ANNUAL REPORT OF THE

BEAN IMPROVEMENT COOPERATIVE

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

VOLUME 64
2021

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THE LXIV

Report of The

BEAN IMPROVEMENT COOPERATIVE

No. 64 May 2021

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Coordinating Committee

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SITE REGULARLY UPDATED

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RESEARCH PAPERS FOR 2021

Cover: Wild and domesticated seed type diversity of tepary bean *(Phaseolus acutifolius)*. Both wild and domesticated genomes were released in 2021. Photo courtesy of Tim Porch.

THE 64th ANNUAL REPORT OF THE BEAN IMPROVEMENT COOPERATIVE

Despite the worldwide trials we continue to encounter due to the pandemic, our work continues and becomes even more critical. The vital role of common bean in human nutrition and health drives our effort to improve *Phaseolus* species resilience, productivity, quality, and nutrition. This publication represents this broad collaboration worldwide.

The BIC Coordinating Committee consulted regarding the pandemic and our BIC Biennial Meeting planned for 2021. We arrived at the conclusion that it would be prudent to have a virtual meeting in 2021 and the first announcement of this meeting is included in this report. Additional information will be announced by the organizers at the University of Saskatchewan. In addition, we would like to encourage members to consider attending the 2022 Canadian Pulse Research Workshop (CPRW) in Windsor, Ontario, Canada, during the first week of November, 2022. The organizers are incorporating BIC and NAPIA presentations, posters, and communities into the program.

Given that the 2021 BIC Meeting will be virtual, we will plan to postpone the BIC Awards nominations announcement until the 2022 BIC Report and the awards banquet until the 2022 CPRW meeting. Please consider your colleagues for these nominations including the BIC Meritorious Service Award, the BIC Achievement Award, and the BIC Technical Merit Award.

Please share information about the BIC with interested colleagues who might like to attend the 2021 virtual meeting or who would like to join the BIC as members. Given that travel is not an issue, we hope that meeting attendance increases, especially from members in Africa, Europe, and Latin America. We continue to accept updates to the Research Techniques page of the BIC website. Your contributions to update these methods and to include new methods are much appreciated. We have begun posting bean-specific job announcements on the BIC webpage.

The BIC continues to conduct business by email, postings on the webpage, and through the online publication of this Annual Report. A site for members to download the report will be provided and older issues are posted on the BIC webpage. Feel free to contact us with any new ideas, contributions, or updates for the BIC website or this Annual Report. Members are asked to ensure that email addresses are current and to periodically review the web page for information on meetings, deadlines and critical dates. We are always open to new ideas to make the BIC a more effective organization and any suggestions can also be shared with members of the Coordinating Committee.

Warm regards,
Tim Porch, BIC President

BIC COMMITTEE MEMBERSHIP - 1957 to 2020

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

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, Sandste
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

BIC Genetics Committee Meeting Minutes

Location: Virtual meeting hosted by Carlos Urrea (U. of Nebraska, Scottsbluff)
Date: Friday, August 21, 2020, 2:30 - 4:00 pm

Committee Members and Guests present:
Bett, Kirstin (k.bett@usask.ca) – University of Saskatchewan
Cichy, Karen (Karen.cichy@usda.gov) – USDA-ARS, East Lansing, MI
Gepts, Paul (plgepts@ucdavis.edu) – University of California, Davis
Gomez, Francisco (gomez225@umn.edu) – University of Minnesota
Harris, Donna (dharri50@uwyo.edu) – University of Wyoming
Heitholt, Jim (Jim.Heithlot@uwyo.edu) – University of Wyoming
Hoyos-Villegas, Valerio (Valerio.hoyos-villegas@mcgill.ca) – McGill University
Karasov, Alexander (akarasev@uidaho.edu) – University of Idaho
McClean, Phillip (Phillip.mcclean@ndsu.edu) – North Dakota State University
Miklas, Phil (**Chair**; phil.miklas@usda.gov) – USDA-ARS, Prosser, WA
Munoz-Amatriain, Maria (maria.munoz_amatriain@colostate.edu) – Colorado State University
Myers, James (james.myers@oregonstate.edu) – Oregon State University
Osorno, Juan (juan.osorno@ndsu.edu) – North Dakota State University
Ostdiek, David (dostdiek4@unl.edu) – University of Nebraska
Pastor-Corrales, Talo (talo.pastor-corrales@usda.gov) – USDA-ARS, Beltsville, MD
Porch, Tim (timothy.porch@usda.gov) – USDA-ARS, Mayaguez, PR
Raatz, Bodo (b.raatz@cgiar.org) – CIAT, Colombia
Urrea, Carlos (currea2@unl.edu) – University of Nebraska
Wallace, Lyle (lyle.wallace@usda.gov) – USDA-ARS, Pullman, Washington

Old Business:

Approval of the Genetics Committee meeting minutes from 2019

Decision: The Genetics Committee minutes were approved from the meeting held at the Hotel Radisson in Fargo, ND on Wednesday Nov 6, 2019. Motion by Paul Gepts, seconded by James Myers, with AIF.

Introduction to the Bean Gene List

Decision: Phil Miklas will review the introductory text at the beginning of the Bean Gene list provided by Phil McClean, that includes new genomic tools such as reference genomes and gene annotation lists and will then share with the committee.

SNP and SCAR markers

Bodo Raatz has agreed to share his SNP marker list developed at CIAT, and Phil Miklas, Phil McClean, and Talo Pastor-Corrales have provided their SNPs pre-publication to make available to the community on the BIC webpage. Bodo Raatz, Tim Porch and Phil Miklas will organize the SNPs for posting with instructions for use with the Intertek platform.

bc-u gene identification (from Phil Miklas)

Three *bc-u* -like loci identified: *bc-u* (original), *bc-ub* (linked with *bc-u*), and *bc-uc* (on another chromosome linked with *bc-2*). Miklas will propose symbols to the committee once the paper is drafted. The *bc-1*^{2} and *bc-2*^{2} symbols will be moved to the Obsolete gene list. A table will be developed with new lines that have all iterations of combinations. New differentials will need to be developed.

Ppd **candidate gene** (item from Jim Kelly)
The red/far-red photoreceptor gene PHYTOCHROME A3 (PHYA3) was identified as a candidate for the *ppd* gene on Pv01 (Kamfwa et al., 2015; Weller et al., 2019). Jim Kelly proposes that the *ppd* gene be renamed PHYA3.
Decision: The committee proposes to retain the *ppd* gene name and to include PHYA3 as a candidate gene. This candidate could be described as a strong candidate for the gene, but we don't yet have conclusive proof that it is the gene.

QTL naming for rust paper (item from Phil Miklas)
A consensus for appropriate symbols for quantitative resistance to the rust pathogen was requested, while BR, RU, RST, RUST, RUS were mentioned. The manuscript is pending but the authors will likely use RUST1.1, RUST3.1, etc.

Molecular evidence for new gene symbol in rules section (item from Jim Kelly)
Currently, new gene symbol evidence must include the following (i to iv. Below). The suggestion is to make the physical map position (iv) mandatory instead of preferred.

i. data from one generation to formulate a hypothesis
ii. data from subsequent generations to test that hypothesis
iii. for hyper-variable pathogens: family mean testing (F2:3 progenies, or recombinant inbred lines – RILs), and use of multiple, specific races of the pathogen to separate effects of individual genes in gene clusters
iv. molecular marker data and genetic linkage map and physical map (preferred) positions when available

An extensive consultation took place about whether molecular marker data, linkage map and physical map information should be mandatory for a new gene symbol or whether genetic information is sufficient. Should large clusters of genes be approached differently from smaller clusters? You would need recombination within a cluster in order to separate out genes. Resistance specificity can be defined to a specific region of the genome (member of a cluster) instead of specifying by recombination. There is also an issue of defining or naming the clusters since sometimes they are Mbs in size. For example, the Pv04 cluster is full of genes and there is little recombination, so the genes are very difficult to separate. Stavely found recombination between *Ur-3* and *Ur-11*, but in most cases there is no recombination or the required population sizes are extremely large. Decisions were deferred to the new business section (below).

New business
Membership
Current members: Bett, Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, Kelly, McClean, Miklas (Chair), Osorno, Porch, and Urrea. We thank **Jim Kelly** for his service as member and chair of the Genetics Committee. He will now rotate off the committee as he has now retired.
New members: We welcome **Valerio Hoyos-Villegas**.

New Gene Symbol (item from Kirstin Bett)
$\boldsymbol{P^{sd}}$ is an allele of the *P* (Pigment) gene with order of dominance $P>p^{sd}>p$) (Islam et al., 2020). It replaces the *sd* gene (symbol) that conditions the slow darkening seed coat trait in pinto (Elsadr et

al. 2011) and carioca beans (Alvares et al., 2019). *P*^{sd} encodes a bHLH transcription factor with two transcript variants but only one is involved in proanthocyanidin (PA) biosynthesis. An additional glutamate residue in the activation domain, and/or an arginine to histidine substitution in the bHLH domain of the *P*^{sd} -1 transcript in the slow darkening cultivar is likely responsible for the reduced activity of this allele compared to the allele in a regular darkening cultivar, leading to reduced PA accumulation. Unlike small *p* that shuts down pathway, it just scales it down. So replacement symbol would be *P*^{sd}. A linked KASP marker can be used that is presented in the Alvares et al. (2019) publication. The Alvarez publication can be added to the gene list. How does it relate to *p*^{gri}?—they have not looked at this. P. McClean says coding sequence is exactly the same as the wildtype for *p*^{gri}, so it is not likely to be *p*^{gri}.
Decision: Accept *P*^{sd} as a new gene symbol and allele of the *P* (Pigment) gene with order of dominance *P*>*P*^{sd}>*p*). *P*^{sd} will replace the *sd* symbol that conditions the slow darkening seed coat trait in pinto.

New Gene Symbols (item from Maria Celeste Gonçalves)
Maria Celeste Gonçalves has published one paper and they are working on submitting another. She requests adding a single anthracnose and angular leaf spot resistance gene *CoPv01*^{CDRK}/*PhgPv01*^{CDRK} from California Dark Red Kidney to the BIC gene list from a PLOS_One paper, with permission requested post-publication.
Decision: the *CoPv01*^{CDRK}/*PhgPv01*^{CDRK} symbol was not accepted.

The other item was a review of anthracnose genes and candidate genes published in First Look in Crop Science: "Integration of anthracnose resistance loci and RLK and NBS-LRR-encoding genes in the Phaseolus vulgaris L. genome." Two linked clusters with separation of about 100,000bp (<1cm) were characterized, but the segregation data indicates two independent loci with considerable recombination.

The consultation on gene clusters continued. There have been different approaches taken. Juan Jose Ferreira has a proposal for how to handle clusters. Kelly came up with a different method for working with clusters. Are they multiple genes or simply alleles of the same gene is the question?

Phil McClean shared that Prakken was able to define and separate out particular phenotypes, striping from mottling, within the C locus. These appear to be a cluster of MIB genes.
Decision: Add a section to the bean gene list for clusters. These can be delimited by physical map locations. As a work in progress, genes can be moved in and out of this list as studies are completed.

FIRST ANNOUNCEMENT FOR THE BIENNIAL BIC/NAPIA 2021 MEETING
Virtual Meeting hosted by the U. of Saskatchewan
Nov 2-3, 2021

BIC and NAPIA will be held during Concurrent sessions on Nov 2 and Nov 3, 2021

The meeting will be held virtually (on-line) and the meeting links and information will be sent to BIC members and posted on the BIC website: http://www.bic.uprm.edu/. The meetings will be held early in the morning Pacific Standard Time (PST) for a four-hour period in order to make attendance feasible for those joining in Africa and Europe.

Registration

Details on Registration will be posted on BIC website: http://www.bic.uprm.edu/. An effort is being made to promote the participation of all students and researchers internationally, thus the registration will be subsidized by the BIC and the registration will include two years of BIC membership. The pricing of the registration will be shared at a later date.

Abstracts

Talks will focus on the participation of students and postdocs, while an electronic poster session will be open to all. The deadline for both talk and poster abstracts is August 31, 2021.

Contacts

Local Host: Kirstin Bett (k.bett@usask.ca)

BIC business contact: Tim Porch (timothy.porch@usda.gov)
NAPIA business contact: Bunyamin Taran (bunyamin.taran@usask.ca)

Schedule for the BIC/NAPIA 2021 Meeting

The meeting will include plenary talks, BIC and NAPIA talks, virtual coffee breaks to provide space for networking, and an e-poster session.

Business meetings

Business meetings, including the W-4150, the Phaseolus Crop Germplasm Committee, and the Genetics Committee Meeting, will be held separately, during the summer of 2021. The dates and times will be shared after consultation with the committee membership.

IN MEMORY OF LUIS FERNANDO ALDANA DE LEÓN

Dr. Luis Fernando Aldana de León passed away surrounded by his family and friends on May 10th 2020. Dr. Aldana was a plant breeder who developed his professional career at the Institute of Agricultural Science and Technology (ICTA) in Guatemala. Additionally, he was professor at Universidad de San Carlos in Guatemala where he taught plant breeding, plant genetics, and experimental design. Dr. Aldana was born Guatemala, completed his bachelor's degree at the University of San Carlos in 1981 with Dr. Porfirio Masaya on the genetic and chemical control of white fly, the vector of *Bean golden yellow mosaic virus* (BGYMV). At the beginning of his career, he participated in a collaborative project between ICTA and CIAT to develop greater tolerance to BGYMV, leading to the release of important varieties such as 'Suchitan' and 'Jutiapan.' In 1985, Fernando completed his Master's degree with Dr. Don Wallace at Cornell University on halo blight and in 1995 he completed his Ph.D. degree on heat tolerance in wheat at South Dakota State University.

Dr. Aldana returned to ICTA to work in the wheat breeding program where he developed and released wheat varieties such as 'ICTA Don Vale', 'ICTA Sibilia', and 'ICTA Cumpalé.' Since the late 1990's, he worked on the development of improved climbing bean varieties which are planted with maize by farmers in the highlands of Guatemala. Thanks to his previous work and dedication, ICTA released the first two climbing bean varieties in 2017: 'ICTA Labor Ovalle' and 'ICTA Utatlán' in collaboration with North Dakota State University and the USAID-Legume Innovation Lab. Dr. Beebe from CIAT and Dr. Aldana cultivated an almost 40-year friendship that resulted in several genetic improvements of much benefit for bean growers everywhere today. In close collaboration with Dr. Beebe, Dr. Aldana led the effort to develop 'Super Chiva', a black bean variety for higher altitudes and enriched for iron. Super Chiva was among the first higher nutrient content bean varieties. Through this effort, Dr. Aldana was able to address Guatemala's chronic malnutrition challenges. Additional breeding material are at their final stages of selection and testing thanks to all his previous work with climbing beans, which historically have received less breeding effort compared to bush-type beans. In 2010, he authored an ICTA manual for the production of beans and bean seed in Guatemala.

Dr. Aldana was in his element in the field. He loved evaluating his genetic material and sharing his knowledge with others. He instilled his love of breeding and evaluation in his students, making famous the quote of Dr. Norman Borlaug: "To produce the land it is necessary to leave the office, go into the field, get the hands dirty and to sweat, it is the only language understood by the soil and the plants." In his office at ICTA Labor Ovalle, where he worked his last years in the bean and wheat breeding programs, he had a photograph with Dr. Norman Borlaug, and another photograph where he was welcoming Dr. Sanjaya Rajaram. Dr. Aldana collaborated with many world-renowned researchers, but he was humble, noble, and dedicated to his work. He always emphasized his gratitude to ICTA for giving him the opportunity to grow professionally.

Dr. Aldana's greatest legacy goes beyond the products of his research and professional relationships. In addition to being a man dedicated to his job and to his family, he was a friend and a leader within his local religious community and always made sure everybody knew about his service and commitment to God. Dr. Aldana will be greatly missed by friends and colleagues, especially in those fields around Quetzaltenango, Guatemala.

IN MEMORY OF DAGOBERTO GARZA GARCIA

Dagoberto 'Dago' Garza García died November 28, 2020, at the age of 60. Dago was born on May 28, 1960, in Ciudad Mante, Tamaulipas, northeast of Mexico. His agility and physical condition helped him to be an outstanding basketball and volleyball player. He obtained a B.S. degree in Agronomy from the Autonomous University of Tamaulipas and his M.S. in Seed Production from the Colegio de Posgraduados in Montecillo, México.

In August 1984, he joined the National Institute of Agricultural Research, INIA, today the National Institute of Forestry, Agricultural and Livestock Research (INIFAP). He began working with oilseeds, and in 2008, he joined the Bean Improvement Program at the Valle de México Experimental Station of the INIFAP. During his participation in the program, he worked with the interdisciplinary group for the improvement of the common bean (*Phaseolus vulgaris* L.), and participated in the development of varieties of different market classes such as 'Altiplanomex', 'Albicampo', 'Primavera-28', 'Azufradoro', 'Azufradomex', 'Mayomex', 'Huitel-143', and 'Xicuco'.

His spirit as an agricultural researcher led him to alternate his work on common beans with the collection of native genotypes and the improvement of pumpkin (*Cucurbita* spp.). Together with his brother, Ramón Garza García, he collected and characterized mante (*Pouteria campechiana* (kunth) Baheni), a native fruit that gives the name to the city where they were born, and currently they maintain an area planted with the collected genotypes, seeking to preserve the diversity of this species. In the same way, they formed a nursery for soyate plants (*beaucarnea recurvata* Lemaire) from seeds of this species endemic to the region. Soyate is a threatened species, with a distribution limited to the states of San Luis Potosí and Tamaulipas.

In recent times, the focus of his research was to know and use the genetic diversity of beans to develop new varieties. Dago collected native bean germplasm and established cross-breeding blocks using outstanding genotypes uncommon among market classes. In the state of Hidalgo, Mexico, from 2014 to 2020, he carried out the evaluation of different bean genotypes to promote the production of this crop in different parts of the state. His closeness to bean-producing farmers led him to understand their preferences and needs, and to improve native genotypes to incorporate disease resistance. This is how Huitel-143 and Xicuco, the last two varieties that he released, were developed. Both are of the type called San Franciscano. Additionally, he worked with string beans and released 'Luciomex', the first Mexican variety of string beans. He had a great capacity for observation, making findings related to the morphological characteristics of flowering in the common bean crop.

Dago is survived by his wife, María de Jesús Ponce de León Vázquez, and his son, José Dagoberto Garza Ponce de León.

IN MEMORY OF ROBERT GEHIN

Robert Gehin was born in 1959 in Madison, Wisconsin. He spent his childhood and youth in Madison, graduating from Belleville High School in 1977. He went on to complete his B.S. degree at the University of Wisconsin-Platteville and his M.S. degree in Plant Breeding and Plant Genetics at the University of Wisconsin-Madison. His M.S. degree advisor was Dr. Fred Bliss, who has commented that Rob had a reserved nature and was a successful breeder.

Rob began working with the Ferry Morse Company in 1981. As the company evolved into Harris Moran and then HM.Clause, Rob held positions including station manager, spinach breeder, and bean breeder. While working with Limagrain seed companies, Harris Moran and HM.Clause, he was granted over 33 variety patents for garden beans, including market leaders 'Wyatt', 'LaSalle', and 'Desoto'. Rob was awarded numerous honors throughout his career for his outstanding leadership and contributions to the HM.Clause business. Rob had a unique talent of offering insight to complex discussions; these insights were based on his skills of observation and thoughtfulness, which ultimately made Rob very successful and effective as a breeder.

Rob made significant advances in snap bean breeding including the release of varieties that set the standard for upright non-lodging garden beans. He also collaborated with the research community. He attended the BIC meetings faithfully and was on the local organizing committee of the 50-year anniversary BIC meeting in Madison, Wisconsin in 2007, contributing significantly and ensuring that it was a successful event. Rob always made sure that Limagrain sponsorship was in place to support the BIC meetings as he felt strongly about this commercial support. He was also generous in inviting academic colleagues for meals during the BIC meetings.

Family, sports, woodworking and Alaska summed up the passions in Rob's life. In 1981 Rob married Brenda Flanagan and established a family with his sons Andrew and Thomas. He coached youth soccer, baseball, and wrestling as hobbies and as a service to his community. He also enjoyed bicycling and woodworking. His wife, sons, and five grandchildren survive him.

IN MEMORY OF TOMMY DEAN GREBB

Tommy D. Grebb died peacefully September 1, 2020, after a 11-year battle with Parkinson's. He was 69 years old. He was born in Greeley, CO, August 26, 1951, to Don and Violet Grebb. When Tom was 5 years old his family moved to Quincy, WA, to farm. Before graduating from high school in 1969, Tom joined the Quincy Fire Department as a volunteer, and continued to serve for 25 years. In the early 1970's, Tom started his own construction business, putting in hundreds of miles of concrete irrigation ditches throughout Central WA.

With the partnership of his parents and brother, Central Bean Co., Inc. opened its doors in 1983. With Tom's oversight and creative vision for growing the business, the company was well known in the dry bean industry for its high-quality beans and seed production capabilities. Central Bean became one of the first seed companies to offer 'Identity Preservation' and to become 'Food Alliance' certified. While running Central Bean, Tom found time through the years to serve on the Quincy City Council, U.S. Jaycees (both locally and at the State level), Rotary International, WA State Ag-Forestry program, Class X, and the U.S. Dry Bean Council (USDBC).

With Tom's great interest in the science side of dry beans he directed the USDBC's efforts toward supporting dry bean research. To better serve this role, he attended Bean Improvement Cooperative meetings on a regular basis to learn about the research and to get to know the scientists directly involved in dry bean breeding and improvement. In addition to the BIC biennial meetings, Tom attended many of the W-150 and W-1150 Regional Dry Bean project annual meetings from 1990 to 2010. During these meetings, Tom provided useful insights and perspectives from the Industry's point of view. Tom served as a steering committee member on numerous bean research consortiums (such as the Bean CAP) and grant programs, which served the greater Grain Legume community as well as dry beans. As a member of the USDBC, Tom made many trips to Washington D.C. to lobby congress for funding to support bean research. Tom worked tirelessly in lobbying for support of dry bean research which directly led to significant funding increases for the four USDA-ARS programs in 1995. In 2005, he successfully lobbied Washington State's Legislators for increased funding for the USDA-ARS project in Prosser, WA, only to have it fade away in a continuing resolution. He also played a prominent role in gaining funding for genomic research in Grain Legumes in the early 2000's. In addition, his company Central Bean has been an important partner across the years for Foundation seed production for several public and private dry bean programs. They were always willing to take the risk of growing a new variety that would benefit the bean industry.

Working with food industries such as Food Alliance, Bon Appetite, Chipotle Mexican Grill, Taco Time NW, Truitt Brothers, Bush Beans, and NW Harvest added to his passion of promoting local farmers. He always said the best beans are grown in the Columbia Basin. To further support bean production in the region Central Bean spun off Haricot Farms which Tom used to explore sustainable growing practices and to successfully introduce several unique, environmentally friendly no-till and minimum till dry bean farming methods to central Washington.

Many of us in the Bean Research Community got to know Tom well and enjoyed our times with him during and after the meetings, or when visiting his bean seed production fields in Washington. He was a knowledgeable person to talk 'beans' with and easy and enjoyable to be around. The bean research community is better off because of Tom's contributions and support.

GENOME-WIDE ASSOCIATION OF RESISTANCE TO ANGULAR LEAF SPOT, COMMON BACTERIAL BLIGHT AND BACTERIAL WILT IN COMMON BEAN ACCESSIONS

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INTRODUCTION

Angular leaf spot (ALS) caused by *Pseudocercospora griseola* (Sacc.) Crous and Braun, common bacterial blight (CBB) caused by *Xanthomonas campestris* pv. *phaseoli* Smith (Dye), and bacterial wilt (BW), caused by *Curtobacterium flaccumfaciens* pv. *flaccumfaciens*, are severe diseases affecting common bean worldwide (Singh and Schwartz, 2010; Viteri et al., 2015). Consequently, new sources of durable resistance for ALS, CBB, and BW are highly desirable for effective breeding efforts. Thus, the identification of new sources of resistance to these diseases is a major priority in breeding programs. The objective of this study was to perform GWAS for common bean resistance to ALS, CBB, and BW under natural occurrence in the field.

MATERIALS AND METHODS

A total of 109 accessions of common beans belonging to the Nupagri's Active Bank of Germplasm were evaluated under field conditions for ALS, CBB, and BW. An experimental design in 11×11 square lattice was used with three replications. The plot consisted of 12 plants sown in a 1-m row, with 0.5 m spacing between rows. The ALS, CBB, and CW symptoms were evaluated using the disease severity scales (1 to 9) proposed by Pastor-Corrales et al. (1995), Inglis et al. (1988), and Maringoni and Camara (2006), respectively. A total genomic DNA was extracted from the trifoliolate leaves of each accession using the DNeasy Plant Mini Kit (Qiagen) following the manufacturer's instructions. The DNA samples were screened with 4,633 SNP DNA markers using the BARCBean6K_3 Illumina BeadChip (Song et al., 2015) by following the Infinium HD Assay Ultra protocol (Illumina, Inc., San Diego, CA, USA) at the Soybean Genomics and Improvement Laboratory of the USDA-ARS, Maryland, MD, USA. To understand the genetic basis of ALS, CBB, and BW resistance, a genome-wide association study (GWAS) was performed via fixed and random model circulating probability unification (FarmCPU) with a covariate added by 3 PCs, using R (Liu et al., 2016).

RESULTS AND DISCUSSION

The results revealed two SNPs significantly associated with resistance to angular spot located on chromosome Pv09 (Figure 1). Mahuku et al. (2009) reported an ALS resistance gene on Pv09 (ALS9.1 GS) in a complementary mode of action with the gene ALS4.2 GS located at Pv04 in the common bean G5686. Two SNPs were found significantly associated with resistance to common bacterial blight: ss715649204 located at Pv04, and ss715641094 located on Pv02 (Figure 1). CBB resistance has been reported across all bean chromosomes (Singh and Miklas, 2015; Viteri et al., 2015). Regarding BW, resistance association analysis allowed the identification of four SNPs: ss715647585 located on Pv03, ss715645243 on Pv07, ss715643118 on Pv10, and ss715648083 on Pv11 (Figure 1).

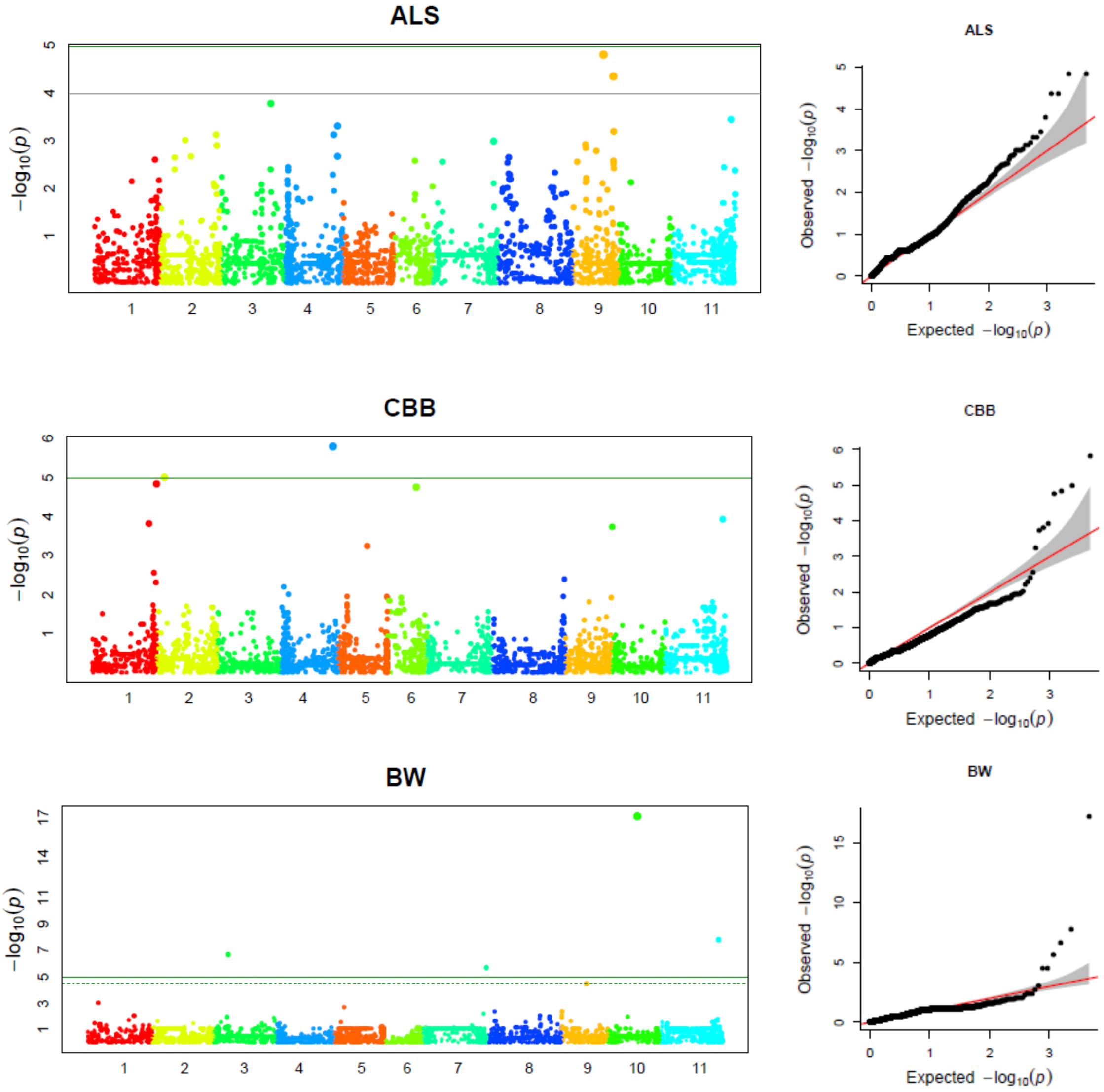

Figure 1. Manhattan and Quantile-quantile (QQ) plots showing the candidate SNP associated with angular leaf spot (ALS), common bacterial blight (CBB), and bacterial wilt (BW) resistance. The green line is the significant threshold calculated via Bonferroni correction with α = 0.05 and p= 1.08 10^{-5}.

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FINE MAPPING OF ANTHRACNOSE RESISTANCE ALLELE *Co-1*^{4} IN THE COMMON BEAN CULTIVAR AND 277

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INTRODUCTION: Among the main limitations faced by the common bean, anthracnose (ANT) caused by the fungus *Colletotrichum lindemuthianum* (Sacc. & Magnus) Briosi &Cavara, causes considerable losses in production and depreciation of the quality of grains when in favorable disease development conditions (Pastor-Corrales et al., 1995). The most effective strategy for anthracnose control is the use of resistant cultivars (Gonçalves-Vidigal et al., 2011). The genetic identification of more specific information about resistance genes in different cultivars provides an additional database of sources of variability, and consequently, they generate information about the use of markers for marker-assisted selection (Song et al., 2015). The Andean cultivar AND 277 is an important source of anthracnose resistance for breeding programs as it exhibits a wide spectrum of resistance, conferring resistance to both Andean and Mesoamerican races. In addition, it presents resistance to the highly virulent races 2047 and 3481. Therefore, the objectives of this study were to fine-map the anthracnose-resistance locus in AND 277 and to identify DNA markers tightly linked to the *Co-1*^{4} allele, previously mapped on Pv01 (Gonçalves-Vidigal et al., 2011).

MATERIALS AND METHODS: The genetic basis of ANT resistance was studied using 149 F_{12} RILs derived from the cross between Rudá and AND 277 (RILs RA). Seedlings with the first fully expanded trifoliolate were inoculated with race 3481 of *C. lindemuthianum* to determine inheritance of the disease reaction. Inoculum of ANT was produced on young green common bean pod medium incubated at 22°C for 14 days and with a final concentration of 1.2×10^6 conidia mL^{-1} used for inoculation. After inoculation, seedlings were placed in a mist chamber for 72 h at 20 ± 2°C, with a photoperiod (12 h lighting/12 h darkness), and relative humidity over 95%. The ANT symptoms were evaluated using the disease severity scale (1 to 9) proposed by Pastor-Corrales et al. (1995). Plants with disease reaction scores between 1 and 3 were considered resistant, whereas plants with scores from 4 to 9 were considered susceptible. Total genomic DNA was isolated using the DNeasy Plant Mini Kit (Qiagen, CA, USA) following the manufacturer's instructions. The DNA samples were screened using the BARCBean6K_3 Illumina Bead Chip (5,398 SNPs) at the Soybean Genomics and Improvement Laboratory, USDA-ARS-BARC-W (Beltsville, MD, USA), using the Illumina Infinium genotyping platform ® HD Assay Ultra as described by Song et al. (2015). The BeadChip was imaged using the Illumina BeadArray Reader and automatic allele calling for each locus was performed using the Genome Studio software v2.0 (Illumina, San Diego, CA, USA). All allele calls were visually inspected and any errors in allele calling due to improper cluster identification were corrected. The genetic linkage maps were created using the software MapChart (Voorrips et al., 2002). A fine linkage map was developed by adding twelve new SSR markers and two STS markers previously mapped on Pv01.

RESULTS AND DISCUSSION: Genetic mapping of AND 277 resistance allele against race 3481 using 149 RILs RA positioned the *Co-1*^{4} locus in a region of 1.4Mb flanked by SNP markers ss715645251 and ss715645250, at the positions of 50,301,592 bp and 51,726,047 bp, respectively on Pv01 (Figure 1A). Further, fine-mapping using an additional twelve SSRs and two STS markers showed that the resistance allele in AND 277 was located between the markers ss715645251 (50,301,592 bp) and BARCPVSSR01356 (50,342,103 bp) (Figure 1B), spanning a region of 40.51 Kb. According to the reference genome, this genomic region contains two gene models: Phvul.001G243800, which encodes a serine/threonine-protein kinase-like protein ccr3-related and Phvul.001G243900, which encodes a double clp-n motif-containing p-loop nucleoside triphosphate hydrolases superfamily protein. Our results validate previous studies conducted by Alzate Marin et al. (2003**)** and Gonçalves-Vidigal et al. (2011) indicating that the ANT resistance gene in AND 277 cultivar is an allele of *Co-1* locus mapped at the end of chromosome Pv01. Furthermore, Zuiderveen et al. (2016) also identified the SNP ss715645251 (50,301,592 bp) associated with race 3481 resistance in the Andean Diversity Panel. In conclusion, the markers identified in this study by fine-mapping, ss715645251 and SSR BARCPVSSR01356, are important tools for breeding programs aiming to obtain new cultivars containing the *Co-1*^{4} allele through marker assisted selection. Therefore, it is concluded that the ss715645251 and SSR BARCPVSSR01356 markers will be important tools for breeding programs aiming to obtain cultivars with the *Co-1*^{4} allele through marker assisted selection.

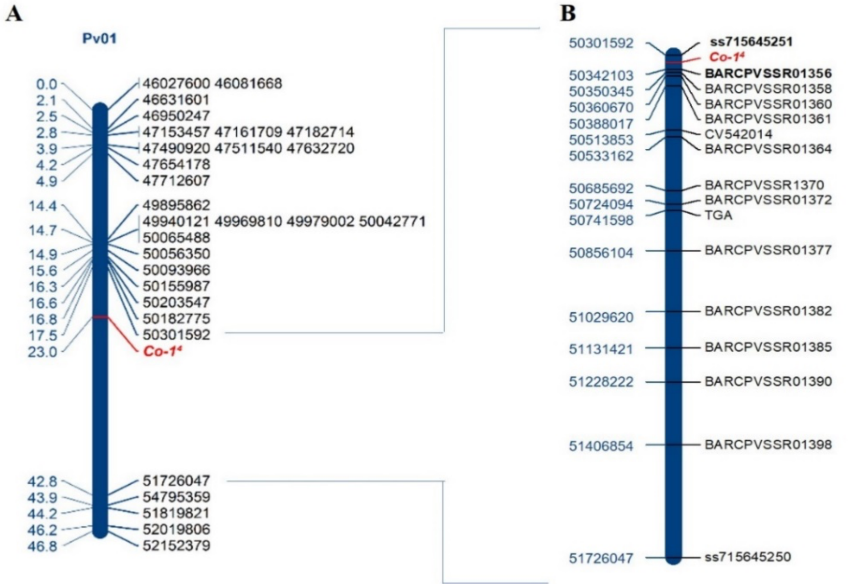

Fig 1. 1A **-** Genetic map of common bean linkage group Pv01 containing the anthracnose resistance allele and SNP markers used to genotype the F_{12} population Rudá × AND 277. The genetic distances in centimorgans (cM) are shown on the left side, and the physical positions (bp) on the right side. The map was built with MapChart (Voorrips et al., 2002**);** 1B **–** Fine-mapping the *Co-1*^{4} allele using SSR and STS markers positioned in region of 40.511 Kbp.

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BROAD-SPECTRUM RESISTANCE IN THE ANDEAN COMMON BEAN LANDRACE G19833 TO MESOAMERICAN AND ANDEAN RACES OF *COLLETOTRICHUM LINDEMUTHIANUM*

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INTRODUCTION

Anthracnose, caused by *Colletotrichum lindemuthianum* (CL), is a major disease of common bean especially in the Americas and Africa. The wide-ranging virulence diversity of CL segregates into two groups, one Mesoamerican and another Andean, that correspond to the Middle American and Andean gene pools of common bean, respectively. There is a preponderance of Mesoamerican races of CL in Brazil, Mexico, Central America, and the USA (Nunes, 2013), where Middle American common bean varieties predominate. Genetic resistance in common bean to CL is conferred mostly by single and dominant genes (Kelly & Vallejo, 2004). Several Mesoamerican genes, such as *Co-4*^{2,} confer broad resistance to all Andean and to most Mesoamerican races of CL (Kelly & Vallejo, 2004; Singh & Schwartz, 2010). Finding genes of Andean origin with resistance to the highly virulent Mesoamerican and Andean CL races is important for the development of durable resistance to the virulence-variable CL pathogen. We report here that the Andean landrace G19833 (Chaucha Chuga) confers broad-spectrum resistance to a diverse group of CL races that included 13 Mesoamerican and seven Andean races. Because G19833 was used to sequence the reference genome of common bean (Schmutz et al., 2014), there is a large amount of sequence information associated with this landrace. G19833 has also been reported to be resistant to many races of the bean rust pathogen (Hurtado-Gonzales et al., 2017) and resistant to angular leaf spot, Ascochyta blight, and anthracnose (Broughton et al., 2003).

MATERIALS AND METHODS

The reactions of G19833 and of the 12 CL common bean differential cultivars to 20 races of CL were evaluated during 2020 at the Soybean Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD, USA. The races used in this study (their origin in parenthesis) were: 4 (Ec. 2.0), 7 (Ec. 7.0), 9 (Mx. 63.0), 17 (Br. 1.1), 19 (Mx. 40.1), 23 (Eur. 10.0), 31 (Eur. 13.0), 39 (NL. 1.0), 55 (D.R. 1.1), 89 (US 90.0), 127 (C.R. 3.0), 321 (Mx. 7.1), 449 (Mx. 3.1), 453 (Mx. 5.1), 469 (Mx.38.1), 1545 (Gu. 8.0), 1601 (Hd. 22.1), 1993 (Hd. 8.1), 2047 (C.R. 1.0), and 3481 (C.R. 2.0) (Table 1). We used a spore concentration of 1.2×10^6 per ml for each of the races. We inoculated simultaneously the primary leaves of 10 plants of G19833 and eight plants of each of the control cultivars with four races of CL. To identify the location of the races the tip of the primary leaf was cut while the other primary leaf remained uncut. Two races were inoculated on each leaf on the abaxial side using a cotton swab. All inoculated plants were transferred to a mist chamber for 48 hours and then relocated to a greenhouse bench. The plants were evaluated for their anthracnose reaction about 10 days after inoculation using a 1-9 scale, where scores 1-3 were resistant and scores 4-9 were susceptible.

RESULTS AND DISCUSSION

G19833 was resistant to all 13 Mesoamerican races (9, 17, 89, 127, 321, 449, 453, 469, 1545, 1601, 1993, 2047 and 3481) and to six of the seven Andean races (7, 19, 23, 31, 39 and 55) but G19833 was susceptible to Andean race 4 from Ecuador (Table 1). None of the differential cultivars were resistant to all 20 races of CL; however, the Middle American differential cultivar G 2333, with three anthracnose resistance genes (*Co-3*^{5}, *Co-4*^{2}, *Co-5*^{2}), like G19833, was also susceptible to one race only, the Mesoamerican race 3481 from Costa Rica. Thus, in this study, G19833 and G 2333 were the most resistant Andean and Middle American common beans, respectively. Although G19833 was resistant to all 13 Mesoamerican races, it is important to emphasize that G19833 confers resistance to two highly virulent Mesoamerican races, such as race 2047, which overcomes the resistance of 11 of the 12 differential cultivars and race 3481, the only race that overcomes the resistance of G 2333. It is also important to underscore that G19833 protects the following anthracnose resistance genes (differential cultivar in parenthesis): *Co-1* (Michigan Dark Red Kidney), *Co-1*^{2} (Kaboon), *Co-1*^{3} (Perry Marrow), *Co-1*^{5} (Widusa), *Co-2* (Cornell 49242), *Co-3* (Mexico 222), *Co-4* (TO), *Co-3*^{3} and *Co-4*^{3} (PI 207262), *Co-5* (TU), *Co-3*^{5}, *Co-4*^{2}, and *Co-5*^{2} (G 2333), *Co-6* and *co-8* (AB 136) and *Co-11* (Michelite). Hence, this study suggests that there is great value in the anthracnose resistance of G19833 for the protection of common bean cultivars against widespread and broadly virulent Mesoamerican races of CL.

Table 1. Reaction of the Andean landrace G19833 and of the 12-anthracnose differential common bean cultivars to seven Andean and 13 Mesoamerican races of *Colletotrichum lindemuthianum*

Common bean cultivars*	Races of *Colletotrichum lindemuthianum**																			
	4	7	9	17	19	23	31	39	55	89	127	321	449	453	469	1545	1601	1993	2047	3481
G19833	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
Michelite	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
MDRK	R	S	R	R	S	S	S	S	S	R	S	R	R	R	R	R	R	R	S	R
Perry Marrow	S	S	R	R	R	S	S	S	S	R	S	R	R	S	S	R	R	R	S	R
Cornell 49242	R	R	S	R	R	R	S	R	R	S	S	R	R	R	R	S	R	S	S	S
Widusa	R	R	R	S	S	S	S	R	S	S	S	R	R	R	S	R	R	R	S	S
Kaboon	R	R	R	R	R	R	R	S	S	R	S	R	R	R	R	R	R	R	S	R
Mexico 222	R	R	R	R	R	R	R	R	R	S	S	S	S	S	S	R	S	S	S	R
PI 207262	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	R	S	S	S
TO	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S	R	R	S	S	S
TU	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S	R
AB 136	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S	S
G 2333	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S

*Cultivars and races of *C. lindemuthianum* highlighted in blue are Andean; the others are Mesoamerican. MDRK: Michigan Dark Red Kidney.

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INHERITANCE OF ANTHRACNOSE RESISTANCE IN THE ANDEAN COMMON BEAN CULTIVAR BRSMG REALCE

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INTRODUCTION

Anthracnose, caused by the fungus *Colletotrichum lindemuthianum* (Sacc. and Magn.), is one of the most important diseases affecting the common bean (*Phaseolus vulgaris* L.) in Brazil. Based on the level of susceptibility shown by the cultivars, the occurrence of environmental conditions favorable to the development of the disease, and the amount of initial inoculum present, losses in the seed yield and quality can range from 80 to 100% (Singh & Schwartz, 2010). Anthracnose resistance in common bean is mainly controlled by major dominant genes from *P. vulgaris* Mesoamerica gene pool (List of Genes – *Phaseolus vulgaris* L; http://www.bic.uprm.edu). The "rajado" seeded Andean cultivar BRSMG Realce has shown wide and durable resistance in Brazil, including resistance to the *C. lindemuthianum* pathotypes 65, 73, 81, 91, 475, and 479 (Melo *et al.*, 2014). The pathotypes 65, 73, and 81 are currently the most prevalent in Brazilian bean fields. The main goal of the present work was to identify the inheritance of anthracnose resistance in the Andean cultivar BRSMG Realce.

MATERIALS AND METHODS

Controlled crosses were carried out at Embrapa Arroz e Feijão between the Andean resistance source BRSMG Realce and the Mesoamerican carioca seeded cultivars BRS Notável and BRS FC104. BRSMG Realce was always used as female parent. All F_1 plants were tested with SSR markers, in addition to the parents, to confirm them as hybrids. The checked hybrids were advanced up to the F_2 generation. Approximately 150 and 300 F_2 seeds from the crosses BRSMG Realce × BRS Notável and BRSMG Realce × BRS FC104, respectively, were sown in polystyrene trays containing commercial soil substrate (Plantmax®), resulting in 128 and 275 F_2 plants, respectively. The *C. lindemuthianum* isolates Cl 1988 (pathotypes 81) and Cl 1322 (pathotype 475) were used to inoculate the F_2 populations from crosses BRSMG Realce × BRS Notável and BRSMG Realce × BRS FC104, respectively. In addition to the parents, IPA 7419 was also tested and used as a susceptible control. All plants screened were inoculated with a conidial suspension at seven days after sowing, in the V2 stage (Pastor-Corrales et al., 1992). The conidial suspension (1.2×10^6 conidia mL^{-1}) was obtained as described by Cárdenas et al. (1964). The conidial suspension was applied to the abaxial and adaxial surfaces of primary leaves with a hand sprayer until runoff. After the inoculation, all plants were kept in a moist chamber for 45 h, with a photoperiod of 12 h light/dark and temperature adjusted to 20 ± 2ºC. The humidity was controlled by nebulization and maintained at approximately 95%. After that, nebulization was turned off and the inoculated plants were kept in a controlled environment with the same temperature and photoperiod described above. The symptoms were evaluated at seven days after the inoculation, following the score scale of 1-to-9, where plants that showed scores 1-to-3 were considered resistant and plants with scores 4-to-9 were considered as susceptible (Pastor-Corrales & Tu, 1989).

RESULTS AND DISCUSSION

The observed symptoms in the susceptible genotypes were fully attributed to the infection caused by the fungus *C. lindemuthianum*, showing the effectiveness of the inoculation procedure. BRSMG Realce showed an average score of 1 when tested with both pathotypes 81 and 475, while BRS Notável, BRS FC104, and IPA 7419 presented average scores of 9. The results from the screening of the two F_2 populations tested in this work indicated that a single dominant gene governs inheritance of anthracnose resistance in the Andean cultivar BRSMG Realce – *Co-Realce* (Table 1). The population BRSMG Realce × BRS FC104 is currently being genotyped with SNP markers for genetically mapping the resistance locus *Co-Realce*.

Table 1. Inheritance of anthracnose resistance in the Andean "rajado" seeded common bean cultivar BRSMG Realce.

Pathotype[a]	Crosses	Ratio	No. Observed		No. Expected		χ^2	p-value
			R	S	R	S		
81	BRSMG Realce[b]	1:0	12	0	12	0	-	-
	BRS Notável[c]	0:1	0	12	0	12	-	-
	IPA 7419[d]	0:1	0	12	0	12	-	-
	F_2 (BRSMG Realce x BRS Notável)	3:1	101	27	96	32	1.04	0.31
475	BRSMG Realce[b]	1:0	12	0	12	0	-	-
	BRS FC104[c]	0:1	0	12	0	12	-	-
	IPA 7419[d]	0:1	0	12	0	12	-	-
	F_2 (BRSMG Realce x BRS FC104)	3:1	215	60	206	69	1.48	0.22

[a]Races of *Colletotrichum lindemuthianum*; [b]Resistant parent; [c]Susceptible parent; [d]Susceptible control; R – Resistant; S – Susceptible.

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PEROXIDASE ACTIVITY IN BEAN GENOTYPES (*PHASEOLUS VULGARIS* L.) WITH DIFFERENT RESPONSE TO COMMON BACTERIAL BLIGHT

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INTRODUCTION

Xanthomonas axonopodis pv. *phaseoli* is the etiological agent of bacterial common bacterial blight (CBB), one of the most important diseases affecting productivity of common bean (Silva *et al.* 2020). Some studies have shown that in seedling leaves of rice (Reimers *et al*., 1992), and dry beans (Silva *et al.* 2020) infected by *X. oryzae* pv *oryzae* or *Xanthomonas axonopodis* pv. *phaseoli*, respectively, peroxidase (POX) activity increases. This increment peaked while bacterial multiplication was restricted. These results suggest that POX activity in the presence of H_2O_2 may oxidize phenols to produce toxic compounds.

The bean breeding Program of CEVAMEX-INIFAP seeks to develop varieties with resistance to CBB, the most common disease in the cultivation of beans in the High Valleys area of the Central plateau of Mexico. Therefore, the purpose of the study was to examine if seeds of varieties resistant to *Xanthomonas axonopodis* pv. *phaseoli* showed higher activity of POX than susceptible ones. This activity is easy to detect and to quantify; which are two desired characteristics for screening a large volumes of materials. The objective of this study was to characterize the activity of POX in the seed of four common bean varieties with different levels of resistance to *Xanthomonas axonopodis* pv. *phaseoli*.

MATERIALS AND METHODS

Four varieties were used including two Flor de Mayo (FM) types, one Bayo (B) and one Cranberry (C). Flor de Durazno (FM) and Cacahuate-72 (C) are susceptible to common blight, while MAM-38 (FM) and Bayo Azteca (B) are resistant. The four varieties were sown in rows of 4 m in length. The plants of each variety were harvested and hand threshed. The seeds were kept at room temperature until seed moisture decreased to 12%.

From each variety, 15 healthy grains without fissures in the coat were selected. At the time of analysis, they were ground in a cyclotec mill with a 0.5 mm mesh and homogenized. A total of 250 mg was taken from each sample. Determination of the peroxidase activity was carried out according to a modified version of the method described by Kato and Shimizu (1987). The activity was quantified in a Thermo Scientific enesys 10s UV / VIS spectrophotometer at a wavelength of 470 nm and at a temperature between 20-25 °C for 150 seconds, at 15-second intervals starting from time zero. Analyzes were carried out in triplicate. Activity of POX in the whole grain of the genotypes is expressed in units of enzymatic activity (U) POX (Δ A470 g bean flour^{-1} min^{-1}). Where the change in absorbance (Δ A470) with respect to time is associated. Absorbance increment occurs due to the formation of tetraguaiacol, in the presence of guaiacol and hydrogen peroxide.

RESULTS AND DISCUSSION

POX activity was different between bean genotypes resistant and susceptible to common bacterial blight (Fig. 1).

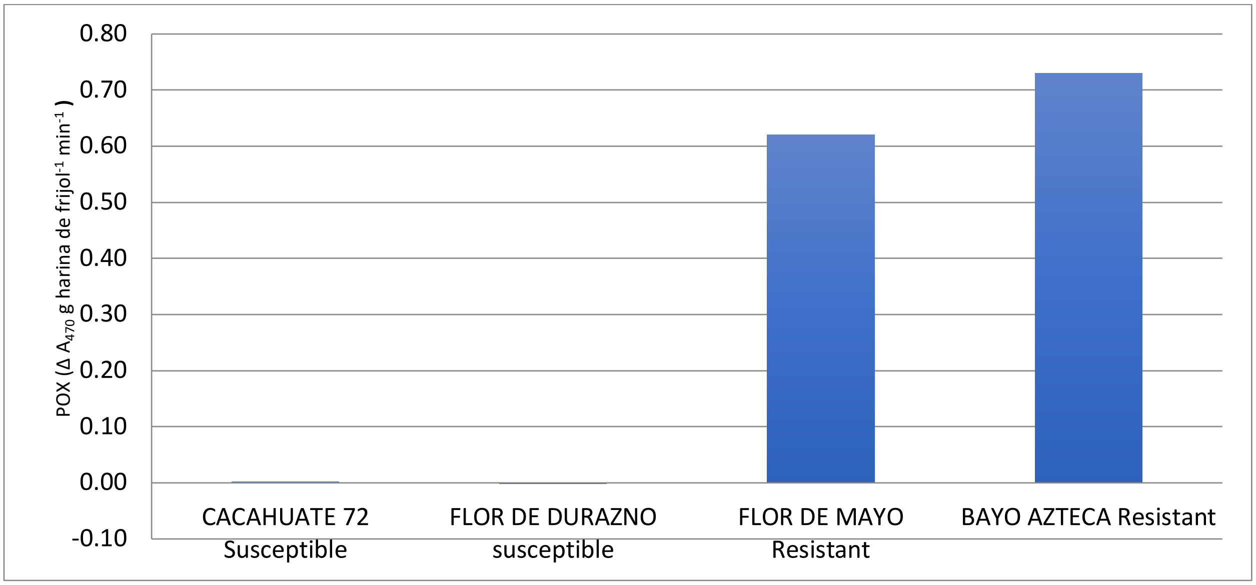

Figure 1. POX activity in bean genotypes with different response to common blight attack.

Bayo Azteca, and Flor de Mayo M-38 varieties with resistance to common blight showed the highest peroxidase activity of 0.73 and 0.62 U. In contrast, the susceptible varieties Flor de Durazno and Cacahuate-72 showed scarcely detectable peroxidase activity (<0.002 U). Even though the resistance mechanisms to *Xanthomonas axonopodis* pv *phaseoli* in these varieties has not been determined, this result suggests a possible association of the peroxidase activity detected in the bean seed with the resistance response to this disease. More studies are required to corroborate this hypothesis, since the measurement of the activity of this enzyme in seed could represent an indirect selection parameter for common bacterial blight.

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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 2020, field and/or greenhouse evaluations were used to screen thirteen common bean lines for putative sources of white mold disease resistance in adapted backgrounds. Evaluations were conducted at multiple sites located in six states (CO, MI, NE, ND, OR, WA) and in one province in Canada (Quebec). Collectively, these 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 resistance in adapted and unadapted bean germplasm, and requires only a small number of seeds to confirm resistance. Thirteen bean lines were evaluated, plus G122 (with partial resistance), Bunsi (mostly field avoidance) and Beryl (susceptible) that were included as the control lines. Greenhouse evaluations were conducted at all locations except ND.

Field tests were conducted in all locations except CO, which is too dry to produce consistent disease pressure. Nine bean lines were evaluated in addition to the three controls described above. Unfortunately, data was collected from only three of the locations due to multiple causes, most commonly a lack of disease pressure as a result of hot, dry weather during the summer growing season. A coating of ash from severe wildfires in the western U.S., and insect damage to the planted seed were also factors in the loss of data. As in years past, this illustrates the necessity of multiple sites for generating data despite weather or other natural complications in field trials.

RESULTS AND DISCUSSION: Although no lines scored as more resistant than the partially resistant control G122 in either the greenhouse or field trials in 2020, three lines (SR16-1, SR9-5 and ND122454(2131)) out-performed the moderate control, Bunsi, in the greenhouse screenings (Table 1). These three were also among the six lines (Adams, ND122454(2131), SR16-2, SR9-5, Eiger and ND132162) that performed equally to G122 in the field screening, including one (SR9-5) for which this was the second year of performing equally to G122 in the field (Table 2). In the past five years, several lines had field performance no different from the partially resistant G122, with two of them showing consistent performance across years (Table 3). In the field trials in 2020, all nine of the trial lines outperformed the partially resistant G122 control line, which combined with information on their performance in the greenhouse trials, indicate that these lines either possess resistance or escape mechanisms in the field.

Table 1. Greenhouse test mean disease ratings* in 2020 with control lines highlighted in blue.

Line	NE	WA	CO	OR	CAN	MI	Mean	Grouping**
G122	5.08	4.08	3.92	3.60	6.91	6.60	5.03	a
SR16-1	5.18	5.42	5.92	3.30	6.58	5.20	5.27	a b
SR9-5	5.42	5.42	5.83	3.00	7.08	5.30	5.34	a b c
ND122454(2131)	4.25	4.50	5.33	3.70	6.83	7.90	5.42	a b c
Bunsi	6.83	5.90	6.31	4.10	7.00	5.40	5.92	a b c d
R17604	6.42	5.50	7.54	4.20	6.83	8.00	6.41	a b c d e
Beryl	5.92	6.25	8.46	4.00	5.75	8.40	6.46	a b c d e
Charro	6.25	5.58	7.46	4.20	7.42	8.00	6.49	a b c d e
SR16-2	7.25	6.00	7.18	3.90	7.90	7.20	6.57	a b c d e
Adams	6.33	7.08	6.62	4.60	9.00	8.60	7.04	b c d e
PT16-23-6-B	9.00	6.92	8.38	3.30	7.58	7.50	7.11	c d e
PT16-23-8-B	8.92	6.83	8.17	4.60	8.17	8.50	7.53	d e
Eiger	8.75	6.92	9.00	4.20	8.00	8.70	7.59	d e
NDF141506	8.75	7.00	8.62	3.70	8.73	8.90	7.62	d e
ND121315	9.00	7.67	8.85	4.30	8.08	9.00	7.82	e
ND132162	8.75	7.33	9.00	4.70	9.00	8.90	7.95	e

* Petzoldt & Dickson scale: 1-3 = resistant, 4-6 = intermediate, 7-9 = susceptible
** P = < 0.01; LSD = 1.832

Table 2. Field test mean disease ratings* 2019 with control lines highlighted in blue.

Line	NE	MI	Mean	Grouping
G122	2.0	2.0	2.0	a
Adams	2.0	2.3	2.2	a
ND122454(2131)	2.0	2.7	2.4	a
SR16-2	2.0	3.3	2.7	a
SR9-5	4.0	2.3	3.2	a
Eiger	3.0	3.7	3.4	a
ND132162	2.0	4.7	3.4	a
Charro	4.0	4.3	4.2	a b
NDF141506	4.0	4.3	4.2	a b
PT16-23-6-B	3.0	6.7	4.9	a b
Bunsi	3.0	7.7	5.4	a b
Beryl	5.0	9.0	7.0	b

LSD = 3.583
*CIAT scale- 1-9; 1= no disease, 9 = dead plant

Table 3. Lines with field performance no different from the partially resistant line (G122) in one or more years (repeated years highlighted in yellow).

	2016	2017	2018	2019	2020
Adams					X
ND122454(2131)					X
SR16-2					X
Eiger					X
ND132162					X
SR9-5				X	X
NDF120287				X	
N14229			X		
VCP-13 (NE5-16-98)		X	X		
NE5-16-101		X			
N14229		X			
B15430		X			
NDZ14083		X			
ASS 1865	X				
R12844	X				
R13752	X				
PS08-039-A5	X				
USPT-WM-12	X				

MAPPING OF A RUST RESISTANCE LOCUS IN ANDEAN COMMON BEAN LANDRACE G19833

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INTRODUCTION

The Peruvian landrace G19833 (Chaucha Chuga) was used to sequence the reference genome of common bean (Schmutz et al., 2014). This resulted in a large quantity of sequence information, corroborating the importance of G19833 for genomic studies of common bean. G19833 is also resistant to numerous highly virulent races of the common bean rust pathogen (Hurtado-Gonzales et al., 2017). The broad-spectrum rust resistance of G19833 could be used in the development of common bean cultivars with comprehensive and durable rust resistance. In this study, we characterized the inheritance of rust resistance of G19833. In addition, we used high throughput genotyping with the BARCBEAN12K BeadChip and Kompetitive allele specific PCR (KASP) genotyping technology to map this prospective new rust resistance locus in G19833.

MATERIALS AND METHODS

A total of 650 F_2 plants from the G19833 (resistant) × Olathe (susceptible) cross were inoculated with four races [16-1 (52), 31-1 (53), 30-1 (55), and 37-1 (84)] of the bean rust pathogen. The cultivars Aurora (*Ur-3*), Early Gallatin (*Ur-4*), Golden Gate Wax (*Ur-6*), Pompadour Checa 50 (*Ur-9*), PI 181996 (*Ur-11*), and PI 260418 (undetermined R genes) were included as controls. All inoculated plants were incubated in a mist chamber ($20 \pm 1^\circ$ C and 95% humidity) for about 18 hours. Then, the plants were transferred to a greenhouse bench. Ten days later, the plants were evaluated for their reaction to the four races using a 1–6 scale (Stavely and Pastor-Corrales, 1989). A total of 187 F_2 plants were genotyped with 11,292 SNP markers using the BARCBEAN12K BeadChip. This data was used to map the rust resistance locus in G19833. We then developed the KASP markers SS120 (218,204 bp) and SS147 (1,433,996 bp) flanking the rust resistance locus to genotype the 650 F_2 plants that were phenotyped with the four races. F_2 plants showing recombination between the SS120 and SS147 KASP markers were then genotyped with other KASP markers designed for the genomic region containing the rust resistance locus in G19833.

RESULTS AND DISCUSSION

The parents G19833 and Olathe were resistant and susceptible, respectively, to all four races of *U. appendiculatus*. An F_2 plant that was resistant or susceptible to one race, was also resistant or susceptible to the other three races, respectively. The resistant reaction of F_2 plants was a tiny sporulating pustule (TP) that often included faint chlorotic spots. Conversely, the susceptible reaction was a large sporulating pustule. Based on their rust reaction, the 650 F_2 plants segregated into two groups: 472 resistant and 178 susceptible fitting a 3 (R): 1 (S) ratio ($\chi^2 = 1.971$, P value = 0.1603), indicating that the resistance in G19833 was conferred by a single and dominant gene. Genotyping 187 F_2 plants with the BeadChip and performing filtering analysis enable the selection of 4,133 SNP markers that were mapped on the 11 common bean chromosomes spanning an 894.51 cM genomic region. The rust resistance gene was mapped on the upper arm of chromosome Pv04 that was linked at 0.0 cM of the SNP markers Chr04_1038110_T/C (1,038,110 bp) and

Chr04_1105555_A/G (1,105,555 bp) (Figure 1a). Genotyping 650 F_2 plants with flanking KASP markers SS120 and SS147, identified 54 recombinant plants that were used for genotyping with nine additional KASP markers that positioned the rust resistance locus in a 543,696 bp genomic region flanked by the SS291 (612,831 bp) and SS299 (1,156,527 bp) KASP markers (Figure 1b).

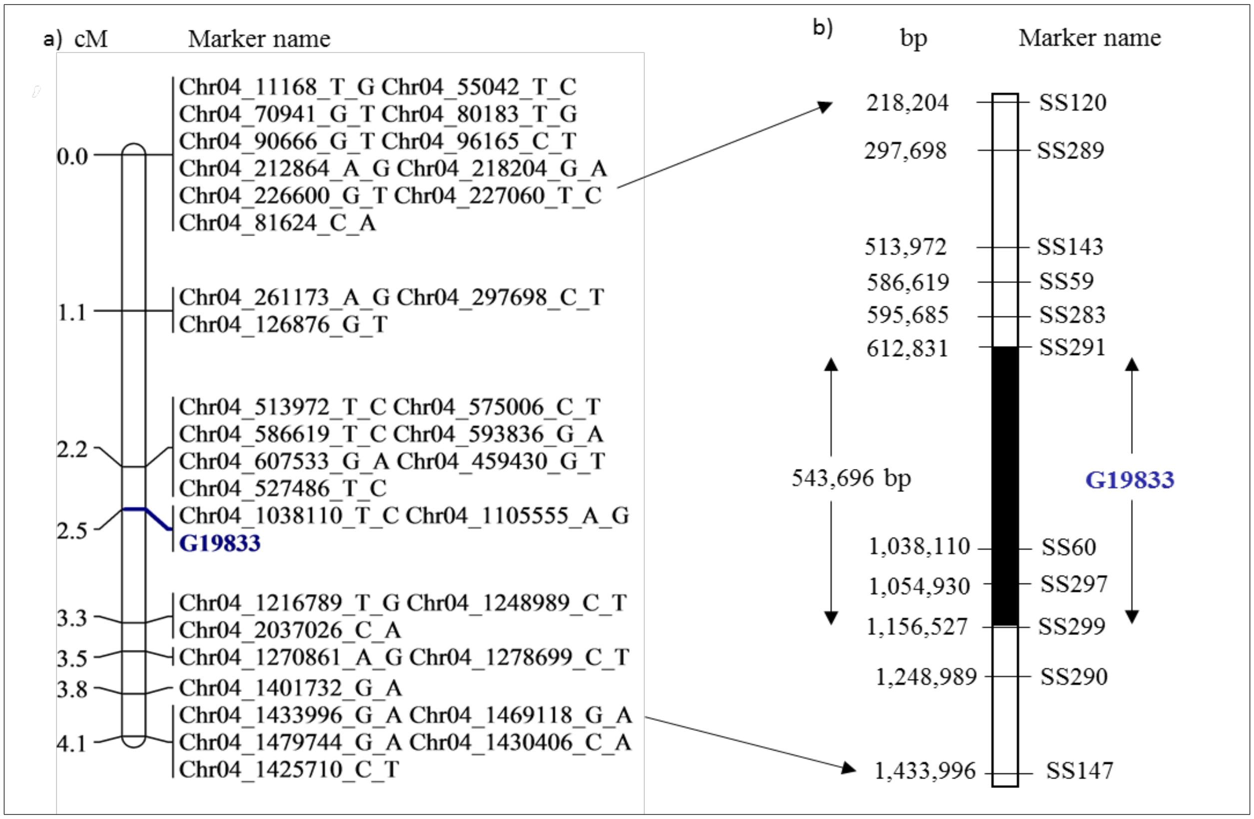

Figure 1. Genetic and physical maps of the rust resistance locus in Andean G19833 (Chaucha Chuga) located on chromosome Pv04 of common bean. a) Genetic map constructed using 187 F_2 plants inoculated with races 16-1 (52), 31-1 (53), 30-1 (55), and 37-1 (84) of the bean rust pathogen and genotyped with the BARCBEAN12K BeadChip. b) Physical map using 54 F_2 recombinant plants genotyped with KASP markers. Marker positions were based on the reference genome of common bean v 1.0.

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RESISTANCE TO *Cowpea mild mottle virus* IN THE EMBRAPA CARIOCA SEEDED COMMON BEAN CULTIVAR BRS SUBLIME

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INTRODUCTION

In Brazil, the *Cowpea mild mottle virus* (CPMMV) was firstly reported in common bean in 1980, in Campinas, São Paulo (Costa *et al*., 1983). The most common symptoms are a mild mosaic along or between the leaf veins and leaf crinckling. In susceptible soybean genotypes, strong stem necrosis is also observed. The symptoms of CPMMV was clearly identified in common bean fields grown with the cultivar BRS FC401 RMD that presents effective resistance to *Bean golden mosaic virus* (BGMV) (event Embrapa 5.1), but it is susceptible to CPMMV (Souza *et al*., 2018). Both viruses are transmitted by the whitefly (*Bemisia tabaci*). Sources of resistance to CPMMV have been identified through greenhouse and field screenings carried out at Embrapa Arroz e Feijão. The main goal of the present work was to elucidate the genetic inheritance of the CPMMV resistance present in BRS Sublime, an Embrapa cultivar with carioca seed type identified as the most promising CPMMV resistance source in Brazil so far.

MATERIALS AND METHODS

Controlled crosses were carried out at Embrapa Arroz e Feijão between the resistance source, BRS Sublime, and the transgenic line CNFCT 16207 (event Embrapa 5.1), susceptible to CPMMV. CNFCT 16207 was always used as the male parent. All F_1 plants were tested with event-specific molecular markers for transgene presence identification to confirm them as hybrids. The checked hybrids were advanced up to generations F_2 and $F_{2:3}$. All plants were maintained in an insect-proof net house. A total of 180 F_2 individual plants and 180 $F_{2:3}$ progenies (2,160 seedlings; 12 seedlings/progeny), in addition to the parents, were mechanical inoculation with a CPMMV isolate (strain CPMMV:BR:GO:14 – GenBank MK202583) at 8 days after planting, according to Alves-Freitas *et al*. (2019). For inoculation, leaves from the transgenic BGMV-resistant common bean line CNFCT 16207, showing severe symptoms of crinkling, were ground in 0.1 M phosphate buffer with 0.1% sodium sulfite, and was applied using carborundum 500 mesh. The inoculum was rubbed on the first trifoliate leaf (Cheruku *et al*., 2017). Four-to-five weeks after inoculation, all plants were scored for CPMMV severity. The scoring scale used to evaluate virus severity ranged from 1 (absence of disease symptoms and signs of pathogens) to 9 (80-100% disease severity or plant death) (Melo, 2009). Plants showing scores of 1-to-3 were considered resistant, and those scoring 4 or higher were considered susceptible. Chi-square (χ^2) tests ($p \leq 0.05$) were performed for goodness of fit to test the deviation of the observed segregation data from the theoretically expected Mendelian segregation ratio.

RESULTS AND DISCUSSION

All tested plants of BRS Sublime were resistant to the isolate CPMMV:BR:GO:14 and all plants of CNFCT 16207 were susceptible. From the 180 F_2 individual plants evaluated, 128 plants showed resistant reactions and 52 were susceptible. The segregation for resistance to CPMMV in the F_2 population showed a goodness of fit of 3 resistant: 1 susceptible (3R: 1S; $\chi^2 = 1.45$, P = 22.8%). Regarding the 180 $F_{2:3}$ progenies tested for CPMMV reaction, 45 shown non-segregating resistance, 88 progenies segregated for CPMMV reaction, and the other 47 progenies shown non-segregating susceptibility (1RR: 2Rr: 1Rr; $\chi^2 = 0.13$, P = 93.5%). Results from both generations indicated that a single dominant gene controls the inheritance of CPMMV resistance in common bean cultivar BRS Sublime. This is the first report of a genetic inheritance study for CPMMV resistance in common bean. The populations used in the present work are being genotyped with SNP markers to genetically map the CPMMV resistance locus present in BRS Sublime.

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ADAPTATION AND DISEASE RESISTANCE OF TROPICAL BLACK BEAN ELITE BREEDING LINES

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INTRODUCTION: Diseases, drought and acidity of the soils are the main factors that limit bean production in Chiapas and Veracruz, Mexico. This situation becomes more critical since most of the landraces and improved cultivars, such as Negro Jamapa, are cultivated in both federal states are susceptible to one or more of these limitations. The objective of this study was to identify high-yielding black bean breeding lines, resistant to diseases and with better adaptation to field conditions than three varieties currently used in Veracruz and Chiapas.

MATERIALS AND METHODS: During 2019 and 2020, in seven environments of Veracruz and Chiapas, Mexico, 11 elite black bean breeding lines and three improved cultivars, Negro Jamapa, Negro Medellín and Verdín, were evaluated in a RCBD with three replications. With the use of CIAT´s general disease reaction scale from 1 to 9 (Schoonhoven and Pastor-Corrales, 1987) the genotype reaction to the incidence of web blight and rust in some environments of Veracruz, and bean golden yellow mosaic virus (BGYMV) in Villa Corzo, Ocozocoautla and El Gavilán in Chiapas, as well as grain yield was determined. Individual analysis of variance of the incidence of each disease and the combined analysis of seven environments for grain yield were performed. Correlation analyses were also made between the incidence values of each disease with the seed yield of the genotypes. The AMMI model was used to identify the most outstanding genotype for their seed yield performance and stability across environments.

RESULTS AND DISCUSSION: In the combined analysis of variance, the Jamapa Plus/XRAV-187-3-4-4 breeding line was the most productive, with an average seed yield statistically similar to that of the Jamapa Plus/XRAV-187-3-1-2 breeding line, but higher than the rest of the genotypes. Both breeding lines showed field resistance to web blight and rust (scores between 2.67 and 3.33), as well as low incidence of BGYMV, diseases that significantly reduced grain yield (Table 1). The AMMI analysis showed that Jamapa Plus/XRAV-187-3-1-2 (G9) showed the least interaction with the environment (CP 1= -0.1531), which indicates the highest stability throughout the test environments, much higher than that of the control varieties, and that of the most productive breeding line, Jamapa Plus/XRAV-187-3-4-4 (G11) (Figure 1). This last breeding line obtained a CP = 9.6827, which indicates specific adaptation to certain environments; this is important if such high yielding genotype presents stability through years in those environments (Acosta et al., 2012).

Table 1. Average yield (kg ha^{-1}) & disease incidence (scale 1 to 9) of 14 black bean genotypes.

Genotype	Average SY	WB 1	Rust 2	BGYMV 3	BGYMV 4	BGYMV 5
Papaloapan/SEN 46-2-6	1252.90	3.33	3.67	3.67	4.67	3.67
Papaloapan/SEN 46-3-2	1298.90	2.00	4.00	4.00	5.33 *	3.67
Papaloapan/SEN 46-7-7	1328.62	4.33	4.00	2.00	1.33	3.00
Papaloapan/SEN 46-7-10	1235.48	4.33	3.67	2.67	3.00	4.33
Papaloapan/SEN 46-7-12	1260.95	4.33	3.67	3.00	3.33	4.33
Negro Citlali/XRAV-187-3-1-5	1126.48	5.67 *	2.33	3.00	2.00	4.00
Negro Citlali/XRAV-187-3-1-6	1273.95	5.33 *	3.00	1.67	2.00	1.33
Negro Citlali/XRAV-187-3-1-8	1201.95	4.67 *	4.67 *	3.33	2.33	4.67
Jamapa Plus/XRAV-187-3-1-2	1379.38*	3.33	2.67	3.33	3.33	5.00
Jamapa Plus/XRAV-187-3-4-1	1328.90	2.00	2.33	5.00 *	6.33 *	6.67 *
Jamapa Plus/XRAV-187-3-4-4	1542.24*	3.00	3.33	3.00	2.33	4.33
Negro Medellín	1086.33	4.33	5.67 *	4.00	4.67	5.33
Negro Jamapa	1021.29	6.00 *	5.00 *	3.67	5.00	4.67
Verdín	1326.57	3.00	5.33 *	2.33	2.33	3.00
ANOVA	**	**	**	**	**	**
LSD (0.05)	193.99	1.476	1.521	0.800	1.217	0.961
Correlation (r) disease *vs* SY		-0.81**	-0.61*	-0.56*	-0.76**	-0.55*

SY=Seed yield. WB=Web blight. BGYMV=Bean Golden Yellow Mosaic Virus. 1=Orizaba, Ver., summer 2019, rainfed. 2=Orizaba, Ver., W-S 2020, irrigated. 3=Villa Corzo, Chis., F-W 2019-20, residual moisture. 4=Ocozocoautla, Chis., F-W 2019-20, residual moisture. 5=El Gavilán, Ocozocoautla, Chis., F-W 2019-20, residual moisture. *$P \leq 0.05$, **$P \leq 0.01$. *Disease incidence values statistically higher according to the LSD test (0.05).

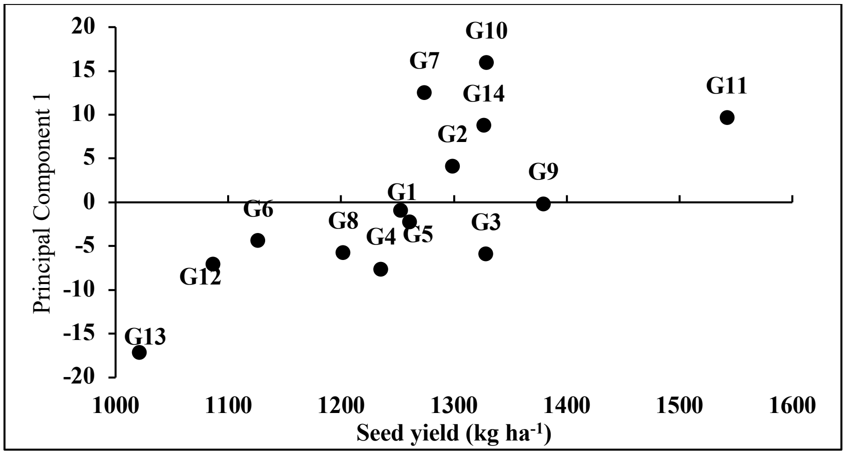

Figure 1. Principal effects and observed interaction of seed yield of 14 black bean genotypes.

CONCLUSIONS: Two breeding lines were identified with higher seed yields than the controls and showed high levels of disease resistance. Jamapa Plus/XRAV-187-3-1-2 (G9) showed wide adaptation to tropical areas of Veracruz and Chiapas, and Jamapa Plus / XRAV-187-3-4-4 (G11) had better adaptation in stress environments due to web blight and rust in Orizaba, Veracruz, and acid soils of low fertility and BGYMV incidence in Villa Corzo, Chiapas.

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ENTOMOFAUNA AND DAMAGE ASSOCIATED WITH THE CULTIVATION OF DRY BEAN IN THE CENTRE REGION OF COTE D'IVOIRE

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is the most widely consumed dry vegetable in the world (Djeugap et al., 2014). Its global production was estimated at 20.4 million tons in 2008 for a cultivated area of 26.47 million hectares in the temperate and tropical regions of America, Africa and Asia (Wortmann, 2006). Breeders at the National Centre for Agronomic Research (CNRA) and CIAT are working hard together for the reintroduction of bean grain legume in Côte d'Ivoire, a crop which is tending to disappear in the country. They have undertaken evaluation and selection of high-performance dry bean varieties with high yields and tolerance to biotic and abiotic factors. In order to set up effective pest control measures, an inventory of the main pests and their damage has been carried out.

MATERIALS AND METHODS

The plant material consisted of 35 dry bean accessions. The insects were captured manually twice a week using pliers and mowing nets, and the ecological parameters used to analyse the data was the relative abundance for each pest group. According to Zaime and Gautier (1989), this component is expressed by the ratio between the number of individuals of a species (Ni) considered and the total number of individuals of all species combined (N): Ar (%) = (Ni/N) x 100. The pods of the plants at the center of each elementary plot were counted and inspected for infested or damaged pods. The rates obtained were subjected to an analysis of variance using Statistica version 7.1 software. The comparison of the means was carried out using the Student-Newman - Keuls test at the 5% threshold.

RESULTS

The insects collected belong to eight Orders divided into 25 families and 45 species. The specific richness of the species varied according to the Orders. The actions of the insects on the plants were noted and summarized in Table 1. The main pests were, respectively, *Medydhia quaterna,* striped foliage beetle which transmits the cowpea mottle virus (relative abundance (Ar) = 24.18 ± 3.21%), *Riptortus dentipes*, probably the most destructive of all the pests of developing pods of cowpea (Ar= 36.12 ± 6.03%) and *Maruca testulalis,* bean pod borer and insect pest of others legume crops such as the pigeon pea, cowpea, mung bean and soybean (Ar = 84.14 ± 7.20%) (Figure 1). Damage to the pods caused by sucking pests and borers varied according to the accessions. For the HARI29/GHA19 accession, which was the most attacked, the percentages of pods attacked by borers and sucking pests were 14.48 ± 8.56 % and 55.73 ± 17.06 %, respectively. The other most damaged lines were HARI03/FER18, HARI07/GHA18, HARI01/KEN16 and HARI25/GHA19. The accessions that were less attacked by both groups of pests were HARI02/KEN18, HARI17/GHA19, HARI21/GHA19, HARI23/GHA19, HARI24/GHA19, HARI31/GHA19 and

HARI35/GHA19. The percentages of pods attacked by borers in these accessions ranged from 3.27 ± 0.72 to 5.10 ± 0.70% and for sucking pests ranged from 20.76 ± 4.82 to 26.21 ± 12.27%.

Table 1. Specific richness of the Insect Orders harvested from dry bean plants in the first crop cycle

Orders	Number of families	Number of Species	Species proportion (%)	Action on the plant
Heteropterans	6	16	35.56	Suckers, predators
Beetles	4	9	20.00	Defoliators, flower eaters
Orthopterans	4	6	13.33	Defoliators
Lepidoptera	3	4	8.89	Borers, defoliators
Hymenoptera	2	3	6.67	Pollinators, predators
Diptera	2	3	6.67	Leaf eaters, predators
Homoptera	3	3	6.67	Leaf miner, suckers
Thysanoptera	1	1	2.22	Flower eaters

Medythia quaterna (Defoliators)

Riptortus dentipes (sucker)

Larva of *Maruca testulalis* (Borer)

Figure 1. Main pests belonging to different insect groups

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RESISTANCE TO TERMINAL DROUGHT OF IMPROVED OPAQUE, BLACK BEAN BREEDING LINES

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INTRODUCTION: In the humid tropical conditions of southeastern Mexico, the small opaque black common bean is a subsistence crop, produced mainly by small farmers with low use of inputs; its productivity and profitability are low, due in large part to the combined effect of biotic and abiotic factors that limit production. With respect to the latter, terminal drought is the most important factor that reduces the grain yield of the vast majority of the varieties grown in this wide region of the country. The objective of this study was to assess the agronomic performance of a group of improved opaque, black bean breeding lines cultivated under conditions of terminal water stress imposed by withholding field irrigation during the flowering stage of the crop.

MATERIALS AND METHODS: During the winter-spring cycle (February-May) of 2017, two yield trials were conducted in the same experimental site in El Rubí, Medellín de Bravo, located in the central coastal region of Veracruz, Mexico. In both trials, 12 opaque improved black bean lines and the commercial cultivars "Negro Comapa" and "Negro Grijalva" were evaluated, in a RCBD with three replications. The experimental plots consisted of three rows, 5 m long and 0.80 m apart. One of the yield trials was conducted with irrigation throughout the crop cycle, applied at 07, 17, 34, 45, 54 and 63 days after sowing. The other trial was conducted under terminal drought conditions imposed by withholding irrigation from the beginning of the flowering stage; therefore, in this trial, the genotypes only received the first three irrigations. In addition, soil samples were taken weekly at a depth of 0 to 40 cm to monitor the usable soil moisture and corroborate the terminal drought condition. Days to flowering and physiological maturity, production of total dry biomass (kg ha^{-1}), harvest index, grain yield (kg ha^{-1}) and yield components (number of pods per plant and 100 seed weight) were determined. The percentage of reduction due to water stress was determined for each trait. Individual ANOVA´s were carried out for each trait and for each soil water condition. Drought susceptibility index (DSI) (Fisher and Maurer, 1978) and the relative efficiency index (REI) (Graham, 1984) of each genotype were estimated.

RESULTS AND DISCUSSION: Table 1 shows that flowering did not vary between soil water conditions, the average was 36 days, mainly because in that period of time the two yield trials were conducted under the same soil humidity conditions. In contrast, the other characteristics were affected to a greater or lesser extent by the suspension of irrigation from the beginning of flowering. The average days to maturity was eight days lower under drought stress in comparison to the full irrigation condition. Grain yield was the trait most affected by the drought condition, with an average reduction of 34%, largely because the number of pods produced per plant was reduced by more than 25%, and by more than 15% in biomass production. Therefore, there was an average reduction of 21.4% in the harvest index. In turn, the 100 seed weight was the yield component least affected by terminal drought. Seed yield varied significantly among genotypes ($p \leq 0.01$) in both soil water conditions. Jamapa Plus/XRAV-187-3-1-2 (11) breeding line obtained high seed yields (2,270 kg ha^{-1}) in the irrigated condition and was the most productive (1,536 kg ha^{-1}) under terminal drought (Figure 1). Although these seed yields were statistically similar to both check cultivars, Negro Comapa (13) and Negro Grijalva (14), this breeding line obtained the highest productive efficiency REI=2.28 (higher than both check cultivars), under both irrigated and drought conditions. This same breeding line had a DSI<1.0 (0.94), which indicates its tolerance to terminal drought stress as well.

Table 1. Average values and percentage of reduction of plant traits of 12 improved black bean breeding lines and two control cultivars evaluated under full irrigation and terminal drought conditions in the winter-spring 2017 season in El Rubí, Medellín de Bravo, and Veracruz, Mexico.

Plant traits	Average values		Reduction %
	Irrigated	Drought†	
Flowering (DAP)‡	36.3	36.2	0.28
Maturity (DAP)	79.3	71.0	10.47
100 seed weight (g)	19.3	17.1	11.40
Pods/plant	18.2	13.6	25.28
Seed yield (kg ha^{-1})	1526	1002	15.28
Total dry biomass (kg ha^{-1})	5464	4629	34.34
Harvest index (HI)	0.28	0.22	21.43

†= Terminal drought imposed at flowering phase. ‡= Days after planting

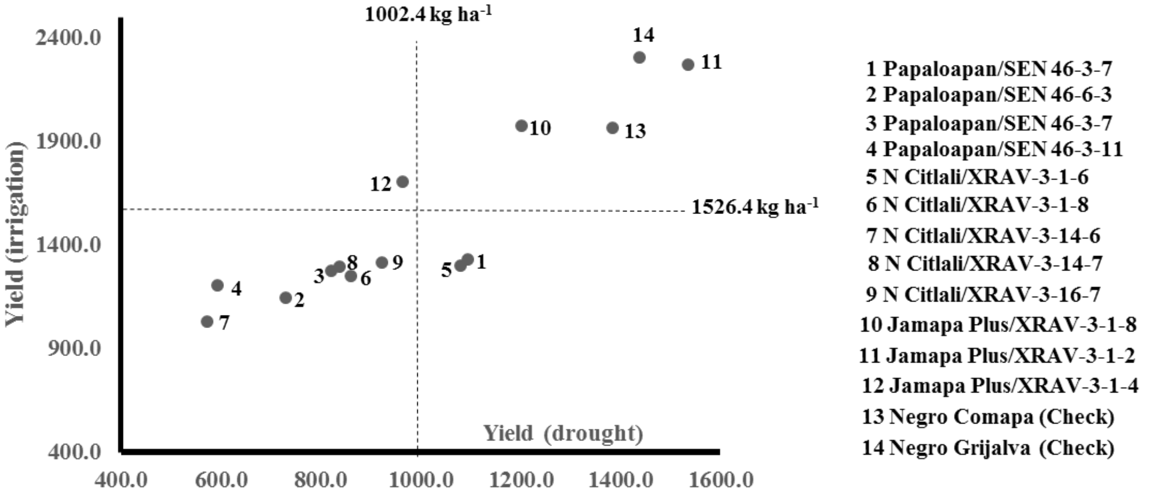

Figure 1. Seed yield (kg ha^{-1}) of 12 improved black bean breeding lines and two check cultivars, grown under terminal drought and full irrigation during the winter-spring 2017 season in Veracruz, Mexico.

CONCLUSIONS: Improved opaque black breeding lines with outstanding response in seed yield and its components were identified under both soil water conditions, fully irrigated and terminal drought stress. Jamapa Plus/XRAV-187-3-1-2 stood out for presenting a drought susceptibility index DSI <1.0 and of a relative efficiency index REI > 2.2.

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RESPONSE OF COMMON BEAN (*PHASEOLUS VULGARIS*) GENOTYPES TO NON-STRESS AND DROUGHT STRESS IN THE SOUTHERN HIGHLANDS OF TANZANIA

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INTRODUCTION

Drought stress is the most serious of all the factors that limit bean production and yield stability in drought-prone areas. It’s a major factor which reduces the quality of crops and limits yield (Acosta-Diaz et al., 2009). Common bean is among the species that need moist soil for proper growth and development. Drought resistance is conditioned by many traits including rooting pattern (Beebe at al., 2006). Although beans can support adverse conditions of lower than expected rainfall over short periods, prolonged drought causes irreversible damage. Seasonal fluctuations in bean production could effectively be reduced through development or introduction of stable genotypes that yield well in good and poor rainfall seasons. The objective of the study was to identify high yielding, drought tolerant bean genotypes adapted to a wide range of environments.

MATERIALS AND METHODS

Two field experiments were conducted on clay loam soils at Tanzania Agriculture Research Institute in Uyole. The geographical position of Uyole is 8^0 53’S $33^0$39’E with an altitude of 1778m.a.s.l. These trials were planted during the dry period and under irrigated conditions. The experimental design was a Randomized Complete Block Design replicated 2 times. Water stress occurred at flowering and two weeks after 50 % flowering while the experiment had a non-stressed control and 130 genotypes randomly occupied the plot. The plot size was single row 4m long with the spacing of 50cm x 10 cm. The whole trial was irrigated to field capacity after sowing (about 35mm every 10 to 14 days). Irrigation was done using hose pipe from planting to flowering initiation and an effective water stress was imposed at flowering until the week before physiological maturity. Soil moisture content in both trials was determined using the standard cup to collect soil samples before irrigation at each irrigation interval and at a depth of 0-20cm. Moisture was determined by calculating the percentage of soil moisture as compared to dry soil. Crop development was monitored by seed yield in kg/ha. Analysis of variance (ANOVA) was done using GENSTAT to determine whether the treatments effects were significant.

RESULTS AND DISCUSSION

The treatments consisted in the omission of irrigation to the drought experiment during reproductive development to maturity. The results show the effect of induced water stress (8 to 11% available moisture) that accelerates the development of beans (Table 1). This was expressed by the premature development of flowers and the subsequent production of small fruits, hastening physiological maturity. In addition, there is evidence for substantial genotypic variation for this trait. The use of visual scores for general vigor and reduced leaf senescence, combined with an estimate of number of pods/plants at maturity, is suggested for the identification of promising stress resistant genotypes. 130 common bean genotypes were tested while the results for the best entries and controls is summarized in Table 2. The yield parameter was reduced significantly by soil moisture stress. The yields ranged from 1031-3547 and 669-1496kg/ha without and with moisture stress, respectively. There were significant differences among treatments in seed production. There were significant differences among treatments in seed yield/ha. The lowest yield was produced when water was withheld. Twenty (20) promising genotypes were selected for further evaluation in different agro-ecologies.

Table 1. Moisture content of soils in the experimental site at TARI Uyole

S/N	Plant growth stage	Non-stress		Drought stress	
		% moisture by weight	Amount of water (mm)	% moisture by weight	Amount of water (mm)
1	14 days at reproductive	24.3	24.4	8.3	14.0
2	21days of reproductive	30.8	33.1	10.1	10.7
3	7 days before maturity	27.3	27.2	11.0	11.2

Table 2. Performance bean genotypes evaluated at TARI Uyole

S/N	Bean genotypes	Without drought stress	With drought stress
		Grain yield (kg/ha)	Grain yield (kg/ha)
1	KG 30-29	1620	828
2	CZ 102-38	1566	920
3	KG 111-36	1615	669
4	KG 111-37	3112	980
5	CZ 114-51	2638	1496
6	KG 114-178	1534	874
7	KG 114-180	2057	1200
8	CZ 108-53	1739	1136
9	CZ 113-15	1031	716
10	KG 111-183	2969	1284
11	KG 111-35	3547	1068
12	CZ 114-47	2872	1226
13	KG 114-185	2207	1260
14	KG 15-6	1279	774
15	CZ 102-36	1641	1017
16	CZ 102-39	2504	966
17	CZ 102-59	2059	1093
18	CZ 112-14	1935	944
19	CZ 113-81	1860	908
20	Kablanketi (check)	1921	996
	Means (130 lines)	1855	969
	LSD 5%	3232	1384

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QTL MAPPING OF SIZE AND COLOR TRAITS IN BEAN PRIMARY LEAVES

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Phenotypic variation for size and color of the primary leaves among bean cultivars is observed at in the seedling stage. In this work we looked for the QTL associated with these characteristics in two recombinant inbred populations.

MATERIALS AND METHODS

Plant Material. Two RIL populations were evaluated. The XC population (115 $F_{7:8}$ lines) was obtained from the cross between the genotypes 'Xana' and 'Cornell 49242', and the XB population (145 $F_{6:7}$ lines) was generated from the cross between the lines 'Xana' and 'BAT93'. Two genetic maps with 762 and 497 marker loci were available in the XC and XB populations, respectively (Murube et al., 2020).

Phenotyping. The populations were evaluated two times in the greenhouse (September – December 2020) using a randomized complete-block design with two replicates per line. A replicate was a 1.5 l pot with 2- 4 plants per line. Six traits of the primary leaves were recorded using Tomato Analyzer V3 software (Brewer et al., 2006): i) ***Leaf dimensions*****:** Leaf Area (LeafA; cm^2), Leaf length (LeafL; cm), Leaf width (LeadW; cm), ii) ***Leaf color traits*****:** Color was measured in the CIELab color space; LeafCol.L (L*), LeafCol.a (a*) LeafCol.b (b*). In addition, chlorophyll content was estimated using SPAD 502 Plus Chlorophyll Meter (LeafClo). SPAD values were measured two times per seedling. Phenotyping was carried out when the primary leaves were fully extended and the first trifoliate leaves were not developed.

QTL mapping. The mixed-model based on composite interval mapping implemented in QTLNetwork 2.1 software was used to detect QTL with individual effects (Yang et al., 2008). QTL with an estimated heritability of additive effects (h^2) greater than or equal to 0.05 were considered.

RESULTS AND DISCUSSION

The three parents exhibited different phenotypes for the primary leaf (see Figure 1). A continuous distribution was detected for the seven traits measured and, no significant deviations from the corresponding normal distributions were observed. Significant differences between Xana and the others two parents were found for four traits (see Figure 1 and Table 1). Pearson´s correlation coefficients for leaf dimensions were positive and significant in both populations (LeafA, LeafL, LeafW). Correlations were also significant among the three leaf color traits and chlorophyll content. The comparison between the parents and the RILs showing the maximum and minimum values reveal the existence of significant transgressive segregants for the seven traits.

QTL analysis revealed 8 single QTL for primary leaf size, 5 in the XC population and 3 in the XB population (Table 2). QTL LeafW07_5.1-XC and LeafA07_5.7-XB, involved in leaf size, were co-located on the chromosome Pv07. Very close on chromosome Pv06 (< 2Mbp) were located the QTL LeafW06_24.6-XC, LeafA06_26.3-XB, and LeafW06_26.3-XB. QTL analysis also showed 10 QTL for primary leaf color, 5 in the XC population and 5 in the XB population (Table 2). At the beginning of chromosome Pv03 three QTL for leaf color, LeafCol.a03_3.81-XC, LeafCol.b03_3.81-XC and LeafCol.L03_5.5-XB, were detected. Finally, three QTLs were identified for chlorophyll content (Table 2).

Nested populations allow the verification of the genetic control in the common genotype and analysis of more variation than in a single biparental population. This work adds knowledge about the genetic control of morphological characters in common bean and reveals the variation in the detection of QTL depending of genetic background.

Figure 1. Primary leaf phenotype in the parents Xana, Corenll49242 and BAT93.

Table 1. Observed means in the three parents and significant differences. Different letters in a row mean significant differences at $p < 0.05$ (Tukey tests).

Trait	Xana	Cornell	Bat93
LeafA (cm^2)	93.35c	65.87b	46.04a
LeafW (cm)	10.98c	8.69b	6.95a
LeafL (cm)	12.31b	12.18b	10.29a
LeafCol.L	41.34a	40.7a	40.58a
LeafCol.a	-13.75a	-13.18a	-13.49a
LeafCol.b	18.34a	17.91a	18.32a
Leaf.Clo	39.263a	26.241b	27.446b

Table 2. Single QTL with individual effects for primary leaf size and color traits identified by mixed–model based composite interval mapping analysis (MCIM) in the XC and XB RIL population using the QTL Network 2.0 software. F-value, F values of additive effects; A, additive effects (positive values are contributed by alleles from the parent Xana); h^2, heritability of additive effect.

		Position			QTL traits		
QTL name	Pop	LG	Start	End	F-value	A	h2
LeafClo01_2.1	XB	Pv01	2110013	2270849	9	0.74	0.06
LeafCol.L01_11.7	XB	Pv01	11769806	14695596	13.6	-0.45	0.07
LeafCol.a01_18.2	XB	Pv01	18267802	25680602	10.3	0.26	0.08
LeafCol.b01_25.6	XB	Pv01	25680602	32434150	8.7	-0.69	0.09
LeafA01_49.6	XC	Pv01	49794342	49647334	9	7.87	0.11
LeafClo02_7.2	XB	Pv02	7275527	11948592	13.2	1.10	0.11
LeafCol.a03_3.81	XC	Pv03	3463864	3815468	19.3	-0.47	0.17
LeafCol.b03_3.81	XC	Pv03	3463864	3815468	16.9	0.97	0.15
LeafCol.L03_5.5	XB	Pv03	5522867	6337788	16.1	0.50	0.12
LeafCol.L02_50	XC	Pv03	50112053	50473308	13.3	-0.64	0.12
LeafW06_24.6	XC	Pv06	24307828	24685018	14.3	0.41	0.07
LeafA06_26.3	XB	Pv06	26310415	27276706	11.2	5.59	0.06
LeafW06_26.3	XB	Pv06	26310415	27276706	12.7	0.33	0.06
LeafClo06_28.9	XC	Pv06	28976317	29420790	13.4	1.18	0.12
LeafClo07_1.5	XC	Pv07	1591518	2157016	9.7	0.80	0.09
LeafW07_5.1	XC	Pv07	5158486	5493421	20.6	0.51	0.13
LeafA07_5.7	XB	Pv07	5761992	6595207	13.7	6.56	0.09
LeafClo08_2.7	XC	Pv08	2742918	2862500	9.2	0.72	0.08
LeafCol.L08_57	XB	Pv08	57066309	57285128	23.2	0.65	0.13
LeafCol.L08_60.2	XC	Pv08	60283020	61226786	16.7	0.60	0.1
LeafCol.b09_20	XC	Pv09	20019010	20267504	10	0.56	0.07
LeafW09_21.4	XC	Pv09	21435696	21644891	14.9	-0.50	0.14
LeafA11_3.91	XC	Pv11	3913307	4636303	9.2	5.79	0.05

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IDENTIFICATION OF QTL ASSOCIATED TO POD LENGTH IN THE COMMON BEAN RIL POPULATION TU/MUSICA

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INTRODUCTION: Bean pods show wide phenotypic variation for length, width, curvature, cross section and color. Pod phenotype is particularly important in beans consumed as immature pods (snap or green beans), so establishing the genetic control that underlies the phenotypic variations in pod traits arouses a special interest. In order to elucidate the genomic regions conditioning pod length in common bean, QTL mapping was carried out in a recombinant inbred line population, TUM, in which the parents show extreme pod size differences.

MATERIALS AND METHODS

Plant Material. The TUM population was generated by single seed descend from the cross between the lines TU and Musica (175 $F_{6:7}$ lines). The parent TU has purple and short pods, while Musica has very large and flat pods (Figure 1). Musica is a snap bean line with green pods. The parents show indeterminate growth habit. This population was genotyped and, a genetic linkage map (data pending publication) with 842 SNP markers obtained by Genotyping-by-Sequencing (Enshire et al. 2011) was created.

Phenotyping. A total of 175 $F_{6:7}$ recombinant inbred lines and parental lines were phenotyped in the greenhouse using a randomized complete block design during four different seasons (Spring 2019 and Autumn 2018, 2019, 2020). Each season represented a single replicate of a single 1-m row plot including 8-10 plants per line. Fresh pods were harvested at the beginning of the R8 growth stage when pods had reached maximum length. Pod length was recorded in 10 fresh pods per line using the software Tomato Analyzer V3 (Brewer et al., 2009).

QTL mapping. QTLNetwork v2.1 (Yang et al., 2008) was used to identify single-locus and epistatic interaction effects. An experiment-wise significance level of 0.05 was designated for candidate interval selection, putative QTL detection, and QTL effect determination. Both testing and filtration window size were set at 10 cM, with a walk speed of 1 cM. Significant QTLs were determined by the critical F-value after 1000 permutation tests with a confidence level of 95%.

RESULTS AND DISCUSION

A continuous distribution was detected for pod length and no significant deviations from the corresponding normal distribution were observed. The parents TU and Musica had a mean of 10.2 cm and 24.2 cm for pod length, respectively. The RIL population showed a mean of 15.1 cm with a variation between 7.63-25.35 cm. QTL analysis revealed 7 single-locus QTL located on chromosomes Pv01, Pv03, Pv04, Pv06, Pv07 and Pv08 (Table 1). In all case, alleles contributed by the parent Musica increased the phenotypic value and, the estimated h^2 of additive effects ranged between 0.03 and 0.25. The highest estimates for additive effect were found for the QTL PL04_37.4 and PL06_18.1. Three QTL exhibited significant epistatic interactions among them (see Table 2). Exploration of the physical positions of the QTL in the bean genome V2 revealed co-locations with previously reported QTL for pod traits:

- PL01_28.9 co-located with PL01.1XB (29932212-33789966) detected in the XB RIL population (Murube et al., 2020)
- PL01_47.8 was located next to PL1MA (47329645-47409645) reported by González et al. (2016)

- PL04_37.8 co-located with PL4PP (41879167-41959167) reported by Yuste-Lisboa et al. (2014). QTLs need to be validated in different genetic backgrounds and environments before they are used in plant breeding. This work verified the role of three genomic positions in the genetic control of pod length and, it identified a region on chromosome Pv06 with an important contribution to this trait; the region between 18115056-18368785 Mbp (QTL PL06_18.1).

Table 1. QTLs for pod length identified in the TUM RIL population by QTLNetwork v2.1.

		Physical positions				
QTL name	**LG**	**Start**	**End**	**F-Value**	**A**	**h^2**
PL01_28.9	Pv01	28994707	30773753	21.7	-0.65	0.11
PL01_47.8	Pv01	47813205	48085334	6.3	-0.42	0.11
PL03_13.1	Pv03	13162474	28684062	11.0	-0.34	0.03
PL04_37.8	Pv04	37813610	46100169	29.9	-1.67	0.10
PL06_18.1	Pv06	18115056	18368785	21.5	-1.17	0.25
PL07_7	Pv07	7075094	7149998	10.9	-0.36	0.03
PL08_10.1	Pv08	10122344	10655061	23.6	-0.73	0.04

LG = Linkage group; Start and End = physical QTL position indicated in base pairs; A = additive effect. Negative additive values are contributed by alleles from the parent Musica; h^2 = heritability of additive effect.

Figure 1. Pod phenotypes in the parental lines at R8 growth stage.

Table 2. Epistatic QTLs detected in the TUM RIL population by QTLNetwork v2.1.

QTL_i	**LG**	**QTL_j**	**LG**	**AA[1]**	**h^2**
PL01_28.9	Pv01	PL03_13.1	Pv03	0.1958	0.0043
PL03_13.1	Pv03	PL06_18.1	Pv06	0.2364	0.0020

[1] P-value < 0.001

QTL_i and QTL_j = The two QTLs involved in epistatic interactions; AA = additive x additive epistatic effect; h^2= heritability of additive x additive epistatic effect.

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EFFECTS OF BETWEEN-ROW SPACING AND IN-ROW PLANT DENSITY ON YIELD OF A TYPE II BEAN WITH FIELD RESISTANCE TO WHITE MOLD

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INTRODUCTION: In general, yield of dry beans with indeterminate type II growth habit are improved when high plant population is used. However, high plant population may favor diseases, especially white mold (WM). Hence farmers prefer using 0.4-0.5 m between rows and 10-13 plants m^{-1}. However, line CNFC 10720 exhibited field resistance to WM (Lima et al., 2020) and 13 plants m^{-1} did not increase WM disease for this line relative to lower densities (Lima et al., 2019). In this 2019 study, the between-row spacing (BRS) used was 0.50 m and 13 plants m^{-1} was the highest in-row plant density (IRPD) tested. The objective with this study was to evaluate the effects of an increase in plant population for a type II beans with partial field resistance to WM on yield and diseases.

MATERIALS AND METHODS: Sprinkler irrigated trials were established in fields naturally infested with *S. sclerotiorum*, during the fall-winter season (2018 and 2019) and during the winter-spring season of 2020 in the Zona da Mata region, State of Minas Gerais, Brazil. The 2019 and 2020 trials were established in a high fertility soil. We combined BRS (0.25 or 0.50 m) and IRPD (7, 10, 13 or 16 plants m^{-1}) using carioca line CNFC 10720 with type II growth habit. The experimental design was a randomized complete block with four replications. Either four (0.5 m) or six (0.25) 4 m-long rows were used per plot. Except for the 2020 trial, a basal fertilization with $N-P_2O_5-K_2O$ (24-84-48) was applied in the furrow at sowing. In 2020, only a topdressing of nitrogen was applied (200 kg ha^{-1} of urea), which was also applied in the other two trials. Insects were controlled by using recommended insecticides.

RESULTS AND DISCUSSION: White mold pressure was low in the 2019 and 2020 trials and absent in the 2018 trial. Mean grain yield in each of the three trials ranged from 1,591 (plants suffered stress due to lack of water during part of the reproductive phase) to 3,121 kg ha^{-1} (Table 1). In the 2018 trial, BRS x IRPD interaction was significant for yield. With the BRS of 0.25 cm, effect of IRPD on yield was not significant (Figure 1). However, with the BRS of 0.50 m yield at 13 plants m^{-1} was 30 % higher than the average yield for the other IRPDs. In the 2019 trial, yield at 0.25 m between rows was 31% higher than yield at 0.50 m. In the 2020 trial, either BRS or IRPD affected yield significantly. Yield at 0.25 m was 702 kg ha^{-1} higher than yield at 0.50 m. The highest mean yield was obtained with 16 plants m^{-1}, but this IRPD did not differ significantly from yields at 10 and 13 plants m^{-1}. These results are in line with those of Lima et al. (2019) and they highlight the potential to increase the yield of type II beans by increasing plant population, especially by decreasing the between-row spacing. However, new studies under moderate to high WM pressures are needed to better understand the effects of BRS and IRPD on yield of a field resistant genotype to WM such as line CNFC 10720.

Table 1. Effects of between-row spacing (BRS) and in-row plant density (IRPD) on yield of line CNFC 10720 in three field trials established in the State of Minas Gerais, Brazil.

Factor	Grain yield (kg ha^{-1})		
	2018	2019	2020
Between-row spacing (BRS)			
0.25 m	1658	2492	3472
0.50 m	1523	1908	2770
In-row plant density (IRPD)			
7 plants m^{-1}	1528	1945	2960 b[1]
10 plants m^{-1}	1509	2248	2986 ab
13 plants m^{-1}	1698	2461	3232 ab
16 plants m^{-1}	1628	2144	3306 a
		p value	
BRS	0.075	<0.001	<0.001
IRPD	0.238	0.102	0.019
BRS x IRPD	0.013	0.663	0.390
Mean	1591	2200	3121
CV (%)	13	18	8

[1] Tukey's test, 5%.

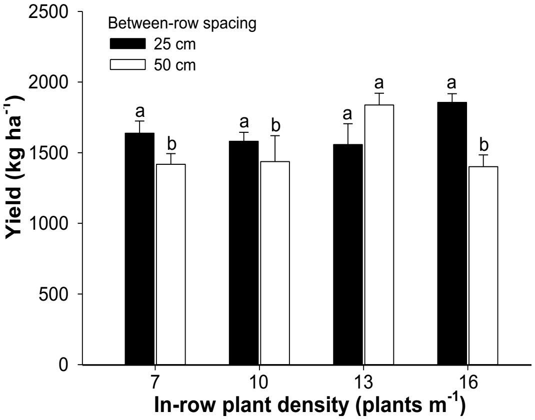

Figure 1. In-row plant density and between-row spacing interaction on yield of the dry bean line CNFC 10720. Mean ± SE.

ACKNOWLEDGMENTS: CNPq and FAPEMIG for financial support.

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EVALUATION OF REDUCED PLANT POPULATIONS IN MICHIGAN BLACK BEANS

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INTRODUCTION

Dry edible bean (*Phaselous vulgaris* L.) production practices have been shifting in Michigan for many years. Since the early 2000's an increasingly larger portion of Michigan's dry bean acres are grown in narrow rows (50-55 cm). As dry bean producers have adopted the narrower row systems standard seeding rates have decreased. Between 2015 and 2020, grower seeding rates have decreased by 10% in black and navy beans (MBC, 2020). This decrease in seeding rate has also been supported by multiple studies. Plant populations from 196,365 to 352,772 plants per hectare often have no direct impact on dry bean yield (Sprague and Homes, 2013; Varner, 2012). However, little research has been conducted on populations lower than 196,000 plants per hectare in dry bean. While seed cost can annually be one of a producer's largest input cost, research done in soybean (*Glycine max* L.) has also documented increased plant productivity in high management production systems under plant populations lower than current standards (Kessler et al., 2020). Altogether, these factors indicate there is value in further understanding dry bean response to reduced plant populations in narrow row production systems. The objective of this study was to identify black bean response to populations below 196,000 plants per hectare on highly productive soils in Michigan's Saginaw Valley.

MATERIALS AND METHODS

In 2020, a black bean yield trial was established near Frankenmuth, MI with four treatments. Treatments were arranged in a randomized complete block design with four replications. For all treatment, plots consisted of four 6-M rows spaced 50 cm apart. 'Zorro' black beans were seeded in all plots at a rate of 321,100 seeds per hectare on June 16, 2020. Seven days after emergence, plants were mechanically thinned to create three separate levels of simulated stand loss when compared to the untreated control (untreated: 288,990 plants per hectare). Stands were thinned to create uniform populations of 192,660; 160,550; and 96,330 plants per hectare in 50-cm rows. Standard agronomic practices were followed after stands were thinned for the remainder of the growing season. At maturity, the center two rows of each plot were harvested with a Wintersteiger Quantum combine. Seed yield was recorded and adjusted to 18% moisture.

RESULTS AND DISCUSSION

The 2020 growing season was conducive for high dry bean yields. Average yield across all plant populations was 3,439 kilograms per hectare. Dry bean yield was only significantly reduced when compared to the control by the 96,330 plants per acre treatment (Figure 1). When stands were reduced to 96,330, a 66% reduction when compared to the untreated population (288,990), yield was reduced by 17% ($\alpha \leq 0.05$). No differences in yield were documented for populations of 288,990, 192,660, and 160,550 plants per hectare. These results indicate that even when dry beans are planted at 55% of current production standards, yield loss may not occur when growing conditions are conducive for high plant productivity. Given the uniform plant spacing, plants were able to increase branching and total pod set per plant. However, important considerations in commercial production should be made to weed control under reduced planting populations. As plant populations dropped below 160,550 plants per acre a visually noticeable delay in canopy closure occurred.

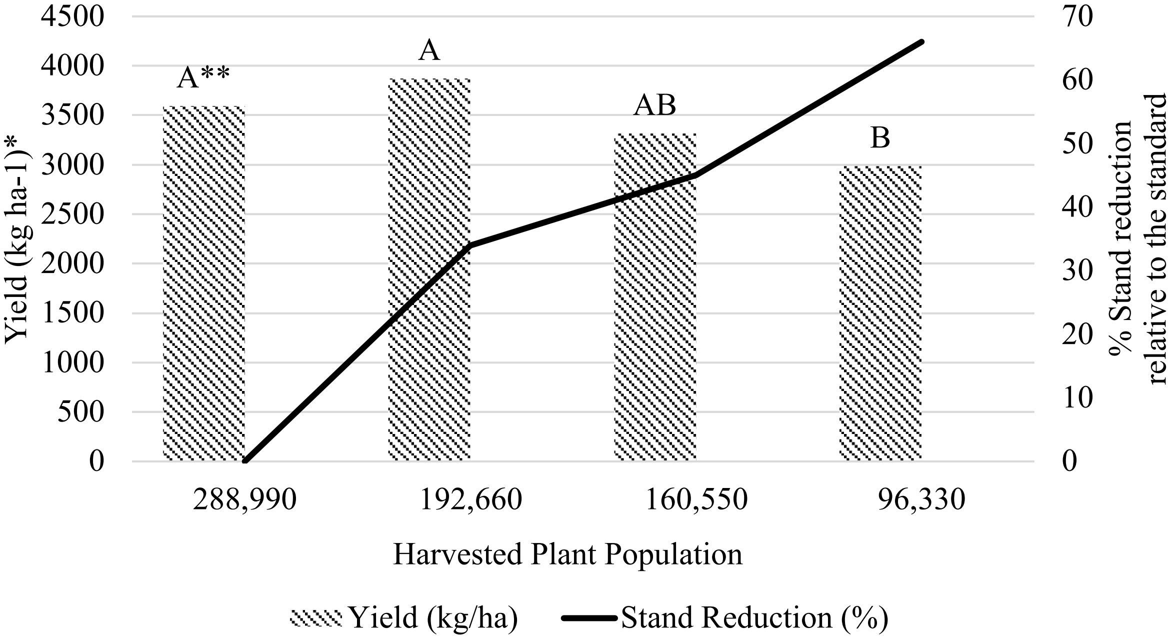

Figure 1. Yield for Zorro black beans at standard and reduced plant populations in 50-cm rows.
*Yield columns followed the same letter are not significantly different ($\alpha \leq 0.05$).
**Yield is in kilograms per hectare adjusted to 18% moisture.

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EFFECTS OF PLANT DENSITY ON YIELD IN TWO BEANS VARIETIES

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INTRODUCTION: Despite being less cultivated in Brazil, pod bean cultivars (*Phaseolus vulgaris* L.) of determinate growth habit are easier to manage and harvest, and reduce production costs. In the field, there is a growing demand for plants with higher productive performance conducted in sustainable production systems, which can be obtained by using a population density that optimizes crop yields, with less use of inputs. Thus, the aim of this study was to evaluate the response of two pod bean varieties in response to changes in plant population density.

MATERIALS AND METHODS: The experiment was carried out at the State University of Londrina, at Londrina/PR – Brazil. The pod bean Feltrin Macarrão Napoli® cultivar was sown on 11th September 2019 and harvested on 2nd February 2020, followed by sowing of Isla Macarrão Baixo® cultivar on 16th May 2020 and harvested on 1st August 2020. Both cultivars were submitted to densities of 33,333, 55,555, 77,777, 100,000 and 122,222 plants per hectare. Treatments were arranged in a randomized block design with three replications. The experimental plots consisted of four lines of two meters, spaced at 0.90 m (5.4 m^2 in a total of 74 m^2 for the entire experiment), with the two central lines of each plot used for experimental analysis. From the experimental area, 10 plants were harvested per plot, and the characteristics of plant height, leaf area, number of trifoliolates, pods per plant, pod mass per plant, average pod mass, pod length and pod yield were evaluated. The data were submitted to regression analysis ($p < 0.05$).

RESULTS AND DISCUSSION: For the cultivar Feltrin Macarrão Napoli plant population density significantly affected plant height, number of trifoliolates, pods, as well as the pod mass per plant. Other characteristics were not affected by population densities. Plant height grew linearly up to 122,000 plants ha^{-1} in population density (Figure 1). For the Isla Macarrão Baixo cultivar, the population increase up to 122,000 plants ha^{-1} linearly increased the yield of pods, however, it linearly reduced the number of trifoliolates and pods per plant, as well as the mass of pods per plant (Figure 2). The other characteristics evaluated were not influenced by population increase. It was not possible to establish an optimal range of plant population for both cultivars evaluated such as obtained by Almeida et al. (2017), which obtained maximum plant yield on a density of 160,000 plants ha^{-1} working with different cultivars of snap beans. Similar results were obtained by Abul-Soud et al. (2018), that related lower density of plants m^{-2} showing a significant positive effect on vegetative growth characteristics and yield components of snap bean. It is recommended that more studies should be carried out with populations above 122,000 plants ha^{-1}, in order to find the population inflection point (minimum optimal plant density) associated with maximum pod yield.

Figure 1. Number of trifoliolates (A), plant height (B), number of pods (C) and pod mass (D) per plant of cultivar Feltrin Macarrão Napoli, according to different plant densities.

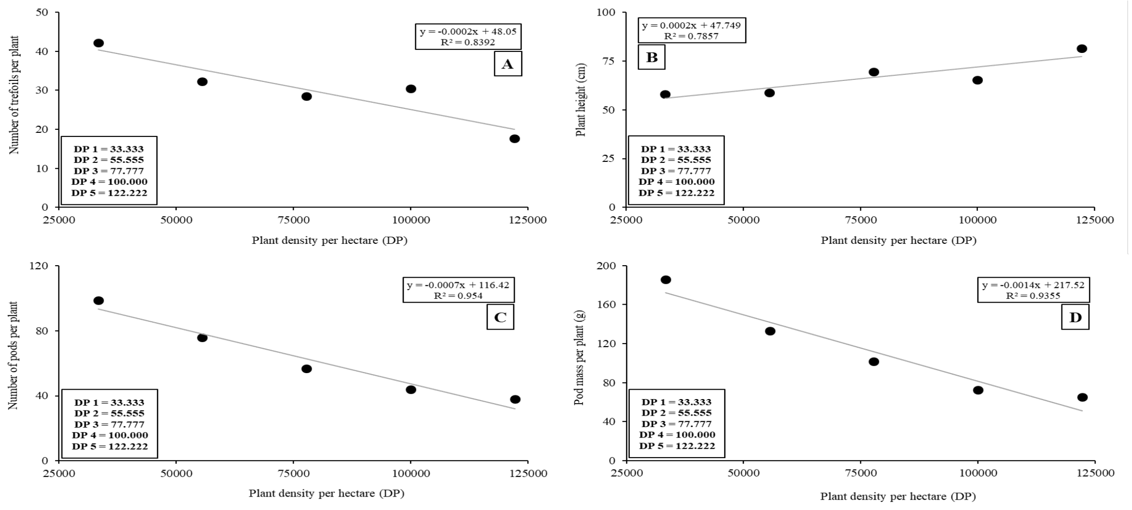
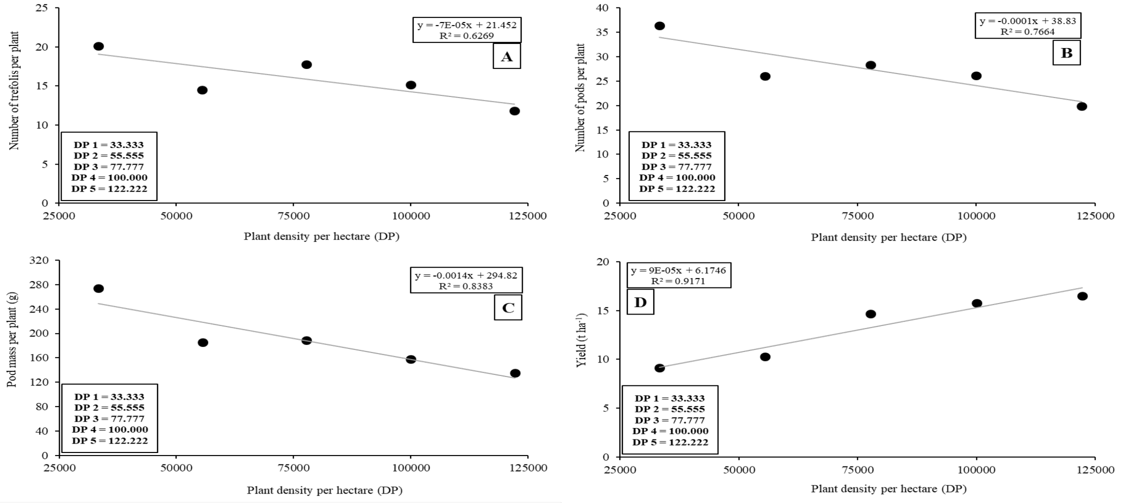


Figure 2. Number of trifoliolates (A), number of pods (B) and mass of pods (C) per plant and yield (D) of the cultivar Isla Macarrão Baixo, according to different plant densities.



CONCLUSIONS: Increasing plant population up to 122,000 plants ha^{-1} did not affect Feltrin Macarrão Napoli yield whereas Isla Macarrão Baixo yield was linearly augmented. Both cultivars presented modifications on plant growth parameters in response to population growth. It was not possible to obtain the optimal range of plant population for the varieties analyzed.

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GROWTH ANALYSIS TO DETERMINE THE INITIAL RELATIVE DEVELOPMENT STAGE (RDS) IN COMMON BEAN CULTIVARS

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INTRODUCTION

The common bean (*Phaseolus vulgaris*) is produced throughout the territory of México, in its different commercial classes, mainly flor de mayo, black, peruvian and pinto. It is broadly produced because it is one of the main food crops used in the population's diet due to its high protein content, averaging about 10 kg per capita consumption (SIAP, 2020), and this allows for additional economic benefits for agricultural producers (Borja-Bravo et al., 2018). Due to the complex response of crops to variations in water deficits, the use of empirical functions are usually applied to estimate yields based on the level of water deficit applied during part or all of the crop cycle (Flores-Gallardo et al., 2013). Therefore, the use of biological simulation models is feasible to estimate potential production and identify production-limiting factors or to analyze changes in crop water management (López-Cruz et al., 2005). However, the data observed in the field are important for modeling crop yields and obtaining data close to the reality of production obtained by the agricultural producer. Therefore, fractions of gross mass assimilated for production are known to be distributed in the leaves, roots, stems and storage organs (fr(org)) as a function of the relative development stage (RDS) of the crops. The objective of this experiment was to determine the fresh weight (FW) and dry weight (DW) of different bean cultivars by means of a growth analysis with future data supplementation for bean yield modeling based on obtaining field observed data.

MATERIALS AND METHODS

The experiment was established on 7th August 2019, at the Montecillo Campus of the Colegio de Postgraduados, with the following geographical coordinates 19° 27' 41.7" N, -98° 54' 8.7" W and 2241 m altitude. Nine cultivars of common bean were sown: three pintos (Saltillo, Centauro and PID 1), three blacks (San Luis, Jamapa and NOD 1) and three flor de mayos (M38, FM14011 and Media Oreja) in pots with a soil with texture class sandy loam with a total of 15 plants for each variety to evaluate its FW and DW. The initial FW and DW measurement was performed 20 days after planting (DAS), for which the plant was dissected into its different organs (leaf, stem and root) to be dried later on in a pressure drying stove for 24 hours (Figure 1).

Figure 1. Bean cultivars set in pots (left), FW and DW weighing process (right).

RESULTS AND DISCUSSION

The RDS for each cultivar requires continuous measurements of the FW and DW at least 10 days apart from each measurement from sowing. Another option is to perform measurements for each phenological stage of the crop (vegetative and reproductive), although the latter will depend on the simulation (daily, decenal or monthly). New measurements will be made with the purpose for having data throughout the growing cycle and simulations can be performed to model common bean yield. However, this information initially launches the development and supplementation of an RDS database on common bean cultivars. Table 1 presents the average FW and DW data for each bean cultivar evaluated in the experiment.

Table 1. Weight result (in grams) in growth analysis for each common bean cultivar.

Cultivar	FW (gr)			DW (gr)		
	L	S	R	L	S	R
Pinto Saltillo	0.99	0.78	0.39	0.14	0.08	0.05
Pinto Centauro	1.22	1.10	0.47	0.15	0.12	0.06
PID 1	1.19	0.93	0.96	0.15	0.09	0.11
Negro San Luis	1.83	0.78	0.77	0.25	0.10	0.13
Negro Jamapa	1.01	0.68	0.47	0.16	0.08	0.05
NOD 1	1.24	0.82	0.50	0.20	0.11	0.11
Flor de Mayo - M38	1.02	0.82	0.42	0.14	0.09	0.05
MF14011	1.23	0.85	0.29	0.18	0.13	0.06
Flor de Mayo - Media Oreja	1.45	0.91	0.79	0.20	0.10	0.08

FW = fresh weight; DW = dry weight:, L = leaf; S = steam; R = root.

CONCLUSIONS

The data obtained are a starting point for development of a database on the organ distribution fractions of the common bean cultivars and its future complementation for use in crop yield modeling.

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EVALUATION OF BLACK BEAN BREEDING LINES FOR SYMBIOTIC NITROGEN FIXATION POTENTIAL IN MICHIGAN

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INTRODUCTION: Common bean (*Phaseolus vulgaris L.*) is an important legume crop that has been characterized as an inefficient fixer of atmospheric nitrogen compared to other legumes (Bliss, 1993). A symbiotic relationship between bean roots and Rhizobia bacteria in the soil allows beans to form nodules that fix nitrogen from the atmosphere through a process known as symbiotic nitrogen fixation (SNF). SNF is under complex multigenic control and is also influenced by biotic factors in both the bean plant and rhizobia bacteria including total plant biomass, root and shoot weight, nodule number and weight, as well as abiotic factors in the environment such as soil moisture, pH, temperature, and nutrient availability (reviewed by Dwivedi et al., 2015). Although common bean is an inefficient fixer, significant genetic variation exists for improving SNF potential. Recent studies have documented this variation in specific subsets of bean germplasm including Andean beans (Kamfwa et al., 2015) navy bean (Farid et al., 2016), black bean (Heilig et al., 2017), heirloom types (Wilker et al., 2019) and under varied nitrogen inputs (Reinprecht et al., 2020). The objective of this study was to identify black bean breeding lines that perform equally well or better under low nitrogen conditions as a basis for superior nitrogen-fixation ability.

MATERIALS AND METHODS: In 2019 and 2020, paired black bean yield trials were established near Frankenmuth, MI with 42 and 36 entries, respectively. Entries included all advanced breeding lines from the MSU program, in addition to commercial checks, and the non-nodulating mutant navy bean R99 (Park and Buttery, 2006). Plots consisted of four 6 m rows spaced 50 cm apart in a 6x7 or 6x6 lattice with four replications each for both low nitrogen (0# N) and standard N (48# N/acre) treatments. Standard agronomic practices were followed with exception of nitrogen rate. At maturity, plots were trimmed to 4.6 m and the center two rows of each plot were harvested with a Wintersteiger Classic plot combine. Seed yield was recorded and standardized to 18% moisture.

RESULTS AND DISCUSSION: In 2019, seed yield and plant growth were limited by rainfall during the middle of the growing season. Yields ranged from 10.7 to 25.3 cwt/acre without nitrogen fertilizer application and 16.6 to 24.5 cwt/acre with 48# N/acre (data not shown). The mean yield of the fertilized trial was slightly higher (21.7 cwt/acre) compared to the trial without fertilizer (19.3 cwt/acre). However, two black bean lines with exceptionally high seed yield, B17207 and B16504, demonstrated equivalent or higher yield potential under low N conditions. In 2020, rainfall was more abundant during the critical reproductive phase, resulting in yields of 1.2 to 37.1 cwt/acre without nitrogen, and 8.3 to 38.7 cwt/acre with fertilizer. R99 was the lowest yielding entry in both trials but failed to properly set pods or mature normally across all reps without fertilizer. This may suggest ambient nitrogen levels were too low to support seed development, since R99 matured normally and set seed in the adjacent trial with fertilizer. Mean yields of fertilized and non-fertilized trials were very similar (29.9 vs 29.5 cwt/acre). Two black bean lines with high seed yield, B19309 and B16504, had similar or higher yield potential under low N conditions.

Furthermore, combined analysis of data across both seasons to assess stability under contrasting field conditions for 18 lines tested in both years revealed that five lines produced equivalent or better seed yield without nitrogen. These included the cultivar Zenith, B16504, B17897, B18204, and B18232 (Figure 1). Interestingly, four of these breeding lines are all half sibs with Zenith as the common parent. Another interesting observation is the dataset includes a pair of near isogenic lines: B16504 averaged 11.8% higher yield without fertilizer, while the cultivar Adams averaged 9.2% lower yield without fertilizer. Further investigation of these two lines is warranted as Adams was a late generation reselection of B16504 made to fix anthracnose resistance gene *Co-4*^{2}, but appears to also differ in SNF potential.

Additional data on plant biomass at flowering and at harvest were collected in 2019, as well as N^{15} analysis of seed to facilitate calculation of percent nitrogen derived from atmosphere (%Ndfa). It will be interesting to determine if lines with equivalent or higher yields without fertilizer also correlate with increased %Ndfa. UAS flights were also conducted at critical timepoints during both seasons and images will be analyzed to determine if that technique is useful for rapidly assessing field variation for SNF. Similar trials will be conducted in the future and may be expanded to other market classes. Given increasing environmental concerns in the Saginaw Bay watershed where most beans in Michigan are grown, there exists a need to enhance our ability to efficiently identify superior yielding lines that will fix higher levels of nitrogen that partitions to yield to encourage reduced fertilizer use and associated runoff.

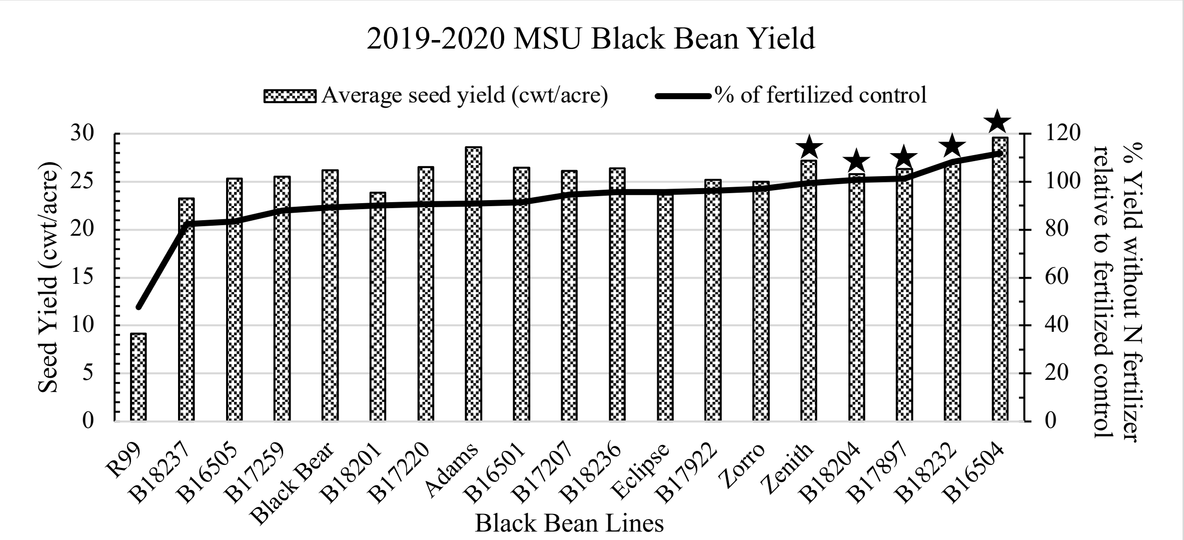

Figure 1. Overall average seed yield (cwt/acre) of 18 black beans and R99 non-nodulating control grown at Frankenmuth, MI from 2019-2020. Right axis depicts the 2-year average yield with no fertilizer as a percentage of fertilized control.

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NITROGEN ACCUMULATION IN COMMON BEAN CO-INOCULATED WITH *Azospirillum brasiliense* AND *Rhizobium tropici* UNDER AN AGROECOLOGICAL GROWING SYSTEM

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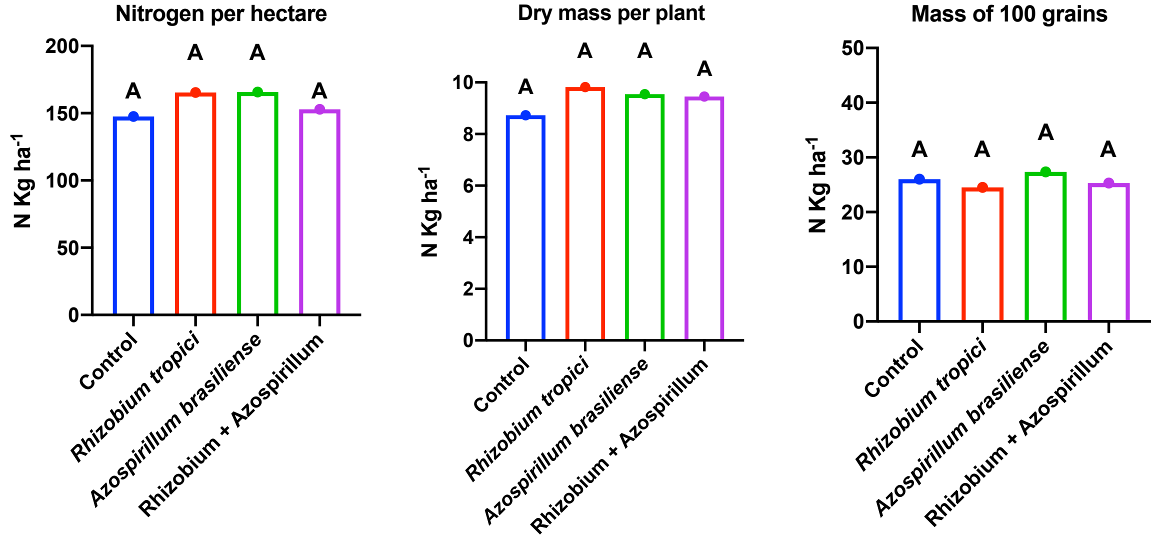
INTRODUCTION: Common bean (*Phaseolus vulgaris* L.) is one of the most consumed vegetables in the world thanks to its ability to be cultivated in different environments and due to its nutritional value, especially its high protein levels. For the formation of these proteins, the vegetable must be provided with a high supply of nitrogen (N) , which can be obtained by the plant mainly by mineralization of organic matter, addition of nitrogen fertilizers (which represent high costs and environmental degradation) and biological nitrogen fixation (BNF), a process by which bacteria in symbiosis with plants convert the N present in the atmosphere into a form that can be used by the plant. The objective of this work was to evaluate the efficiency of BNF by bacteria of the genera *Rhizobium* and *Azospirillum*, inoculated separately and combined, in the common bean variety IPR Tangará, identifying which inoculation this variety responds best to in agroecological production systems.

MATERIALS AND METHODS: The experiment was carried out at the State University of Londrina school farm, located in the city of Londrina-PR, Brazil, located at 23°55'46" S and 50°52'23" W, with an altitude of 508 meters, annual average temperature of 20 ºC and 1588 mm of rainfall. Prior to the installation of the experiment, soil samples were collected at a depth of 0-20 cm for chemical analysis, which demonstrated no need of correction or addition of fertilizers in the area. Using the common bean genotype IPR TANGARÁ, a randomized block experimental design with 4 treatments was used. The first treatment was a control (without inoculation), the second treatment was inoculated only with *Rhizobium tropici*; the third treatment was only inoculated with *Azospirillum brasilense;* and the fourth treatment was co-inoculated with *R. tropici* and *A. brasilense*, with 5 repetitions and 5 blocks. There were 20 experimental plots in total, each consisting of 8 lines, 5 meters long, spaced by 0.45 m, with 10 plants per linear meter. The useful area was formed by the 4 central lines, eliminating 1 m from the ends of each line. Sowing was carried out using enough seeds to obtain a density of 10 to 12 plants per linear meter on March 19, 2018. The emergence occurred seven days after sowing. At the full flowering stage (R6), five plants were collected in the useful area of each plot, with the N content determined. Harvest of the useful area was carried out at 100 days after sowing (DAS) and the mass of 100 grains and the dry mass of plants were obtained. Data were evaluated through analysis of variance using the F test and submitted to the Tukey test at 5% probability.

RESULTS AND DISCUSSION: There was no significant difference regarding the accumulation of N in the aerial part expressed in Kg ha^{-1} (Figure 1). Hungria et al. (2013) also found no differences between non-inoculation, nitrogen fertilization, inoculation without nitrogen fertilization, inoculation with *A. brasilense*, inoculation with *R. tropici* and co-inoculation in common bean cultivated in the 2009/10 rainy season in Londrina for the nitrogen content of the shoot.

Figure 1. Nitrogen accumulation (N), dry mass per plant and mass of 100 grains in the aerial part of the bean plant due to the inoculation of *Rhizobium tropici* and *Azospirillum brasiliense* alone and co-inoculated compared to a non-inoculated treatment in an agroecological system.



The means among treatments do not differ according to the Tukey test at 5% significance.

Regarding the weight of 100 grains and dry weight per plant, there was no significant difference in the evaluation of the inoculation of *R. tropici* and of *A. brasiliense* alone and co-inoculation compared to non-inoculation (Table 3). This is mainly due to the high incidence of anthracnose disease, caused by the pathogen *Colletotrichum lindemuthianum*, during the reproductive stage. Gitti et al. (2012) found no differences between inoculation and non-inoculation of bean seeds with *A. brasilense* on the number of pods. Thus, it was observed that environmental conditions, such as the high inoculum of the fungus *C. lindemuthianum* and a high competition with the tiririca (*Cyperus rotundus* L.) weed directly influenced production components, determining no difference among treatments and low productivity.

CONCLUSION: The inoculation of *R. tropici* and *A. brasiliense* alone and co-inoculated did not provide differences regarding the accumulation of N, dry matter per plant and mass of 100 grains on common bean IPR Tangará.

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BEHAVIOR OF BEAN YIELD COMPONENTS AS A FUNCTION OF NITROGEN FERTILIZATION

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INTRODUCTION

Beans (*Phaseolus vulgaris* L.) are an important food due to nutritional and medicinal properties. The national average of beans planted in the spring-summer under rainfed conditions is 0.770 t ha^{-1} (SIAP, 2018), which is insufficient to satisfy the national demand. For this reason, agronomic practices include nitrogen fertilization (N) which is decisive in increasing crop yield. The magnitude of the response will depend on the initial level of N in the soil (Cedano et al*.,* 2000) and the amount of nitrogen supplied. Under rainfed conditions, a maximum increase of 100 kg ha^{-1} has been reported (Escalante et al., 2020). The objective of the study was to determine the effect of N on phenology, number of pods, number of grains and grain yield.

MATERIALS AND METHODS

The dry bean cultivar Cacahuate 72 was planted on May 9, 2018 in Montecillo, Municipality of Texcoco, State of Mexico, Mexico (19 ° 29 'N, 98 °53'W and 2250m altitude) with a temperate climate. In the first 30 cm of the profile, the soil is a clay loam, with 20 ppm NO3, pH of 7.5, and 2.4% moisture. The distance between rows was 0.80 m and between plants 0.30 m; population density was 4.16 plants m^{-2}. The treatments consisted of the application of: 0, 20, 40, 60, 80 or 120 kg of N ha^{-1} (50% before sowing and 50% at the first weeding). The N source was urea (46% of N). Irrigation was applied a total of 10 times. The experimental design was randomized blocks with four repetitions. Following the criteria indicated by Escalante and Kohashi (2015), the days to occurrence of phenological phases were recorded. At physiological maturity, 20 plants were taken per treatment and repetition to record per m^{-2}: the number of pods with grain (PN), grains (GN), grain size (GS, g) and the number of grains per pod (GP). An analysis of variance, Tukey's test of comparison of means and a regression analysis were applied to the variables under study using SAS software version 9.1 (SAS, 2003). The seasonal mean of the high and low temperatures obtained from the agrometeorological station of the Postgraduate College, Campus Montecillo, municipality of Texcoco, State of Mexico Mexico, were also recorded.

RESULTS AND DISCUSSION

In general, during the development of the crop, high temperature was 24 °C and the mean low temperature was 8 °C. There was no effect of N on days to emergence, flowering and or physiological maturity, (8, 40 and 90 days from sowing, respectively). With the exception of GS and GP (on average 0.293 g and 4.7), the PN, GN and GY were affected by the supply of N, showing a response that adjusted to a second degree polynomial: $Y = A + BX + CX^2$ (Table 1), where the maximum PN, GN and GY was achieved with 80 kg of N ha^{-1}, with 135 and 637 m^{-2} and 200 g m^{-2}, respectively. Multiple regression analysis indicates that the GY responded to the model, $GY= -3.2 + 0.75PN + 0.16\ GN$ with $R^2 = 0.98$ **.

Table 1. Regression equations for PN, GN and GY as a function of nitrogen supply (x). Montecillo, Mexico, Summer, 2018.

Variable	Equation	R^2
PN	$y = 99.0950 + 0.9232x - .0073x^2$	0.86
GN	$y = 513.4 + 3.6321x - 0.0312x^2$	0.80
GY	$y = 152 + 1.2393x - 0.0102x^2$	0.82

The R^2 was significant at 0.05.

CONCLUSIONS

The nitrogen supply did not cause changes in the days to occurrence of phenological phases. The number of pods, grains and the yield showed a similar response that was adjusted to a second degree polynomial, finding the maximum values at 80 kg of nitrogen ha^{-1}. The multiple regression model that involved grain yield as a function of number of pods and grains, showed an R^2 of 0.98 **.

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EVALUATION OF THE RHIZOBIAL POTENTIAL OF SOILS IN CÔTE D'IVOIRE WITH REGARD TO COMMON BEAN

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INTRODUCTION

Common bean belongs to the family Fabaceae and it scientific name is *Phaseolus vulgaris*. It is now widely cultivated as a major food crop in many tropical and subtropical areas. Common bean is a major grain legume consumed worldwide for its edible seeds and pods. In most countries, bean cultivation remains traditional, resulting in lower yields due to uncontrolled cultivation practices (Katungi et al., 2010). Furthermore, poor availability of essential plant nutrients, especially nitrogen, is one of the yield limiting factors in grain legumes (Kochian et al., 2004). Common bean has high nitrogen and phosphorus requirements for expressing its genetic potential. However, common bean also has the ability to fix and use atmospheric nitrogen offsetting its soil fertility and mineral nutrition requirements.

MATERIALS AND METHODS

Through trapping tests, five introduced dry bean accessions were used to check for the presence of rhizobia in soils sampled in twelve localities in Côte d'Ivoire. At the end of this test, six nodules were sampled from each accession and in each locality in order to extract the bacteria they contained (Figure 1). Data was analyzed using STATISTICA version 7.1 statistical package.

Figure 1. Rhizobium bacteria trapping trial by dry bean varieties.

RESULTS AND DISCUSSION

The results obtained at the end of this study showed that the bean varieties tested nodulated in the soils of all localities except those of Korhogo (North), Daloa (West) and Béoumi (Centre). However, in the localities of Bouaké (Centre) and Sinématiali (North), only plants from the accessions HARI17 and HARI27 showed nodules. Thus, with an average number of 17.03 ± 29.34 nodules per plant, the accession HARI21 had the highest nodulation potential among the five evaluated (Table 1). With respect to the isolation of rhizobia, a total of 197 isolates of morphological aspects representative of bacteria belonging to the genus Rhizobia were extracted from nodules of bean plants. They were composed of colonies that were circular in shape, convex or flat, regular in outline with a smooth surface, transparent, translucent or opaque, and whitish in colour and varying in size from 2 to 7 mm in diameter (Figure 2).

Table 1. Average number of nodules per plant according to the localities

Bean lines	**Average number of nodules per plant and per city**												**Means (nods/plant)**
	Ykro	**Btro**	**Bflé**	**Skss**	**Fké**	**Bké**	**Ggnoa**	**Djbo**	**Sine**	**Kgo**	**Dloa**	**Bmi**	
HARI17/GHA19	36	36	0	26	8	25	17	24	0	0	0	0	14
HARI21/GHA19	13	7	92	45	42	0	4	6	0	0	0	0	17
HARI22/GHA19	16	12	0	0	15	0	4	16	0	0	0	0	5
HARI27/GHA19	15	10	3	22	5	0	5	70	1	0	0	0	11
HARI35/GHA19	13	15	0	31	10	0	10	28	0	0	0	0	8

Legend:

***Ykro**: Yamoussoukro, **Btro**: Botro, **Bflé**: Bouaflé, **Skss**: Sakassou, **Fké**: Ferkéssédougou, **Bké**: Bouaké, **Ggnoa**: Gagnoa, **Djbo**: Djébonoua, **Sine**: Sinématiali, **Kgo**: Korhogo, **Dloa**: Daloa, **Bmi**: Béoumi.*

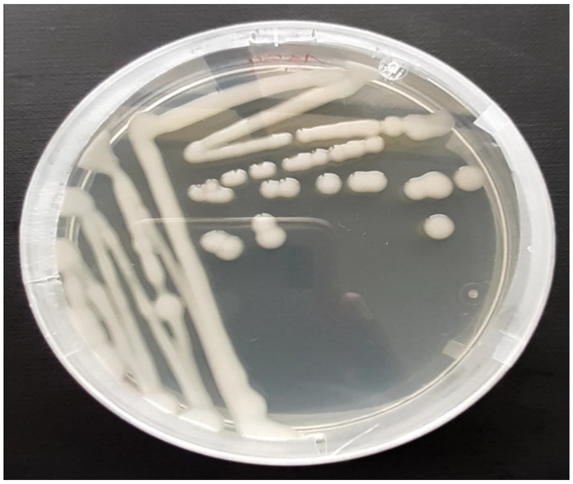

Figure 2. Bacterial colonies obtained after purification

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NITROGEN FERTILIZATION ENHANCES SEED IRON AND ZINC CONCENTRATION IN BEAN LINES

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INTRODUCTION

Soil has considerable influence on nutrient content of grains. One objective of current biofortification research efforts is to develop bean cultivars that are rich in iron and zinc for production in bean growing and consumption areas in Africa. Nitrogen (N) deficiency is the most important constraint to bean production in sub-Saharan Africa (Wortmann et al., 1998). Losses due to N deficiency are estimated at 389,000 t per year. About 50% of soils in bean growing areas in eastern Africa and 30% in southern Africa are low in nitrogen. Thirty-eight lines were selected for high mineral density from germplasm accessions, introductions, advanced lines and varieties grown in East and Central Africa in 2003/2004 (Kimani and Warsame, 2019). The role of N application in maximizing the expression of genetic variability for iron (Fe) and zinc (Zn) concentration in common bean is not well known. Studies were therefore initiated to determine the role of specific environmental factors in determination of seed iron and zinc concentration. The objective of this study was to determine the effect of N application on seed iron and zinc concentration.

MATERIALS AND METHODS

Ten bean lines were grown in field experiments at four nitrogen levels in three locations in Kenya during the long rainy (April-July) and short rainy (Oct-Feb) seasons. The 10 test lines were selected to include lines with both high and low seed Fe and Zn, seed colour and seed size. The four N levels were 0, 50, 100 and 150 kg N ha-^{1}. The trials were conducted at Thika (1548 masl) and Kabete (Field 16, 1849masl) during the short rainy season, and at Kakamega (1583 masl) and Kabete (Field 10, 1794 masl) in the long rainy season. Soils at Kabete are humic nitisols (FAO, 1990; Jaetzold and Schmidt, 2010), slightly acidic (pH 5.5) and deficient in available phosphorus and nitrogen. Soils at Thika are eutric nitosols and acrisols, and low in nitrogen and phosphorus. At Kakamega the soils are Dystro-mollic nitisols, low in phosphorus. Soil samples were collected at each site before planting. Leaf samples were collected before flowering. Seed samples for mineral analyses were taken at harvest. Ground samples were digested with hydrogen peroxide, sulphuric acid and salicylic acid following methods of Novozamsky et al. (1983) and Okalebo et al. (2002), and read on an atomic absorption spectrophotometer (Perkin-Elmer Corporation, USA). The factorial experiment was laid out in a split plot design with three replicates. Genotypes were the main plots and N levels the subplots. Each test line was sown in four, 3 m rows. Data was collected from the inner two rows. Seed iron and zinc concentration was analyzed at the National Agricultural Research Laboratories, Nairobi, Kenya. Genstat (9 edition) software was used for data analysis.

RESULTS AND DISCUSSION

Nitrogen fertilization up to 100 kg N ha^{-1} increased bean yields at all test sites over the two seasons. Application of up to 100 kg N ha^{-1} significantly increased seed iron concentration across sites and seasons (Table 1). Mean grain iron concentration across sites and seasons varied from 91.7 ppm for cv. AND 620 to 71.4 ppm for cv. Nakaja. Nitrogen fertilization (up to 100 kg N ha^{-1}) significantly ($P<0.05$) increased seed zinc concentration (Table 2). Mean grain zinc concentration varied from 26.1 ppm for Nakaja to 35.6 ppm for genotypes MLB 49 89A and 36.7 ppm for VNB 81010. Significant genotype x environment interactions for grain mineral concentration were detected.

Table 1. Effect of nitrogen fertilization on grain iron concentration in ten bean genotypes grown in four environments in Kenya.

Nitrogen level kg ha^{-1}	Fe concentration (ppm)				
	Kabete Field 16	Thika	Kabete Field 10	Kakamega	Mean
0	65.4^{b}	61.4^{b}	66.7^{b}	68.9^{b}	65.6
50	72.7^{b}	69.7^{b}	106.0^{a}	72.3^{b}	80.2
100	103.6^{a}	135.9^{a}	94.3^{a}	95.1^{a}	107.2
150	74.7^{b}	61.7^{b}	63.7^{b}	76.5^{b}	69.2
Mean	79.1	82.2	82.7	78.2	

* LR= long rain season; SR= short rain season; means followed by the same letter are not significantly different at 5% probability level.

Table 2. Effect of nitrogen level on seed zinc concentration of ten bean lines grown in four environments in Kenya.

Nitrogen level (kg ha-^{1})	Zinc concentration (ppm)				
	Kabete Field 16	Thika	Kabete Field 10	Kakamega	Mean
0	23.1c*	22.0b	27.6b	27.7a	25.1
50	28.9b	26.4a	33.7a	28.4a	29.4
100	33.4a	27.1a	32.9a	29.2a	30.7
150	24.4c	23.6b	27.2b	26.8a	25.5
Mean	27.5	24.8	30.4	28.0	

* Means followed by the same letter down the column are not significantly different at 5% probability level.

These results confirmed our previous trials which suggested that grain mineral concentration is influenced by the interactions between genotypes and the environments in which they are grown (Kimani, 2005).

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DISTANCE BETWEEN ROWS AND NITROGEN FERTILIZATION IN SNAP BEANS (*Phaseolus vulgari*s L)

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INTRODUCTION

The consumption of green beans (*Phaseolus vulgaris* L.) in Mexico is less common than that of dry beans, despite their nutritional value. Salinas et al. (2013), indicates an average green bean production with bush-type cultivars planted on May 7, density of 6.25 plants m^{-2} and 415 mm of rain during development of the crop of 0.452 kg m^{-2} with 113 green beans m^{-2}. However, this yield is considered insufficient to satisfy the domestic demand of 1.1 kg *per capita*. Thus, more appropriate agronomic practices are required to increase yield. Some studies indicate that this can be achieved by reducing of the distance between rows (Escalante *et al.*, 2015a) and foliar fertilization (Escalante *et al.,* 2020). However, studies on the combination of between row spacing and nitrogen fertilization to the soil are not abundant for green beans. The objective of the study was to determine the effect of distance between rows and soil nitrogen fertilization on phenology and production of green beans.

MATERIALS AND METHODS

The green bean cultivar "Strike" was sown on August 22, 2019, in the Montecillo municipality of Texcoco State of Mexico (19 ° 29´N and 98 ° 53´W and 2250 m altitude) where the climate is temperate (García, 2004) under field conditions with irrigation. The soil was a clay-loam, with 50 kg of assimilable N, a pH of 7.0 and no salinity problems. The treatments consisted of sowing in single or double rows (RD) 0.80 m apart, and 15 cm between plants, generating a population density of 12 and 24 plants m^{-2}. Nitrogen fertilizer (100 kg per ha^{-1}) was applied to the soil, 50% before sowing and the rest 25 days later. The control treatment included no application of N. The experimental design was divided plots with four repetitions. A single harvest was made. The variables under study were days from planting to each phenological stage (Escalante and Kohasi, 2015b), number of green beans (PN) and fresh weight of green beans (PY) per m^2. An analysis of variance and the Tukey test of means were performed. Mean maximum and minimum temperatures, rainfall and evaporation were recorded.

RESULTS AND DISCUSSION

Emergence occurred at 8 days after sowing (das) and flowering occurred at 30 das. The maximum temperature ranged from 26 to 30 ^{0}C and the minimum between 12 and near zero, the latter at the end of the crop cycle. Only significant differences were found due to the main effects of RD and N. By reducing RD and with the density of 24 plants m^{-2}, PN and PY increased by 86% and 31%, respectively. With N, these increases were 76 and 82%, respectively. The highest PN and PY (184 m^{-2} and 731 g m^{-2}, respectively) was achieved with an RD of 0.40 m (24 plants m^{-2}), and the lowest PN (70 m^{-2}) and PY (273 gm^{-2}) with an RD of 0.80 m (12 plants m^{-2}) without application of N (Table 1). This indicates that by reducing RD and increasing the population density, addition of N to the soil is required to support a larger number of plants and achieve a high yield.

Table 1. Number and yield in green beans (g m^{-2}) as a function of the distance between the row and nitrogen fertilization in beans (*Phaselus vulgaris* L). Montecillo, Texcoco, Mexico.

Treatments (RD+NF)	**PN m^{-2}**	**PY (g m^{-2})**
0.40 +100N	184 a	731 a
0.40 + 0N	150 ab	583 ab
0.80 + 100N	124 bc	449 b
0.80 + 0N	70 c	273 c
Tukey 0.05	58	165
Mean	134	509

In columns, values with similar letter are statistically the same. RD = row distance; NF = nitrogen fertilization; PN = number of green beans; PY = green bean yield.

CONCLUSIONS

In the study region, days to occurrence at phenological phases were not affected by changes in distance between rows and nitrogen fertilization. On the other hand, reducing the distance between rows from 0.80 m to 0.40 m and with nitrogen fertilization, the number and yield in green beans increased.

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PHOSPHORUS ENHANCES GRAIN IRON AND ZINC CONCENTRATION IN BEAN LINES

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INTRODUCTION

Biofortification seeks to alleviate micronutrient deficiencies through the development, production and consumption of mineral rich varieties on-farm and across agricultural regions. For the last two decades, bean programs in east, central and southern Africa have been developing nutrient rich and stable bean varieties which can contribute to the alleviation of micronutrient malnutrition in the region. Initial activities focused on screening available germplasm for genetic variation in iron and zinc (Kimani et al., 2005; Blair et al., 2010). These studies showed that considerable variation exists to increase seed iron concentration by more than 80% and zinc by 50%. Thirty-eight promising lines were selected following screening of landraces, advanced lines and varieties grown in eastern Africa (Kimani and Warsame, 2019). However, stability of micronutrient density in bean cultivars across environments is not well known. Productivity and stability in the diverse bean growing environments is influenced by many environmental factors. Soil fertility factors are among the most important. Soils in most bean growing environments in East, Central and Southern Africa are deficient in soil phosphorus (P) (Wortmann et al., 1998). Blair et al. (2009, 2010) showed that concentration of iron and zinc in seeds is influenced by several quantitative loci. It would therefore be expected that these traits are influenced by environmental factors. To test this hypothesis, a study was conducted to determine the influence of applied soil P on seed iron and zinc concentration.

MATERIALS AND METHODS

Ten bean lines were grown at four levels of phosphorus fertilization at three locations in Kenya during the short rain season (November to February) and during the long rain season (April- August). The bean lines included nine with high levels of iron and/or zinc, and a check (M211). Treatments were four levels of P (0, 25, 50, 75 kg P ha^{-1}). Source of P was triple super phosphate (46% P_2O_5) fertilizer. Fertilizer was applied in the furrows and thoroughly mixed with the soil before planting. The factorial experiment was laid out in a split-plot design with three replicates. Varieties were the main plots and P levels the subplots. A plot consisted of 3 m rows. Spacing was 45 cm between rows and 10 cm within rows. The trial was conducted at Thika (1548 masl) and Kabete (Field 16, 1849 masl) during the short rain season, and at Kakamega (1583 masl) and Kabete (Field 10, 1794 masl) in the long rain season. Soils at Kabete are humic nitisols slightly acidic (pH 5.5) and deficient in available phosphorus and nitrogen (Jaetzold, Schmidt and Shisanya, 2010). Soils at Thika are eutric nitosols and acrisols, and low in nitrogen and phosphorus. At Kakamega soils are Dystro-Mollic nitisols, low in phosphorus. Soil samples were collected at each site before planting. Leaf samples were collected before flowering. Seed samples for mineral analyses were taken at harvest. Ground samples were digested with hydrogen peroxide, sulphuric acid and salicylic acid following the methods of Novozamsky et al. (1983) and Okalebo et al. (2002), and read on an atomic absorption spectrophotometer (Perkin-Elmer Corporation, USA). Data was collected on phenology, disease incidence, 100-seed mass and grain yield following the CIAT standard scale (Schoohoven and Pastor-Corrales, 1987). Genstat (2005) software was used for analyses of variance.

RESULTS AND DISCUSSION

Results of soil analyses showed that available phosphorus ranged from 12.9 to 14.4 ppm in the Kabete Field 16, 18.0 to 25 ppm in Thika, 13.5 to 16.9 ppm in the Kabete Field 10 and 13.3 to 17.3 ppm in Kakamega. The available P in the soils from the four environments is generally rated low to deficient. P application up to 25 kg ha-^{1} significantly increased grain yield. Mean bean yields in all four environments increased with increasing rates of P fertilizer application up to 25 kg P ha^{-1} rate. Highest yields at the 25 kg P ha^{-1} rate were achieved at Kakamega (2799 kg ha-^{1}), followed by the Kabete Field 10 (2417 kg ha-^{1}), the Kabete Field 16 (2221 kg ha-^{1}) and the lowest at Thika (1086 kg ha-^{1}). However, higher P levels depressed grain yield. Application of up to 50 kg P ha-^{1} increased seed iron concentration in 10 bean genotypes, but higher levels depressed Fe concentration (Table 1). Seed zinc concentration was increased by fertilization with up to 50 kg P ha-^{1} (Table 2). AND 620 and Maharagi Soja had the highest grain iron concentration across locations and seasons. VNB 81010 had the highest zinc concentration at all test sites and seasons. These results suggest that soil factors can influence grain mineral concentration. Genotypes AND 620, Maharagi Soja, MLB 49 89A, and VNB 81010 combined high levels of iron and zinc, and probably have favorable alleles for these micronutrients.

Table 1. Seed iron concentration of ten bean lines grown at four levels of P fertilization in four environments in Kenya.

P level	Seed Fe concentration (ppm)				
(kg ha-^{1})	Kabete Field 16	Thika	Kabete Field 10	Kakamega	Mean
0	54.0^{c*}	58.2^{b}	57.5^{c}	63.5^{b}	58.3
25	76.3^{b}	66.8^{b}	86.4^{b}	86.3^{a}	79.0
75	91.1^{a}	86.4^{a}	107.3^{a}	84.6^{a}	92.4
100	52.6^{c}	66.5^{b}	68.8^{c}	66.7^{b}	63.7
Mean	68.5	69.5	80.0	75.3	73.4

* Means followed by the same letter are not significant at 5% probability level.

Table 2. Effect of phosphorus level on seed zinc concentration of ten bean lines grown in four environments in Kenya.

Phosphorus level (kg ha-^{1})	Kabete Field 16	Thika	Kabete Field 10	Kakamega	Mean
0	23.9^{b*}	21.7^{b}	22.3^{c}	25.2^{c}	23.3
25	25.8^{b}	26.4^{ab}	25.0^{b}	29.0^{ab}	26.6
50	30.2^{a}	29.0^{a}	28.9^{a}	30.7^{a}	29.7
75	24.1^{b}	23.0^{b}	27.3^{ab}	27.9^{b}	25.6
Mean	26.0	25.0	25.9	28.2	26.3

* Means followed by the same letter are not significant at 5%probability level.

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GENE EXPRESSION PATTERNS OF SOAKING DRY BEANS (*Phaseolus vulgaris* L.) WITH CONTRASTING COOKING TIMES USING WEIGHTED GENE COEXPRESSION ANALYSIS

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INTRODUCTION: Although long cooking time is a barrier to eating dry beans (*Phaseolus vulgaris* L.) and is a heritable trait, there are few genetic resources available to study it (Bassett *et al*., 2020). Soaking, a technique used to lower the cooking times of beans, also influences genetic expression and enzyme activity, in particular genes and enzymes that affect pectin solubility and cotyledon cell wall thickness (Bassett *et al*., 2020; Martinez-Manrique *et al*., 2011). This study investigated the relationship between soaking and gene expression in brown and yellow beans with contrasting cooking times using RNA-sequencing (RNA-seq). Gene ontology analysis was used to identify gene functions and discover gene expression pathways within co-expression modules.

Genotype	Picture	Average Cooking Time (mins)
ADP0037 (a.k.a. W6 16488)		33.0
ADP0027 (a.k.a. Incomparable)		60.3
ADP0512 (a.k.a. Ervilha)		26.0
ADP0468		46.0

Table 1: Genotypes arranged by color and cooking time.

MATERIALS AND METHODS: Four dry bean genotypes with contrasting cooking times were selected for this study (Table 1). The genotypes were harvested in duplicate in Entrican, MI, 2018 using a Hege 140 plot combine harvester. Fresh seeds were soaked for 0, 3, 6, 12, and 18 hours, then cooked with a Mattson pin-drop cooker. RNA extraction was performed in triplicate on uncooked seeds soaked for 0, 3, 6, 12, and 18 hours using a Spectrum Plant Total RNA kit. Residual genomic DNA was removed with the Sigma On-Column DNase digestion kit and the Turbo DNA-free kit. Libraries were constructed robotically at the Cornell University Sequencing facility using the Lexogen QuantSeq FWD kit. Raw expression data was fed into a data analysis pipeline (Fig. 1) that produced significant gene ontology (GO) terms.

RESULTS: Weighted gene correlation network analysis (WGCNA) resulted in five modules correlated with changes in cooking time in soaking brown beans and five in yellow beans. According to topGO, the genes in these modules had functions related to carbohydrate metabolism, cell wall metabolism, auxin/ABA signaling, and ATP metabolism, much like what has been observed in flooded seedlings (Butsayawarapat *et al*., 2019; Borrego-Benjumea *et al*., 2020; Nakayama *et al*., 2017; Ren *et al*., 2017; Sharmin *et al*.,

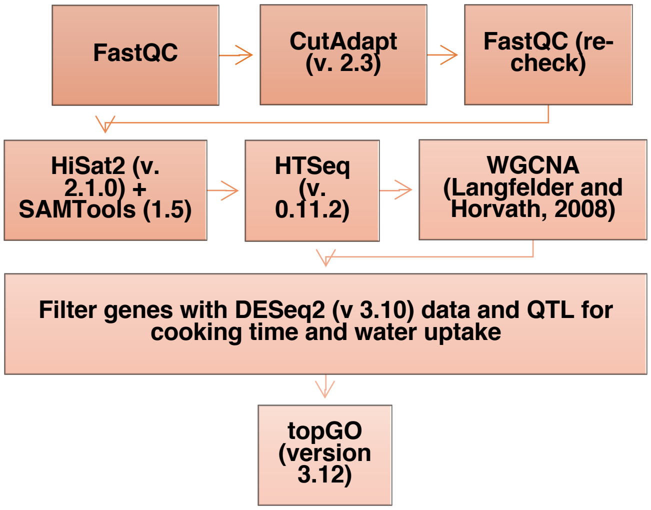

Figure 1: Pipeline used to check the quality of the data, identify the transcripts, count the number of transcripts, normalize the gene counts, and identify differentially expressed genes (DEGs).

2020; Wang *et al*., 2019). Candidate genes for the fast-cooking trait and the slow-cooking trait were identified within WGCNA modules from brown and yellow beans. No candidate genes for cooking time were expressed in both brown and yellow beans at any soaking time point. For example, *xyloglucan endogtransglucosylase 6* (*XTH6*) was expressed in slow cooking brown beans at hour six of soaking, but not in slow cooking yellow beans at hour six. This indicates that the brown and yellow beans might have different mechanisms controlling cooking time.

We asked if we could more quickly identify the candidate genes by combining brown and yellow bean expression data, then filtering it with DESeq2 data prior to performing WGCNA. The topGO results of the combined, filtered data set were identical to those obtained from separated, unfiltered data, but genes previously associated with the fast-cooking trait were forced into associating with the slow cooking trait. It is possible that pre-filtering with DESeq2 data forced genes into co-expression modules that would not otherwise have been together. Moreover, filtering resulted in a single, highly correlated module, which violates the scale-free topology assumption of the WGCNA algorithm.

CONCLUSIONS: DESeq2 and WGCNA detected differentially expressed genes and co-expressed gene modules in brown and yellow beans with contrasting times during soaking. In the future, candidate genes will be produced by overlapping the DESeq2 and WGCNA data with QTL for cooking time and protein concentration, which could assist breeders hoping to breed for faster cooking times. Furthermore, filtering WGCNA data is not recommended for plant-based RNA-seq data, in accordance with previous recommendations for human data (Langfelder and Horvath, 2008).

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COOKING ATTRIBUTES, TASTE PROFILE AND SENSORY ANALYSIS FOR COMMON BEAN (*PHASEOLUS VULGARIS* L.) ADOPTION IN THE NORTHERN PART OF COTE D'VOIRE

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INTRODUCTION

The implementation of food and agriculture security policy in the country had allowed the diversification and promotion of food crops. Among the grain legumes, common bean contains more than 20% proteins and is also a key source of minerals in the human diet, especially iron and zinc and other essential micro-nutrients that are found in low amounts in the cereal and root crops (Wang et al., 2003). Côte d'Ivoire had produced 4,761 tons of green beans and 25,950 tons of cowpeas in 2008 (PNIA, 2017). Current national statistics on dry bean production were not be available as the crop is in danger of disappearing. The objective of this study undertaken by the Vegetable and Protein Research Program (VPRP) of the National Center for Agronomic Research (CNRA) was to assess the preference between common bean and cowpea through cooking time, tasting and ascending hierarchic classification to boost dry bean variety adoption.

MATERIALS AND METHODS

For the taste tests, four dry bean varieties (Figure 1) and three cowpeas varieties were used. Fifty (50) people were selected to evaluate different varieties of beans and cowpeas. Among the attributes assessed were the cooking time of 5 kg of bean grain, the color of the grain and dishes, and the smell and taste of the meal. The evaluation of the rating cards will allow for two levels of classification, first the choice made by the panel member between beans and cowpeas, and second the classification of the four dry bean varieties by order of preference. Data was analyzed using the STATISTICA version 7.1 statistical package.

HARI11/GHA18 **HARI25/GHA19** **HARI13/GHA19** **HARI35/GHA19**

Figure 1. Seeds of four (4) dry bean varieties used in the taste tests.

RESULTS AND DISCUSSION

The results from this study showed that dry bean was largely preferred over cowpea (Figure 2A). Indeed, 50% of the tasters chose dry beans instead of cowpeas (24%). Of the four bean varieties proposed, HARI11/GHA19 white seeded bean had a cooking time of 112 minutes (Figure 3B) was the first choice followed by HARI25/GHA19, HARI13/GHA19 and HARI35/GHA19, respectively (Figure 2B). The ascending hierarchical classification revealed four groups of tasters. Groups 3 and 4 were the most active in selecting bean varieties (Figure 3A).

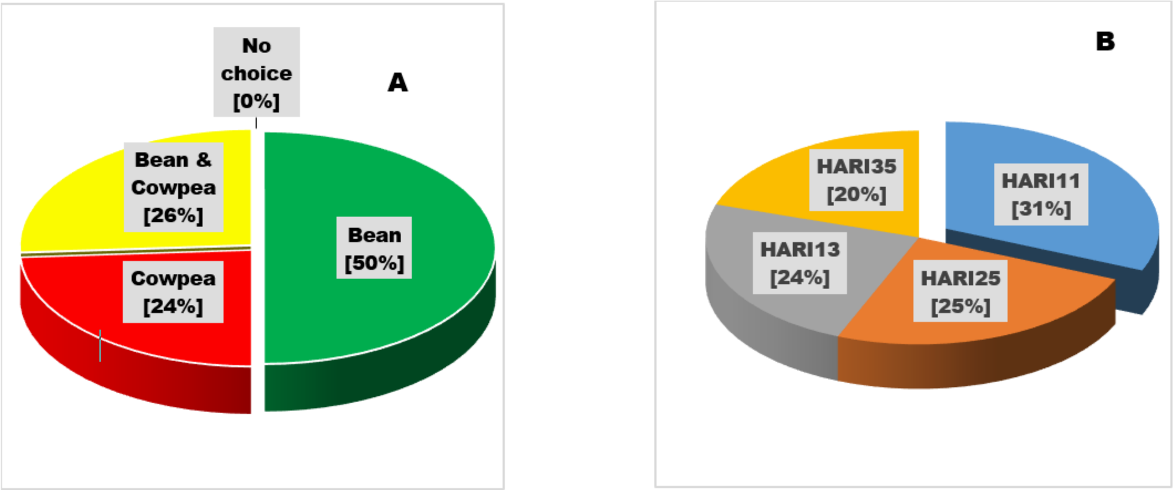

Figure 2. Percentages of preferences between dry bean and cowpea (A), and classification of four dry bean varieties according to the tasters' choice (B).

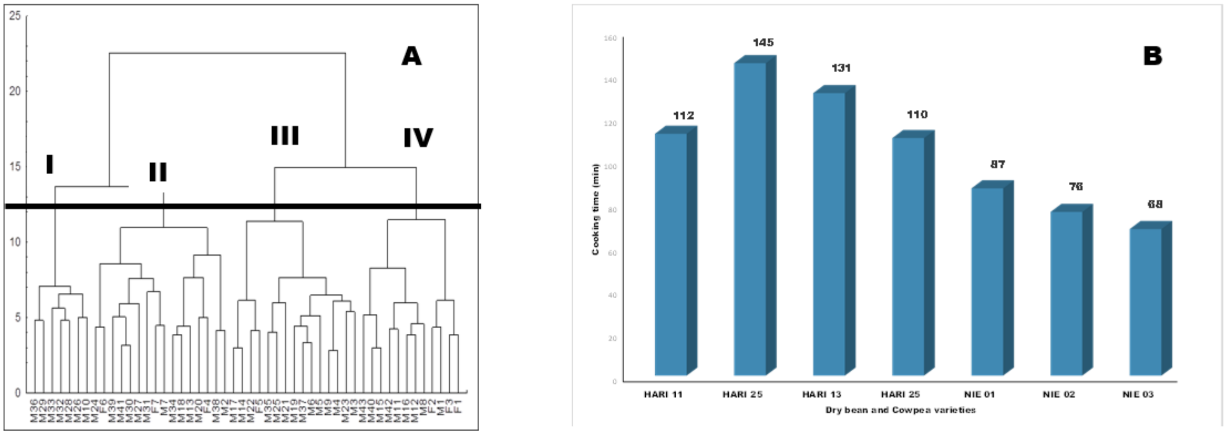

Figure 3. Hierarchical ascending classification of fifty (50) bean and cowpea tasters: (A). Cooking time of 5 kg of seeds for four varieties of dry beans and three varieties of cowpea (B).

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EVALUATION OF VIGOR TESTS FOR THE SELECTION OF BEAN GENOTYPES WITH HIGH SEED VIGOR

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INTRODUCTION: Bean landraces are a good option for use in breeding programs due to their special characteristics such as seed quality and vigor of the seedlings. The process of coevolution and adaptation to environmental changes could provide desirable genes and identify genotypes for hybridization programs (Bevilaqua et al., 2014). The high performance of seeds is very important for obtaining good stands of plants in cropping systems and seedlings with high performance. Work developed by Ribeiro et al. (2008) evaluating 32 bean cultivar cultivars for potential agricultural and nutritional use, showed that some of them stand out for nutritional composition and certain agronomic characteristics. The objective of this work was to evaluate the seed quality of bean cultivars grown in different environments in relation to commercial cultivars, to identify those with the highest physiological potential of their seeds.

MATERIALS AND METHODS: Seeds of 15 bean genotypes were evaluated, including breeding lines and landraces, and BRS Intrepido, for black grain, and Carioca, colored grain as checks. The seeds were from the 2012 trial of cultivars of the South Brazilian network, conducted in the municipalities of Sobradinho and São Luiz Gonzaga, in Rio Grande do Sul. In the first municipality, the sowing season was in October and the harvest was carried out in January. In the second, in the second cropping season, the sowing season was in January and the harvest was carried out in April. The fertilization was performed with NPK fertilizer, using 300 kg ha^{-1} of formula 10-30-10. Harvesting was performed by harvesting the plants, followed by drying in ambient air. The seeds were submitted to germination tests, according to Brazil (2009), accelerated aging, cold, electrical conductivity, shoot length and seedling root, described in Krzyzanowski (1999). The data obtained from the performed tests were submitted to analysis of variance and the means compared by the Scott-Knott test at 5% probability.

RESULTS AND DISCUSSION: The analyzes carried out showed high quality seeds in landraces and breeding lines, where in all tests they were statistically superior to the commercial cultivars used as controls. These results demonstrate the potential of using these varieties in the development of cultivars of quality and with greater resistance to adverse conditions during the establishment stage of the crop. The genotypes presented different results in both sites, indicating the presence of interaction of the genotype with the environment. The germination test was efficient in separating the genotypes for differences in seed performance, unlike tests of accelerated aging and cold, which were not efficient in separating the genotypes in the level of vigor, in both places. This fact may lead to the need for methodological adjustments in the performance of these vigor tests for the species. The seedling root length vigor test was the one that showed the greatest sensitivity for the separation of genotypes into vigor classes, being an excellent test in the variety selection.

In Sobradinho, the genotypes TB 0307 and TB 0325 stood out for high germination, while in São Luiz Gonzaga, Iolanda and Vinho stood out. In Sobradinho, TB 0222, TB 0305, Iberico and TB 0221 stood out for their high root growth, all of black grain. In this local, we can highlight TB 0221 and TB 0226, the first of black grain and the second of red grain. In São Luiz Gonzaga, the most notable were Iberico, TB 0226, TB 0307 and TB 0222, with different types of grain. This fact can be attributed to the presence of seed dormancy in some genotypes, which is corroborated by the fact that the phenotype was repeated in the two sites under very different cultivation conditions for TB 0226.

TB 0221 and TB 0325 can be highlighted in terms of high vigor, low electrical conductivity and high root growth of the seedlings at both cultivation sites. However, the first showed root growth below the best treatments. The genotypes Iolanda and Carioca, colored seed, and TB 0305 and Ibérico, both black seeded, stood out in relation to the vigor tests in Sobradinho, but this was not repeated in São Luiz Gonzaga. The genotypes TB 0305, Iberico and TB 0221 were distinguished for high root growth at both sites. The conductivity test presented discrepant data in relation to the other tests, because genotypes superior for vigor in the other tests were those that presented the highest values of electrical conductivity. This fact contradicts data by Kryzanowski et al (2004), that high-vigor seeds have low electrical conductivity.

Table 1. Results of germination (G), accelerated aging (AA), cold test (CT), seed electrical conductivity (EC), seedling root length (SRL) in landraces (LR) and lines of the breeding program of beans in Sobradinho (1fst) and São Luiz Gonzaga (2 sec), RS.

Genotypes	Grain Color	G		AA		CT		EC		SRL	
		............................%............................						.....µsi/cm2....		.........cm..........	
TB 0222 (BL)	black	92b	95c	79b	96a	92a	97a	37,9c	42,5c	14,7a	8,0c
TB 0325 (BL)	black	94a	94c	87a	93a	90a	97a	51,8a	59,2a	11,4b	10,0b
TB 0305 (BL)	black	88b	94c	85a	80a	86a	77c	43,6b	40,1d	14,0a	14,0a
TB 0221(BL)	black	87c	96b	90a	93a	96a	98a	24,4e	36,5d	13,4a	14,3a
TB 0324 (BL)	black	89b	92c	85a	91a	87a	94a	53,9a	58,2a	11,0b	8,6c
BRS Intrepido	black	81d	96b	71b	93a	86a	97a	35,6c	42,0c	12,5b	6,5e
Carioca	brown	90b	94c	89a	86a	78a	94a	50,2a	45,2c	12,5b	13,4a
Guabiju (LR)	black	89b	92c	91a	89a	88a	96a	30,5d	48,8b	12,2b	5,3e
Iberico (LR)	black	92b	82d	81b	91a	91a	94a	35,8c	50,8b	13,3a	13,4a
Iolanda (LR)	red	89b	99a	86a	98a	88a	94a	28,5d	36,3d	12,0b	11,1b
TB 0220 (LR)	black	91b	89c	71b	88a	90a	95a	43,9b	54,5a	11,0b	11,9b
TB 0225 (LR)	black	84c	95c	82b	85a	89a	96a	33,7c	50,6b	11,2b	11,1b
TB 0226 (LR)	red	75d	90c	90a	92a	82a	96a	38,8c	45,7c	11,4b	6,7d
TB 0307 (LR)	red	96a	94c	76b	97a	78a	99a	47,4b	40,6d	12,1b	3,9e
Vinho (LR)	purple	86c	99a	79b	91a	90a	87b	21,6e	25,8e	11,4b	12,6a
Cv%		3,2	4,9	8,4	7,9	6,4	5,5	6,2	6,5	10,2	9,0

Means followed by the same letter do not differ significantly for the Scott- Knott test at 5% probability.

CONCLUSIONS: The tests of accelerated aging and cold were not efficient in separating the bean genotypes according to vigor levels, with a strong interaction of the results with the site. The seedling root length was the most effective test for vigor classification. TB 0221, TB 0305, and Iberico presented the most consistent results at both sites.

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SELECTION OF CARIOCA COMMON BEAN LINES WITH SLOW SEED COAT DARKENING

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INTRODUCTION

Common beans (*Phaseolus vulgaris* L.) from the Carioca market class are the most consumed in Brazil. Studies related to darkening of the seed coat in Carioca beans are of great importance for breeding programs since the change in seed color has a detrimental effect on bean quality, triggering a rejection by consumers, and leading to a decrease in crop value (Pereira et al., 2017). Rapid darkening occurs due to gradual chemical changes from oxidation and dehydration during grain storage. The main changes are associated with the presence of polyphenolic compounds in the seed coat, which are converted into visible pigments with a high concentration in carioca beans with regular darkening (Beninger et al., 2005; Islam et al., 2020). The genetic control of slow darkening (SD) is conditioned by a single recessive *sd* gene, which has been considered a basic requirement in breeding programs that aim to develop cultivars with the slow darkening trait (Junk-Knievel et al., 2008; Silva et al., 2008). Carioca cultivars with slow darkening have been developed and are available for farmers in Brazil, including BRSMG Majestoso (Silva et al., 2008) and BRSMG Madrepérola (Araújo et al., 2012). The finding of new genetic sources of slow darkening plays an important role in accelerating the pace of improvement in carioca beans. The objective of this study was to select promising slow seed coat darkening carioca common bean lines.

MATERIALS AND METHODS

Carioca Claro is a common bean cultivar from the carioca market class originally from the state of Mato Grosso, Brazil that has the genetic characteristic of slow darkening of the seed coat after harvesting. IPR Juriti and Pérola, on the other hand, are commercial cultivars from the carioca market class broadly cultivated in Brazil which present regular darkening (*RD*). At the Núcleo de Pesquisa Aplicada à Agricultura (Nupagri) from the Universidade Estadual de Maringá, Brazil, crosses between the Carioca Claro (*SD*) and the cultivars IPR Juriti (*RD*) and Pérola (*RD*) were performed. F_1 seeds were planted in the greenhouse to obtain the next generation. The F_2 seeds were sowed in pots with soil that was previously sterilized and fertilized. Bean plants were kept in a greenhouse until they produced $F_{2:3}$ seeds through the self-pollination of single F_2 plants. We obtained a total of 84 $F_{2:3}$ families from the Carioca Claro × IPR Juriti cross and 88 $F_{2:3}$ families from the Carioca Claro × Pérola cross. After harvesting, seeds of the $F_{2:3}$ families were maintained in a cold room at 48% relative humidity and 10±2ºC temperature for 12 months. After storage, these families were phenotypically evaluated for their seed coat darkening according to the methodology described by Silva et al. (2008).

RESULTS AND DISCUSSION

Of the tested 84 $F_{2:3}$ families from the Carioca Claro (*SD*) × IPR Juriti (*RD*) cross, only 22 exhibited slow darkening (*SD*). Regarding the 88 $F_{2:3}$ families from the Carioca Claro (*SD*) × Pérola (*RD*) cross, 19 families exhibited slow darkening (*SD*) of the seed coat. Figure 1 shows the $F_{2:3}$ families that exhibited the seed coat slow darkening (*SD*). The observed segregation of both populations adjusted to a 3 *RD*: 1 *SD* ratio as expected for a gene with recessive effect (χ^2= 0.63 and 0.54, and *p*-value=0.80 and 0.46, respectively). The slow darkening of the seed coat is expressed through the maternal tissue, thus the phenotyping of seeds in the $F_{2:3}$ generation is used to determine the phenotype of an F_2 plant (Silva et al., 2014). This maternal expression, combined with recessive inheritance, delays the breeding progress for the SD trait. It is worth mentioning that several Carioca and Pinto cultivars, and lines exhibiting desirable seed color traits, often do not have optimum agronomic performance (Pereira et al., 2017; Arns et al., 2018; Miklas et al., 2020). Therefore, we selected the 41 slow darkening lines derived from the Carioca Claro × Pérola and Carioca Claro × IPR Juriti crosses to evaluate for agronomic performance in field assays, creating an opportunity to identify lines that combine the slow seed coat darkening from Carioca Claro and the high seed yield and size, plant architecture, and broad adaptation from Pérola and IPR Juriti cultivars.

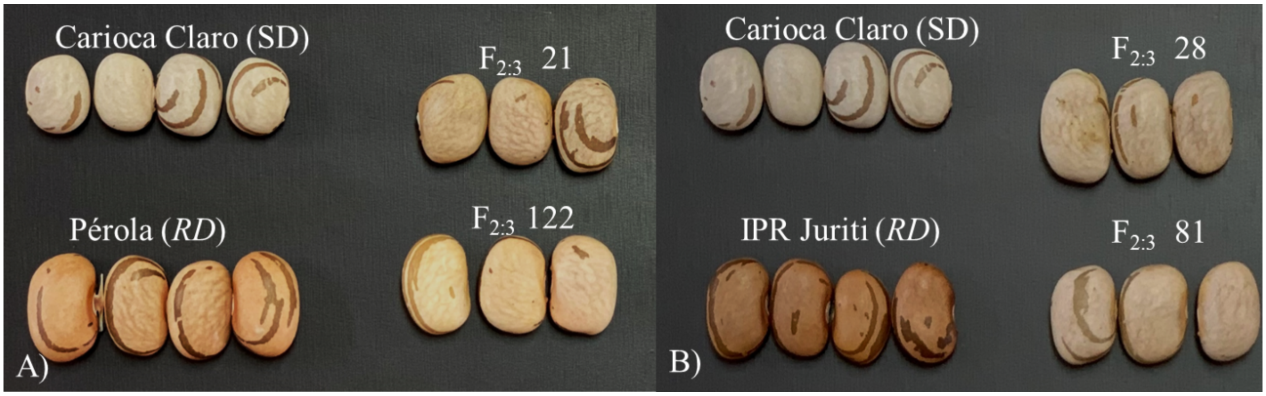

Figure 1. Seeds of cultivars and $F_{2:3}$ families 12 months after harvesting. A) Carioca Claro (*SD*), Pérola (*RD*) and the *SD* $F_{2:3}$ families (21, 122). B) Carioca Claro (*SD*), IPR Juriti (*RD*) and $F_{2:3}$ families (28 and 81). Carioca Claro and the $F_{2:3}$ families showed light cream color for seed coat after storage. Pérola and IPR Juriti exhibited dark seed coat after storage.

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NUTRITIONAL AND BIOCHEMICAL CHARACTERIZATION OF ANDEAN COMMON BEAN ACCESSIONS

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the main sources of food in terms of caloric intake and nutrients worldwide, especially in developing countries in East Africa and Latin America that include common beans in their diet (Celmeli et al., 2018). Improving common beans to increase nutritional content of the grain is one of the main strategies to reduce the problems caused by malnutrition worldwide (Blair, 2013). In this context, the aim of the present study was to characterize common bean accessions of Andean origin for nutritional and biochemical characteristics.

MATERIALS AND METHODS

Twelve common bean accessions of Andean origin (G6416, KID44, BRS Ártico, IPR Garça, Gordo, LP01, LP02, BRS Realce, DRK 15, BRS Embaixador, BRS Radiante and Vermelho de Imbituba) were evaluated in the present study. The experiments were carried out at the Research Stations of the Instituto de Desenvolvimento Rural do Paraná (IDR-Paraná) in the cities of Londrina and Guarapuava. The experimental design used was a completely randomized block with three replications. The following nutritional and biochemical characteristics were determined: protein content in grains (Prot), calcium (Ca), potassium (K), phosphorus (P), magnesium (Mg), sulfur (S), manganese (Mn), copper (Cu), iron (Fe), zinc (Zn), condensed tannins (CT), total flavonoid content (TFC), total phenolic content (TPC) and antioxidant activity (DPPH). The data were submitted to analysis of variance (ANOVA) and a hierarchical grouping of Ward associated with the heatmap was performed using the Mahalanobis distance. All statistical analyzes were performed using R software (https://www.r-project.org/).

RESULTS AND DISCUSSION

The analysis of variance showed a significant effect ($P < 0.01$) of the accessions for all evaluated traits, indicating the presence of genetic variability for nutritional and biochemical quality among the studied accessions. In addition, there was also a significant effect ($P < 0.05$) of the environments for the characteristics P, K, Ca, S, Mg, Cu, TPC and TFC, indicating that the evaluated characteristics showed differential responses according to the environment. There was no significant interaction ($P > 0.05$) between genotype–environment for any of the traits, inferring that the differential response of the accessions was not dependent on the environments. The presence of genetic variability for nutritional characteristics has already been reported in common beans worldwide (Blair, 2013). The clustering analyses separated the evaluated accessions into three distinct groups (Figure 1). Group 1 (blue) was composed by the accessions G6416, KID44, BRS Ártico and IPR Garça. This group was characterized by presenting the highest averages for the characteristics Fe, Mn and Prot; however, they also had the lowest averages of Cu, Zn, CT, TFC, TPC and DPPH. Group 2 (green) was composed of the accessions Gordo, LP01 and LP02, this group being characterized by presenting the lowest averages for P, Ca, Mg and K, and high averages for Cu, Zn, CT, TFC, TPC and DPPH. Group 3 (orange) was formed by four accessions (BRS Enhance, DRK 15, BRS Ambassador, BRS Radiante and Vermelho de Imbituba). These accessions stood out from the others because they presented the highest averages for the characteristics P, Ca, Mg, K, Cu, Zn, CT, TFC, TPC and DPPH. The accessions that stood out in this study can be used as parents in common bean breeding programs aimed at developing cultivars with higher nutritional and biochemical quality in the grains.

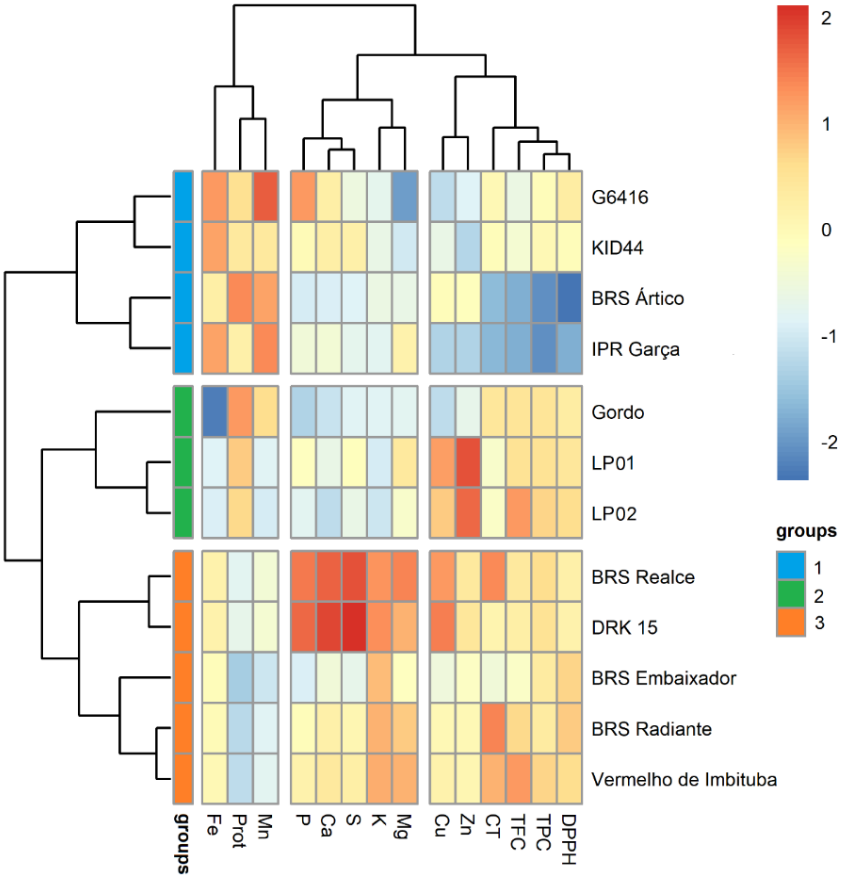

Figure 1. Ward clustering associated with a heatmap of 12 Andean common bean accessions evaluated for nutritional and biochemical characteristics.

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GENETIC DIVERSITY IN CARIOCA COMMON BEANS TO SEED COAT DARKENING AND OTHER TECHNOLOGICAL TRAITS

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is an important source of protein, minerals, unsaturated fatty acids, fibers and vitamins. This crop has great economic and social importance in Brazil, as it is a food that is present in the daily meals of the Brazilian population, in addition to being one of the main sources of income for small farmers. Among the commercial groups, the carioca group represents approximately 70% of Brazilian common bean production and the cultivars of this group differ in relation to the time of seed coat darkening. The early seed coat darkening of the grains decreases the market acceptance by consumers and several studies have demonstrated the existence of genetic variability for this trait, allowing the selection of genotypes with slow seed coat darkening. Thus, the objective of the present work was to verify the genetic diversity in common beans of the carioca group for the early seed coat darkening and other characteristics in relation to the technological and biochemical quality of grains.

MATERIALS AND METHODS

Twelve Mesoamerican common bean accessions from the carioca commercial group (IPR Tangará, IPR Quero-Quero, IPR Campos Gerais, IPR Curió, IPR Andorinha, IPR Sabiá, BRS Estilo, BRS Notável, BRSMG Madrepérola, IAC Sintonia and Agronorte 09) were evaluated. The field experiment was conducted at the Research Station of the Instituto de Desenvolvimento Rural do Paraná (IDR-Paraná), in the city of Ponta Grossa, state of Paraná-BR, using a completely randomized block design with three replications. A sample of 200 grams of grains was selected from each repetition for grain analysis. The following traits were evaluated: cooking time (CZ), grain color (C), total soluble solids in the broth (TS), total phenolic compounds (TPC), total flavonoids (TFC) and antioxidant activity (DPPH). These traits were evaluated at times 0 and 72 hours after being submitted to an accelerated seed coat darkening protocol described by Junk-Knievel et al. (2008). The data were submitted to principal component analysis (PCA) using the R software.

RESULTS AND DISCUSSION

Knowledge of the nutritional value and cooking quality of cultivars, combined with resistance to storage are fundamental in studies of genetic plant breeding, especially in the selection of new cultivars that must serve the producer and the consumer. In the PCA the first two components explained 64.1% of the total variance (Figure 1). In the bidimensional graph, two groups were formed, defined according to the time of submission to the accelerated seed coat darkening protocol, 0 and 72 hours. The traits that most contributed to the separation of the accessions were total soluble solids in the broth (TS) and cooking time (CZ). The accessions that showed greater stability in relation to seed coat darkening were BRS Madrepérola, BRS Notável and BRS Estilo, IPR Andorinha, IAC Sintonia and IPR Sabia. The process of accelerated seed coat darkening affected the technological and biochemical quality of the evaluated accessions, showing that accessions more susceptible to seed coat darkening, besides being less attractive to consumers, also present a lower technological quality related to cooking and biochemical compounds.

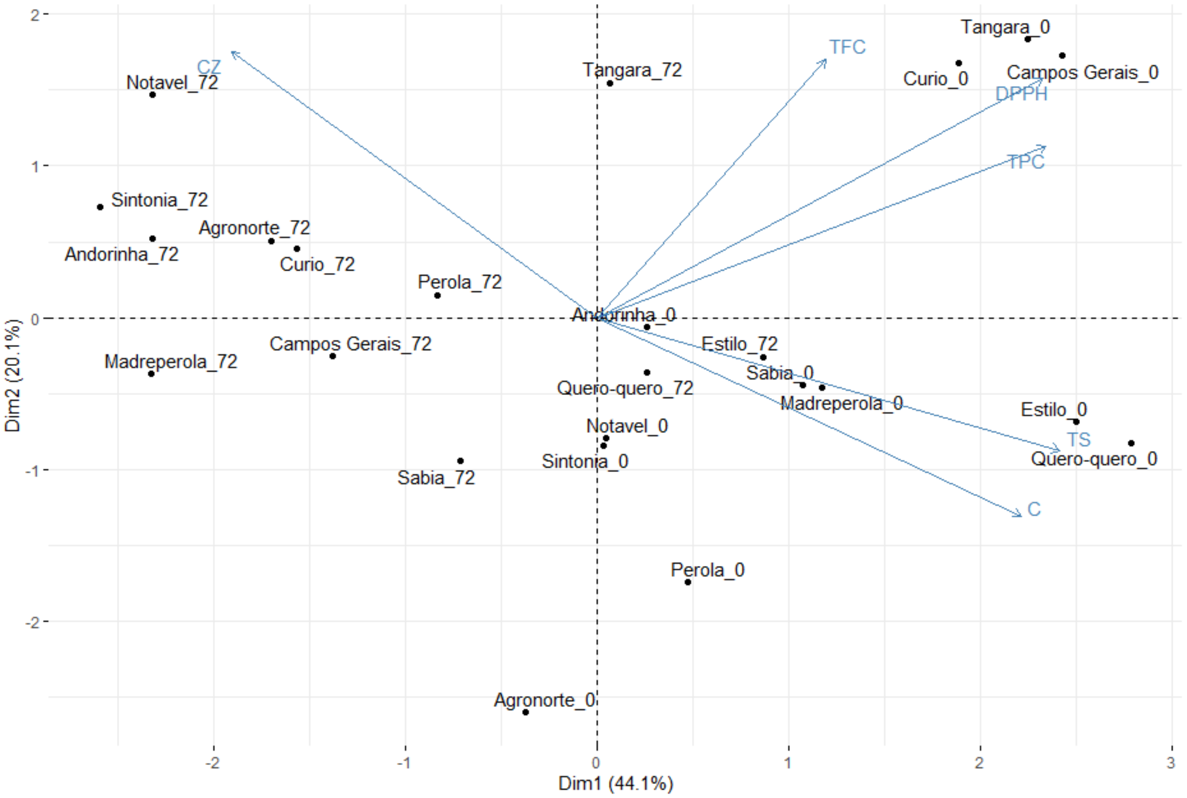

Figure 1. Bidimensional representation of Principal Component Analysis (PCA) of common bean accessions submitted to an accelerated seed coat darkening protocol and evaluated for grain color and technological traits.

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CHROMOSOME-LEVEL GENOME ASSEMBLY OF COMMON BEAN (*Phaseolus vulgaris*) USING PACBIO HIFI AND HI-C TECHNOLOGIES

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INTRODUCTION: Having a complete and accurate genome assembly is crucial for comparative and functional genomic studies. However, abundant repetitive sequences found in eukaryotic genomes often fragment short read assemblies. Long-read assemblies produce much longer contigs which still need additional scaffolding to achieve chromosomes. Recently, Pacific Biosciences (PacBio) high fidelity long reads sequencing, known as HiFi, and scaffolding technologies such as Hi-C and Optical maps, have allowed to produce assemblies with greatly improved contiguity and accuracy (Burton et al., 2013; Lam et al., 2012). In common bean, two reference genomes have been published, corresponding to Andean and Mesoamerican genotypes, G19833 and BAT93, respectively (Schmutz et al., 2014; Vlasova et al., 2016). However, the BAT93 assembly presents low contiguity and is highly fragmented. Even if this resource made it possible to progress in *P. vulgaris* genetics, it lacked contiguity and completeness required for structural variation analysis, including NLR gene evolution study, the largest class of disease resistance genes in plants (Richard et al., 2018). Here, we generated a highly contiguous chromosome-level genome assembly of the genotype BAT93 using PacBio HiFi sequencing and compared two scaffolding tools (optical mapping and Hi-C).

MATERIALS AND METHODS: High molecular weight DNA from BAT93 young trifoliate leaves was sequenced using 1 SMRT cell of PacBio Sequel II system. In parallel, Bionano optical maps and Hi-C chromosome conformation capture data were generated. Finally, an assembly using HiFi long reads was generated and scaffolded using either optical maps or Hi-C data.

Table 1. Assembly statistics of the BAT93 genome

		Scaffolding tools	
	PacBio HiFi assembly	Optical mapping	Hi-C
Assembly length (Mb)	631	566	569
Contig number	1585	-	-
Scaffold number	-	1495	1441
N50 (Mb)	8.6	28.1	52.3
L50 (contig/scaffold number)	26	8	6
Longest contig/scaffold (Mb)	29	51.9	63.8
Scaffolds > 10 Mb	-	22	11

Mb, Megabase

RESULTS AND DISCUSSION: HiFi long reads were assembled into 1585 contigs, corresponding to 631 Mb and 31X genome coverage. Strikingly, the total size of the contigs (631 Mb) is very close to the expected size of common bean genome based on flow cytometry (637 Mb) (Arumuganathan and Earle, 1991). Then, we performed scaffolding using Bionano optical mapping data, and obtained 22 scaffolds longer than 10 Mb with an N50 of 28.1 Mb and an assembly size of 566 Mb. Even if this method allowed us to triple the N50 value, we did not obtain chromosome-level scaffolds. We therefore performed scaffolding based on Hi-C data, an alternative scaffolding tool. As expected for common bean, 11 chromosomes were built as single scaffolds using Hi-C data, with a N50 of 52.3 Mb and an assembly size of 569 Mb (Table 1). The remaining unplaced scaffolds were very short (less than 1 Mb) and contained mostly repetitive sequences. In conclusion, scaffolding based on Hi-C data was more efficient than optical mapping data to reach a chromosome-level assembly, since it enabled the reconstruction of the 11 expected chromosomes in single and highly continuous scaffolds (Figure 1).

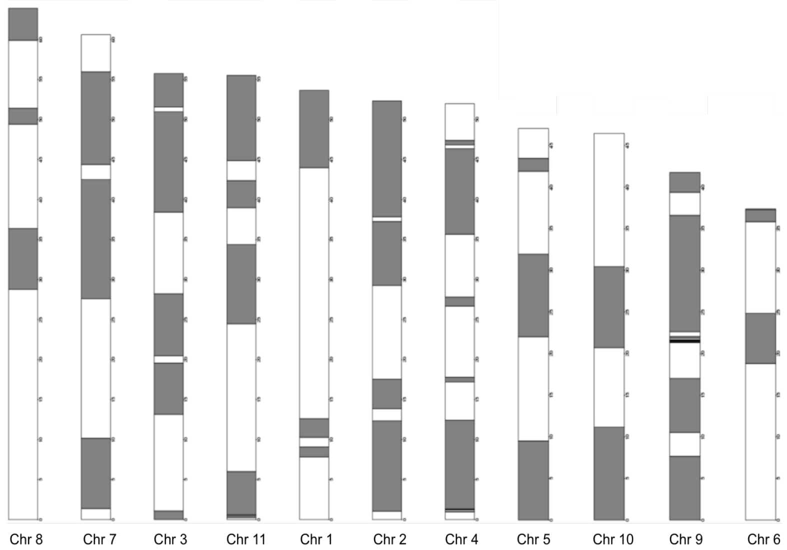

Figure 1. Assembly overview of the 11 chromosome scale scaffolds of BAT93 after Hi-C scaffolding. Chromosome numbers were assigned based on the G19833 genome (Schmutz et al. 2014). White and gray blocks represent boundaries between contigs. Scale in Mb is presented to the right of the chromosomes.

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A PROPOSAL FOR COMMUNITY-LED DEPOSITION AND CURATION OF *PHASEOLUS* DATA AT THE LEGUME INFORMATION SYSTEM

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ABSTRACT: The number of genomic resources for *Phaseolus* and the legume family have undergone unprecedented growth in recent years. Many of these resources, including marker-trait associations, have been assigned to a range of genome assemblies and genetic maps that may not be readily comparable among experiments. This obstructs the accessibility of many promising results, particularly for those working with different genetic data types or distinct species. The Legume Information System (LIS) offers a continuously updated, highly integrated platform for comparing genetic and phenotypic data among distinct genomes assemblies and species. Recent updates in the data deposition system (available at https://legumeinfo.org/submit_data) now facilitate the process of adding QTL mapping or GWAS data to the repository. These data can then be quickly and easily compared using a variety of LIS tools. We propose here a community-led curation of genotypic and phenotypic data that will greatly increase the impact of deposited data among *Phaseolus* research labs and across the legume community.

BACKGROUND AND RATIONALE: The increasing number of genetic and genomic resources available in *Phaseolus* offers widespread opportunities, but also creates a complex and decentralized body of work distributed among a variety of sources that are difficult to compare and assemble as illustrated by several useful reviews and compilations (e.g., Pérez de la Vega et al., 2017). Nevertheless, these resources are intrinsically limited in their capacity to remain up-to-date as new results are published. Platforms such as the Legume Information System (LIS) integrate numerous forms of data and offer tools to easily extract relevant data. Online tools such as LIS can be continuously updated to reflect the state of the art in the field. A community-led agreement to submit marker-trait associations and other data to LIS would create a single comprehensive repository for finding these data. The benefits of this would include increasing the accessibility and impact of the submitted data.

LIS was developed as a collaboration between the National Center for Genome Resources and the USDA Agricultural Research Service (Gonzales et al., 2005, Berendzen et al., 2021). The platform offers a variety of genetic and genomic tools for more than 20 legume species. These resources include genome browsers, tools for accessing gene annotation and expression data, trait and map databases, and numerous comparison tools. The system has the capacity to curate the marker information included previously in the PhaseolusGenes database (which will cease to operate) and the extensive data sets being generated in the genus *Phaseolus*, with the eventual goal to integrate them into their pre-existing system of comparative tools.

From this perspective, it is important to note that LIS recently updated its data submission portal (https://legumeinfo.org/submit_data). The portal now includes example data sets that can be used as templates for future submissions. Under this proposal, submission by the authors of QTL mapping and GWAS results to LIS as a routine part of the publication process in *Phaseolus* is strongly encouraged. These data can be reviewed by LIS developers and rapidly incorporated into the database. This will create a single comprehensive source for marker-trait data in the genus. Community participation will distribute the curation workload and promote the visibility of the results deposited in the system.

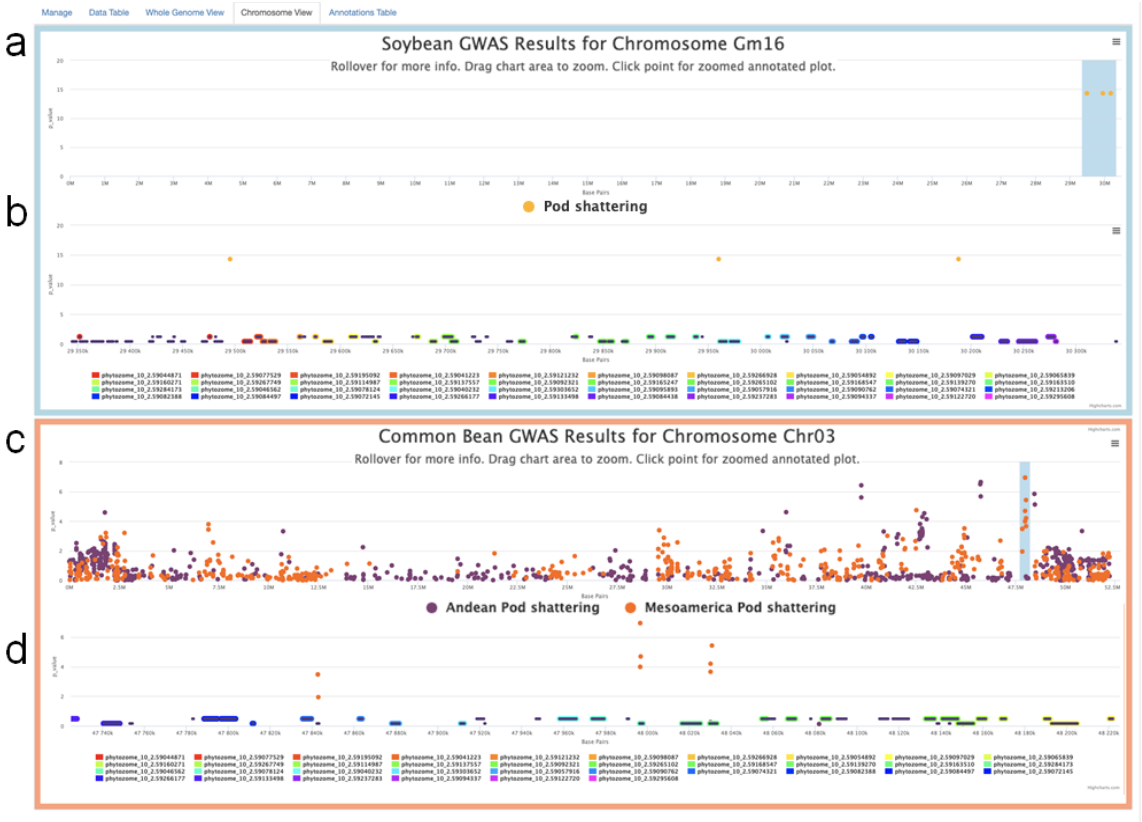

Figure 1. Example of interspecies comparisons using the LIS interface. A) A pod-dehiscence QTL (*PDH1*) maps to soybean chromosome Gm16. B) Zoomed-in view of the soybean *PDH1* QTL. C) The syntenic region of common bean (on chromosome Pv03) also includes a major pod shattering QTL *PvPdh1*. D) Zoomed-in view of the common bean QTL. Submitting data to LIS will maximize the accessibility and impact of data across populations and studies. ZBrowse based on Ziegler et al. (2015).

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USE OF ARTIFICIAL INTELLIGENCE FOR THE CLASSIFICATION OF LIMA BEAN ACCESSIONS FOR ANTHRACNOSE RESISTANCE

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INTRODUCTION: Machine Learning is a subarea of Artificial Intelligence (AI), which automates the construction of analytical models, becoming a powerful tool for solving problems in a non-linear way. With machine learning it is possible to produce models more quickly and automatically that are capable of analyzing data in greater quantity (Big data), of more complexity and with more accuracy (Biamonte et al. 2017). In this sense, recent studies have shown that machine learning has great potential to detect diseases in plants through spectral information and images, presenting advantages for non-destructive tests. This approach is also able to compare genotypes in terms of disease susceptibility levels. The aim of this present study is to propose a method for assessing the levels of resistance to anthracnose in lima bean accessions using algorithms based on Artificial Intelligence.

MATERIALS AND METHODS: Thirty lima bean accessions from the *Phaseolus* Active Germplasm Bank of the Federal University of Piauí (UFPI) were evaluated. The accessions UFPI 251 and UFPI 669 were used as checks, and were identified by Cavalcante et al. (2012) as highly resistant and highly susceptible, respectively. The experiment was carried out in a greenhouse, in the municipality of Teresina, State of Piauí, in February 2020. The accessions were sown in pots, ten per accession, totaling 25 inoculated plants. The inoculation with the *Colletotrichum truncatum* isolate was carried out on two leaves at the same stage of development, removed from each accession. All leaf samples were digitized. Then, the accessions of lima bean were sown in the experimental area of the Department of Plant Science/UFPI and submitted to natural infestation. The plots consisted of 4 rows of 5 plants each, with 1m spacing, in a total of 20 plants. The images obtained by the digital camera were subjected to the standardization of RGB colors and formatted for the dimensions 150 x 150. Then, the total set of images was divided into sets for training and testing, in the proportion of 20% for testing and 80% for training. The model selection was carried out through the application of different neural network architectures by the Python tensorflow library. Accuracy (ACC) was considered a model selection parameter.

RESULTS AND DISCUSSION: The 238 images obtained in the field presented leaves with symptoms and without symptoms of anthracnose and were classified as susceptible (“S”) and resistant (“R”) (Figure 1).

Figure 1. Images of resistant (R) and susceptible (S) leaves photographed in the field.

The "Transfer learning" approach was used to improve the accuracy of the network, for which training information was obtained from the VGG19 network. The selected model consisted of a pooling layer and a dense hidden layer with 100 neurons, using the Relu function. For the output layer, the most effective function was "softmax" with two neurons. In regards to precision, the model obtained better results with the "adam" optimizer. The final accuracy of the test was approximately 80%, with high classification sensitivity for resistant genotypes. This is an initial prototype that needs new adjustments in the network with the insertion of more training data and refinement of parameters. However, it shows that the use of machine learning methods with computer vision is promising for the evaluation of diseases in lima bean, as it promotes a method of rapid and inexpensive evaluation (Carvalho 2009; Costa et al. 2016). The present model can be implemented as an integrated tool with mobile devices for evaluation in the field that can assist in rapid phenotyping in terms of anthracnose resistance of accessions in germplasm banks, after successive training steps.

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ROOT SIZE IN AYOCOTE (*Phaseolus coccineus* L.) PLANTS

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INTRODUCTION: *P. coccineus*, one of the five domesticated species of the genus, is a legume with underexploited potential and little knowledge available concerning its root dimensions. Its roots can be fleshy or woody, globose or fusiform, frequently branched, pluriannual, growing vertically to horizontally to one-meter-long and 2-5 cm thick (Freytag and Debouck, 2002). This species is cultivated as an annual or perennial crop (Hernández-Xolocotzi et al., 1979). It has an extensive fleshy root system, comprised mainly of a taproot, many secondary roots, and corms which make it a perennial (Mata and Salas, 2014). The ayocote plant possibly evolved in areas of high evaporation occasioned by summer rainfall in the subtropical areas of Sierra Madre Oriental, Sierra Madre Occidental and the Neo-Volcanic Axis in Mexico. The aim of this paper was to learn about its root size and its relation with its regrowth capacity.

MATERIALS AND METHODS: Ten Mexican native varieties of *P. coccineus* were sown on March 23, 2013 in Texcoco, Edo. de Mexico (7 plants per replication with one row per accession). Data on latitude, longitude, altitude, minimum and maximum annual temperature of collection sites, and days from sowing to flowering time (Table 1). The seed harvest was completed in October 2013 and on March 10, 2014 (321 days after the sowing date) when data on root length and weight of three plants were collected. Finally, on March 30, 2015 (706 days after the sowing date) the percentage of visible regrowth was collected. ANOVA were run in the SAS statistical program and regression graphs in the Sigma v 14 Program.

Table 1. Geographical and climatic characteristics of the ayocote collection sites.

Num.§	Sub province	NL°:' WL °:'	Altitude masl	Min. temp. °C	Max. temp. °C
8276	Lagos y Volcanes del Anáhuac	19°:03' -98°:03'	2300	-1.0	27
8278	Lagos y Volcanes del Anáhuac	19°:03' -98°:03'	2300	-1.0	27
8211	Carso Huasteco	19°:87' -97°:48'	2025	1.0	23
8389	Neovolcánica Tarasca	19°:57' -102°:32'	2120	1.0	29
8382	Mil Cumbres	19°:387'-100°:15'	1950	-1.0	23
8301	Sierras y Valles de Oaxaca	16°:98' -98°:75'	1800	4.5	33
8376	Mil Cumbres	19°:387'-100°:15'	1950	-1.0	23
8120	Lagos y Volcanes del Anáhuac	19°:32' -98°:23'	2400	4.5	27
8398	Sierras y Valles de Oaxaca	16°:82' -96°:67'	1500	4.5	31
8250	Lagos y Volcanes del Anáhuac	19°:32' -98°:23'	2400	-1.0	27

§Germplasm bank "Centro Nacional de Recursos Genéticos. Tepatitlán, Jalisco, Mexico"

RESULTS: The ANOVA fulfilled the assumptions of homogeneity of variance and normality for flowering time and root length and weight. Days to flowering ranged from 30 to 55 days after sowing and was not related to the regrowth percent, nor the coordinates nor altitude or temperature of collection sites. The regrowth percent was significantly related to length and root weight (Figure 1). On March 30, 2015, accessions 8276, 8376 and 8389 had not visible regrowth, accession 8250 had 57 percent of regrowth (with flowers), and the greatest regrowth was observed in accession 8211.

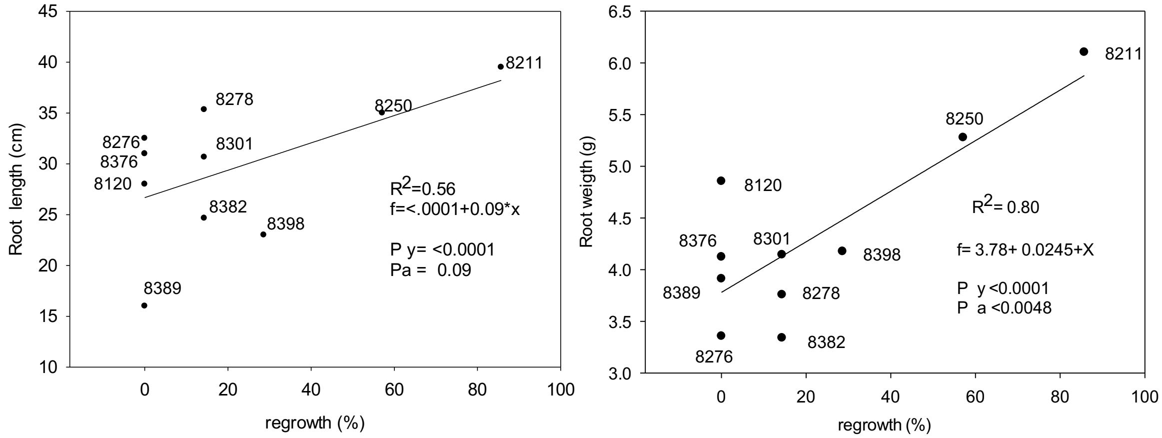

Figure 1. Regression of root length and weight, after seed harvest, with the regrowth percentage of ten native Mexican varieties of ayocote (*P. coccineus*).

CONCLUSION: The heaviest and longest roots of *P. coccineus* plants, after the first life cycle, showed the highest regrowth percentage.

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MULTIVARIATE APPROACH TO THE MORPHOAGRONOMIC CHARACTERIZATION OF Phaseolus lunatus L.

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INTRODUCTION

Lima bean (*Phaseolus lunatus* L.) is characterized by having high genetic diversity and potential for high production (Barbosa & Arriel, 2018; Oliveira et al., 2011). The morpho-agronomic characterization of the accessions available in the germplasm banks is essential to estimate the genetic divergence between the studied genotypes. Gower (1971) proposed a method to estimate the similarity between two individuals using quantitative and qualitative data with continuous and discrete distributions through an algorithm. In this sense, the objective was to promote the morpho-agronomic characterization and estimate the genetic diversity of lima bean accessions from the *Phaseolus* Active Germplasm Bank of the Federal University of Piauí (UFPI) through a multivariate approach.

MATERIALS AND METHODS

The experiment was carried out from January to September 2016 in a greenhouse at the Department of Plant Science of the Federal University of Piauí in the municipality of Teresina, PI. The 22 accessions of lima bean were from the *Phaseolus* Active Germplasm Bank of the Federal University of Piauí (BGP-UFPI). The design was completely randomized, with four replications. The characterization of the accessions was performed based on 25 morpho-agronomic descriptors of lima bean (Bioversity International, 2007). The genetic distance matrix was estimated through the combined analysis of quantitative and qualitative descriptors based on the Gower algorithm (1971). The accessions were grouped by the UPGMA method (Unweighted Pair-Group Method Using an Arithmetic Average). Statistical analyzes were performed using the R program (R Development Core Team, 2018).

RESULTS AND DISCUSSION

Based on the UPGMA cluster, five groups were formed (Figure 1). Group I with accessions UFPI 220 and UFPI 866; group II, comprising accessions UFPI 836, UFPI 865 and UFPI 872; and group III formed by nine accessions (UFPI 879, UFPI 863, UFPI 864, UFPI 857, UFPI 879, UFPI 860, UFPI 868, UFPI 860 and UFPI 879). Groups IV (UFPI 852 and UFPI 867) and V (UFPI 858 and UFPI 862) were formed by two accessions. Quantitative and qualitative characteristics contributed to the grouping. The growth pattern and the color of the pods did not contribute to the formation of the groups, since all the accessions studied have an indeterminate growth pattern and brown colored pods. The accessions of BGP-UFPI were not grouped according to the collection area. In the case of accessions from geographically distinct regions, the grouping may be related to the genetic variability existing between the genotypes. For accesses from nearby regions, the greatest probable similarity was the result of the exchange of seeds between producers.

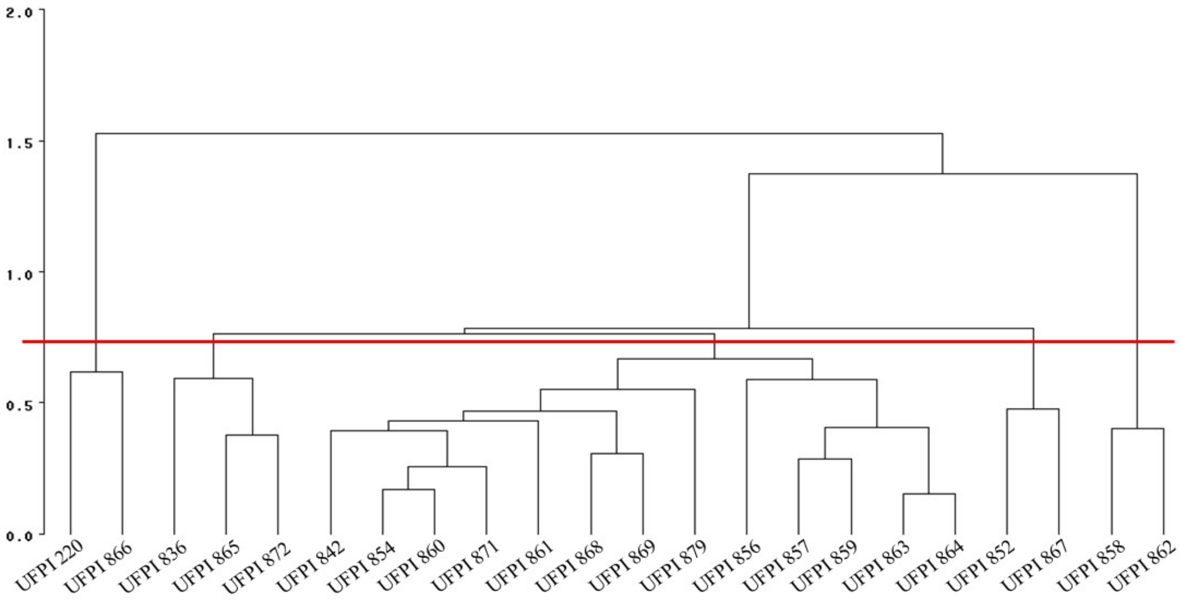

Figure 1. Dendrogram of 22 accessions of fava beans obtained by the UPGMA method based on Gower's distance (1971), using 11 qualitative and 14 quantitative characteristics.

Gower's genetic distance is efficient in discriminating groups and allows the simultaneous analysis of qualitative and quantitative descriptors, helping in the process of characterizing the genetic divergence existing in the germplasm bank. The UPGMA grouping method formed five groups. This indicates genetic variability between lima bean accessions, which can be used in breeding programs in the future.

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RESPONSE OF TEPARY BEANS TO BEAN GOLDEN YELLOW MOSAIC VIRUS AND POWDERY MILDEW

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INTRODUCTION: Severe infections of *Bean Golden Yellow Mosaic* Virus (BGYMV) reduce both the yield and the quality of seed of common beans (*Phaseolus vulgaris* L.). Tepary beans (*Phaseolus acutifolius* A. Gray) develop BGYMV symptoms but the effects of infection on seed yield and other traits can vary between genotypes. Powdery mildew caused by *Erysiphe polygoni* is a frequent disease of common and tepary beans in the Caribbean. The objective of this study was to evaluate the response of elite tepary bean breeding lines and cultivars to BGYMV and powdery mildew.

MATERIALS AND METHODS: Field trials were planted at San Juan de la Maguana, Dominican Republic in December 2018 and 2019. The tepary bean trials used a RCB design with two replications in 2018 and four replications in the 2019 planting. The experimental units were the middle two rows of four row plots planted in 2.5 m row lengths. The field trials were fertilized with a granular fertilizer at the recommended rate for commercial production. No agrochemicals were used to control disease or pest populations. The trials were not irrigated after 50 days after planting. The number of plants with BGYMV and powdery mildew symptoms were counted between 20-30 days after planting. Seed yield, % damaged seed and 100 seed weight were evaluated after harvest.

RESULTS AND CONCLUSIONS: The mean seed yields of the tepary bean lines were 1,418 kg/ha in the 2018 planting and 1,183 kg/ha in the 2019 planting (Table 1). Tep 58A (1,799 kg/ha) and G40001 (1,732 kg/ha) produced the highest seed yields over two years. Several tepary bean lines yielded well despite having large numbers of plants expressing BGYMV symptoms. Tep 54, Tep 64 and Tep 101 had among the lowest % plants with BGYMV symptoms both years. BGYMV can cause seed damage in susceptible common bean plants. The tepary beans were harvested under dry conditions and the overall % damaged seed was low. Several lines, including Tep 58A and G40001, had < 3% damaged seed both years. When harvested under humid conditions, the prostrate habit of tepary beans can result in seed damage. All the tepary lines were infected with powdery mildew. This disease can cause early defoliation and seed yield loss when levels of infection are high. Powdery mildew symptoms appeared both years later in the growing season and premature defoliation was not significant. Tep 93 and Tep 213 had the lowest overall % plants with powdery mildew symptoms. The 2019 planting was more stressful which resulted in lower mean seed yields and 100 seed weights. Tep 97 had the greatest 100 seed weight in both the 2018 planting (17.4 g) and the 2019 planting (14.9 g). Tep 51, Tep 97, Tep 100, Tep 104 had mean 100 seed weights > 15 g in the 2018 and > 13 g in the 2019 plantings. The study demonstrated that some of the tepary bean lines have the capacity to produce good yields of high-quality seed in spite of having large numbers of plants expressing BGYMV and powdery mildew symptoms. Common bean cultivars susceptible to BGYMV in neighboring field trials had much lower seed yields than the most promising tepary beans in this study. Introgression of greater tolerance to BGYMV from tepary to common bean would help to broaden resistance to this important viral disease.

Table 1. Performance of tepary bean lines planted in December 2018 and 2019 in field trials planted at the Arroyo Loro Research Station in San Juan de la Maguana, Dominican Republic.

Genotype	Seed type	Seed yield (kg/ha)			BGYMV (%)		Damaged seed (%)		Powdery mildew (%)		Hundred seed weight (g)	
		2018	2019	Mean	2018	2019	2018	2019	2018	2019	2018	2019
G40001	white	2086	1377	1732	36.3	30.0	2.5	1.8	38.9	27.8	13.7	10.9
Sacaton white	white	1340	941	1141	37.5	28.8	2.8	2.3	33.3	47.2	13.1	10.2
TARS Tep 22	white	1353	1307	1330	28.8	17.5	1.8	1.4	38.9	38.9	14.6	12.5
Tep 51	white	1685	1456	1571	35.0	18.8	4.5	2.5	61.2	38.9	15.8	13.3
Tep 54	white	1663	966	1315	20.0	12.5	2.4	0.7	50.0	41.7	15.4	11.9
Tep 58A	white	2161	1437	1799	27.5	15.0	1.9	2.6	38.9	27.8	14.2	12.7
Tep 64	white	1515	1415	1465	20.0	11.3	4.4	1.7	61.2	27.8	15.2	12.8
Tep 77	white	1374	1231	1303	25.0	10.0	3.1	1.5	44.5	47.2	13.9	11.6
Tep 90	black	980	915	948	30.0	27.5	2.0	1.0	66.7	63.9	17.2	12.6
Tep 93	speckled	1694	1200	1447	40.0	40.0	0.5	3.4	27.8	33.3	14.7	12.3
Tep 94	cream	1408	1050	1229	32.5	18.8	3.9	1.7	55.6	30.6	15.2	11.3
Tep 95	white	1364	1065	1215	36.3	18.8	1.8	0.9	38.9	36.1	14.2	10.5
Tep 96	black spotted	1392	1049	1221	28.8	20.0	0.5	0.6	44.5	30.6	14.2	11.6
Tep 97	black spotted	1272	1245	1259	31.3	31.3	0.9	1.9	55.6	33.3	17.4	14.9
Tep 100	speckled	1237	1102	1170	35.0	27.5	1.2	3.0	50.0	25.0	16.1	13.5
Tep 101	white	1639	1277	1458	17.5	17.5	1.8	2.5	50.0	38.9	17.0	13.5
Tep 102	striped	1343	1272	1308	22.5	16.3	2.4	2.6	77.8	58.3	13.0	10.2
Tep 103	speckled	1143	911	1027	33.8	41.3	2.1	3.1	44.4	27.8	14.6	13.1
Tep 104	Tan pinto	1317	1342	1330	28.8	23.8	3.8	4.7	61.2	30.6	15.6	13.5
Tep 213	mottled black	397	1102	750	47.5	33.8	4.6	3.4	33.3	25.0	12.8	11.8
Mean		1418	1183		30.7	23.0	2.4	2.2	48.6	36.5	14.9	12.2
LSD (0.05)		630	330		13.6	18.9	2.2	1.6	NS	15.5	1.0	1.5
CV (%)		21.2	19.7		21.2	58.0	43.4	54.6	27.5	30.1	3.4	8.5

INTROGRESSION OF DISEASE RESISTANCE INTO HEIRLOOM-TYPE DRY BEANS FOR HIGH VALUE REGIONAL FOOD SYSTEMS

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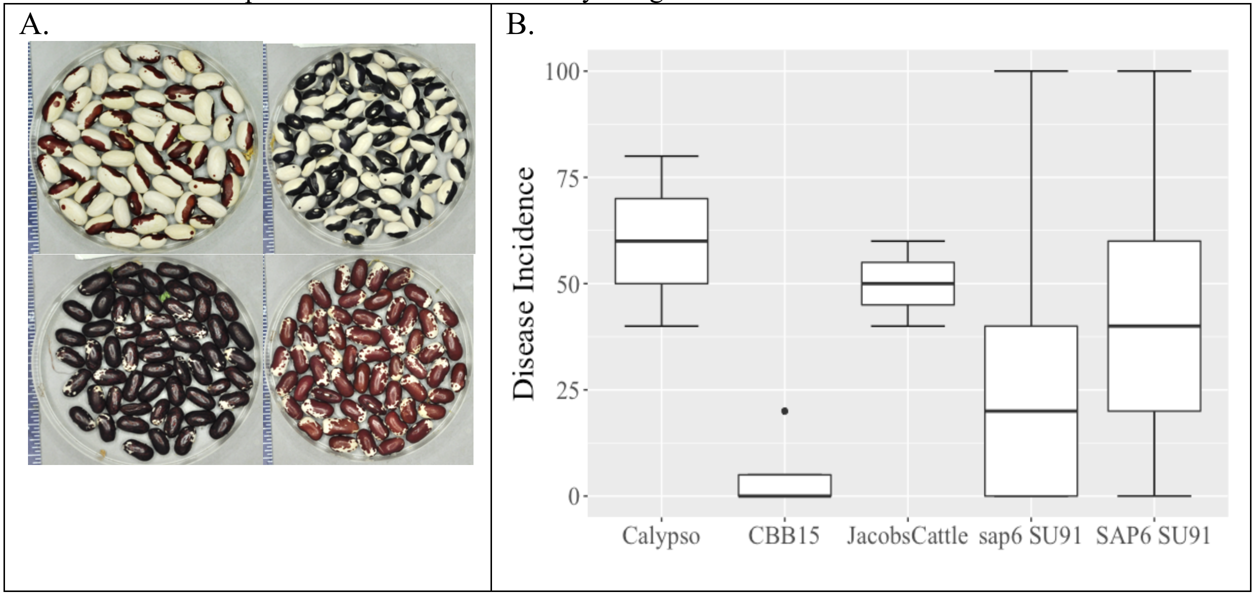
INTRODUCTION: In the Northeastern United States, consumers seek locally grown identity preserved dry beans. A partly colored seed coat pattern, characterized by white markings set on a solid or patterned background is not represented by any major commodity market class (Bassett and Mcclean, 2000). The goal of this breeding work was to develop lines with this novel partly seed coat pattern as well as favorable agronomic traits and resistance to BCMV and common bacterial blight, that would represent a unique product for high value bean production.

MATERIALS AND METHODS: Two heirloom parents were selected; 'Jacob's Cattle', likely t^{cf}/t^{cf} at the *T* locus. and 'Calypso', likely to be *t/t* (Bassett and Mcclean, 2000). They both exhibit type I determinate growth habit and are likely race Nueva Granada (Singh, Gepts, and Debouck, 1991). Each was crossed to the breeding line 'USDK-CBB-15', a dark red kidney developed by Dr. Phillip Miklas of USDA-ARS, which possesses the *I* gene for hypersensitive resistance to BCMV, the *SAP6* and *SU91* loci for partial resistance to common bacterial blight (P. N. Miklas et al., 2006). F_2 plants were screened for the *SU91*, *SAP6* and *I* loci using a combination of dominant SCAR markers in the case of *SU91* and *SAP6* loci (Miklas et al., 2000; Pedraza Garcia et al., 1997) and a co-dominant CAPS marker for the *I* locus (Bello et al., 2014). Plants that had at least one resistance allele for two or more resistance loci were space-planted in the field and subsequently, only plants possessing the partly-colored phenotype (*t/t* or t^{cf}/t^{cf}*)* were advanced. F_3 plants were screened with co-dominant high-resolution melt (HRM) markers for *I*, *SAP6* and *SU91* loci ((Lobaton et al., 2018; Soler *et al.,* 2021) and parameters for advancement as in the F_2 were used. 34 $F_{3:4}$ families, planted in an augmented design with 2 replications and 4 blocks, were screened with markers using the same procedure as in the F_3 generation. Each $F_{3:4}$ family was rated on a whole-plot basis for maturity time, vigor, lodging and disease incidence under natural bacterial blight pressure. Where families were segregating for seed coat pattern, only individual plants with the partly colored phenotype were selected. Foliar disease incidence scores were grouped by bulked F_4 family genotype and a linear mixed model was fitted mixed linear model was fitted to the data using the lme4 package in R. Least-squares means for merged genotype values were calculated using the 'emmeans' function in the emmeans package (Bates et al., 2015). Tukey's Honestly Significant Difference (HSD) was performed using the 'cld' function in the multcomp package (Hothorn and Westfall, 2008) for pairwise comparisons between least squares means at the $\alpha=0.1$ significance level.

RESULTS: 17 $F_{3:4}$ families were observed to be homozygous recessive at the recessive T locus for partly colored seed coat and 13 of these were fixed at the I locus for hypersensitive resistance to BCMV. Eight families were either homozygous or heterozygous for all three disease resistance loci *I*, *SAP6*, and *SU91.* Three families were homozygous for resistance alleles at all four targeted loci. Under natural field bacterial blight pressure, $F_{3:4}$ families had a lower mean disease incidence scores than susceptible parent genotypes, though high variance was observed and these results were not significant at the 0.1 level. Resistance at the *SAP6* locus did not appear to confer additional resistance when compared to lines with resistance at the *SU91* locus only. This could indicate the presence of more virulent strains of *X. campestris* in the region, as *SAP6* only confers resistance to less virulent strains. In future generations, direct selection of families for resistance when uniformly inoculated with *X. campestris* in a greenhouse or field environment is needed, as is selection for yield and other agronomic traits.

Figure 1. A) Seed coat phenotypes of selected F4 families; B) Bacterial blight incidence of parent genotypes and bulked F4 families under natural field disease pressure. The dominant genotype indicates that one or more dominant alleles was present in the bulked F4 family at a given locus.



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HUITEL-143: IMPROVED COMMON BEAN VARIETY OF THE SAN FRANCISCANO NATIVE TYPE FOR THE CENTRAL REGION OF MEXICO

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INTRODUCTION

In Mexican communities part of the genetic diversity of common bean is preserved. In some communities there are local native genotypes that are preferred by consumers in the area because of their organoleptic characteristics; they are recognized by their characteristics colors that they associate with a special flavor.

In the bean program of the Valle de Mexico Experimental Field (CEVAMEX), INIFAP, an objective for common bean improvement has been started to maintain local commercial types, incorporating disease resistance and thus higher yields, and protein content. This is the case with the bean called San Franciscano from the Valle del Mezquital area, in the state of Hidalgo, which is the preferred common bean in the region, however it presents susceptibility to anthracnose, *Colletotrichum lindemuthianum* (Sacc & Magn.) Briosi & Cav. and common bean blight, *Xanthomonas axonopodis* pv. *phaseoli* (Xap) (Smith)., which affects the yield. Its protein content is less than 23%.

The objective of this study was the development of a variety that incorporates anthracnose and common bean blight resistance, and a higher protein content while maintaining San Franciscano-type quality attributes for which is the preferential type in the area.

MATERIALS AND METHODS

'Huitel-143' was derived from a single-cross population that included the local native variety of the San Franciscano type, and Flor de Mayo M-38 as a disease resistant parent adapted to the Mexican highlands. The population was generated in CEVAMEX, in 2010. Pedigree selection combined with mass selection was used. During the first three years, the selection was made for diseases, mainly anthracnose, and common bean blight. In the next three cycles selection was for grain yield, adaptation and a San Franciscano-type seed coat. The selection criteria used in years 7 to 9 were grain yield, seed coat color, fast cooking time, high protein content, and resistance to common bean blight. Subsequently, we continued evaluating seed yield. In the selection process, the line was identified as CV10-143-3C-5C-0C-0C-0C, which was later named Huitel-143.

RESULTS

Agronomic features. Huitel-143 exhibits an indeterminate semi-prostrate growth habit (type III) with short vines and purple flowers; pods are medium-large containing 5 to 6 medium size grains. In the high valleys, it matures in 105 to 118 days. It is resistant to anthracnose, and common bacterial blight, is fast to cook and has a high protein content (>23%).

Adaptation and grain yield. Huitel-143 is a variety with wide adaptation in Valle del Mezquital, and reaches its maximum yield potential at locations with deep soils (clay loam) and with rainfall over 300 mm during its biological cycle. When assessed for three years (2015-2017) over one location; Huitel-143 average yield was 1,429 kg ha^{-1} and exceeded by over 23% the yield of the San Franciscano local native genotype. The highest yield reached by Huitel-143 was 1,772 kg ha^{-1} under rainfall conditions in 2017 at Huitel, Hgo.

Table 1. Commercial yield of common bean cv Huitel-143 and the local native genotype evaluated at Huitel, Hidalgo state from 2015 to 2017

	Yield (kg ha^{-1})	
Year	Huitel-143	Local Native San Franciscano genotype
2015	1,254	559
2016	1,260	1,009
2017	1,772	1,700
Average	1,429	1,089
Yield difference between Huitel-143 and the native San Franciscano genotype	-	-23.80%
Maximum	1,772	1,700
Minimum	1,254	559

Grain quality. Huitel-143 is an improved variety of the native local type for the central region of Mexico. The mean weight of 100 seeds of Huitel-143, is 30 g and the volume is 20.5 ml. This variety shows excellent capacity for water uptake, approximately 100% of its dry weight after 18 hours of soaking; its cooking time is short as well (70 min). Huitel-143 has higher protein content (24-25%) that is higher than the native genotype San Franciscano (22.5%).

Economic advantages. Huitel-143 is an excellent alternative to increase the economic income of common bean producers in the Valle del Mezquital area, in the state of Hidalgo. Because Huitel-143 it is a preferential grain, of San Franciscano type, it has a good price in the regional market.

In memoriam of M.Sc. Dagoberto Garza-García†, who passed away on November 28, 2020. Dago, as a member of the CEVAMEX Common bean Interdisciplinary Group, made important contributions for the improvement of common bean varieties for the High Valleys of the Central Plateau. Huitel-143 arose from the appreciation of the great genetic diversity that Mexico has in common bean, as well as the closeness and empathy with the farmers of the area who seek to preserve the materials they have inherited from their ancestors.

PERFORMANCE OF COMMON BEAN GENOTYPES IN VALUE FOR CULTIVATION AND USE (VCU) TRIALS

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INTRODUCTION

Common bean breeding programs seek to identify cultivars that meet both farmers' needs as well as consumer preferences. Such programs rely on the knowledge of region-specific problems and of issues that may arise during cultivation under different production systems and growing seasons. The introduction of new, more productive, and more resistant cultivars has led to higher yield and, thus, to a more efficient production process (Embrapa, 2019). The objective of this study was to perform superior grain lines using the REML/BLUP method for common bean traits of interest in Value for Cultivation and Use (VCU) trials carried out in Maringá, Paraná, Brazil.

MATERIALS AND METHODS

Eighteen genotypes, fourteen lines, and four common bean commercial cultivars (IPR Uirapuru, IPR Campos Gerais, BRS Esteio, and Pérola), were evaluated in the Centro Técnico de Irrigação (CTI) at Universidade Estadual de Maringá, Paraná, Brazil. The experimental design was a randomized complete block with three replications. Each experimental plot consisted of four 5.0 m lines, spaced at 0.5 m. The two central lines were evaluated, eliminating one meter from both ends. The genetic parameters were estimated using the statistical Model 21 (REML/BLUP) using the software Selegen (Resende, 2016), and the lines were selected based on the harmonic mean of the relative performance of the genetic values (HMRPGV).

RESULTS AND DISCUSSION

Selective accuracy values were classified as moderate to high with an average of 0.85, especially for grain yield and 100 seeds weight traits, for which magnitudes were 0.97 and 0.98. In addition, the heritability of the genotype mean was 0.93 and 0.96, respectively. High values of selective accuracy indicate high confidence in the evaluation and in the genetic value predicted for the individual. This reliability factor is a function of the coefficient of genotypic determination associated with the trait under evaluation, which corresponds to the coefficient of heritability, in an intra-population selection process (Resende and Duarte, 2007). In studies to predict genotypic values and estimate genetic parameters in common beans using the REML/BLUP methodology, Chiorato et al. (2008) estimated a heritability value of grain yield based on lines averaging 75% using REML/BLUP, which is lower than the estimate shown in the present study, which is 93%. The results revealed that BRS MG UAI, GEN 45-2F-293 P, TB 03-11, CHP 01-182-48, CNFC 15097, and LP 09-33 were superior (Table 1). Their new estimated average grain yields reach levels above 3,000 kg ha^{-1}. Based on that, these genotypes are the most promising to be released as new commercial cultivars indicated for use by growers in the Maringá area.

Table 1. Performance of the 18 common bean genotypes evaluated in the VCU assay for the prediction parameters of genotypic effects (g), genotypic values free of interaction (u + g), genetic gain, and new average (Kg ha^{-1}) for grain yield.

Order	Lines/Cultivar	g[1]	$u + g$[2]	Gain	New average
1	**BRS MG UAI**	**960.23**	**3,606.24**	**960.23**	**3,606.24**
2	**GEN 45-2F-293 P**	**407.48**	**3,053.49**	**683.86**	**3,329.86**
3	**TB 03-11**	**382.28**	**3,028.29**	**583.33**	**3,229.34**
4	IPR Uirapuru*	362.53	3,008.54	528.13	3,174.14
5	**CHP 01-182-48**	**355.89**	**3,001.90**	**493.68**	**3,139.69**
6	**CNFC 15097**	**262.31**	**2,908.32**	**455.12**	**3,101.13**
7	IPR Campos Gerais*	245.25	2,891.26	425.14	3,071.15
8	**LP 09-33**	**120.86**	**2,766.87**	**387.1**	**3,033.11**
9	BRS Esteio*	84.56	2,730.57	353.49	2,999.5
10	SM 03-12	12.08	2,658.09	319.35	2,965.36
11	LEC 02-16	-106.02	2,539.99	280.68	2,926.69
12	IAC Netuno	-159.68	2,486.32	243.98	2,889.99
13	Pérola*	-220.14	2,425.87	208.28	2,854.29
14	IPR Tangara	-244.68	2,401.33	175.93	2,821.93
15	LEC 01-16	-378.6	2,267.41	138.96	2,784.97
16	LP 11-117	-417.42	2,228.59	104.18	2,750.19
17	CHP 04-239-52	-780.54	1,865.47	52.14	2,698.15
18	TB 02-19	-886.39	1,759.62	0.00	2,646.01

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HIGH YIELDING COMMON BEAN IMPROVED LINES DERIVED FROM RECURRENT USE OF OUTSTANDING PARENTS IN CROSSING BLOCKS

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INTRODUCTION: Lines showing broad adaptability and higher yield potential have been selected to be used as parents in breeding programs in North-Central México. Selected germplasm includes landraces and improved cultivars derived from the Mesoamerican, Durango and Jalisco races. Some cultivars belonging to Nueva Granada race have also been included to improve the azufrado and peruano commercial classes. Using selected cultivars as parents in INIFAP´s breeding programs has resulted in the development of multiple improved common bean lines showing higher yield potential across production areas in México (Rosales et al., 2009). Other specific traits have also been improved including plant architecture, drought and disease resistance, seed size, slow seed coat darkening (pinto beans) and the accumulation of bioactive compounds in black seeded cultivars (Rosales et al., 2015). The objective was to identify cultivars for use as recurrent parents in common bean breeding programs.

MATERIALS AND METHODS: An observation nursery was sown at the Campo Experimental Valle del Guadiana in Durango, México. Common bean bred lines (420) were included for azufrado (37), flor de mayo (10), black (30) and pinto (343) seed commercial classes. Lines were sown at July 10th 2020, including a commercial control in each seed class, such as Azufrado Higuera, Flor de Mayo M38, Jamapa and Pinto Saltillo. Lines were sown in a single row, 5 m in length and 0.80 m apart. Fertilizer was mechanically incorporated at the rate of 35-50-00 (for N-P_2O_5-K_2O) and foliar fertilizer was also applied during the flowering period and pod set. Irrigation was applied one time in order to avoid severe water stress in plants and to obtain high expression of the seed yield potential. Insecticide (Dimethoate) was sprayed twice for the control of common bean pod weevil (*Apion* spp.). Data was registered for the number of days to flowering and maturity (days after sowing = DAS), disease reaction, yield and seed size (CIAT, 1987). At maturity, a sample was obtained in each line for seed yield determination. Plant sample consisted of one row, 4 m in length by 0.80 m in width (3.2 m^2). Plants in each field sample were threshed and seed cleaned and weighted for yield estimation and then a sub-sample was taken for seed size determination (100 seeds weight). Common parents were then identified in the genealogy of the high yielding lines selected in each seed class. Selection was performed according to high seed yield and seed size compared to the average in each commercial class, as well as precocious to intermediate maturity and high levels for disease resistance.

RESULTS AND DISCUSSION: Improved lines in pinto and azufrado groups showed precocious flowering (41 to 43 DAS) and maturity (96 to 97 DAS), which is an important trait related to adaptation in areas with short growing season. Flor de mayo (pink) and black seeded lines registered intermediate to full-season growth cycle, related to higher risk for terminal drought and freeze damage caused by low temperatures registered at the end of the growing season in the Mexican Highlands (Rosales *et al*., 2009). Absence of symptoms were observed for anthracnose and rust; but moderated (4) to generalized (6) symptoms were registered for common bacterial blight (CBB). Highest level for seed yield average was registered in pinto group (4201 kg/ha), showing fluctuation among 3117 kg/ha to 5966 kg/ha. Lowest yield average (3252 kg/ha) was obtained for the azufrado group due to its genetic origin and the recent start of genetic improvement program for this commercial class in North-Central México. Lower seed size was observed for some improved lines compared to the control, mainly in the azufrado group (Azufrado Higuera = 44.0 g/100 seeds *vs*. the improved lines 29.2 to 44.1 g/100 seeds). In the pinto class most of the improved lines overpassed the seed size of the control (Pinto Saltillo = 34.1 g/100 seeds) and the highest value was 47.5 g/100 seeds. Results suggests that significant advances have been obtained for seed yield and size in pinto common bean bred lines, mainly due to recurrent use of high yielding parents (Pinto Villa and Pinto Saltillo) combined with cultivars producing larger seeds (Pinto Centenario and Pinto Bayacora) in crossing blocks. Advances have also been observed in breeding lines with opaque black seeds showing low number of days to maturity, improved disease resistance, higher yield and acceptable seed size according to the market requirements (18 to 25 g/100 seeds). In the flor de mayo group, improved lines resulted similar to the commercial check (Flor de Mayo M38), due to selection restrictions imposed by the narrow genetic base and market requirements for seed size and coat color. Improved lines in azufrado group showed higher seed yield compared to the check (Azufrado Higuera), but seed size needs to be increased. Outstanding parents were Pinto Villa, Pinto Saltillo, Jamapa, and Pinto Centenario. Selection criteria are required for efficient breeding programs implemented in México in order to obtain bean cultivars with enhanced acceptance among producers, brokers, industrializers and consumers.

Table 1. Traits evaluated in common bean germplasm grown under irrigation in Durango, México.

Cultivar	**[1]DF**	**A**	**R**	**B**	**DPM**	**Seed Yield kg/ha**	**100 Seeds Weight (g)**
[2]PTVilla/PTSaltillo-48	41	1	1	5	97	5966	31.8
PT16031/PTCentenario-34	38	1	1	5	97	5604	36.9
Pinto Saltillo (Control)	43	1	1	5	99	4151	34.1
Group Average	**41**				**97**	**4201**	**37.9**
[2]NGO16028 (FrijoZacN101/NPNL//Jamapa/NPNL)	47	1	1	5	101	4927	24.5
NGO16039 (NPNL/N8025//NG Vizcaya/Méx 332)	45	1	1	5	98	4624	22.6
Jamapa (Control)	40	1	1	4	103	3050	17.9
Group Average	**46**				**99**	**3904**	**25.2**
[2]FM14002 (FMM38/FMayo1/2 Oreja-2)	48	1	1	4	103	4449	33.8
FM14011 (FMM38/FMayo1/2 Oreja-11)	46	1	1	4	100	4410	30.0
Flor de Mayo M38 (Control)	50	1	1	4	103	4574	25.4
Group Average	**48**				**101**	**3776**	**30.3**
[2]AZ17023 (L31-AZ16111-7)	41	1	1	6	93	4469	38.6
AZ17024 (L12-AZ16100-1)	42	1	1	6	95	3838	34.9
Azufrado Higuera (Control)	41	1	1	6	97	703	41.1
Group Average	**43**				**96**	**3252**	**37.5**

[1] DF = days to flowering; Reaction to A = anthracnose, R = rust, B = CBB, and DPM= days to physiological maturity.

CONCLUSIONS: Cultivars showing potential for use as recurrent parents in breeding programs were: Pinto Villa, Pinto Saltillo and Jamapa. Advances in common bean improvement have been restricted by selection for seed commercial appearance, plant archetype and cultivar growth cycle.

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MAPPING OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH YIELD COMPONENT AND ENVIRONMENT INTERACTIONS IN COMMON BEAN

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INTRODUCTION

Studies of quantitative traits are complex, especially when genotypes (G) are grown in different environments (E), due to the significant G × E interaction (Kearsey and Pooni, 1996). The objective of this study was to map quantitative trait loci (QTL) related to yield components in black common beans supported by QTL × E interaction.

MATERIALS AND METHODS

A total of 208 recombinant inbred lines (RILs) derived from the cross between Awauna UEM and IPR88 Uirapuru (AU) were evaluated in 2017, 2018, and 2019 at the experimental locations of the Universidade Estadual de Maringá, Paraná, Brazil. The experimental design was a triple lattice 15 × 15 and each experimental plot consisted of one line with 24 plants. The following traits were investigated: plant height (PH), first pod height (FPH), number of pods per plant (NPP), number of seeds per pod (NSP), seed mass (SM, mean dry mass of 100 seeds), and grain yield per plant (GYP). Analysis of variation and G × E interaction, between years, and for all years (All) were performed using linear mixed model of REML/BLUP in Selegen (Resende, 2016). The RILs and parental DNA samples were genotyped using the BARCBean6K_3 Illumina Bead Chip (5,398 SNPs) (Song et al., 2015). The BeadChip was imaged using the Illumina BeadArray Reader and automatic allele calling for each locus was performed using the Genome Studio software v2.0 (Illumina, San Diego, CA, USA). All allele calls were visually inspected and any errors in allele calling due to improper cluster identification were corrected resulting in 288 polymorphic SNPs. The QTL mapping was estimated using the software QTL IciMapping 4.2 (Meng et al., 2015) and QTLs were designated according to Miklas and Porch (2018).

RESULTS AND DISCUSSION

Analysis of variance showed significant differences across RILs and significant G × E interactions (α: 1 and 5%) for all evaluated traits, years, and combination of years. Therefore, it was necessary to adjust the phenotypic averages, and attenuating environmental effects that reduce the range of variation in the population that would restrict the detection of QTL. In addition, the new averages avoid any misunderstanding between environmental effects and QTLs, resulting in coherent values of estimated phenotypic variation explained (PVE) (Resende et al., 2008; Resende et al., 2012). A linkage map of 590.3 cM was created with an average density of 2.05 cM / marker. Six putative QTLs were mapped, one of them co-located for PH and FPH, and another co-located for PH, NPP, and GYP (Table 1), suggesting pleiotropic effects or linked genes (Haggard et al., 2015). QTLs $SM8^{AU}$ and $SM10^{AU}$ were found as putative, however, they present significant G × E and high contribution of additive effects (AA) in the total phenotypic variation explained (PVE).

Table 1. Significant QTL found in single environments

Trait	QTL	Agr. year	Chr.	Left marker	Righ marker	Range LOD	Range PVE
PH	PH4^{AU}	17;18	4	ss715649973	ss715647823	3.2 to 3.33	2.03 to 2.43
PH	PH1^{AU*}	19	1	ss715646884	ss715645259	3.47	8.88
NPP	NPP1 ^{AU}	19; All	1	ss715646884	ss715645259	3.7 to 4.72	9.6 to 10.13
FPH	FPH4 ^{AU}	17;18;19	4	ss715649973	ss715647823	3.32 to 3.79	2.0 to 2.69
SM	SM8^{AU}	17;18;19; All	8	ss715646109	ss715646101	7.75 to 12.58	8.27 to 14.25
	SM10^{AU}	18; All	10	ss715645516	ss715650584	2.96 to 3.02	2.76 to 2.95
GYP	GYP1^{AU}	19; All	1	ss715646884	ss715645259	2.97 to 2.98	6.78 to 7.87

*: designed in this study as non-putative; Agr. year: agricultural year; Chr: Chromosome.

In other words, the contribution of the environmental effect (AAbyE) in the PVE is substantially small (Tables 1 and 2). This result indicates a potential use of SM8^{AU} and SM10^{AU} to develop markers for marker-assisted selection (MAS).

Table 2. QTL with significant environmental interaction in multi-environments

QTL	Chr	Left marker	Right marker	LOD Score			PVE		
				Total	AA	AAbyE	Total	AA	AAbyE
SM8^{AU}	8	ss715646109	ss715646101	37.41	33.86	3.55	12.1	11.49	0.61
SM10^{AU}	10	ss715645516	ss715650584	7.27	6.09	1.19	2.29	1.77	0.51
PH1^{AU}	1	ss715646884	ss715645259	4.58	2.55	2.03	3.12	2.59	0.54

In summary, the majority of putative QTL had their total PVE relatively lower than the respective heritability ($\widehat{h^2}$) of the evaluated traits (data not shown). This suggests that phenotypic performance may be affected by Epistatic QTL (E-QTL) or by the QTL × E interaction (Wang *et al*., 2012). The PH1^{AU} reported in Tables 1 to 3 presents PVE lower than its $\widehat{h^2}$, indicating that its phenotypic performance is affected by the QTL × E interaction (Table 2). However, the epistatic effects stood out from the environmental effect, since additive effects (AA) effects have a greater weight in total PVE (Table 3), suggesting that, in this case, epistasis is a more influential genetic factor than environmental interactions.

Table 3. Significant digenic epistatic QTLs in multi-environments

Scanning position for digenic epistatic QTL					LOD Score			PVE		
QTL	Chr	Scan	Left marker	Right marker	Total	AA	AAbyE	Total	AA	AAbyE
PH1^{AU}	1	1st	ss715646884	ss715645259	9.05	5.26	3.8	4.06	2.71	1.35
PH11^{AU}	11	2nd	ss715647468	ss715649886						

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PROMISING LINES OF COMMON BEAN BASED ON ADAPTABILITY AND YIELD STABILITY

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INTRODUCTION

Common beans are grown in different environments under very heterogeneous conditions. Consequently, the objective of common bean breeding programs is to develop productive and widely adaptable cultivars. Therefore, the use of refined statistical models such as the Restricted Maximum Likelihood / Best Linear Unbiased Prediction (REML/BLUP) is a tool widely used by breeders to identify promising lines (Ramalho and Araújo, 2011). The objective of this study was to identify superior elite lines of common beans in relation to adaptability and stability of grain yield via mixed models.

MATERIALS AND METHODS

Fourteen elite lines and four commercial common bean cultivars (Pérola, IPR Sabiá, IPR Uirapuru, and BRS Esteio) were evaluated under field conditions in 17 environments in Paraná State, Brazil. The experiments were carried out in Maringá (Northern), Santa Tereza do Oeste (Western), Dois Vizinhos (Southeastern), Guarapuava (Mid-South), and Ponta Grossa (Southern) regions of Paraná state, during the summer seasons of 2018/19 and 2019/20, and in the autumn-winter seasons of the years 2019 and 2020. The experimental design was based on a completely randomized block with three replications. The genetic parameters were estimated by REML/BLUP, and the significance of the estimated effects were estimated via deviance analysis. The lines were selected based on the harmonic mean of the relative performance of the genetic values (HMRPGV). Adaptability and stability were analyzed using the statistical Model 54 (REML/BLUP) and the Selegen software (Resende, 2016).

RESULTS AND DISCUSSION

Deviance analysis showed a significant effect of grain yield, indicating that lines exhibit genetic variability and that they perform differently across environments. The heritability of the genotype mean ($\hat{h}^2_{mc}$) showed a high value of 0.86. Similarly, the precision value (Acgen) was 93%, which is a high index according to Resende and Duarte (2007). Thus, these values show success in the selection of common bean lines based on the predicted genotypic values (Santos et al., 2018). The genotypes that exhibited high grain yield and wide production stability (u+g) were IPR Sabiá, LP 13-84, CHP 01-182-12, LP 13-624, and CHP 04-239-0 (Table 1). Furthermore, the results showed that these same lines were classified as more stable and adaptable (HMRPGV), with grain yields 1.09 and 1.08 times higher than the overall average (Table 1). In conclusion, these four lines can be considered promising cultivars and can be recommended to Parana growers for commercial purposes.

Table 1. Performance of 14 common bean elite lines and four cultivars for genotypic effect, adaptability, and stability of grain yield (Kg ha^{-1}) evaluated in 17 environments in Paraná State, Brazil

Order	Lines/Cultivars	u+g[1]	HMRPGV[2]	HMRPGV*GM[3]
1	IPR SABIÁ	3,004.57	1.11	3,041.55
2	**LP 13-84**	**2,991.87**	**1.09**	**2,997.62**
3	**CHP 01-182-12**	**2,970.91**	**1.09**	**2,988.13**
4	**LP 13-624**	**2,950.71**	**1.08**	**2,969.21**
5	**CHP 04-239-01**	**2,942.25**	**1.08**	**2,960.05**
6	IPR UIRAPURU	2,934.40	1.06	2,912.01
7	BRS ESTEIO	2,896.81	1.05	2,885.65
8	IAC Linhagem 110	2,846.07	1.04	2,854.79
9	PÉROLA	2,814.56	1.02	2,804.50
10	FAP-F3-2 SEL	2,806.04	1.02	2,794.83
11	TB 17-03	2,755.94	0.99	2,732.35
12	SM 1510	2,749.08	0.99	2,718.67
13	TB 17-02	2,615.15	0.94	2,583.93
14	LEC 04-16	2,551.90	0.89	2,461.26
15	SM 0511	2,516.44	0.89	2,439.12
16	CNFRs 15558	2,459.61	0.84	2,320.41
17	UEM 266	2,303.40	0.80	2,212.21
18	CNFRj 15411	2,186.57	0.68	1,878.43

[1] Genotypic effect, [2] Harmonic Mean of the Relative Performance of the Genetic Values; [3] HMRPGV * global mean. Global mean: 2,738.70 Kg ha^{-1}.

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AGRONOMIC EVALUATION AND SEED YIELD OF IMPROVED COMMON BEAN CULTIVARS SOWN IN DURANGO, MÉXICO

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INTRODUCTION: The state of Durango is a leader in the generation of common bean cultivars with high productivity, consumer preference and commercial impact in México (Rosales et al., 2019). Common bean is the most important plant-based food product in Durango, which contributes to the family economy and social welfare. The main factors limiting common bean productivity include water scarcity, soil erosion and low soil fertility, as well as plant diseases, pests and weeds. This plant species needs to be incorporated into production programs under irrigated conditions in order to ensure the domestic supply in Durango (20,000 t/year) and additionally, contributions for productive sustainability will also be achieved. New improved common bean cultivars with pinto and black grains were generated, showing adaptation under irrigation conditions. Two cultivars released in 2020 were named PID 1 and NOD 1. PID 1 is a pinto bean cultivar flowering 44 days after sowing (DAS), resistant to anthracnose and rust, matures at 98 DAS, yields 2.7 t/ha under irrigation and has medium to large seed size (35-43 g/100 seeds) (Rosales et al., 2020a). NOD 1 has opaque black seeds, flowers at 50 DAS, is resistant to anthracnose and rust, matures at 105 DAS, and has an average yield of 3.0 t/ha under irrigation and the seed size is small to medium (18-28 g/100 seeds) (Rosales et al., 2020b). Improved bean varieties need to be evaluated in commercial plots to determine yield, commercial acceptance and consumption preferences. The objective was to evaluate agronomic adaptation and yield performance of two improved cultivars in commercial plots established at different sites in Durango, México.

MATERIALS AND METHODS: Two improved cultivars (PID 1 and NOD 1) were sown in three commercial plots established under irrigation in Durango (2) and La Soledad (1), in the state of Durango, México. Cultivars and commercial checks (Pinto Saltillo and Negro San Luis) were sown from July 10th to July 13th 2020, in one commercial plot (1 ha) per site, with rows 100 m in length and 0.80 m apart. Fertilizer was incorporated into the soil during first mechanical cultivation at the rate of 35-50-00 (N-P_2O_5-K_2O). Irrigation and insecticide (Dimethoate) were applied one to three times in order to avoid severe water stress in plants and to control the bean beetle (*Epilachna varivestis*) and the bean pod weevil (*Apion* spp.). At maturity, five to six plant samples were taken per cultivar for seed yield determinations. Plant samples consisted of two rows, 5 m in length, by 0.80 m in width (8.0 m^2). Plants obtained in each field sample were threshed and the seeds cleaned and weighed for yield estimation, and then a sub-sample was taken for seed size determination (100 seed weight). For each location, the analysis of variance was obtained using a completely randomized design with five to six replications. When statistically significant differences were observed, means comparisons were performed using Tukey's test ($p \leq 0.05$). For the analysis of variance and means comparison the SAS ver. 9.4® computer program was used.

RESULTS AND DISCUSSION: The days to flowering were lower in the pinto bean cultivars (39-44 DAS), compared to NOD 1 (44-47 DAS) (Table 1). In the Durango 2 site, doubtful symptoms (2) were observed for the incidence of anthracnose and in La Soledad for rust in both pinto cultivars. Across locations, all cultivars showed intermediate (5) to generalized (6) symptoms for the incidence of common bacterial blight (CBB), which is the most frequent disease in Durango. Early to intermediate maturity was registered in pinto beans (94-97 DDS) compared to black beans (100-108 DAS), showing intermediate to full-season life cycle. In the Durango 1 plot, seed yield was similar between cultivars, reaching 3,003 kg/ha in PID 1, followed by NOD 1 and Pinto Saltillo. Pinto Saltillo seed yield (2,883 kg/ha) was statistically similar to PID 1 and both exceeded NOD 1 at the Durango 2 site. In La Soledad, higher yield values were observed in the NOD 1 cultivar (1,421 kg/ha) and Negro San Luis (1,194 kg/ha), both exceeding the pinto improved cultivars (720 to 964 kg/ha). The low yields observed at this location were due to limited access to irrigation water, low precipitation levels (193 mm) and irregular rainfall. In all the plots, it was observed that at least one improved cultivar suprassed the average yield of common bean, under irrigation conditions, reported for Durango from 2015 to 2019 (1,382 kg/ha). Seed weight was reduced 4 g/100 seeds in PID 1 across sites but exceeded Pinto Saltillo in all the plots. NOD 1 produced seeds of acceptable size for its commercial class (Jamapa) (18-25 g/100 seeds).The genetic improvement of common bean in irrigated areas and the adoption of improved cultivars will contribute to a significant increment in seed yield and production stabilization, also reducing the use of water. Bean is a useful plant species under irrigation and its cultivation increases yield, reduces irrigation (compared to corn) and increases the economic benefits for the farmer.

Table 1. Traits evaluated in common bean improved cultivars grown under irrigation in Durango, México.

Cultivar	DF	A	R	B	DPM	Yield (kg/ha)	100 Seeds Weight (g)
						Durango 1	
PID 1	41	1	1	6	97	3003	36.8^{a}
NOD 1	44	1	1	5	102	2952	23.2^{c}
Pinto Saltillo	42	1	1	6	97	2829	33.2^{b}
						Durango 2	
Pinto Saltillo (t)	41	2	1	6	97	2883^{a}	30.9^{b}
PID 1	40	2	1	6	94	2873^{a}	35.4^{a}
NOD 1	47	1	1	5	102	2084^{b}	19.1^{d}
Negro San Luis (t)	49	2	1	5	108	1891^{b}	27.3^{c}
						La Soledad	
NOD 1	46	1	1	6	100	1421^{a}	22.7^{c}
Negro San Luis	52	1	1	6	108	1194^{ab}	25.9^{c}
Pinto Saltillo	39	1	2	5	94	976^{bc}	29.1^{b}
PID 1	44	1	2	5	94	729^{c}	32.4^{a}

DF = days to first flower; reaction to A = anthracnose, R = rust, and B = common bacterial blight; DPM = days to physiological maturity.

CONCLUSIONS: Agronomic and yield performance observed in PID 1 reinforced its utility to improve disease resistance and seed quality compared to Pinto Saltillo. NOD 1 showed low days to maturity, improved seed quality and similar yield to Negro San Luis. Traits observed in PID 1 and NOD 1 could be used to encourage cultivar adoption in the Highlands of México.

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YIELD PERFORMANCE AND MARKET PREFERENCE FOR IMPROVED COMMON BEAN CULTIVARS DEVELOPED IN DURANGO, MÉXICO

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INTRODUCTION: PID 1 and NOD 1 improved common bean cultivars were released in 2020 mainly for irrigated areas in the state of Durango, México. Since 2010, difficulties were observed for cultivar adoption by producers, mainly due to the high level of preference observed for Pinto Saltillo. The objective was to evaluate preference, yield and agronomic performance of improved common bean cultivars in a commercial plot established in the state of Durango, México.

MATERIALS AND METHODS: A plot was established in the state of Durango at La Soledad, in the Canatlán municipality. Cultivars were sown on July 13th 2020, in a plot of a cooperating producer (Carlos Olguín Chávez) and a group of 25 local farmers, showing interest for new common bean cultivars. Four cultivars were sown (Pinto Saltillo, PID 1, NOD 1 and Negro San Luis) in a 1 ha plot. A survey was carried out before sowing (seed preference) and other during the seed filling period (plant archetype). In the grain preference survey, all varieties were presented to the producers in seed samples, packed in open 10 kg clear polypropylene sacks. The characteristic evaluated was the commercial appearance of the grains, visually qualified. After this first survey, cultivars were sown in strips, consisting of 24 to 40 rows, 100 m in length and 0.80 m apart. A second survey was carried out under field conditions, during the seed filling period and producers expressed their opinion regarding the plant archetype, growth habit, pod load and pod distribution, visually qualified. In both surveys four categories were used: 1= the best, 2= middling good, 3= middling bad, and 4 = the worst. Fertilizer was mechanically incorporated at the rate of 35-50-00 (for N-P_2O_5-K_2O) and foliar fertilizer was also sprayed during the flowering period and pod set. Light irrigation was applied three times to avoid severe water stress in plants. Insecticide (Dimethoate) was sprayed twice for the control of common bean pod weevil (*Apion* spp.). Data were taken for days to flowering, physiological maturity and disease resistance (CIAT, 1987). At maturity, six plant samples were harvested in each cultivar for seed yield determination. Plant samples consisted of two rows, 5 m in length by 0.80 m in width (8.0 m^2). Plants in each field sample were threshed and the seed cleaned and weighed for yield estimation and then a sub-sample was taken for seed size evaluation (100 seeds weight). The analysis of variance was obtained under a completely randomized design with six replications and mean comparisons were performed using Tukey's test ($p \leq 0.05$), in both cases using the SAS ver. 9.4® computer program.

RESULTS AND DISCUSSION: The highest level for seed preference was registered for Pinto Saltillo (13 producers = 52 %), followed by PID 1 (11 producers = 44 %). In contrast NOD 1 registered the lowest preference level (19 producers = 76 %) and was considered as the worst on the basis of seed market quality (Figure 1a). Results were related to high preference for production and consume of pinto bean seeds (mainly Pinto Saltillo) in most of the productive and consume areas of the state of Durango. Recent release of the cultivar NOD 1 was related to the low acceptance of its opaque black seeds by local producers. Under field conditions different response was observed and the NOD 1 cultivar was considered as the best by most of the producers (15 producers = 60 %) based on its erect plant archetype, growth habit, pod load and pod distribution (Figure 1b). Significant differences ($p \leq 0.05$) were observed among cultivars for seed yield and seed size (Table 1). Pinto Saltillo showed precocious flowering (39 days after sowing; DAS), while Negro San Luis was considered as a late flowering (52 DAS) cultivar. Symptoms were ausent (1) for anthracnose in all the cultivars, doubtful for rust (2) in both pinto cultivars and intermediate (5) to generalizated (6) for common bacterial blight in all the cultivars. Pinto seeded cultivars also showed precocious/intermediate maturity (94 DAS), compared to black seeded varieties (100 to 108 DAS). The cultivar NOD 1 reached the highest yield value (1421 kg/ha), which was consistent with the producer´s preference for pod load under field conditions. The PID 1 cultivar (32.4 g/100 seeds) showed the highest seed weight and resulted preferent over the rest of the cultivars, due to the market demand for large (36 to 45 g/100 seeds) pinto grains. Phenology, plant archetype, pod load, yield and seed size were considered as important selection criteria for genetic improvement in common beans with enhanced commercial quality and acceptance among producers, brokers, industrializers and consumers.

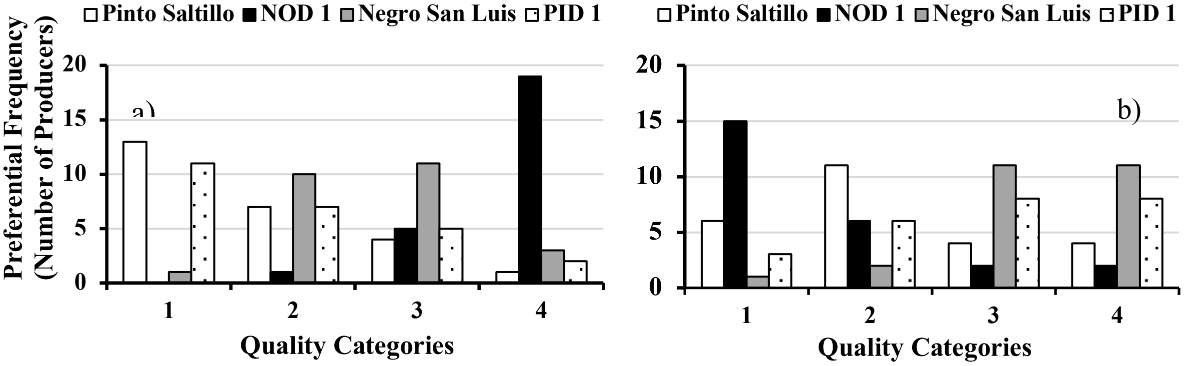

Figure 1. Seed (a) and plant (b) preferential quality in four common bean cultivars sown at La Soledad, Dgo., México. (n= 25). 1= the best, 2= middling good, 3= middling bad and 4= the worst.

Table 1. Traits evaluated in common bean cultivars grown under irrigation in La Soledad, Dgo., México.

Cultivar	[1]DF	A	R	B	DPM	Seed Yield kg/ha	100 Seed Weight (g)
NOD 1	46	1	1	6	100	1421^{a}	22.7^{c}
Negro San Luis	52	1	1	6	108	1194^{ab}	25.9^{c}
Pinto Saltillo	39	1	2	5	94	976^{bc}	29.1^{b}
PID 1	44	1	2	5	94	729^{c}	32.4^{a}
Mean	**45**				**99**	**1080**	**27.5**
Coefficient of Variation (%)						19.8	4.9

[1]DF= days to flowering; Reaction to A= anthracnose, R= rust, B= common bacterial blight, DPM= days to physiological maturity. [a-c]Different letters indicate significant differences among cultivars according to Tukey's test ($p \leq 0.05$).

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2020 FINANCIAL STATEMENT
BEAN IMPROVEMENT COOPERATIVE

BALANCE AS OF January 1, 2020			**$ 30,017.00**

INCOME

2020 and 2021 Dues	$	5,280.00	
Tom Grebb Memorial Fund	$	4,000.00	
Bank Interest	$	0	
TOTAL INCOME	$	9,280.00	

EXPENSES

Labor charges	$	0	
Postage, Copy Charges and Office Supplies	$	28.60	
Pdf & Book editing and publishing fees	$	680.90	
PayPal Fees	$	129.86	
Bank Fees	$	48.00	
TOTAL EXPENSE	$	887.36	

BALANCE AS OF December 31, 2020			**$ 38,409.64**