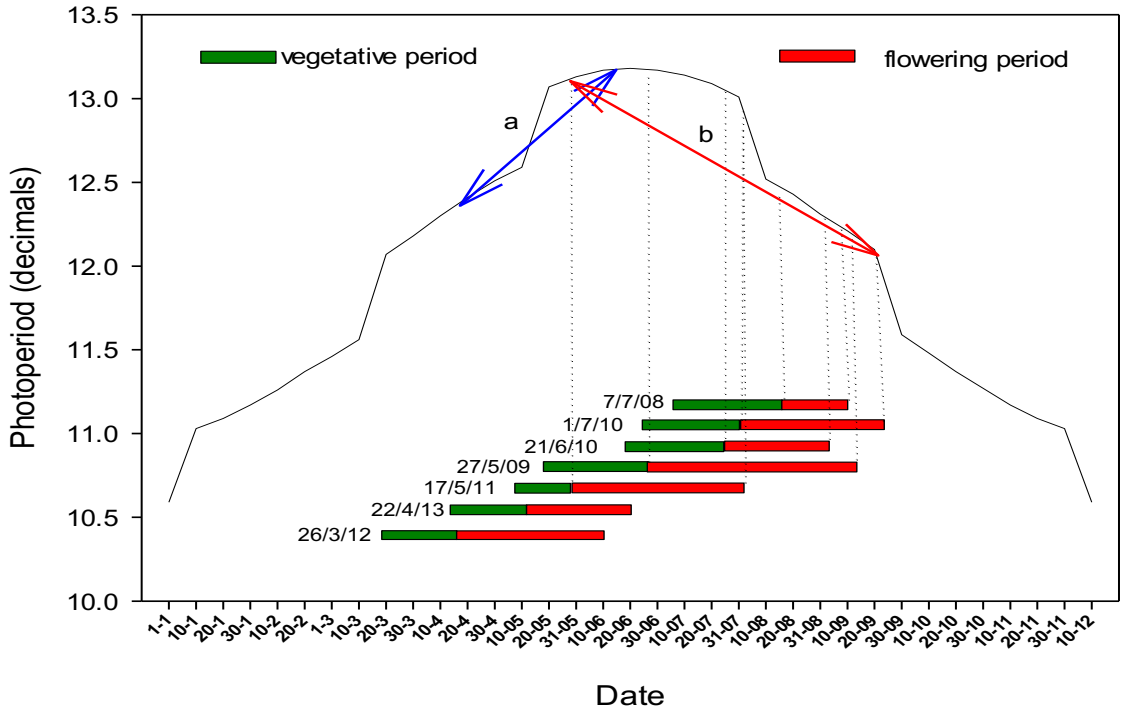

Figure 1. Average duration of vegetative (green) and flowering period (red) of *P. coccineus* landraces in seven different sowing year/date in Texcoco, Mexico. In each year the sowing date was different. Blue arrow indicates the trend during early sowing dates, March and April, while the red arrow indicates the trend of sowing dates from May onwards.

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ROOT SPROUTS OF *PHASEOLUS COCCINEUS* L. PLANTS AND ITS ORIGIN SITES

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INTRODUCTION: Plant conservation and evolution is based on *de novo* plant replacements like seed germination, but the sprouts are a persistent form in different ecosystems (Bond and Midgley 2001). Plant persistence in the field is due to sprouts that arise from root buds. Root sprout emergence in the *P. coccineus* plant is a reproductive strategy that may have evolved in response to the environment. In Mexico, this plant is grown as an annual in sub humid climates with frosts in winter, or as a perennial in hot and sub humid climates in frost free areas (Hernández X., *et al*, 1979). This report identifies cultivars that developed root sprouts, and the climate of its origin sites.

MATERIALS AND METHODS: In 2012, we regenerated seed of 70 Mexican cultivars (collected from 16° to 21°NL and from 96° to 102°WL). The new seeds were sown on April 22, 2013 in Texcoco, Mexico. The harvest was completed and the root was kept in the ground. In March 10, 2014, nondestructive root samplings were carried out. The climate type of the collection sites was obtained from García and Conabio (1998). We then completed a principal component analysis (PCA).

RESULTS AND DISCUSSION: The 42 sprouting cultivars originate from sites with temperate humid and subhumid climates, and 28 that did not sprout, to sites with temperate subhumid, semiarid temperate and semi warm subhumid climates. The PCA which included geographical and climatic variables of the source sites and sprout weight explained 70 % of variability. The first one 34 % with latitude, longitude, altitude and min. temperature; the second, 25 % with sprout fresh weight; and the third one, 11% with root crown diameter. Spatial distribution in Fig. 1 by quadrants: on the left, S of Puebla and N of Oaxaca, on the right, N of Pue., Mex., Gto., Tlax., Qro., and Mich.

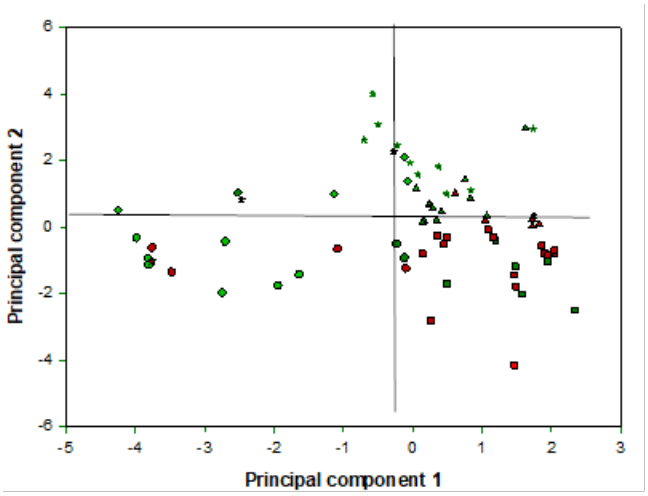

Figure 1. Principal component analysis spatial distribution of 70 Mexican *P. coccineus* cultivars according to its root sprouting capacity.

The left map (Fig. 2) grouped cultivars in the temperate and sub humid tropic (16° 47’ to 20° 02’ NL, and 96° 40’ to 98° 02’ WL) in Pue. and Oax., as well as high mountains of Ver., in sites with a minimum annual temperature from -3 to 5°C in a range of 820-2720 m in the southeast of the Eastern Sierra Madre. The right map grouped 46 cv., also from the temperate zone, but it also included cv from the arid zone of N of Gto., center of Pue., west of Mex., and Mich., Tlax., and Qro. states, in sites between 18° 52’- 21° 27’ NL and 97° 22 -102° 19’ WL, and with minimum annual temperatures from -3 to 1ºC and a range from 1500 to 2320m in the Transversal Neo Volcanic Axis. The maps show geographical overlaps in the distribution of cultivars with and without root regrowth.

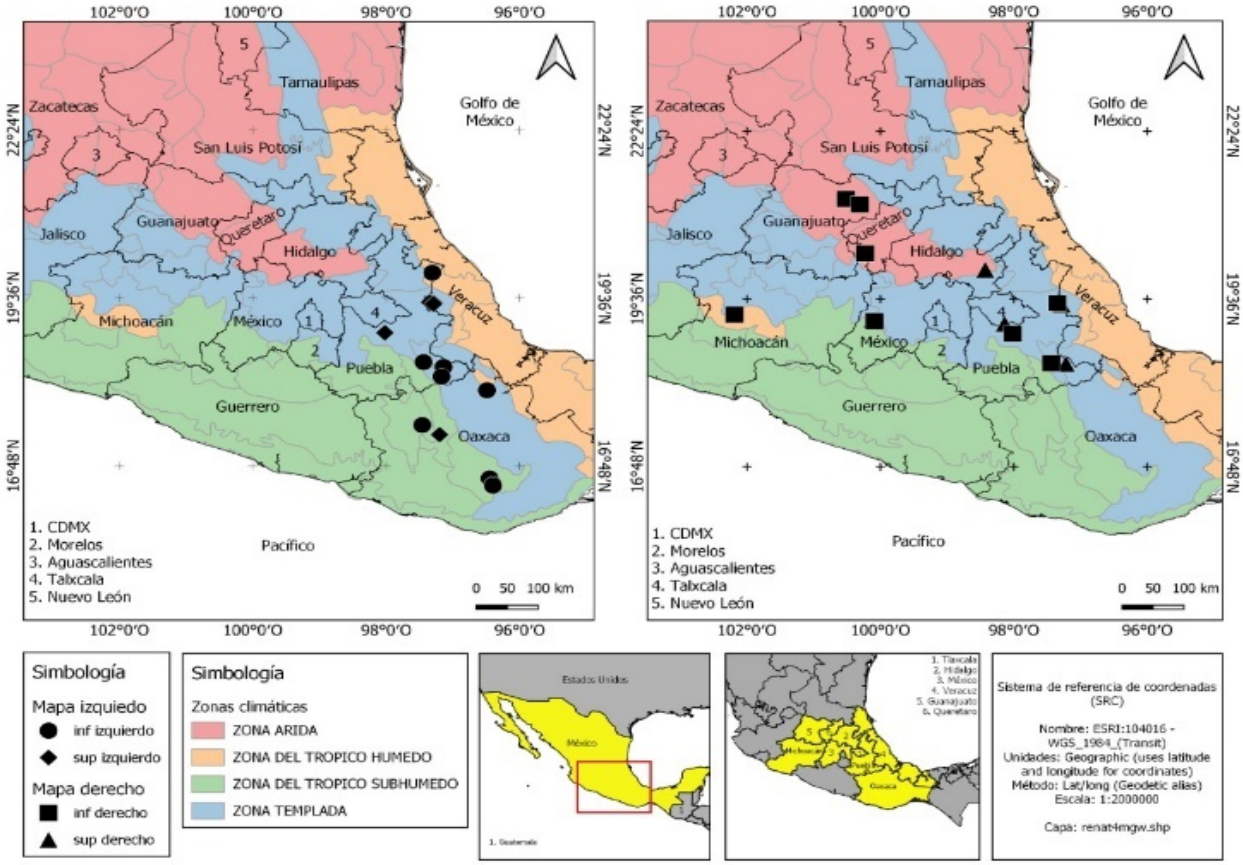

Figure 2. Distribution of 70 ayocote cultivars in different climatic zones of Mexico.

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2022 FINANCIAL STATEMENT
BEAN IMPROVEMENT COOPERATIVE

BALANCE AS OF January 1, 2022		**$ 37,583.96**
INCOME		
2022 Membership dues and Registrations	$ 3,687.17	
BIC Meeting Sponsorships	$ 0.00	
Bank Interest	$ 0.00	
TOTAL INCOME	$ 3,687.17	
EXPENSE		
Labor charges	$ 0.00	
Postage, Copy Charges and Office Supplies	$ 20.00	
Pdf & Book editing and publishing fees	$ 530.40	
Reimbursement to NAPIA for 2021 meeting	$ 3,255.00	
BIC Student Awards (2021 meeting)	$ 654.99	
PayPal Fees	$ 61.55	
Bank Fees	$ 24.00	
TOTAL EXPENSE	$ 4,545.94	
BALANCE AS OF December 31, 2022	**$ 36,725.19**	