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ANNUAL REPORT OF THE
BEAN IMPROVEMENT
COOPERATIVE



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

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Cover Image: Dry bean seed production field near Twin Falls, Idaho. Photo taken by Joyana Baumann, NDSU Foundation Seedstocks.

TABLE OF CONTENTS

LXIX Annual Report of the Bean Improvement Cooperative	xii
BIC Coordinating Committee Membership - 1957 to 2025	xiii
2025 BIC Award Recipients.....	xviii
Past Award Recipients.....	xxv
BIC Genetics Committee Minutes	xxix

RESEARCH PAPERS FOR 2026

ORAL PRESENTATIONS (2025 BIC MEETING)

GENETIC IMPROVEMENT OF NAVY BEAN CULTIVARS RELEASED IN SOUTHWESTERN ONTARIO BETWEEN 1940 -2011	1
Alireza Navabi ¹ , Andrew J. Burt ² , Chris Gillard ² , Manilal William ² , K. Peter Pauls ²	
ROOT ARCHITECTURE, SEED SIZE, AND SEEDLING ESTABLISHMENT IN WILD ANDEAN AND MIDDLE AMERICAN BEAN ACCESSIONS	3
Paige Smith ¹ ; Viviana Ortiz Londoño ² , Miranda J. Haus ²	
HIGH-THROUGHPUT SCREENING APPROACH TO ENHANCE SYMBIOTIC NITROGEN FIXATION IN DRY BEANS.....	5
Deevita Srivastava ² , Casey Nichols ¹ , Erica Maul ¹ and Mia Haugan ¹ , Juan M. Osorno ² , Barney A. Geddes ¹	
PROJECT LIMA!: DEVELOPMENT OF RESOURCES TO ACCELERATE LIMA BEAN BREEDING FOR AGRONOMIC AND QUALITY TRAITS	7
Travis Parker ¹ , Jaclyn Adaskaveg ¹ , Sarah Dohle ² , Stephanie English ³ , Emmalea Ernest ⁴ , Andrew Farmer ³ , Jean-Xavier Guinard ⁵ , Michelle Heer ⁶ , Jenna Hershberger ⁷ , Bao-Lam Huynh ⁸ , Diego Jarquin ⁹ , Yukina Murata ⁵ , Antonia Palkovic ¹ , Varma Penmetsa ¹ , Francis Reith ⁴ , Phil Roberts ⁸ , Sangita Subedi ⁷ , Marilyn Warburton ² , Donna Winham ⁶ , Christine Diepenbrock ¹ , Paul Gepts ¹	
GENOTYPIC AND MULTI-ENVIRONMENT PHENOTYPIC EVALUATION OF THE LIMA USDA NPGS COLLECTION.....	9
Jaclyn Adaskaveg ¹ , Andrew Farmer ² , Jenna Hershberger ³ , R.Varma Penmetsa ¹ , Ivan Garcia- Lopez ¹ , Emmalea Ernest ⁴ , Julian Garcia-Abadillo ⁵ , Xiangming Zhou ⁵ , Diego Jarquin ⁵ , Sarah Dohle ⁶ , Antonia Palkovic ¹ , Travis Parker ¹ , Christine Diepenbrock ¹ , Paul Gepts ¹	
EVALUATING A COMMON BEAN/TEPARY BEAN INTERSPECIFIC POPULATION FOR AGRONOMIC AND QUALITY TRAITS	11
Sassoum Lo ^{1#*} , Jonathan M. Berlinger ^{1#} , Margaret Riggs ¹ , Santos Barrera-Lemus ^{2†} , Earl Ranario ³ , Heesup Yun ³ , Lars Lundqvist ³ , Astrid Lao ¹ , Anisha Yodtare ⁴ , Milton Valencia-	

Ortiz⁴, Kesevan Veloo⁴, Jesus Linares⁵, Travis Parker¹, Paul Gepts¹, Sindhuja Sankaran⁴,
 Antonia Palkovic¹, Karen Cichy⁶, Timothy Porch⁷, Philip Miklas⁸, Carlos Urrea², Brian
 Bailey¹, J. Mason Earles³, Christine Diepenbrock¹

SENTINEL TRIALS FOR ON-FARM BEAN DISEASE ASSESSMENT: A STRATEGIC TOOL
 TO GUIDE BREEDING FOR SMALLHOLDER AGRICULTURE 13

E. Espitia¹, F. Kato², P. Paparu³, C. Mukankusi², A. Nkuboye³, G. Mosquera^{1*}

USE OF TWO GENOMIC APPROACHES TO IDENTIFY QTLs FOR COMMON
 BACTERIAL BLIGHT RESISTANCE IN PHASEOLUS VULGARIS L. CRANBERRY
 MARKET CLASS 15

Gaiti A. 1, Kúhn L. , Fourie D. , Miklas PN. , Ferreira JJ., Campa A., Avite E., Pasquali M.
 1, Pozzi CM. 6

HIGH THROUGHPUT PHENOTYPING OF BRUCHIDS RESISTANCE IN A BEAN
 ANDEAN DIVERSITY PANEL -CASE *ZABROTES SUBFASCIATUS*..... 17

María Isabel Gómez-Jiménez¹, Hector Fabio Buendía¹, Cristian Tirado¹, José Polania¹,
 Stephen Beebe¹, Jennifer Wilker¹

PINPOINTING CANDIDATE GENES IN A QUANTITATIVE TRAIT LOCUS ASSOCIATED
 WITH RESISTANCE TO BACTERIAL BROWN SPOT IN ADZUKI BEANS..... 19

Omorieg UE, Wally, Pauls, KP

GENOMIC INSIGHTS INTO IRON AND ZINC BIOFORTIFICATION IN COMMON BEAN:
 LEVERAGING CROP WILD RELATIVES AND INTROGRESSION MAPPING..... 21

S. Diaz, S. Cruz, J. Lobaton, D. Duarte, S. Beebe, J. Wilker

A FRAMEWORK FOR GENOMIC SELECTION IN DRY BEAN BREEDING: FROM GBS
 TO SNP CHIP DEVELOPMENT..... 23

Jose C. Figueroa-Cerna¹, Nusrat Khan¹, Phillip E. McClean¹, Rian Lee¹, Jayanta Roy¹, Juan
 M¹. Osorno

DEVELOPING PROTEIN-RICH DRY BEANS (*PHASEOLUS VULGARIS* L.) THROUGH
 GENOMIC PREDICTION 25

Carly J. George¹, Jose Figueroa-Cerna¹, Nusrat Khan¹, Phillip E. McClean¹, Juan M.
 Osorno¹

GENETIC MAPPING, PROXIMAL SENSING, AND CROP MODELING OF NUTRITIONAL
 AND AGRONOMIC TRAITS IN A COWPEA MAGIC POPULATION ACROSS THREE
 CALIFORNIAN ENVIRONMENTS 27

Jonathan M. Berlinger^{1#*}, Sassoum Lo^{1#}, Ismael Mayanja², Isaac Kazuo Uyehara¹, Hamid
 Kamangir², Margaret Riggs¹, Astrid Lao¹, Antonia Palkovic¹, Bao-Lam Huynh³, Brian Bailey¹, J.
 Mason Earles², Christine Diepenbrock¹

HIGH-THROUGHPUT PHENOTYPING AND DEEP LEARNING FOR POD-BASED YIELD PREDICTION AND RUST SCREENING IN DRY BEANS 29

Maria Roberta de Oliveira¹, Juan M. Osorno¹, Jithin Mathew², Anup Das², Christian Perdigon², Paulo Flores²

EVALUATION OF MULTIPLE BOTRYTIS SPECIES CAUSING CHOCOLATE SPOT ON FABIA BEAN (*VICIA FABIA*) IN THE MID-ATLANTIC AND FUNGICIDE MANAGEMENT OPTIONS..... 31

Marian Grskovich, Dr. Douglas Higgins

GENOME-WIDE ASSOCIATION STUDY TO IDENTIFY GENOMIC REGIONS ASSOCIATED WITH RESISTANCE TO SOYBEAN CYST NEMATODE HG TYPE 2.5.7 IN DRY BEANS 33

Dalvir Singh¹, Prabhat Poudyal¹, Gurminder Singh¹, Rekha Neupane¹, Jose Figueroa-Cerna², Juan M. Osorno², Guiping Yan¹

VALIDATION OF MOLECULAR MARKERS FOR APHANOMYCES ROOT ROT RESISTANCE IN COMMON BEAN (*PHASEOLUS VULGARIS* L.) 35

Rebecca O. Arias¹, Ken Kmiecik², Douglas Rouse², Mikah Fowler², Shelby Ellison¹

MARKER-ASSISTED BACKCROSSING TO INTRODUCE THE NON-DARKENING TRAIT INTO CRANBERRY BEAN (*PHASEOLUS VULGARIS*) VARIETIES 37

Sajida Noor, K. Peter Pauls

REACTION OF COMMON BEAN CULTIVARS AND BREEDING LINES TO ROOT ROT CAUSED BY *FUSARIUM OXYSPORUM* F. SP. *PHASEOLI* 39

Isabella Mendonça Arruda¹; Vania Moda-Cirino¹

IRON NUTRITION FROM GREAT NORTHERN BEANS: THE ABSENCE OF FLAVONOIDS AND EFFECTS OF CANNING..... 41

Raymond Glahn¹, Jason Wiesinger¹, Karen Cichy², Phil Miklas³, Juan M. Osorno⁴, Carlos Urrea⁵

BREEDING POPPING BEANS FOR TEMPERATE U.S. PRODUCTION..... 43

James R. Myers¹, Emma Landgraver¹, Joel Davis¹, Shinji Kawai¹, Brigid Meints², James Heitholt³, Jill Keith⁴, Carol Miles⁵, Girish Ganjyal⁶, Mahvash Rezaey⁶, Alex Karasev⁷, Gardenia Orellana⁷, José Hernández⁸, and Karen Cichy⁹

INTRODUCING A WEB APP FOR DRY BEAN STAND COUNTING 45

Aliasghar Bazrafkan^{1*}, Valerio Hoyos Villegas¹

POSTER PRESENTATIONS (2025 BIC MEETING)

SELECTION OF LIMA BEAN (*PHASEOLUS LUNATUS*) GENOTYPES FOR TOLERANCE TO DROUGHT STRESS..... 47

Carlos German Muñoz Perea¹; Yolanda Potosi²; María Isabel Chacón Sanchez³

HEAT STRESS IN BEANS: REPRODUCTIVE RESILIENCE AND SINK STRENGTH AS KEYS TO YIELD STABILITY	49
Jorge Aragon ¹ ; Cristian Tirado ¹ ; Hector F. Buendia ¹ ; Jose Polania ^{1*} ; Jennifer Wilker ¹	
GENOME-WIDE SELECTION FOR DROUGHT TOLERANCE IN MESOAMERICAN BEAN GENOTYPES	51
Santos, Elizeu David ^{1,2} ; Arruda, Isabella Mendonça ¹ ; Santos Neto, José dos ¹ ; ALVES, Daniel Soares ¹ ; Gepts, Paul ³ ; Moda-Cirino, Vania ¹	
FOUR NEW LIMA BEAN RIL POPULATIONS FOR EXPLORING AGRONOMIC AND SEED APPEARANCE TRAITS.....	53
Emmalea Ernest ^{1*} , Francis Reith ¹ , Ekaterina Hampton ¹ , Christine Diepenbrock ² , Antonia Palkovic ² , Jaclyn Adaskeveg ² , Varma Penmetsa ² , Andrew Farmer ³ , Stephanie English ³ , Paul Gepts ²	
ASSESSING THE ROLE OF POLLEN RELEASE AND STIGMA EXSERTION IN LIMA BEAN YIELD.....	55
Ekaterina Hampton ¹ , Emmalea Ernest ¹ , Ashish Reddy Mulaka ² , Yin Bao ²	
PRESENCE OF NEW BEAN ANTHRACNOSE RACES IN NORTHERN SPAIN	57
A Campa, E Portilla*, M Suárez-Fernández, JJ Ferreira	
POPULATION DYNAMICS OF <i>MEGALUROTHRIPS USITATUS</i> IN COMMON BEAN IN GUATEMALA.....	59
Inelda Z. Tuj ¹ , Astrid J. Racancoj ¹ , Angela N. Miranda ¹ , Jose Figueroa-Cerna ²	
IDENTIFYING GENOMIC DIVERSITY AMONGST NORTH AMERICAN <i>SCLEROTINIA SCLEROTIORUM</i> ISOLATES: A STEPPINGSTONE TOWARDS IMPROVED WHITE MOLD SCREENING	61
Marysia Zaleski-Cox ^{1*} , Tanya Copley ² , Lone Buchwaldt ³ , Valerio Hoyos-Villegas ¹	
PREDICTION OF WHITE MOLD SEVERITY AND YIELD UNDER DISEASE PRESSURE IN DRY BEANS FROM UAS DATA	63
John Hawkins ¹ , Aliasghar Bazrafkan ¹ , Valerio Hoyos-Villegas ^{1*}	
IDENTIFYING EARLY ROOT TRAITS FOR IMPROVED FUSARIUM ROOT ROT RESISTANCE IN FIELD GROWN <i>PHASEOLUS VULGARIS</i>	65
Asia Hawkins ^{1,2,3} , Weijia Wang ⁴ , Paige Smith ⁴ , Miranda Haus ^{2,4,5}	
DISEASES RESISTANCE, ADAPTABILITY AND STABILITY OF COMMON BEAN LINES IN MULTI-ENVIRONMENT TRIALS IN PARANÁ, BRAZIL.....	67
Jaqueline B. Silva ¹ , Pedro S. Vidigal-Filho, Maria Celeste Gonçalves-Vidigal ¹ , Giselly F. Lacanallo ¹ , Mariana Vaz Bisneta ¹	
FINE MAPPING OF THE ANTHRACNOSE RESISTANCE GENE <i>CO-PA</i> IN THE ANDEAN COMMON BEAN CULTIVAR PALOMA	69

J. V. Silva Alves¹; M. C. Gonçalves Vidigal¹; G. Figueredo Lacanallo¹; M. Vaz Bisneta¹; L. L. F. Segal Xavier²; H. Ruifeng²; Q. Song²

THE PAN-GS CONSORTIUM: LEVERAGING COLLECTIVE BREEDING PROGRAM DATA FOR DURABLE GENOMIC SELECTION MODEL	71
Lovepreet Singh ¹ Robert McGee ² , Isabella Chiaravallotti ² , Jamie Larsen ³ , Anfu Hou ⁴ , Parthiba Balasubramanian ⁵ , Peter K. Pauls ⁶ , Mohsen Y. Najafabadi ⁶ , Lyndsay Schram ⁶ , Evan M. Wright ¹ , Juan M. Osorno ⁷ , Jose F.-Cerna ⁷ , Diego Jarquin ⁸ , Julián G-A. Velasco ⁸ , Virginia M. Moore ⁹ , Erika F. Everest ⁹ , Carlos Urrea ¹⁰ , Karen Cichy ¹¹ , Phil N. Miklas ¹¹ , Timothy Porch ¹² , Bodo Raatz ¹³ , Jennifer Wilker ¹⁴ , Winnyfred Amongi ¹⁵ , Clare Mukankusi ¹⁵ , Valerio Hoyos-Villegas ^{1,6*}	
EXPLORING THE GENETIC CONTROL OF SEED COAT COLOR IN A RIL POPULATION DERIVED FROM A RED X RED CROSS.....	73
E. Portilla [*] , C. García-Fernández, A. Campa y J.J. Ferreira	
IDENTIFICATION OF ANTHRACNOSE RESISTANCE LOCI INTROGRESSED FROM <i>P.</i> <i>COCCINEUS</i> INTO <i>P. VULGARIS</i> COMBINING BSA AND WGS	75
E Portilla ^{1*} , A Gaiti ² , A Campa ¹ , JJ Ferreira ¹	
UNDERSTANDING HEAT TOLERANCE IN <i>PHASEOLUS VULGARIS</i> THROUGH COMPARATIVE GENOMICS.....	77
Leah Tomey ^{1,2} , John P. Hamilton ^{2,3} , Kathrine Mailloux ² , Joshua C. Wood ² , Brienne Vaillancourt ² , Timothy Porch ⁴ , C. Robin Buell ^{1,2,3,5}	
TOWARD A NAVY BEAN PANGENOME FOR DISSECTING COMMON BACTERIAL BLIGHT RESISTANCE AND TEPARY BEAN INTROGRESSIONS	79
Mohammad Erfatpour ¹ , Gregory Perry ¹ , Maryam Vazin ¹ , Karl Peter Pauls	
USE OF MOLECULAR MARKERS TO FIX THE <i>BC-3</i> GENE IN ANDEAN LARGE- SEEDED CLIMBING BEANS	81
Héctor F. Buendía [*] , Elizabeth Portilla, Bodo Raatz, Christian Cadena, Jennifer Wilker Alliance of Bioversity International, CIAT	
GENOME-WIDE ASSOCIATION MAPPING OF ANTHRACNOSE RESISTANCE AND RELATED TRAITS IN ONTARIO DRY BEANS.....	83
Aashvi Patel ¹ , Sajal Ahlawat ¹ , Lyndsay Schram ¹ , Mohsen Yoosefzadeh Najafabadi ^{12*}	
THIRTY-FIVE YEARS OF GENETIC GAIN IN DRY BEAN BREEDING: EVIDENCE FROM MULTI-ENVIRONMENT TRIALS IN NORTH DAKOTA AND MINNESOTA	85
Nusrat Khan ¹ , Sara D. Long ¹² , Sara Wheatley ¹² , Jose C. Figueroa-Cerna ¹ , Juan M. Osorno ¹	
GENETIC DIVERSITY OF ANDEAN COMMON BEAN CULTIVARS AND BREEDING LINES REVEALED BY MORPHOAGRONOMIC TRAITS	87
Isabella Mendonça Arruda ¹ ; Elizeu David dos Santos ¹ ; José dos Santos Neto ¹ ; Vania Moda- Cirino	

REBUILDING CONFIDENCE IN BEAN INOCULANTS: IDENTIFYING CROP SPECIFIC RHIZOBIA IN COMMON BEAN VARIETIES FOR SUSTAINABLE NITROGEN FIXATION

..... 89

S.U. Attanayake*, K. E. Bett¹, I. J. Oresnik, I², G. C. diCenzo³, A. Vargas¹

EVALUATING A BREEDING PANEL OF HISTORICAL COMMON BEAN (*PHASEOLUS VULGARIS*) LINES FOR EFFECTS OF INDIRECT SELECTION 91

Grace Sidberry^{1,2}, C. Robin Buell³, K. A. Cichy^{4,5}, Miranda J. Haus^{1,2}

DEEP LEARNING AND COMPUTER VISION FOR HIGH-THROUGHPUT PHENOTYPING OF CANNING QUALITY TRAITS IN DRY BEANS 93

Lovepreet Singh¹ Om Sai Krishna Madhav Lella¹, Evan M. Wright¹, Karen Cichy^{1,2}, Valerio Hoyos-Villegas^{1*}

ADDITIONAL RESEARCH PAPERS FOR 2026

NOTICE OF NAMING AND RELEASE OF AD 1, A HIGH YIELDING AND DISEASE RESISTANT AZUFRADO COMMON BEAN CULTIVAR 95

Rigoberto Rosales-Serna^{1*}, Sergio Arellano Arciniega², Esteban Salvador Osuna Ceja², Saúl Santana Espinoza³

COMMON BEAN PRODUCTIVE PREFERENCES IN THE STATE OF DURANGO MÉXICO 97

Leslie Carnero Avilés¹, José Carlos Monárrez González¹, Rigoberto Rosales-Serna¹, Saúl Santana-Espinoza^{2*}

YIELD RESPONSE OF COMMON BEAN BRED LINES SELECTED IN THE BREEDING PROGRAM DEVELOPED IN DURANGO, MÉXICO 99

Rigoberto Rosales-Serna^{1*}, Rubén Bañales-Cárdenas², Ixchel Abby Ortiz-Sánchez², Cynthia Adriana Nava-Berumen³, Sonia Valdez-Ortega²

PRODUCTIVE IMPORTANCE OF NATIVE AND IMPROVED CULTIVARS OF COMMON BEAN IN THE SEMIARID HIGHLANDS OF MÉXICO 101

Saúl Santana Espinoza¹, Rigoberto Rosales-Serna²

SEED PRODUCTION FOR PREFERENT COMMON BEAN CULTIVARS IN THE SEMIARID HIGHLANDS OF MÉXICO 103

Rigoberto Rosales-Serna¹, Saúl Santana-Espinoza^{2*}

PROMISING GERMPLASM FROM AN INTERSPECIFIC DIVERSITY PANEL 105

Tim Porch¹, Ali Soltani², Stephanie Cosme¹, Giovanni Lorenzo¹, Robin Buell³, Consuelo Estevez de Jensen⁴, David Lowry²

YIELD POTENTIAL OF CYCLE I LINES DERIVED FROM THE UFV BLACK COMMON BEAN RECURRENT SELECTION PROGRAM 107

Mateus Miranda Correia¹ Danilo Vencio Rodrigues¹ Yara Paola Lopez Gamarra¹ Núbia Xavier Nunes¹ Pablo Dias Aymara¹ Thiago Henriques Moreira¹ Lisandra Magna Moura²

Vanessa Aparecida Pereira Batista² Isabela Rodrigues Miranda² Lorena Freitas Talamoni²
 Lucas Bitencourt Faria² Hudson Faleiro Castro² Thiago Henrique Barbosa Silva² Reberth
 Renato da Silva¹ José Eustáquio de Souza Carneiro¹ Pedro Crescêncio Souza Carneiro¹

POD QUALITY, YIELD AND DISEASE RESISTANCE OF NEW TROPICALLY ADAPTED
 VEGETABLE RUNNER BEAN LINES..... 109

Kimani P.M. , S.N Njau

BREEDING RUNNER BEAN FOR CANNING INDUSTRY IN EASTERN AFRICA111

Kimani P.M.¹ and S.N Njau¹, Mwangi Njiru², Steve Omondi³

AGRONOMIC PERFORMANCE OF CARIOCA COMMON BEAN LINES FROM THE
 FIRST CYCLE OF RECURRENT SELECTION AT UFV FOR FUSARIUM WILT
 RESISTANCE.....113

Danilo Vencio Rodrigues¹ Yara Paola Lopez Gamarra¹ Núbia Xavier Nunes¹ Mateus
 Miranda Correia¹ Pablo Dias Aymara¹ Thiago Henriques Moreira¹ Lisandra Magna Moura²
 Vanessa Aparecida Pereira Batista² Isabela Rodrigues Miranda² Lorena Freitas Talamoni²
 Lucas Bitencourt Faria² Hudson Faleiro Castro² Thiago Henrique Barbosa Silva² Reberth
 Renato da Silva¹ José Eustáquio de Souza Carneiro¹ Pedro Crescêncio Souza Carneiro¹

OPTIMIZATION OF THE EVALUATION TO SEED SIZE AND SHAPE OF COMMON
 BEAN LINES115

Everton da Silva Cardoso¹, Lorena Caroline Dumbá Silva¹, Vinícius Quintão Carneiro¹,
 Elaine Aparecida de Souza¹, Jussara Mencalha¹, Heloisa Oliveira dos Santos¹

TERMINAL DROUGHT TOLERANCE AND PRODUCTIVE EFFICIENCY OF TROPICAL-
 ADAPTED BLACK BEAN GENOTYPES117

O. H. Tosquy-Valle^{1*}, R. Zetina-Lezama¹, L. A. Fadda¹, J. L. Anaya-López², M. V. Vázquez-
 Hernández¹

SPATIAL DISTRIBUTION AND NICHE SUITABILITY OF COMMON BEAN POD WEEVIL
 IN NORTH-CENTRAL MÉXICO119

Leslie Carnero-Avilés¹, Rigoberto Rosales-Serna^{1*}, Pablo A. Domínguez-Martínez¹, Ramón
 Garza-García², Saúl Santana-Espinoza³, José F. Rodríguez-Rodríguez⁴

DISTRIBUTION OF *MACROPHOMINA PHASEOLINA* INFECTING COMMON BEANS
 AND OTHER CROPS IN MEXICO 121

V. H. Ramos-García^{1, 2}, M. A. Reyes-Lara³, A. C. González-García⁴, H. R. Gill-Langarica⁴,
 J. G. García-Olivares⁴ & N. Mayek-Pérez^{4*}

SCREENING OF POWDERY MILDEW (*ERYSIPHE VIGNAE*) RESISTANCE IN A TEPARY
 BEAN DIVERSITY PANEL 123

Ihann Rosado¹, Tim Porch², Robin Buell³, Consuelo Estevez de Jensen¹

GENOME-WIDE ASSOCIATION STUDY OF WHITE MOLD RESISTANCE IN COMMON
 BEAN..... 125

Ram Neupane*¹, John Hawkins¹, Alvaro Soler-Garzón³, Phillip N Miklas², Valerio Hoyos-Villegas

REACTION OF COMMON BEAN LINES TO RACES 65 AND 89 OF *COLLETOTRICHUM LINDEMUTHIANUM*..... 127

Rhyan Vilas Boas Carvalho¹, Alex Naves Ferreira¹, Elaine Aparecida de Souza¹

THE *UR*-3 AND *UR*-7 LOCI REVEAL CANDIDATE GENES FOR RUST RESISTANCE IN COMMON BEAN 129

Alvaro Soler-Garzón, ²Giseli Valentini, ²Marcial Pastor-Corrales, ²Ruifeng He, ³Phil Miklas

INHERITANCE OF ASHY STEM BLIGHT RESISTANCE IN BLACK COMMON BEAN UPR-MP-42 131

Diego M. Viteri, Angela M. Linares-Ramírez, Ediezel Figueroa

EVALUATION OF DRY BEAN BREEDING LINES FOR WHITE MOLD RESISTANCE IN THE GREENHOUSE AND FIELD USING MULTI-SITE SCREENING NURSERIES..... 133

Evan Wright¹, Halima Awale¹, Phillip Miklas², James Myers³, Juan Osorno⁴, Carlos Urrea⁵, Michael Wunsch⁴, Valerio Hoyos-Villegas¹

GENETIC VARIABILITY OF GERMPLASM OF BEANS CULTIVATED IN OAXACA, MEXICO..... 135

A. L. García-Narváez¹, J. L. Chávez-Servia², S. Hernández-Delgado¹, N. Mayek-Pérez^{1*}

SNP DISCOVERY AND QTL MAPPING IN POPPING BEAN 137

Price P. A. Akiina, Ilyas Ahmad, Donna K. Harris

A PRACTICAL HAPLOTYPE GRAPH FOR TEPARY BEAN 139

John P. Hamilton^{1,2}, Yi-Wen Wang^{1,3}, Joshua C. Wood¹, Kathrine Mailloux¹, Brieanne Vaillancourt¹, Consuelo Estévez de Jensen⁴, Tim Porch⁵, C. Robin Buell^{1,2,3}

THE COMPLEX *C* LOCUS: GENOMIC ORGANIZATION IN THE ANDEAN GENEPOOL 141

Alvaro Soler-Garzon¹, Phillip E. McClean², Rian Lee², Jayanta Roy², Phillip N. Miklas³

APPLICATIONS OF YIELD AND SUITABILITY MODELS FOR COMMON BEAN IN THE MEXICAN TROPICS AND SUBTROPICS..... 143

L. A. Fadda¹, O. H. Tosquy-Valle^{1*}, F. J. Ibarra-Pérez¹

LARGE SCALE ENVIRONMENTAL GENOME-WIDE ASSOCIATION STUDY OF LANDRACES OF COMMON BEAN (*PHASEOLUS VULGARIS* L.): CURRENT PROGRESS 145

Correa, M.*¹, Ospina, J. 1, Franco, J.2, Sonder, K. 3, Wenzl, P. 1, Carvajal-Yepes, M.1

PHENOMICS-DRIVEN EARLY DETECTION AND BREEDING FOR ANTHRACNOSE RESISTANCE IN ONTARIO DRY BEANS..... 147

Philip Lorenc 1, Sajal Ahlawat 1, Lyndsay Schram 1, Mohsen Yoosefzadeh Najafabadi 12*

PILOT PRODUCTION OF TYPE IV CLASSIC FLAT WHITES™ USING A LIVING TRELLIS SYSTEM.....	149
Ken Kmiecik	

LOW-COST, HIGH-THROUGHPUT METHOD FOR HYDROGEN CYANIDE DETECTION IN SUCCULENT LIMA BEAN SEEDS.....	151
Sangita Subedi ¹ , Jenna Hershberger	

ADDENDUM

<i>PHASEOLUS</i> EXPLORATION AND COLLECTION IN THE SOUTHWESTERN USA	153
Richard C. Pratt ¹ , Daniel G. Debouck ² , Sarah Dohle ³ , Timothy Porch ⁴ , Luis Guillermo Santos ² , Marcela Santaella ² , Gabriela Guerrero Florez ⁵	

RESISTANCE GENE MAPPING AND TRANSCRIPTOMIC PROFILING OF COMMON BEAN IN RESPONSE TO THE INFECTION BY <i>COLLETOTRICHUM LINDEMUTHIANUM</i>	155
Larissa F.S. Xavier ¹ , Giseli Valentini ² , Marcial A. Pastor-Corrales ¹ , Maria Celeste Gonçalves-Vidigal ³ , Qijian Song ¹ , Ruifeng He ¹	

AGRONOMIC PERFORMANCE, NUTRITIONAL QUALITY AND COOKING TRAITS OF COMMON BEAN GENOTYPES GROWN UNDER TERMINAL DROUGHT CONDITIONS IN SOUTH-CENTRAL CHILE	157
Kianyon Tay ^{1,2} , Nelson Zapata ² , Carlos A. Urrea ³ , Miguel Garriga ² , Abdelhalim Elazab ² , María Dolores López-Belchí ^{2,4}	

SUBJECT MATTER INDEX – BIC 2026.....	159
2025 BIC FINANCIAL STATEMENT.....	160

THE 69th ANNUAL REPORT OF THE BEAN IMPROVEMENT COOPERATIVE

It is both an honor and a pleasure to coordinate the 69th Annual Report of the BIC, which is my second report as president. As all you may know, last year we had our 33rd biennial joint meeting between the BIC and NAPIA (North American Pulse Improvement Association) at Lincoln, NE on November 3-6, 2025. The local meeting organizers were Dr. Carlos Urrea, dry bean breeder at the Univ. of Nebraska-Lincoln, but stationed at the Scottsbluff Research and Extension Center, and Connie Hansen (UNL Event Planner). The event was a success and we had a total 148 participants from more than 12 countries. A workshop focused on Root Rots was also held on November 6th. In addition, the Phaseolus Crop Germplasm Committee (PCGC), BIC Genetics Committee (BGC) and the Multistate W-5150 Committee conducted their annual meetings on November 6th. All these meetings are open to everyone interested in either participating and/or becoming a member of any of these amazing groups. A tour of UNL campus facilities was also held on November 6th. The Frazier-Zaumeyer Distinguished Lectureship was awarded to both Drs. Robin Buell and James Myers. You can read more about their amazing career accomplishments as well as other important awards given during the meeting a few pages down.

Since our 2023 meeting, both BIC and NAPIA decided to alternate the hosting and organization of the joint meeting, so I'm very happy to announce that our next joint BIC/NAPIA meeting will be hosted and organized by NAPIA and the University of Saskatchewan in Saskatoon, Canada during the last week of October, 2027. Details will be shared later as the local organizing committee starts planning this important event. To my knowledge, this is the second time the BIC meeting will be held in Canada after our 2015 meeting at Niagara Falls.

Please share information about the BIC with interested colleagues who might like to attend the 2027 meeting or who would like to join the BIC as members. Also, feel free to contact us with any new ideas, contributions, or updates for the BIC website or this Annual Report. We are especially interested in receiving new or updated methods that can be shared with the general community for the Research Techniques page of the BIC website. The BIC continues to conduct business by email, postings on the webpage, and through the online publication of this Annual Report. We are always open to new ideas to make the BIC a more effective organization and any suggestions can be shared with members of the Coordinating Committee. We wish you a fulfilling and successful year. Warm regards,



**Juan M. Osorno,
BIC President**

BIC COMMITTEE MEMBERSHIP - 1957 to 2025

Coordinating Committee (approximate year of appointment):

Year	Committee Members
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, Wyatt
1983	Coyne, Dickson, Hagedorn, Saettler, Silbernagel, Steadman, Temple, Wallace, Wyatt
1985	Coyne, Dickson, Mok, Saettler, Silbernagel, Steadman, Temple, Wallace, Wyatt
1986	Coyne, Dickson, Mok, Saettler, Schoonhoven, Schwartz, Silbernagel, Steadman, Wallace
1988	Brick, Dickson, Emery, Magnuson, Roos, Schwartz, Singh, Steadman, Uebersax
1992	Dickson, Emery, Grafton, Magnuson, Schwartz, Singh, Stavely, Steadman, Uebersax
1994	Antonius, Dickson, Grafton, Magnuson, Park, Schwartz, Singh, Stavely, Uebersax
1996	Antonius, Grafton, Park, Schwartz, Singh, Stavely, Myers, Kotch, Miklas, Riley
1998	Antonius, Park, Schwartz(ex officio), Singh, Myers, Kotch, Miklas, Riley, Beaver, Vandenberg, Kelly
2000	Antonius, Beaver, Kelly, Kotch, Miklas, Myers, Park, Riley, Schwartz, Singh, Vandenberg
2001	Antonius, Beaver, Kelly, Kotch, Miklas, Myers, Park, Riley, de Ron, Schwartz, Vandenberg
2003	Beaver, Kelly, Kmiecik, Kurowski, Miklas, Myers, Park, Riley, de Ron, Schwartz, Vandenberg
2007	Beaver, Kelly, Kmiecik, Miklas, Myers, Park, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2008	Beaver, Kelly, Kmiecik, Miklas, Myers, Pauls, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2010	Beaver, Kelly, Kmiecik, Miklas, Myers, Pauls, Riley, de Ron, Schwartz, Shellenberger, Vandenberg
2011	Bett, Kelly, Kmiecik, Miklas, Myers, Osorno, Pastor-Corrales, Pauls, Riley, de Ron, Wahlquist
2015	Bett, Cichy, Kelly (ex officio), Kmiecik, Miklas, Myers, Osorno, Pauls, Souza, Trapp, Wahlquist
2020	Bett, Cichy, Kmiecik, Miklas (ex officio), Myers, Osorno, Pauls, Porch, Souza, Trapp, Wahlquist
2021	Bett, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Osorno, Pauls, Porch, Souza, Wahlquist
2023	Bett, Chang, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Osorno, Pauls, Porch
2024	Bett, Chang, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Osorno, Pauls, Porch, Wiersma
2025	Bett, Chang, Cichy, Kamfwa, Kmiecik, Miklas, Myers, Pauls, Porch, Wiersma, Osorno

Awards Committee:

1971	Baggett, Briggs, Burke, Dean, Wallace	1995	Coyne, Dickson, Stavely
1973	Burke, Dean, Mautz, Zaumeyer	1997	Coyne, Schwartz, Stavely
1975	Ballantyne, Frazier, Mauth	2001	Hosfield, Magnuson, Schwartz
1977	Ballantyne, Curme, Frazier, Schuster	2004	Hosfield, Schwartz, Singh
1979	Ballantyne, Schuster, Silbernagel, Temple	2012	Noffsinger, Schwartz, Singh
1981	Abawi, Bliss, Monis, Silbernagel	2014	Beaver, Noffsinger, Urrea
1983	Adams, Bliss, Burke, Dean, Morris	2015	Beaver, Myers, Urrea
1985	Emery, Hagedorn, Sandsted, Schwartz	2022	Myers, Urrea
1987	Emery, Hagedorn, Sandsted	2024	Porch, Urrea
1989	Coyne, Silbernagel, Wallace		

THE BEAN IMPROVEMENT COOPERATIVE

Proudly Presents the

Frazier - Zaumeyer Distinguished Lectureship

to

James R. Myers

Professor Emeritus
Oregon State University

&

C. Robin Buell

Professor of Crop and Soil Sciences
University of Georgia

The **Frazier - Zaumeyer Distinguished Lectureship** was established in 2001 to recognize and honor a distinguished colleague who will present the keynote opening address at the biennial BIC meeting. The individual selected will have made outstanding and pioneering contributions to science that led to the advance of bean research. The Lecture will focus on current topics relevant to the BIC membership. The Lectureship is distinct from the other BIC career Awards, such as the Distinguished Achievement and Meritorious Service Awards. Holders of these awards are not excluded from being awarded the Frazier-Zaumeyer Distinguished Lectureship. The name for the Lectureship honors the original BIC founder members, the late William A. ‘Tex’ Frazier, distinguished bean breeder, and the late William ‘Bill’ Zaumeyer, an equally distinguished bean pathologist. Dr. Tex Frazier, working at Oregon State University, is recognized for his pioneering work in developing the famous Bush Blue Lake snap bean and related germplasm. Dr. Bill Zaumeyer, of USDA-ARS, is recognized for his outstanding contributions to bean pathology.

JAMES R. MYERS

Dr. Jim Myers is Professor Emeritus (previously Baggett-Frazier Endowed Chair of Vegetable Breeding and Genetics) in the Department of Horticulture at Oregon State University. He received a B.S. degree in Horticulture from Kansas State University in 1978, then obtained both M.S. and Ph.D. degrees in Plant Breeding and Genetics (1981 and 1984) from the University of Wisconsin-Madison, where he studied male sterile sterility in peas under the direction of Dr. Earl Gritton. A course from that time that proved important to his career was “Tropical Bean Breeding” from Dr. Steve Temple, who was on sabbatical from CIAT. From 1985 to 1987, he was a postdoctoral fellow and then as a research specialist in a somatic cell genetics laboratory managed by Dr. Glenn Collins at the University of Kentucky. In 1987, Myers took over from Dr. John Kohler the University of Idaho dry bean breeding program in Kimberly. He subsequently moved to the OSU in 1996, where he remained to the present. At OSU, Myers follows two prominent snap bean breeders: Dr. William “Tex” Frazier (1949 – 1973) and Dr. Jim Baggett (1973 – 1995). As his predecessors did, one of Myers’ main responsibilities was to develop improved snap bean cultivars for the processed vegetable industry of western Oregon. The breeding program included not only beans but also other vegetable crops, including edible podded peas, broccoli, winter and summer squash, table beets, peppers, and tomatoes. The major academic focuses of his program have been on breeding for disease resistance, organic agricultural production systems, human nutrition, flavor, taste, and quality. He developed the first snap bean diversity panel that was subsequently supplemented and used in his program to investigate the genetics of root rot and white mold resistance, snap bean leaf and pod color, phenolics, and flavor volatiles.

He has released 34 cultivars, including 14 dry bean cultivars and four germplasm releases, while at the University of Idaho, and 20 cultivars and one germplasm release at OSU. His OSU releases include one snap bean, six tomatoes, three edible podded peas, two table beets, two mild habanero peppers, one broccoli, and five dry bean cultivars. The OSU5630 bush blue lake snap bean, released in 2005, has been grown on about 80% of the acreage used for processing in western Oregon. He will probably be best known as the originator of high anthocyanin ‘Indigo’ tomatoes that are now being grown worldwide.

From 1990 to 2017, Myers provided leadership in breeding in Eastern and Southern Africa for the US-AID funded Bean/Cowpea CRSP. With Dr. Gaylord Mink, he initially studied the epidemiology of bean common mosaic necrosis virus in Eastern and Southern Africa and later developed bruchid resistant germplasm introgressed from tepary bean. This germplasm is being used in the Caribbean, Central America, and Eastern and Southern Africa to breed for bruchid resistance, with three cultivars to date deployed in Tanzania.

His efforts to breed for organic systems spanned more than two decades across several projects. He was project director (2009 – 2023) of the USDA-OREI funded Northern Organic Vegetable Improvement Collaborative, a multi-institutional effort to breed vegetables adapted to organic production systems. This project trained more than 10 graduate students and facilitated the release of at least 22 vegetable cultivars. He has published papers on the effect of selection in organic systems on snap bean microbiome and the snap bean genome. He has coedited 2 books, published 89 peer refereed publications, 16 book chapters, 107 peer reviewed papers and more than 150 invited and contributed papers. He has obtained over \$12 million in competitive grants funds and another \$2.8 million in commodity commission funds. He has advised 12 Ph.D., 16 M.S. and, 1 M.Ag students, and served as a committee member for another 43 students. Myers has facilitated undergraduate student directed research for 32 students. He has taught an upper-level undergraduate-graduate course in Vegetable Systematics and graduate courses in Plant Domestication, Intellectual Property and Organic Plant Breeding (online). Myers was awarded the BIC Distinguished Achievement Award in 1999 and the BIC Meritorious Service Award in 2019. He was elected a fellow of the American Society of Horticultural Science in 2022 and has been recognized with several ASHS Outstanding Publication awards in 2013, 2017, and 2022.

C. ROBIN BUELL

Dr. C. Robin Buell is the Georgia Research Alliance Eminent Scholar Chair in Crop Genomics and Professor of Crop and Soil Sciences at the University of Georgia. She currently serves as Director of The Plant Center at the University of Georgia, leading interdisciplinary efforts to advance plant science through genetics, genomics, synthetic biology, and breeding innovation. In 2025, she was elected to the U.S. National Academy of Sciences for her pioneering contributions to plant genome biology. She has authored nearly 320 publications, received over \$82 million in funding directly to her lab, and given over 250 presentations to scientific and lay audiences. Dr. Buell received her Ph.D. in Biology/Molecular Biology from Utah State University (1992), M.Sc. in Plant Pathology from Washington State University (1988), and B.Sc. in Biology from the University of Maryland (1985). She completed postdoctoral fellowships at Michigan State University and the Carnegie Institution of Washington at Stanford. Her academic appointments include Louisiana State University, The Institute for Genomic Research, and Michigan State University, where she served as Director of the Plant Resilience Institute and was named University Distinguished Professor.

A leading plant genomicist, Dr. Buell's research has transformed our understanding of genome structure, evolution, and function in plants. Her work spans crop species (rice, maize, potato, wheat), model species (*Arabidopsis*), ornamentals (mints, dahlia), trees (poplar, pine) and medicinal plants (periwinkle, cinchona, kratom). Her first exposure to beans was as a faculty member at Michigan State University in which she taught a number of Dr. Jim Kelly's students in Plant Genomics. From these interactions and her later involvement in the Plant Resilience Institute at Michigan State University, she began research on beans, specifically tepary bean. She was a co-leader of the tepary genome project with Phil McClean, Tim Porch, and Kristen Bett publishing the results in *Nature Communications* in 2021. She has continued her research in bean genomics through a long-standing collaboration with Tim Porch on tepary bean genetic diversity and with the first *k*-mer-based genome-wide association study in common bean with Andrew Wiersma and Jim Kelly. Her lab has published multiple research articles in the Bean Improvement Cooperative and the Plant Genome, contributing foundational insights into gene expression, resistance traits, and genome annotation in common and tepary beans.

Dr. Buell is currently leading a USDA-NIFA-funded project in collaboration with Tim Porch and Consuelo Estevez de Jensen, focusing on leveraging the genome of the tepary bean to improve resilience to biotic stress in common bean. This research aims to identify and transfer disease resistance traits from tepary bean into common bean, addressing yield loss due to pests and pathogens. One component of this project is the construction of a Practical Haplotype Graph for tepary bean to organize the tepary bean pan-genome. A current focus in her research group is heat tolerance in common bean and the identification of adaptive alleles for accelerated breeding of heat-tolerant common bean varieties.

She has mentored over 50 graduate students and postdoctoral researchers and developed bioinformatics workshops for plant biologists. Her contributions have been recognized with the McClintock Prize (2021), USDA Honor Awards (2004, 2011), and she is a fellow of both the American Association for the Advancement of Science and the American Society of Plant Biologists. She has served on the editorial boards of *GigaScience*, *Plant Cell*, and *Plant Physiology*, and held advisory roles at the Salk Institute, the Department of Energy, and multiple international genomics initiatives. Dr. Buell continues to advance bean genomics through collaborative research, resource development, and mentoring the next generation of students and postdocs.

THE BEAN IMPROVEMENT COOPERATIVE

Proudly Presents the

Meritorious Service Award

to

in Memory of Phil McClean

North Dakota State University

Fargo, North Dakota

Ken Kmiecik

Ken Kmiecik, LLC

Rigoberto Rosales-Serna

Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias (INIFAP)

Distinguished Achievement Award

to

Kelvin Kamfwa

University of Zambia

Lusaka, Zambia

Travis Parker

University of California

Davis, California

ProVita, Inc.

In Memory of Ron Shellenberger (1943-2015)

Kuna, Idaho

Technical Merit Award

to

Héctor Fabio Buendía

Alliance of Bioversity International and CIAT

Palmira, Colombia

PHILLIP E. MCCLEAN

In Memory of Phillip McClean (1949-2025)

Phillip Edward McClean was born on November 25, 1949, in Pierce, Nebraska. Phil's father was in the US Air Force, so his family lived in many places, including Germany. He attended ~12 different schools by the time he graduated. Driven by a lifelong love of learning, he earned his Ph.D. from Colorado State University in Fort Collins, CO, following studies at Denver Community College and Metropolitan State College. After postdoctoral work at the University of Virginia and the University of Missouri-Columbia, he joined North Dakota State University (NDSU) in November 1985. Dr. McClean served proudly as a faculty member at NDSU for nearly four decades, achieving the rank of Professor since 1998.

During his tenure at NDSU, Dr. McClean became a world authority in common bean genetics and genomics. His research has fundamentally advanced agricultural science and significantly improved global food security. His work, which underlies the development of genetic markers, gene mapping, and genomic tools for improving bean varieties, has touched the lives of millions, particularly in regions where food security is a critical challenge.

Dr. McClean's career is marked by extraordinary research accomplishments, including the development of the first reference genome for the common bean, a landmark achievement cited over 1,500 times. He published more than 100 refereed journal articles, in addition to five book chapters and numerous abstracts. He was a key leader in securing and managing the Common Bean Coordinated Agricultural Project (Bean CAP), the largest single investment in bean research at that time. More recently, he was a mastermind behind the scenes in planning and successfully obtaining the NSF FARMS Engine grant, the largest grant ever obtained by NDSU, which is poised to bring up to \$160 million to North Dakota's agriculture sector. He served as the Director of the Genomics and Bioinformatics graduate program. Dr. McClean contributed to grants worth over \$24 million, with \$9.7 million directly supporting his projects.

At the international level, Dr. McClean actively collaborated with scientists across the globe and served as PI and on advisory boards for the USAID Legume Innovation Laboratory and the Canadian Common Bean Sequencing Project, among others. His work contributed to the international release of over six bean varieties and numerous genomic tools.

His excellence has been repeatedly recognized, including with the Distinguished Research Award from the Bean Improvement Cooperative (1999), the Dermot Coyne Lectureship (2012), the Frazier-Zaumeyer Lectureship (2012), and the Cargill Lectureship from Colorado State University (2014), among others.

Beyond his research, Dr. McClean was an equally exceptional educator and mentor. He embraced new technology to enhance student learning, always seeking to teach what was at the "tip of the arrow." He was a pioneering teacher who developed one of the first course websites and led the NDSU Virtual Cell Animation Project, which produced groundbreaking animations of cellular processes. He has 20 refereed publications related to the development of educational software and has received four awards for his contributions to the field of education. Dr. McClean inspired students to "think about science in a big way." His office door was always open, and he mentored many young scientists, freely giving credit and leading with humility.

Dr. McClean passed away on September 11, 2025, but his legacy and impact will continue for many years.

KEN KMIETIK

After dropping out of the University of Wisconsin Theatre Program, knocking about cooking and traveling on his motorcycle, Ken returned to school in 1975 as a Horticulture Major with the goal of becoming an Extension Specialist in vegetables. As a student, he was hired hourly by Fred Bliss and worked for Steve Beebe. Beans and breeding became woven into Ken's DNA during his long association with Dr. Bliss and his students. In 1979 as part of Fred's program Ken had his first interaction with the Bean Improvement Cooperative operating the slide projector for the BIC meeting in Madison, WI that year.

Ken provided 19 years of professional and technical support to the UW-Madison bean program. Lots of road time, blue slides, pollinations, along with late days in the field and lab with graduate and undergraduate students. In September of 1988 before leaving the University of Wisconsin for UC-Davis Fred Bliss wrote:

Ken, You are a friend and colleague ... Your patience and caring about the students both grad and undergrad who have come through the program are unique. They and I have had a better time at this big University because of you

Sincerely Fred

Ken left the UW to join what was becoming Seminis Vegetable Seeds in April 1998. Eventually he took responsibility for garden bean breeding in the Americas, Australia, and New Zealand. What guided him then, as it does now, was the idea that he supported the needs of his colleagues. Growers, sales reps, and production staff at Seminis replaced the students and staff he had valued in his 19 years at the University. With 30 or so garden bean releases and stepping into help with dry edibles Ken found both success and satisfaction in the 16 years with Seminis. On June 25th 2014 Seminis / Monsanto informed him of his retirement. On July 5th, 2014 Wolf Bertoni, a grower in New Jersey, wrote:

Hi Ken, Its Wolf, I heard the bad news, we've waited a generation for a break through variety and your the only one on the planet to create it (aph resistant snap bean). ... Thanks for everything!!

That same July a grower (John Wallendal) in Wisconsin asked Ken what he might do post Monsanto. Ken replied that he would plant some seed somewhere. John's response was, "How many acres do you need?"

The BIC and its mission of open exchange has never been far from his heart. Ken served on the coordinating committee from 2003 to 2023 and when the BIC celebrated its 50th in 2007 Ken enlisted fellow industry colleagues (Rob Gehin, Roxanne Mainz, Alyson Thorton,) and Michelle Sass of UW to bring the meeting to Madison, WI site of the first BIC meeting.

Since 2015, Ken has had a third career and has become Ken Kmiecik, LLC - breeding and developing beans independently. He also has the good fortune to be working with Professors who were the students of graduate students in the 1980's. Current UW projects include: resistance to Seed Corn Maggot, mapping Aph resistance, and white mold resistance. Ken is also an active participant in the Midwestern based Artisan Grain Collaborative working to incorporate dry edibles into the rotations of mid-sized local grain producers. In this 3rd career Ken would like to become the Mick Jagger of beans ...not sex, drugs, and rock and roll, but still on tour at 80.

RIGOBERTO ROSALES-SERNA

Dr. Rigoberto Rosales-Serna was born in Las Mercedes, Durango, México, on April 4th, 1967. He received his B. S. degree of Ingeniero Agrónomo Fitotecnista (Engineer on Agronomy and Plant Breeding) in 1989 from the Instituto Tecnológico Agropecuario Núm. 1 (ITA # 1), at Villa Montemorelos, Durango, Méx. He earned his MSc degree in Plant Breeding and Genetics in 1996 and his PhD in Botany in 2005, both from the Colegio de Postgraduados in Montecillo, Mexico. The professional activity of Dr. Rosales-Serna began in 1988, when he joined the Edible Legumes Program of the National Institute of Forestry, Agricultural and Livestock Research (INIFAP) as a field assistant. In 1991, he was invited to a Postgraduate Specialization Program in Common Bean, held at the International Center for Tropical Agriculture (CIAT) in Palmira, Colombia. In 2012-2013, occupied a postdoctoral position at Escuela de Biotecnología of Instituto Tecnológico de Monterrey (ITESM), and a sabbatical leave (2023-2024) at CIIDIR-Instituto Politécnico Nacional. In his early career, Dr. Rosales-Serna developed fieldwork to release the Pinto Villa common bean drought-tolerant cultivar, resulting in significant increases in seed yield under drought conditions. Dr. Rosales-Serna has developed 26 common bean varieties in several market classes, such as pinto, bayo, flor de mayo, black, and azufrado. He participated in the development, registration, and technology transfer of the slow darkening Pinto Saltillo cultivar, encouraging the adoption process among farmers in several states (11) of the Mexican Highlands. Pinto Saltillo has been considered an important scientific, productive, and market success, growing on more than 4.6 million hectares from 2014 to 2023 in the Highlands of Mexico, producing over 2.6 million tons of grain. In several countries, Pinto Saltillo has been recognized as a significant gene source for slow darkening seed coats and has been utilized as a donor parent in common bean breeding programs in the USA and Canada. Pinto Saltillo and other varieties developed by Dr. Rosales-Serna reduced cooking time and gas consumption in Mexican homes by 20%, also having a positive impact on the home economy and reducing pollution. Common bean varieties released by Dr. Rosales-Serna also increased seed yield, improving the economic benefits obtained by farmers and the commercial quality of the seeds, thereby alleviating hunger in Mexico and other countries. He collaborated for more than five years as a researcher in México with the Bean/Cowpea Collaborative Research Support Program (CRSP), developing important common bean lines and cultivars with enhanced adaptation under drought conditions (Pinto Mestizo, Pinto Bayacora). Dr. Rosales-Serna published 119 scientific peer-reviewed papers, 310 articles in national and international congresses, 82 research notes, four books, 13 chapters in scientific books, and 119 technological publications, resulting in important advances in common bean knowledge. He advised 29 BS, 4 MSc, and 3 PhD theses, and attended 46 residency stays for undergraduate students. Dr. Rosales-Serna participated in multiple technology transfer and field training events for producers, students, technicians, and government employees. He also participated in organizing scientific proceedings and compiling memories, and was invited as a reviewer-editor for several research journals, including *Revista Fitotecnica Mexicana*, *Agronomía Mesoamericana*, *Polibotánica*, *American Journal of Experimental Agriculture*, and *Journal of Agricultural Science*. Currently, Dr. Rosales-Serna is working on developing agronomic solutions to enhance soil fertility and structure by producing biomass that can be used as organic amendments. Achievements have allowed him to obtain several awards, including two Durango State Awards for Science, Technology, and Innovation in 2009 and 2014, and a second place in the award given by the Mexican Association of Directors in Applied Research and Technological Development (ADIAT, 2010; Mexican Association of Directors in Applied Research and Technological Development). Dr. Rosales-Serna was also awarded as a Distinguished Agronomist by the Colegio de Postgraduados and recognized by the Government of the State of Durango for his “Valuable contribution to the productivity of the state agriculture with his participation in the research of new common bean varieties”. Dr. Rigoberto Rosales-Serna's hard work, dedication, and friendly support inspire his colleagues and friends.

KELVIN KAMFWA

Kelvin Kamfwa is a Senior Lecturer and leader of the Legume Breeding Program at the University of Zambia (UNZA), the largest public university in Zambia. He also serves as the Assistant Dean for Research in the School of Agricultural Sciences at the UNZA.

Kelvin was born and raised in the rural part of Northern Zambia. His early experiences in rural agriculture inspired a lifelong commitment to improving the livelihoods of smallholder farmers through science and innovation. He earned his Bachelor of Science in Crop Science from the UNZA, a Master of Science in Plant Breeding from Makerere University in Uganda, and a PhD in Plant Breeding, Genetics, and Biotechnology from Michigan State University (MSU), where he worked on symbiotic nitrogen fixation under the mentorship of Drs. Jim Kelly and Karen Cichy.

After graduating from MSU, he returned to Zambia in 2016 to take up a position as a lecturer at the University of Zambia, convinced that the skills he had acquired in the US would have the greatest impact in his native country, Zambia, where over 70% of the population depends on agriculture, and access to improved varieties for legume crops is limited.

Kelvin established the first Legume Breeding Program at the University of Zambia in the same year he returned. This program is externally funded, with the overall breeding objective of delivering high-yielding varieties of common bean, cowpea, and soybean to smallholder farmers in Zambia and the southern African region. Kelvin has developed and released varieties that are currently being grown by smallholder farmers in Zambia. Despite the various challenges of running a public breeding program in a developing country like Zambia, where there is limited research support, Kelvin has successfully established an impactful breeding program that has attracted approximately \$600,000 in research funding since 2016, primarily from external partners.

Kelvin's breeding program has graduated 14 MSc students in Plant Breeding and Seed Systems from the University of Zambia, with students from various southern African countries. Currently, he supervises eight MSc and four PhD students working on various topics related to common bean, cowpea, and soybeans.

In recognition of his impact on smallholder farmers through breeding, the Legume Innovation Lab awarded Kelvin the Early Career Grain Legume Scientist award in 2017 at a ceremony held in Ouagadougou, Burkina Faso. The award recognized his early career achievements in grain legume research and his commitment to improving the livelihoods of smallholder farmers in developing countries.

Working with collaborators, Kelvin led the breeding efforts to deploy weevil resistance in breeding lines across various market classes. These lines are currently being tested in Malawi, Mozambique, and Zambia for agronomic performance and could potentially be released as new varieties, another demonstration of the international impact of his breeding program. His team has also accelerated the deployment of resistance genes against major pathogens affecting common bean by integrating molecular tools into conventional breeding.

Kelvin has published 46 peer-reviewed research articles on common bean, demonstrating the impact and contribution of his work in this field. Kelvin's lab has also hosted graduate students from the region, including those from South Africa, Malawi, and Mozambique, to conduct research on the common bean.

TRAVIS PARKER

Dr. Travis Parker is an assistant professional researcher at the University of California Davis, where he specializes in the genetics and breeding of *Phaseolus*. Dr Parker is a native of San Diego County and completed his bachelor's degree in Biology at Cal Poly San Luis Obispo on California's Central Coast. In 2020, he completed a PhD in Plant Biology at UC Davis, where he also finished a postdoc in 2022. His PhD and post-doctoral fellowship were both completed in Professor Paul Gepts' lab.

Dr. Parker's research includes 14 first-author peer-reviewed publications in high-impact journals such as Plant Cell, New Phytologist, Remote Sensing, and The Plant Journal, as well as 3 first-author book chapters. His projects span from genomics and phenomics to plant developmental biology and applied breeding. His work has characterized the genetic basis of traits ranging from seed color to pod shattering and early-season growth vigor. He has also published on novel drone data pipelines, key traits differentiating snap and dry beans, and the development of numerous markers and breeding resources.

As a plant breeder, he has developed and released six common bean cultivars specifically bred for organic systems. These were selected for yield and BCMV resistance on organic farms in the Western United States. In 2024, his variety UC Southwest Gold was awarded a Good Food Award for combining environmental sustainability with high culinary quality. He continues to select breeding lines adapted for sustainable production in regions such as the western United States and Africa.

Dr. Parker is also passionate about teaching. At UC Davis, he designed and taught a course titled "Drones in Agriculture", exploring the integration of aerial imaging technologies into crop science. In 2023, he developed and delivered a workshop series at UC Davis on video editing for scientists. He has given 22 guest lectures and labs, on topics ranging from intellectual property protections to plant reproductive biology. He has given 41 conference presentations across 10 countries and earned first place for the Early Career Poster Award at the National Association of Plant Breeders meeting in 2025. He has a YouTube channel with educational plant science content in four languages.

He greatly values international and intercultural partnerships, collaborating broadly with researchers across Africa, Europe, North and South America. He is committed to the reciprocal exchange of skills and knowledge, believing that communities are strongest when united and advancing together in pursuit of common goals.

Since 2022, Dr. Parker has been the lead scientific advisor for the Kirkhouse Trust's African Bean Consortium and also advises the Trust's cowpea breeding projects. In this capacity, he has made six advisory visits to the continent and has also welcomed four African researchers at UC Davis for extended training visits. In this time, the funded African teams have publicly released four new varieties of common bean, with many more in trials for future release.

PROVITA, INC

In Memory of Ron Shellenberger (1943-2015)

ProVita Inc. was started in 1997 as the dream and passion of Ron Shellenberger. Ron was already an accomplished dry bean breeder from his employment with Rogers Brothers Seed company (later Syngenta) throughout the 70's and 80's; when he decided to start his own plant breeding business in Kuna, Idaho. ProVita started like many American dreams do from scratch in a house and garage, but with the support of some incredible key industry members many of which are still investing and supporting the program to this day. Ron's legacy and foundation for success lives on through his sons and owners of ProVita (Matt, Luke, and Brian Shellenberger).

ProVita, Inc. started its breeding program with a focus on Pintos, Navies, and Great Northerns from 1997-2003; with the addition of Light Red Kidneys in 2003. In 2009 support for Small Reds, Blacks, Pinks, Yellows, Dark Red and White Kidneys, and Cranberries was established.

Much of ProVita's early success on pintos was through improved direct harvestable architecture and yield. There was an acknowledgment early in the program that upright pintos would be the way of the future even if direct harvest wasn't adopted. The improved disease avoidance, quality, and ease of growing were program objectives with the overall hope that direct harvest would be adopted as well. The pinto variety La Paz was instrumental in achieving these goals and helped growers with the widespread adoption of direct harvest of dry beans. La Paz and upright pintos expanded the use of Pintos to areas of North Dakota and US that didn't have dry beans as an option before direct harvest. HMS Medalist was the early successful variety in the navy beans and improved the archetype and yield for growers. Additionally it achieved the difficult task of being broadly adapted and preferred for growers in Michigan, Minnesota, and North Dakota. Objectives and improvements to Great Northerns were around seed quality, upright architecture, and yield. Orion was ProVita's early success in the great northern market class which achieved many of the goals set out to achieve.

ProVita set out to improve the Light Red Kidney genetics with a focus on disease resistance, yield, architecture, and seed quality. Early successes were with the varieties Big Red and Ronnie's Red (which was named by a client in honor of Ron Shellenberger). Big Red brought higher yields and stress/disease tolerances to the early maturing light red kidneys; while Ronnie's Red brought improved direct harvestable architecture and good stress/disease tolerance to the full season maturing segment of the market class.

ProVita has contributed the following varieties for use by the dry bean industry (varieties in bold still being used today): 19 pinto and slow darkening pinto varieties, 9 navy bean varieties, 9 great northern varieties, 6 light red kidney varieties, 7 black bean varieties, 5 dark red kidney varieties, 1 pink variety, 2 small red varieties, and 1 cranberry variety. Use of some of the varieties above have expanded beyond the U.S. to Canada and the European Union.

It has been the great privilege and honor for everyone at ProVita to work with such a great industry. The support from dealers, growers, other private breeders, universities, USDA, and this BIC community have all contributed in the success of our company and for that we are grateful. Private breeders, the USDA, universities and the BIC have been important resources for germplasm exchange as well as knowledge advancement. We look forward to continuing to serve and hopefully improve this dry bean industry we are a part of for many years to come.

HÉCTOR FABIO BUENDIA

Mr. Héctor Fabio Buendía has been a cornerstone of the Bean Program at the Alliance of Bioversity International and CIAT in Colombia since 2000. Originally from Ibagué, Colombia, Héctor earned his degree in Agricultural Engineering from the University of Tolima. He began his career at CIAT as an intern in the molecular lab under Dr. Matthew Blair, where he mastered advanced laboratory techniques, including marker-assisted selection, mapping populations, and QTL identification for both quantitative and qualitative traits. Notably, he contributed to the development of microsatellite markers, which proved instrumental in early studies on population and race structure in common beans.

After eleven years in the lab, Héctor transitioned to the field breeding team led by Dr. Steve Beebe, focusing on agronomic management. Over time, he advanced through various roles to his current position as operations manager. In this capacity, Héctor has consistently demonstrated exceptional leadership, technical expertise, and a remarkable ability to collaborate across disciplines. His contributions have been both strategic and transformative. During the COVID-19 pandemic, he led a major restructuring of the program to improve operational efficiency. He also designed a training program in plant breeding fundamentals for field staff in Colombia and actively participated in CIAT's committee on regenerative agriculture. His training efforts extended beyond Colombia, reaching molecular biologists in Africa, both within the Alliance and in the NARs.

Héctor's deep knowledge of the crop has enabled him to make strategic selections of advanced breeding lines and provide expert guidance on parental combinations. He introduced index selection into the breeding process and routinely applied complex crossing strategies—including simple, double, and triple crosses, as well as advanced backcrosses—to integrate key traits. Under the guidance of Dr. Bodo Raatz and Dr. Karen Cichy (MSU), he has also explored phenotyping for consumer traits such as cooking time and canning quality, helping to establish these platforms in Kawanda, Uganda.

Throughout his career, Héctor has played a key role in developing dry bean varieties at CIAT, including drought-tolerant Andean lines, heat-tolerant interspecific lines, and biofortified types—three of which were recently released in Colombia. He has also contributed significantly to the development of market-specific bean types for Africa, including yellow beans for Tanzania, climbing beans for Rwanda, Uganda, and Burundi, and numerous red-mottled and red lines (DAB, NUA) released across Burundi, Ethiopia, Kenya, Zambia, Mozambique, and Malawi. Additionally, he has played a key role in selecting small red and small white beans now released in Rwanda, Ethiopia, Kenya, Tanzania, Uganda, and Burundi.

In addition to his breeding work, Héctor has co-authored several peer-reviewed publications spanning diverse research areas such as genomic prediction, heat stress physiology and genetics, symbiotic nitrogen fixation, disease resistance, and variety development. His contributions have had a lasting impact on the Bean Program and the broader research community, making him a truly deserving recipient of the BIC Technical Merit Award.

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

Year	Award List
1970	Melvin E. Anderson, Rogers Bros. Seed Co., Plant Pathologist William A. Frazier, Oregon State University, Horticulturist Walter H. Pierce, Asgrow Seed Co., Plant Pathologist William J. Zaumeyer, USDA, Plant Pathologist
1971	Walter H. Burkholder- Cornell Univ., Plant Pathologist James R. Douglass- USDA, Entomologist Howard S. Gentry- USDA, Plant Explorer Charles W. Hungerford- Univ. of Idaho, Plant Pathologist Herbert A. K. Lamprecht- Pl. Breeding Inst. of Sweden, Geneticist John J. Natti- Cornell Univ., Plant Pathologist Melbourne C. Parker- Gallatin Valley Seed Co., Plant Breeder Francis L. Smith- Univ. of California, Agronomist Robert E. Wester- USDA, Plant Breeder
1973	Leslie L. Dean- Univ. of Idaho, Plant Pathologist Nicolas Hubbeling- Inst. of Phyto. Res.- Netherlands, Plant Pathologist
1975	Leslie L. Dean, University of Idaho, Plant Pathologist Nicolaas Hubbeling, Institute of Phytopathological Research, Netherlands, Plant Pathologist M. Wayne Adams, Michigan State University, Plant Breeder Dermot P. Coyne, University of Nebraska, Plant Breeder Shigemi Honma, Michigan State University, Plant Breeder Max L. Schuster, University of Nebraska, Plant Pathologist
1977	Douglas W. Burke, USDA, Plant Pathologist Roelof Prakken, Utrecht University of the Netherlands, Geneticist Clibas Vieira, Federal University of Vicosa, Brazil, Agronomist Barbara J. Ballantyne, New South Wales, Plant Pathologist Donald J. Hagedorn, University of Wisconsin, Plant Pathologist Marshall LeBaron, University of Idaho, Agronomist
1979	Eelco Drijfhout, Agricultural Institute of the Netherlands, Plant Breeder Donald H. Wallace, Cornell University, Plant Breeder Donald R. Wood, Colorado State University, Plant Breeder Leland W. Hudson, USDA, Horticulturist Roger F. Sandsted, Cornell University, Horticulturist
1982	Michael H. Dickson, Cornell University, Plant Breeder Aart van Schoonhoven, CIAT, Entomologist

Year	Award List
	Frederick A. Bliss, University of Wisconsin, Plant Breeder Matt J. Silbernagel, USDA, Plant Pathologist
1983	Axel L. Andersen, Michigan State University, Plant Breeder/Pathologist John D. Aktin, Asgrow Seed Co., Plant Breeder Colin L.A. Leakey, England, Geneticist Alfred W. Saettler, USDA/ARS, Plant Pathologist Arthur P. Sprague, Del Monte, Plant Breeder James R. Steadman, University of Nebraska, Plant Pathologist J.C. "Mike" Tu, Agriculture Canada, Plant Pathologist
1987	Iver L. Jorgensen, Northrup King & Co., Plant Breeder John L. Morris, Rogers/NK Seed Co., Plant Breeder Rosario Provvidenti, Cornell University, Plant Pathologist Shree P. Singh, CIAT, Plant Breeder J. Rennie Stavely, ARS/USDA-Beltsville, Plant Pathologist Daniel Debouck, IBPGR, Rome, Plant Geneticist [Achievement Award] Paul L. Gepts, University of California-Davis, Plant Geneticist [Achievement Award] Pat Barnes-McConnell, Bean/Cowpea CRSP, Director [Achievement Award]
1991	Hubert L. Bannerot, INRA, Versailles, Plant Breeder Cesar Cardona, CIAT, Entomologist Robert B. Colville, Del Monte Foods, Variety Development George L. Hosfield, ARS/USDA, East Lansing, Genetics/Nutrition Oswaldo V. Voysest, CIAT, Agronomy/Germplasm Evaluation James S. Beaver, University of Puerto Rico, Plant Breeder [Achievement Award]
1993	Howard F. Schwartz, Colorado State University, Plant Pathologist Kenneth F. Grafton, North Dakota State University, Plant Breeder [Achievement Award]
1995	George Emery, Ferry Morse, Plant Breeder James D. Kelly, Michigan State University, Plant Breeder Steve Magnuson, Harris Moran, Plant Breeder David Nuland, University of Nebraska, Bean Extensionist Phillip Miklas, USDA-ARS, Prosser, WA, Plant Geneticist [Achievement Award]
1997	James R. Baggett, Oregon State University, Plant Breeder James S. Beaver, University of Puerto Rico, Plant Breeder

Year	Award List
	<p>Phillip McClean, North Dakota State University, Geneticist [Achievement Award]</p> <p>James Myers, Oregon State University, Plant Breeder [Achievement Award]</p> <p>Dermot P. Coyne, University of Nebraska, Plant Breeder [Frazier-Zaumeyer Distinguished Lectureship]</p>
1999	<p>Mark J. Bassett, University of Florida, Plant Geneticist</p> <p>Soon J. Park, Agriculture and Agri-Food Canada, Plant Breeder</p> <p>Mark A. Brick, Colorado State University, Plant Breeder [Achievement Award]</p> <p>Ron Riley, Syngenta, Plant Breeder [Achievement Award]</p> <p>Juan Carlos Rosas, Escuela Agricola Panamericana, Honduras, Plant Breeder</p> <p>Fredrick A. Bliss, Seminis Seeds, Plant Breeder [Frazier-Zaumeyer Distinguished Lectureship]</p>
2001	<p>Steve Beebe, CIAT, Colombia, Plant Geneticist</p> <p>Paul Gepts, University of California, Plant Geneticist</p> <p>Marcial A. “Talo” Pastor-Corrales, USDA-ARS, Beltsville, Plant Pathologist</p> <p>Perry B. Cregan, USDA-ARS, Beltsville, Geneticist, Soybean Genomics [Frazier-Zaumeyer Distinguished Lectureship]</p>
2003	<p>Jorge A. Acosta Gallegos, INIFAP, Mexico, Plant Breeder</p> <p>Phillip N. Miklas, USDA-ARS, Prosser, Plant Geneticist</p> <p>David M. Webster, Seminis Seeds, Plant Breeder</p> <p>A. “Bert” Vandenberg, University of Saskatchewan, Plant Breeder [Achievement Award]</p> <p>Molly Jahn, University of Wisconsin, Plant Geneticist and Dean CALS [Frazier-Zaumeyer Distinguished Lectureship]</p>
2005	<p>Robert L. Gilbertson, University of California-Davis, Plant Pathologist</p> <p>Walter Edwin (Ed) Kee Jr., University of Delaware, Vegetable Specialist</p> <p>Hans Henning Muendel, Agriculture and Agri-Food Canada, Lethbridge, Plant Breeder</p> <p>Matthew W. Blair, CIAT, Colombia, Plant Breeder [Achievement Award]</p>
2007	<p>Maurice Bennink, Michigan State University, Nutritionist [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>Henry Thompson, Colorado State University, Nutritionist [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>Mark Brick, Colorado State University, Plant Breeder</p>

Year	Award List
2009	<p>Phillip McClean, North Dakota State University, Geneticist [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>Kenneth F. Grafton, North Dakota State University, Plant Breeder and Dean, Director, & Vice President of Agriculture</p> <p>Juan Jose Ferreira Fernández, SERIDA Spain, Plant Breeder [Achievement Award]</p> <p>Timothy G. Porch, USDA-ARS, Mayaguez, Plant Geneticist [Achievement Award]</p> <p>Carlos A. Urrea Florez, University of Nebraska, Plant Breeder [Achievement Award]</p>
2011	<p>James D. Kelly, Michigan State University, Plant Breeder [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>James Nienhuis, University of Wisconsin, Plant Breeder</p> <p>K. Peter Pauls, University of Guelph, Plant Geneticist</p> <p>Kirstin E. Bett, University of Saskatchewan, Plant Geneticist [Achievement Award]</p> <p>Thomas Smith, University of Guelph, Research Technician [Technical Merit Award]</p>
2013	<p>Paul Gepts, University of California-Davis, Plant Geneticist [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>Karen A. Cichy, USDA-ARS, East Lansing, Plant Geneticist [Achievement Award]</p> <p>Juan M. Osorno, North Dakota State University, Plant Breeder [Achievement Award]</p>
2015	<p>David M. Kramer, Michigan State University, Photosynthesis and Bioenergetics [Frazier-Zaumeyer Distinguished Lectureship]</p> <p>Maria Celeste Gonçalves-Vidigal, Plant Geneticist [Meritorious Service Award]</p> <p>Gregory V. Varner, Research Director [Meritorious Service Award]</p> <p>Irvin E. Widders, Director of the Legume Innovation Lab [Meritorious Service Award]</p> <p>Deidré Fourie, ARC Grain Crops Institute, Plant Pathologist [Achievement Award]</p> <p>Clare Mukankusi Mugisha, CIAT Uganda, Plant Breeder [Achievement Award]</p> <p>Rian Lee, Research Technician [Technical Merit Award]</p> <p>Evan M. Wright, Research Technician [Technical Merit Award]</p>
2019	<p>James Beaver, University of Puerto Rico, Plant Breeder [Frazier - Zaumeyer Distinguished Lectureship]</p> <p>Juan Carlos Rosas, Zamorano University, Professor and Bean Breeder [Frazier - Zaumeyer Distinguished Lectureship]</p>

Year	Award List
	<p>James R. Myers, Oregon State University, Professor [Meritorious Service Award]</p> <p>Sara F. Rose, Bush Brothers Company, Director of Research [Meritorious Service Award]</p> <p>Frédéric Marsolais, Agriculture and Agri-Food Canada, Research Scientist [Distinguished Achievement Award]</p> <p>Albert Jody Vander Wal, North Dakota State University, Research Technician [Technical Merit Award]</p>
2021	No awards
2023	<p>Karen Cichy, USDA, ARS, East Lansing, Michigan, Research Scientist [Frazier - Zaumeyer Distinguished Lectureship]</p> <p>Raymond Glahn, USDA-ARS, Ithaca, New York, Physiologist [Frazier - Zaumeyer Distinguished Lectureship]</p> <p>Daniel G. Debouck, CIAT, Colombia, Emeritus Scientist [Meritorious Service Award]</p> <p>Antonio M. De Ron, Spanish National Research Council, Ad Honorem Professor [Meritorious Service Award]</p> <p>Emmalea Ernest, University of Delaware, Assistant Professor [Distinguished Achievement Award]</p> <p>Consuelo Estévez de Jensen, University of Puerto Rico, Professor [Distinguished Achievement Award]</p> <p>Aldemaro Clara, CENTA, San Salvador, Bean Breeder [Distinguished Achievement Award]</p> <p>Antonia Palkovic, University of California, Assistant Project Scientist [Technical Merit Award]</p>
2025	<p>James R. Myers, Oregon State University, Professor Emeritus [Frazier - Zaumeyer Distinguished Lectureship]</p> <p>C. Robin Buell, University of Georgia, Professor [Frazier - Zaumeyer Distinguished Lectureship]</p> <p>In Memory of Phil McClean, North Dakota State University, Professor [Meritorious Service Award]</p> <p>Ken Kmiecik, Ken Kmiecik, LLC, Bean Breeder [Meritorious Service Award]</p> <p>Rigoberto Rosales-Serna, INIFAP, Mexico, Bean Breeder [Meritorious Service Award]</p> <p>Kelvin Kamfwa, University of Zambia, Senior Lecturer and Leader of the Legume Breeding Program [Distinguished Achievement Award]</p> <p>Travis Parker, University of California, Assistant Professional Researcher [Distinguished Achievement Award]</p> <p>Provita, Inc. In Memory of Ron Shellenberger (1943-2015), Kuna, Idaho [Distinguished Achievement Award]</p>

Year	Award List
	Héctor Fabio Buendía, Alliance of Bioversity International and CIAT Palmira, Colombia, Operations Manager [Technical Merit Award]

BIC GENETICS COMMITTEE MEETING MINUTES

November 6, 2025; 4-5pm

Lincoln, Nebraska

Committee Members: Branham, Brown, Diepenbrock, Dohle, Ferreira, Gepts, Goncalves-Vidigal, He, Miklas, Osorno, Parker (Chair), Porch, Urrea

Zoom link - Optional (helpfully set up by Christine): <https://ucdavis.zoom.us/j/8208866818>

Meeting ID: 820 886 6818; no password

Minutes Recorded by Emmalea Ernest

Genetics Committee Members (all): Branham, Brown, Diepenbrock, Dohle, Ferreira, Gepts, Goncalves-Vidigal, He, Miklas, Osorno, Parker (Chair), Porch, Urrea

Members Present: Branham, Brown, Diepenbrock, Osorno, Parker (Chair), Urrea

The committee discussed inclusion of *Co-18* (Lateef et al. 2019), and *Co-19* (Badiyal et al. 2024) in the Gene List:

Both are anthracnose genes described in recent publications that are mapping to locations where no previous *Co* loci have been mapped however not all named *Co* genes have been mapped (e.g. *Co-11* and *Co-12*).

Travis Parker made a motion to include *Co-18*, *Co-19* in the gene list. Juan Osorno seconded the motion. The motion was unanimously approved by the committee.

The committee discussed the conventions for gene nomenclature. Should gene names include linkage group and source? E.g., *CoPv01^{CDRK}* vs. *Co-20^{CDRK}*? Or *Co-I²* vs. *Co-I^{Kaboon}*?

Travis Parker made the following motion: Continue using sequential numbering for resistance loci. The first time the gene is named, no superscript needs to be included in the name. Subsequent alleles indicate the origin with superscript. Juan Osorno seconded the motion, and it was unanimously approved by the committee.

The committee discussed the logistics of getting researchers to follow standard naming conventions. Ideally, new names should be submitted to the BIC Genetics Committee before publication. Then the BIC GC chair will send the request to committee members for review/comment. If a committee member is a peer reviewer for a paper publishing a new gene, recommend that the authors contact the committee regarding naming conventions and review. Additionally, the BIC GC committee chair should review the information on the BIC GC webpage regarding gene name submissions

Action Item: Review information on the BIC GC committee web page, especially related to submitting new genes/names to committee for review and what information researchers/authors need to provide.

The committee discussed updates to the tm-shift/gene model table. This table may be accessed through the BIC Genetics Committee page on the BIC website

(https://www.bic.uprm.edu/?page_id=91) New information could be added to this table. There is also a table maintained by CGIAR at this site:

<https://excellenceinbreeding.org/toolbox/tools/kasp-low-density-genotyping-platform>. The committee discussed whether to integrate information from the CGIAR table into the BIC GC table or to direct users of the BIC GC website to the CGIAR website.

Action Item: Add link to BIC GC website linking to CGIAR in some way. Committee recommendation a to link to the CGIAR genotyping-platform page

<https://excellenceinbreeding.org/toolbox/tools/kasp-low-density-genotyping-platform>.

There are some inconsistencies in the existing table on the BIC GC website, and updates may be needed. Updates or new information to add to the table should be emailed to Travis Parker. For new additions, send a revised version of the Excel file that contains the information in a new row.

Discussion

- Lima bean sequences could be added to the table in a new tab.
- Can we make it a requirement that people include new genes or markers presented at the BIC in the table? No – some of the data is too preliminary. Only validated markers that are being used should be added.
- Should the person who compiles the BIC report contact people who might have information that should be added to the table?
- Should there be a presentation at the next BIC meeting about the Genetics Committee and the resources on the website?

Action Items: (1) Add information about the BIC GC, gene naming and GC resources to the email to BIC members asking for reports. Encourage members to submit gene names and marker information. (2) Make an announcement about the BIC Genetics Committee and resources at the next BIC meeting.

Travis will send an email regarding correspondence from Celeste Goncalves-Vidigal.

Membership Updates

Jenna Hershberger, Miranda Haus and Burcu Celebioglu expressed interest in joining the BIC Genetics Committee.

Juan Osorno made a motion that J. Hershberger, M. Haus and B. Celebioglu be added to the BIC GC. Travis Parker seconded the motion. The motion was approved.

Committee Adjourned.

GENETIC IMPROVEMENT OF NAVY BEAN CULTIVARS RELEASED IN SOUTHWESTERN ONTARIO BETWEEN 1940 -2011

Alireza Navabi¹, Andrew J. Burt², Chris Gillard², Manilal William², K. Peter Pauls²

¹ Agriculture and Agri-Food Canada (AAFC) Greenhouse and Processing Crops Research Centre, Harrow, ON, Canada.

² Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.

ABSTRACT

Genetic gain advances achieved through crop breeding efforts can be estimated by evaluating the advances in yield and agronomic parameters of cultivars released over a period of time. The yield and agronomic aspects of 27 navy bean cultivars used between 1940 -2011 in Southwestern Ontario were studied to evaluate the improvements and genetic gains achieved through sixty years of bean improvement efforts. Significant varietal effects and variety environmental interactions were observed for yield, days to maturity, 100 kernel weight, canopy height, harvestability and Common Bacterial Blight (CBB) resistance. More-recently released cultivars had significantly improved yield, possessed predominantly Type II growth habit and were better adapted to Ontario bean growing environments. Bean yields for varieties released in the 1950s were approximately 2.4 t/ha, whereas those released after 2005 had yields greater than 3.4 t/ha, which represents an annual genetic gain of 0.86 t/ha among the 27 navy bean cultivars released between 1940 to 2011.

MATERIALS AND METHODS

Agronomic and disease resistance trials were conducted over three years with 27 navy bean cultivars used in Southwestern Ontario between 1940 -2011. The varieties were analysed for yield, 100 kernel weight, days to maturity, canopy height and harvestability. Additionally, they were tested for their susceptibility to CBB caused by *Xanthomonas axonopodis* pv *phaseoli* and *Xanthomonas citri* pv. *fuscans* as well as anthracnose caused by *Colletotrichum lindemuthianum* (race 73). The 27 cultivars used in the study were genotyped to identify single nucleotide polymorphisms (SNPs) with an Illumina Infinium iSelect Custom Genotyping BeadChip (BARCBEAN6K_3) at Genome Quebec Innovation Center at McGill University, Quebec, Canada.

RESULTS

Similarity comparisons, based on nearly 5,000 single nucleotide polymorphisms (SNPs) indicated that the 27 cultivars formed three distinct clusters (data not shown). The groupings of the individuals in the clusters agreed with their

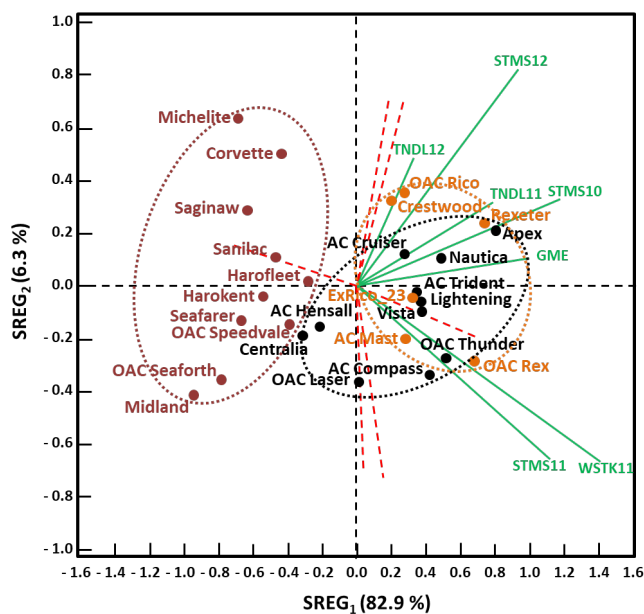


Figure 1. Site regression analysis of genotype and genotype by environment interaction (GGE) of twenty-seven navy bean cultivars grown across seven location/years (in green). The ellipses and font colours identify three groupings of genotypes based on SNP similarities.

pedigrees and highlighted the importance of common parents, such as Seafarer, ExRico, Michelite and Robust in the genetic base of these Ontario grown cultivars.

Most of the yield variation observed in the study resulted from genotype and genotype*environment effects. A site regression (SREG) analysis identified a highly significant PC1 ($p < 0.0001$) that explained 82.9% of the variation observed (Fig. 1). The SREG analysis showed that the most recently released varieties (like Apex and Rexeter) were more adapted to the test sites in Ontario than the earlier introduced navy bean varieties (like Michelite and Saginaw).

Although there were advances in developing improved resistance to CBB, a majority of the varieties showed a high degree of susceptibility. In contrast, the varieties that had lines in their pedigrees with a source of CBB resistance from interspecific hybridization with *Phaseolus acutifolius* (like OAC Rex, Rexeter and Apex) had good resistance to CBB. Most of the more recently released varieties were susceptible to anthracnose, which is another important disease in Ontario. Highly significant correlations were observed between yield and resistance to common bacterial blight and anthracnose, which highlight the importance of developing bean cultivars with yield stability under disease pressure.

Significant advances were made in increasing the yield potential and improving the growth type amenable to mechanized farming operations (Fig. 2). More-recently released cultivars had significantly improved yield, possessed predominantly Type II growth habit and were better adapted to Ontario bean growing environments. An annual genetic gain of 0.86 t/ha was achieved among the 27 navy bean cultivars released between 1940 to 2011.

CONCLUSIONS

The data indicates that there was a gradual improvement in the yield potential of cultivars released between 1940-2011 as well as improvements in agronomic parameters including harvestability and plant architecture. The SREG analysis also indicated that a number of the most-recently released cultivars have yield performances that are adapted to the testing environments in Ontario.

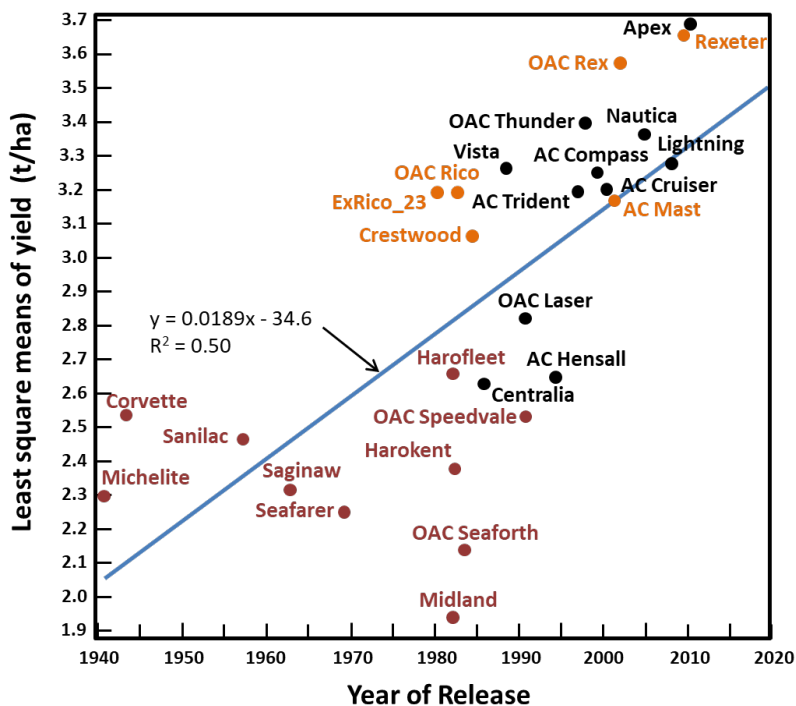


Figure 2. Fig. 2. Combined least square mean values of yield (t/ha) across sites and years plotted against the year of release. The font colours identify three groupings of genotypes based on SNP similarities.

ROOT ARCHITECTURE, SEED SIZE, AND SEEDLING ESTABLISHMENT IN WILD ANDEAN AND MIDDLE AMERICAN BEAN ACCESSIONS

Paige Smith¹; Viviana Ortiz Londoño², Miranda J. Haus²

¹ Plant Resilience Institute Michigan State University, East Lansing, MI, USA; ²Department of Horticulture, Michigan State University, East Lansing, MI, USA

INTRODUCTION:

Two major concerns from the Phaseolus Crop Germplasm Vulnerability Report¹ are genetic vulnerability and the capacity of current cultivars to respond to emerging biotic and abiotic stressors. Wild *Phaseolus vulgaris* accessions represent a major untapped reservoir of adaptive variation, including root traits that govern seedling establishment, resource capture, and interactions with soil environments. *P. vulgaris* was independently domesticated twice in two geographically distinct climates resulting in the Andean and Middle American gene pools. The phenotypic diversity in wild materials may provide novel sources of phenotypic variation, especially within root system traits. Here, we characterize seed traits, early developmental timing, and root architecture to test if they differ between wild Andean and Middle American accessions and cultivation status. We further aim to use this data to ask if climate and soil gradients associated with collection origins help explain structured variation in root phenotypes.

MATERIALS & METHODS:

We evaluated 152 georeferenced wild and landrace *P. vulgaris* accessions in a greenhouse setting. Seeds were imaged and measured for size and shape using ImageJ. Each accession was grown in rhizoboxes (at a 45° angle) and monitored over a 10-day period to capture timing of developmental stages. At the end of the 10 day period, roots were imaged, processed with RootPainter², and quantified using RhizoVision Explorer³ to extract architectural traits. Using the latitude and longitude of each accession's collection region, standardized climate variables (WorldClim⁴ BIO variables) and soil properties (SoilGrids⁵) were collated. Distance-based redundancy analysis (dbRDA) was used to estimate how much variation in root traits could be explained by climate, soil, and spatial factors.

RESULTS:

Seed traits differed between the Middle American and Andean gene pools in accordance with cultivated lines in that Andean accessions were on average larger and less circular than Middle American accessions. Early establishment patterns were not uniform across gene pools in that time to reach developmental stages of seedling establishment was positively correlated with seed size in Andean accessions ($R^2 = 0.3$ to 0.6), whereas the relationship was weaker and less consistent in Middle American accessions ($R^2 < 0.001$ to 0.3). This may suggest gene pool-specific differences in early vigor or nutrient prioritization. Multivariate analyses of 24 root architecture traits indicated that accessions can be separated by both gene pool and cultivation status (wild vs. landrace). Overall, the total root length, convex area, average diameter, and branching patterns contributed most to the variation in the population. Andean roots tended to have fewer, thicker, and shallower roots compared to the Middle American accessions.

WorldClim and SoilGrid data identified that collection regions occupy distinct climate and soil space, with greater climatic diversity among collection regions for Middle American accessions. Climate and soil variables could partially explain root trait variation: climate predictors accounted for approximately 20–32% of variance in root traits in dbRDA models, with climate effects

generally exceeding soil and spatial (geographical) components. The greatest contributors explaining root traits included minimum temperature of the coldest month (BIO6), precipitation of the driest quarter (BIO17), mean temperature of the driest quarter (BIO9), sand fraction, and soil pH.

TABLE 1. Summary of key findings and environmental predictors

Result category	Summary
Seed traits & establishment	Seed traits differ between Andean vs Middle American accessions; seedling establishment is positively associated with seed size in Andean accessions, but not consistently in Middle American accessions.
Root architecture structure	Root architectural traits separate accessions by gene pool and cultivation status (wild vs. landrace) in multivariate space.
Environmental differentiation	Collection regions differ in climate/soil context; Middle American regions span broader environmental diversity.
Variance explained (dbRDA)	Climate explains ~20–32% of variance in root traits; climate effects generally exceed soil and spatial factors.
Top predictors	BIO6 (min temp coldest month), BIO17 (precipitation driest quarter), BIO9 (mean temp driest quarter), sand, and soil pH.

CONCLUSIONS:

These data demonstrate that wild *P. vulgaris* germplasm variation in seed traits, early establishment, and root architecture that aligns with major evolutionary history: specifically gene pool, cultivation status, and collection region. Further work is needed to evaluate the relationship between seed size and establishment specifically on shoot/root coordination as a target trait for early vigor and stress resilience. Most excitingly, the finding that climate variables explain a substantial fraction of root trait variation supports the hypothesis that adaptive root phenotypes are linked to environmental gradients at collection origins. This will allow us to curate a subset of accessions to further characterize under extreme stress conditions relevant to climate change (e.g., cold and drought), potentially translating these traits into breeding pipelines aimed at improving stress resilience.

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HIGH-THROUGHPUT SCREENING APPROACH TO ENHANCE SYMBIOTIC NITROGEN FIXATION IN DRY BEANS

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INTRODUCTION:

Legumes form symbiotic associations with nitrogen-fixing rhizobia, which convert atmospheric nitrogen into a form usable by plants, reducing the need for synthetic fertilizers. Dry beans (*Phaseolus vulgaris*) generally show lower nitrogen fixation. One possible explanation for this reduced efficiency is the broad host range of dry beans, which allows association with diverse rhizobial strains, many of which may be suboptimal nitrogen fixers or poor competitors. As a result, highly efficient rhizobia may fail to dominate nodule occupancy under field conditions.

To address this limitation, we conducted a high-throughput competition experiment using a diverse library of rhizobial isolates obtained from dry bean nodules collected in North Dakota and Minnesota. The goal of this study was to identify rhizobial strains that are highly competitive across different market classes of dry beans and under stress conditions, thereby enabling the selection of elite candidates for improved inoculant development.

MATERIALS AND METHODS:

Bacteria were isolated from root nodules of dry bean plants collected from fields in North Dakota and Minnesota. The nodules were cleaned, crushed, and grown on nutrient plates to obtain individual bacterial strains. Barcoded plasmids present in *E. coli* was transferred into the rhizobial isolates using a conjugation-based method. The resulting strains were mixed in equal amounts and used to inoculate sterilized dry bean seedlings grown under nitrogen-free greenhouse conditions. The experiment was performed on Black (ND Galaxy), Kidney (ND Redbarn) and Pinto (ND Rodeo) along with 400‰ (5.68 gm Na₂SO₄ and 4.8 gm MgSO₄/ kg of soil) and 800‰ 11.36 gm Na₂SO₄ and 9.6 gm MgSO₄/ kg of soil) salinity treatment on black beans. After three weeks, plants were harvested and root nodules were collected to evaluate how well each bacterial strain competed for nodule formation.

RESULTS AND DISCUSSION:

Using a high-throughput plasmid ID-based approach, we simultaneously evaluated the competitiveness of approximately 300 rhizobial isolates in mixed inoculation experiments. This strategy enabled the identification of several rhizobial strains that consistently outcompeted others for nodule occupancy. Notably, some highly competitive strains were found to be specific to particular market classes of dry beans black, pinto, or kidney beans as indicated in Figure 1a (red arrows). This suggests that host genotype plays a role in shaping rhizobial competitiveness.

In addition, certain rhizobial isolates exhibited enhanced competitiveness under salt stress conditions Figure 1a (red box), indicating stress tolerance as an important trait influencing successful symbiosis. Importantly, a subset of rhizobia displayed high competitiveness across all

three bean market classes and maintained their performance under salinity stress (Figure 1d). These strains represent promising candidates for broad-spectrum inoculant development.

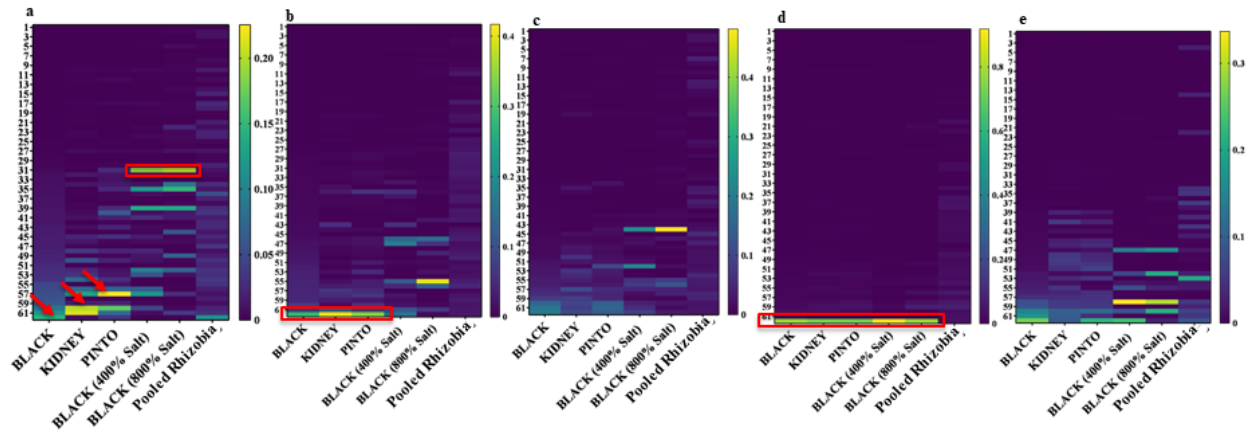


Figure 1. Heat map showing the relative abundance of rhizobial strains in root nodules following the competition assay. Numerical labels indicate the strains competed together. Yellow represents the most abundant (highly competitive) rhizobial strains, while blue indicates low abundance (less competitive) strains. The pooled rhizobia column shows the relative abundance of each strain in the inoculum.

Based on the results of the initial screening, a second round of competition assays was conducted using 11 highly competitive rhizobial strains, along with three known inefficient strains included as controls selected from first set of experiment. This focused competition experiment enabled finer discrimination among top-performing isolates. From this analysis, two rhizobial strains emerged as consistently dominant competitors across three market classes (Figure 2a–c, red boxes). Additionally, three strains demonstrated moderate but reproducible competitiveness, particularly in pinto beans.

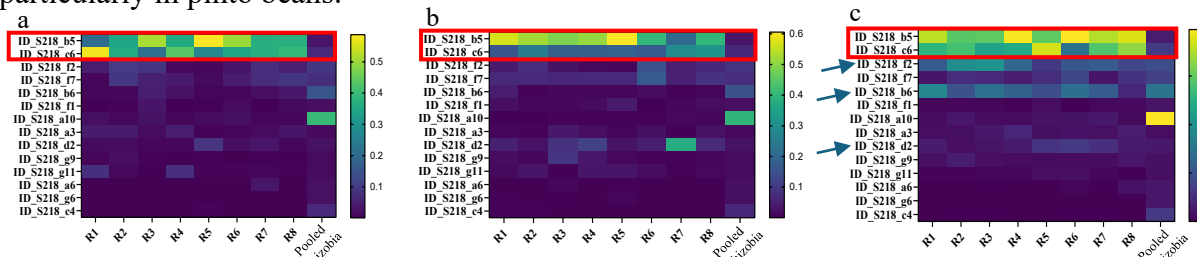


Figure 2. Heat map showing the relative abundance of rhizobial strains in Black (a), Kidney (b), and Pinto (c) bean nodules. Rhizobia highlighted in red boxes are highly competitive across all three bean market classes. Blue arrows indicate rhizobial strains that are highly competitive only in pinto beans.

To further refine candidate selection, the nitrogen fixation efficiency of these five competitive rhizobial strains will be evaluated and compared with well-characterized nitrogen-fixing strains currently used for dry bean inoculation. Integrating competitiveness data with nitrogen fixation performance will allow identification of elite rhizobial partners optimized for dry bean cultivation, with potential applications in sustainable agriculture.

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PROJECT LIMA!: DEVELOPMENT OF RESOURCES TO ACCELERATE LIMA BEAN BREEDING FOR AGRONOMIC AND QUALITY TRAITS

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INTRODUCTION:

Lima bean (*Phaseolus lunatus* L.) is the second most economically important *Phaseolus* species, but significant bottlenecks exist for its production, consumption, and breeding. Here, in a USDA NIFA Specialty Crop Research Initiative (SCRI)-funded project called LIMA!, we address three primary bottlenecks: 1) the Consumer & Grower Information Bottleneck, to understand consumer perceptions and preferences, identify production constraints for lima bean, and promote awareness of the crop; 2) the Pre-Breeding Bottleneck, to promote the accessibility of diverse germplasm through crosses with temperate-adapted lines; and 3) the Germplasm Utilization Bottleneck, to characterize the genetic, genomic, phenotypic, and phenomic diversity of lima bean germplasm (Fig. 1).

RESULTS AND DISCUSSION:

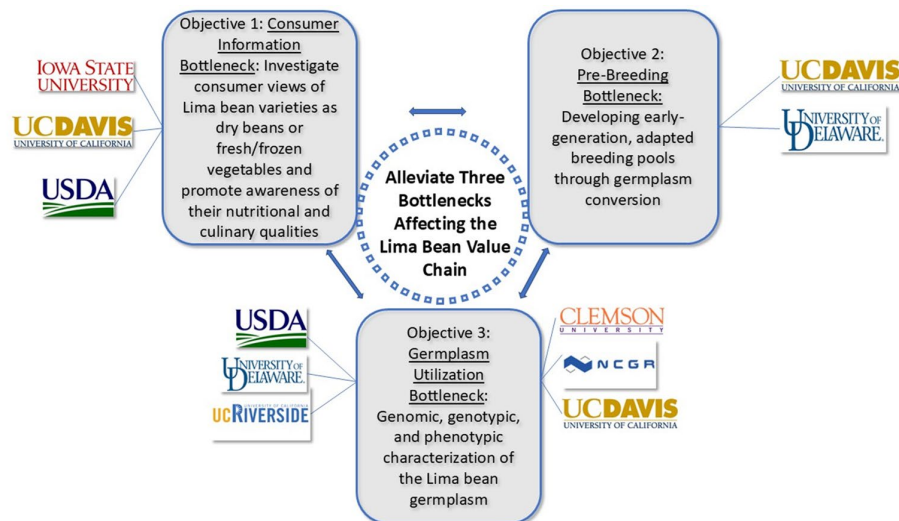
Consumer knowledge and perceptions of lima bean were assessed through a nationwide survey with 2,164 respondents. Lima bean consumption varied regionally, from 43% of respondents in the North-Central U.S. to 74% in the Middle Atlantic region. Lima beans were consumed slightly more by women than by men (42% vs 37%). Baby limas were consumed by more respondents (37%) than large limas (31%). Presentations for agricultural audiences in 2025 occurred in Delaware (3), California (1), New Jersey (1), South Carolina (2), and Washington (4). Novel drone methods and educational resources developed by the project in 2025 include a website ([PlantScienceDroneMethods.GitHub.io](https://plantsciencedronemethods.github.io)), a methods paper (Parker et al. 2025), and four educational YouTube videos (<https://www.youtube.com/@travisarkerplantscience>). In terms of pre-breeding, numerous wide crosses have been made between temperate-adapted lines and diverse tropical or otherwise unadapted materials. For example, USDA-NPGS has created 33 populations derived from 17 exotic donors, including 10 with resistance to both major root-knot nematode species *Meloidogyne incognita* and *M. javanica*. We have characterized candidate mutations for key adaptation and domestication traits, such as photoperiod sensitivity and growth habit, and developed selectable PACE/KASP markers to screen them. These markers have been deployed on adapted/exotic pre-breeding populations. We have grown all available lima beans

(~750 accessions) from the USDA National Plant Germplasm System (NPGS), and following single-seed descent and scoring of descriptive traits, genotyped them using low-coverage, short-read sequencing. Approximately 350 of the genotyped accessions were screened in multi-environment field trials for agronomic and seed compositional/quality traits, and lima core collections were identified that incorporate these and other genotyped accessions. Seven recombinant inbred populations have also been genotyped using RAD-seq and phenotyped to understand the basis of key pathogen resistances, heat tolerance, phenology, plant architecture, and seed quality. Whole-genome sequencing and assembly has been conducted on a subset of interest. Sensory descriptive analyses of succulent and dry lima beans have been conducted for the first time. These have characterized flavor/taste, texture/mouthfeel, and visual appearance profiles and consumer perceptions in detail across a range of lima bean germplasm, with green/yellow-seeded succulent limas and white-seeded dry limas generally associated with “buttery” and “sweet”, resulting in higher overall liking than those with phenolic-pigmented seed coats that were associated with bitter flavors. The project has supported the regeneration and characterization of the lima bean USDA NPGS collection, of which only 30% had sufficient seed available at the start of the project to allow for distributions. Future activities nearing completion include a set of standardized ontology terms for lima bean, as well as a project website available at <https://lima.ucdavis.edu/>.

CONCLUSION:

Resources recently developed by the LIMA! project will benefit stakeholders across the lima bean supply/demand stream, with a broad range of deliverables. These resources will strengthen the lima bean industry and improve options for consumers globally.

Figure 1. LIMA! project overview, including the objectives to address the three major bottlenecks, and institutions involved.



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GENOTYPIC AND MULTI-ENVIRONMENT PHENOTYPIC EVALUATION OF THE LIMA USDA NPGS COLLECTION

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INTRODUCTION

Lima bean (*Phaseolus lunatus* L.) is an economically and agronomically important grain legume. Lima beans were independently domesticated in the Andes (flat, large-seeded types) and Mesoamerica (round, small-seeded or flat, medium-seeded types) (Gutiérrez Salgado, Gepts and Debouck 1995). The USDA National Plant Germplasm System (NPGS at Pullman, WA) maintains a *Phaseolus* collection, including an extensive lima bean collection sourced from around the world with varying levels of improvement. Here, we generated and integrated genotypic and comprehensive field- and laboratory-based phenotypic data for the available accessions in this collection across multiple environments to inform germplasm utilization in breeding as part of the LIMA! Project funded by the USDA SCRI program (see also note here by Parker et al.).

MATERIALS AND METHODS

A total of 810 accessions were genotyped using short-read, low-coverage sequencing. From this genotypic data, the population structure of the panel was evaluated via principal component analysis and fastSTRUCTURE (Raj et al. 2014). A partially overlapping subset of the diversity panel ($n=353$ unique accessions, 141-308 per environment) was evaluated across six trials over two years in Davis, CA, Central Ferry, WA, and Coachella Valley, CA to assess trait performance in contrasting environments (the latter was fall-planted for evaluation of photoperiod-sensitive alongside day-neutral accessions). Agronomic traits such as early-season biomass, growth habit, flowering time, and grain yield were scored in the field, and seed coat color and hundred-seed weight were also recorded. Dry-grain macronutrient traits were measured via benchtop near-infrared spectroscopy (NIRS), including protein, fat, and ash (total mineral) content, using a custom calibration developed with wet chemical reference data. Genome-wide association studies were conducted utilizing the FarmCPU model with the rMVP package in R (Yin et al. 2021). A conditional core collection was established to include a preselected set of 300 genotyped and extensively phenotyped accessions and an additional 100 accessions selected to maximize genetic diversity (Zhou et al., *in review*) building up on the super-saturated method via parallel computing as described in Virdi et al. (2023).

RESULTS AND DISCUSSION

The genotyped collection contained accessions from around the world, with the majority of accessions originating from the United States and Brazil. Population structure among the genotyped collection was explained by origin, accession improvement status, and gene pool. The first principal component explained 46% of variation across genotypes and corresponded to separations between large-seeded and baby-seeded genotypes, representing the Andean and

Mesoamerican gene pools, respectively.

Phenotypic characterization of dry-grain macronutrient traits (protein, fat, and ash content) and hundred-seed weight was conducted on a subset of the collection across three locations and two years (six total environments). Protein showed the most variation across genotypes and environments. Protein and fat contents were negatively correlated across environments. The Coachella Valley location consistently exhibited lower protein and higher fat content across genotypes, distinguishing it from the other two locations. The main and interaction effects of genotype and environment on these traits were also analyzed. Variation in hundred-seed weight was explained primarily by genotype, as expected. In contrast, variation in protein content was explained primarily by the environment.

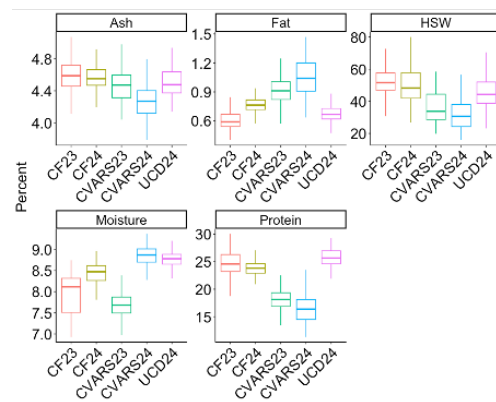


Figure 1. Phenotypic variation across Central Ferry, WA, in 2023 and 2024 (CF23, CF24), Coachella Valley Agricultural Research Station, CA, in 2023 and 2024 (CVARS23, CVARS24), and Davis, CA, in 2024 (UCD24) for seed traits including dry-grain macronutrient traits (ash, fat, protein, and moisture content (%)) and hundred-seed weight (g).

We integrated genotypic and phenotypic data to identify genomic loci associated with agronomic and dry-grain macronutrient traits. We identified loci significantly associated with traits such as growth habit, seed coat color, hundred-seed weight, and dry-grain fat content. Candidate genes are being analyzed in the regions identified from this

study. Finally, from the genotypic and phenotypic information obtained in this study, we established a conditional core collection. We designed this conditional core collection to be constrained to include over 300 lima accessions extensively phenotyped (based in part on seed availability) and then supplemented the collection with 100 accessions that maximized genetic diversity from among the genotyped accessions. Of the various core analyses run, this conditional core analysis incorporated >5 samples from multiple countries in Central and South America that were less represented in other such analyses.

CONCLUSIONS

Overall, this research has provided new genotypic resources to be integrated into the Legume Information System (LIS) and phenotypic resources to be integrated into the USDA-ARS Germplasm Resource Information Network, providing a foundation for molecular breeding efforts and supporting the development of improved lima bean varieties.

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EVALUATING A COMMON BEAN/TEPARY BEAN INTERSPECIFIC POPULATION FOR AGRONOMIC AND QUALITY TRAITS

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INTRODUCTION:

Common bean (*Phaseolus vulgaris* L.) is among the most widely consumed grain legumes and a key source of dietary protein worldwide. However, it is susceptible to drought and high-temperature stresses. Recently, efforts have been made to develop bean cultivars resistant to both high temperatures and drought through interspecific hybridization with closely related species that possess these traits. Therefore, a population of interspecific F5:6 families was developed at the International Center for Tropical Agriculture (CIAT, Cali, Colombia) through the use of bridge lines that removed the requirement of embryo rescue in the crossing of tepary bean and common bean materials (Barrera et al., 2022). In this study, we evaluated this interspecific population across an extensive environmental gradient for agronomic, sensing, and quality traits.

METHODS:

The interspecific population comprising 314 lines, along with parental and other relevant checks for each of common and tepary bean, was evaluated in multi-environment trials under contrasting temperature regimes in California (Kearney as a high-temperature stress environment and Davis as a lower-temperature environment, 2022, 2023) and Tanzania (2023-2025). Previous evaluations of these populations also included drought trials in Scottsbluff, Nebraska (2020, 2021) and heat trials in Puerto Rico (2021) and Texas (2021). Based on agronomic performance in the 2022 California environments, a subset of ~70 lines (including checks from each species) was selected for field evaluation under contrasting temperatures and/or irrigation treatments in Washington, Puerto Rico, Nebraska, and California (in 2024 and/or 2025). Traits collected in the field included flowering time, plant height, and grain yield. Additionally, regular sensing operations were conducted in multiple locations, whether weekly and/or at critical developmental stages. Traits

collected in the laboratory included hundred-seed weight, grain macronutrients (protein, starch, phytate, fat, ash, and moisture percentages) via custom benchtop near-infrared spectroscopy calibrations with wet-chemistry reference analyses on a subset of samples (selected via Kennard-Stone algorithm within each environment assayed), and (on a subset of environments) cooking time via Mattson cooker.

RESULTS AND PLANNED ANALYSES:

We found moderate overlap in best-performing lines and minor evidence of crossover interactions within and across mega-environments. There was also noticeable variation in yield across California locations and years (Figure 1). Drone-based sensing, and in some locations rover-based sensing, are being integrated across environments to extract a diversity of informative features that further our understanding of germplasm performance in contrasting environmental and management conditions. Tepary genotypes were found to have a leaf canopy area fraction more similar to that of cowpea than common bean in Davis 2022, with all species grown in the same field block. Additionally, tepary (PA) genotypes were found to have lower protein (Figure 2) and fat % and lower hundred-seed weight than common bean (PV) and interspecific (IS) genotypes at the two California locations in both 2022 and 2023. In contrast, phytate % was largely uncorrelated with these traits and did not systematically vary across species. Genetic mapping, genomic prediction, and GxE analyses are underway on these data. Overall, our goals are to cross-dissect the GxExM bases of agronomic and grain quality traits, and to assess the effects that introgression of drought and high-temperature tolerance traits from tepary into common bean could have on other traits of interest.

Reference:

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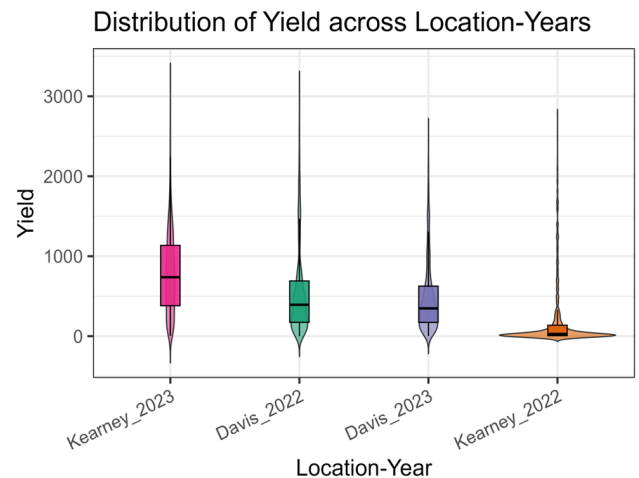


Figure 1: Distribution of yield across location-years

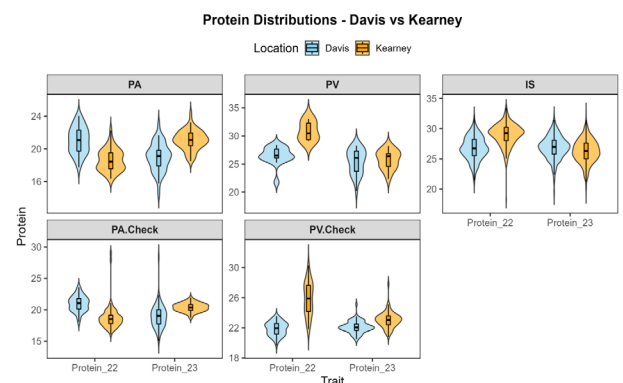


Figure 2: Protein distributions within species

SENTINEL TRIALS FOR ON-FARM BEAN DISEASE ASSESSMENT: A STRATEGIC TOOL TO GUIDE BREEDING FOR SMALLHOLDER AGRICULTURE

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INTRODUCTION

Disease resistance is a key priority in regions where beans are a major crop. Although several resistance loci and molecular markers for Angular Leaf Spot (ALS) have been identified mainly through controlled inoculations with specific pathogen races, there is a gap between these race-specific results and actual on-farm performance. To better understand this relationship, CIAT and NaCRRI implemented a coordinated effort to monitor ALS severity under real farming conditions in Lwengo district, Uganda, an area with high disease pressure and widespread bean cultivation.

METHODS

A bean nursery of 112 genotypes representing elite breeding lines, resistant parents, local varieties, local land races, international differentials, and ALS checks, was evaluated between October 2024 and January 2025, in two farms (Garden 1, 31.350833, -0.392850; Garden 2, 31.216183, -0.400833). The trials were managed using farmer practices, except no fungicide applications. An RCB experimental design was used with three replications. ALS severity from R6 to R8 developmental stages was measured using CIAT's 1-9 scale. Three evaluations were performed on leaves and one on pods. The maximum score from three different evaluations on leaves, and the one on pods were processed to calculate the accumulated probabilities for three phenotypic categories. Range [1,3] were classified as resistant, [4,6] as intermediate, and [7,9] as susceptible.

RESULTS

ALS was the most severe disease observed in both Lwengo farms, followed by rust, prompting a deeper analysis of ALS data. Race structure assessment using universal differentials showed highly aggressive pathogen races, as all tested differentials displayed foliar symptoms—even though two Andean differentials (G11796 and Bolon Bayo) were not included (Table 1). These findings are notable because several resistance loci present in key differentials—such as *Phg-2* in Mexico54 and *Phg-4/5* in G5686—are widely used in breeding programs to develop ALS-resistant varieties. Interestingly, pod damage in these differentials was lower than leaf damage, suggesting that resistance mechanisms may differ between the two tissues. At the variety level, only two of the 18 NARO-released Ugandan varieties showed strong on-farm performance: NABE12C (Andean sugar type climber) and NABE14 (Andean bush), both displayed moderate resistance in leaves and high resistance in pods (Table 1). Complete nursery results can be found at <https://doi.org/10.7910/DVN/UX25WU>.

Table 1. Genotype performance for On-farm infection with ALS at Lwengo district in Uganda.

		Cumulative Probabilities for ALS on leaves						Cumulative Probabilities for ALS on Pods				
Genotype	Loc.	Resistant	Intermed.	Suscept.	Categ.	Genotype	Loc.	Resistant	Intermed.	Suscept.	Categ.	
Andean Differentials												
Don Timoteo	G1	0%	2%	98%	S	Don Timoteo	G1	71%	27%	2%	R	
Don Timoteo	G2	0%	0%	100%	S	Don Timoteo	G2	54%	42%	4%	R	
Montcalm	G1	0%	47%	53%	S	Montcalm	G1	100%	0%	0%	R	
Montcalm	G2	0%	5%	95%	S	Montcalm	G2	86%	13%	1%	R	
Amendoin	G1	0%	80%	20%	I	Amendoin	G1	57%	38%	4%	R	
Amendoin	G2	0%	39%	61%	S	Amendoin	G2	43%	50%	7%	I	
G5686	G1	0%	64%	36%	I	G5686	G1	91%	8%	1%	R	
G5686	G2	0%	98%	2%	I	G5686	G2	64%	33%	3%	R	
Meso American Differentials												
PAN72	G1	0%	5%	95%	S	PAN72	G1	28%	59%	13%	I	
PAN72	G2	0%	0%	100%	S	PAN72	G2	1%	9%	91%	S	
G2858	G1	0%	0%	100%	S	G2858	G1	0%	4%	95%	S	
G2858	G2	0%	0%	100%	S	G2858	G2	0%	0%	100%	S	
Flor De Mayo	G1	0%	0%	100%	S	Flor De Mayo	G1	34%	55%	10%	I	
Flor De Mayo	G2	0%	0%	100%	S	Flor De Mayo	G2	8%	54%	39%	I	
MEXICO54	G1	0%	2%	98%	S	MEXICO54	G1	100%	0%	0%	R	
MEXICO54	G2	0%	0%	100%	S	MEXICO54	G2	61%	36%	3%	R	
BAT332	G1	0%	2%	98%	S	BAT332	G1	55%	40%	5%	R	
BAT332	G2	0%	4%	96%	S	BAT332	G2	84%	15%	1%	R	
CORNELL492	G1	0%	2%	98%	S	CORNELL492	G1	35%	55%	10%	I	
CORNELL492	G2	0%	0%	100%	S	CORNELL492	G2	22%	62%	16%	I	
Best Local Varieties												
NABE 12C	G1	0%	64%	36%	I	NABE 12C	G1	83%	16%	1%	R	
NABE 12C	G2	0%	64%	36%	I	NABE 12C	G2	70%	28%	2%	R	
NABE14	G1	0%	80%	20%	I	NABE14	G1	100%	0%	0%	R	
NABE14	G2	0%	84%	16%	I	NABE14	G2	54%	42%	4%	R	

CONCLUSIONS AND FUTURE IMPACT

1. **Pathogen Diversity:** The pathogen population exhibits high race-level complexity, as reflected in the pronounced level of disease severity across differential genotypes.
2. **Resistance Sources:** Among the known resistance loci, the Andean bush G5686 source appears to be the only one providing a moderate level of foliar disease control under the conditions assessed.
3. **Implications for Management:** Moderate resistance performance could be enhanced through appropriate on-farm practices, seed treatment and strategic application of fungicides as part of an integrated disease management approach.
4. **Acknowledgements:** Funding provided by CG Science Programs and AVISA Project (BMGF)

USE OF TWO GENOMIC APPROACHES TO IDENTIFY QTLs FOR COMMON BACTERIAL BLIGHT RESISTANCE IN *PHASEOLUS VULGARIS* L. CRANBERRY MARKET CLASS

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INTRODUCTION: Common bacterial blight (CBB) remains one of the most damaging and widespread diseases of common bean (*Phaseolus vulgaris* L.). Although several major QTLs for CBB resistance have been identified, only a limited number have been deployed in marker-assisted selection. Among these, resistance QTLs on Pv06 (BC420), Pv08 (SU91), and Pv10 (SAP6) have historically been used to introgress resistance into different market classes (Viteri et al., 2014). However, the effectiveness and transferability of these loci in the cranberry market class genetic background have not been validated. The objective of this study was to identify and validate QTLs controlling CBB resistance in this genetic background using two complementary genomic approaches: classical linkage mapping and QTL-seq based on whole genome sequencing (WGS) data.

MATERIALS AND METHODS: Two populations were evaluated under greenhouse conditions. A recombinant inbred line (RIL) population, PIC257 (Krimson × RS-7), was used for linkage mapping, and an F₂ population (Tintoretto × CXR1) for QTL-seq. Krimson and Tintoretto are susceptible cultivars, whereas RS-7 and CXR1 are resistant lines derived from tepary bean introgressions (Viteri et al., 2014). All parental lines are cranberry type. Plants were inoculated using the multiple-needle method with a *Xanthomonas phaseoli* pv. *phaseoli* isolate. Disease severity was scored at 7, 10, and 14 days after inoculation using the 1–9 scale, and AUDPC was calculated. For linkage mapping, 143 representative RILs were genotyped using WGS data and QTLs were detected by composite interval mapping. For QTL-seq, extreme phenotypes were selected from 210 F₂ plants to form three resistant and three susceptible DNA bulks (10 plants each). ΔSNP-index was computed using the QTLseqr package. Selected QTLs were validated using PCR-based markers in the F₂ population.

RESULTS AND CONCLUSION: CBB resistance showed continuous phenotypic distributions in both populations, consistent with quantitative inheritance. Broad-sense heritability exceeded 0.84 for all disease ratings in the RIL population. Linkage mapping identified three QTLs for CBB resistance (Table 1). A major QTL on Pv08 explained up to 49% of the phenotypic variance and mapped to the distal region associated with the SU91 locus. A second major QTL on Pv06 explained about 25% of the variance and spanned the proximal region of the chromosome. A minor QTL on Pv11 explained 13–14% of the phenotypic variance. QTL-seq confirmed a strong and consistent signal on Pv06 across all resistant-susceptible bulk comparisons, with a ΔSNP-index peak of 0.87 within the first 15 Mb. A second significant signal on Pv08 was detected in three bulk comparisons, consistent with a complementary resistance effect (results not shown).

Marker validation in the F₂ population confirmed strong associations between CBB resistance and indel markers on Pv06, with C6_500 showing the strongest phenotypic separation among genotype classes (Table 2). A significant association with resistance was also detected for the SU91-linked marker on Pv08, which was designed in the coding region of a Niemann–Pick polymorphism gene (NPP_08) (Reinprecht et al., 2024). Effective resistance required the presence of resistant alleles at both Pv06 and Pv08, indicating a strong epistatic interaction between these loci (results not shown). The Pv06 QTL detected in this study appears distinct from the classical BC420 locus, as BC420 SCAR and BC420-CG14 markers were absent in all parental lines (Shi et al., 2012). This suggests the presence of a potentially novel resistance locus.

Table 1. QTLs for CBB resistance identified in RIL population by composite interval mapping. Physical position of peak marker is relative to reference genome v2 G19833.

CBB rating	Pv	QTL interval (cM)	Peak marker	Peak LOD	R ²	QTL size (Mb)
7 DAI	06	0–36	SNP06_14938684	9.27	0.26	21.18
10 DAI	06	0–24	SNP06_14938684	6.87	0.20	19.78
14 DAI	06	0–25	SNP06_14938684	9.25	0.26	19.95
AUDPC	06	0–31	SNP06_14938684	8.80	0.25	20.40
7 DAI	08	80–100	SNP08_62741705	18.66	0.45	1.55
10 DAI	08	78–100	SNP08_62741705	19.67	0.47	2.14
14 DAI	08	80–100	SNP08_62741705	19.31	0.46	1.55
AUDPC	08	79–100	SNP08_62741705	20.71	0.49	1.90
7 DAI	11	56–59	SNP11_7069294	4.26	0.13	1.77
14 DAI	11	57–58	SNP11_7069294	4.46	0.14	–
AUDPC	11	57–59	SNP11_7069294	4.20	0.13	1.44

Table 2. Markers validation and contribute to CBB resistance in F₂ population. Numbers of individuals genotyped (n), mean ± SD of CBB rating at 14 DAI by genotype class (rr, Rr, RR), Kruskal–Wallis (KW) statistic test and chi-square test for 1:2:1 segregation. Phenotypic scores are based on 1-9 rating scale for CBB. Significance: * p < 0.001.

Marker	n rr	n Rr	n RR	mean rr (sd)	mean Rr (sd)	mean RR (sd)	KW p	Chi ² p
C6_500	58	108	45	8.12 (0.85)	5.74 (1.60)	4.38 (1.95)	1.14e-20 *	ns
C6_29100	59	107	45	8.08 (0.88)	5.74 (1.61)	4.38 (1.95)	1.90e-20 *	ns
C6_46200	55	110	46	8.07 (0.90)	5.75 (1.65)	4.61 (2.09)	6.76e-18 *	ns
NPP_08	52	115	43	7.38 (1.24)	5.70 (2.01)	5.67 (2.23)	2.49e-06 *	ns

In conclusion, this study identified two major (Pv06, Pv08) and one minor (Pv11) QTLs controlling CBB resistance in cranberry market class, including a potentially novel major QTL on Pv06, and demonstrated that pyramiding QTLs on Pv06 and Pv08 is required for the resistance.

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HIGH THROUGHPUT PHENOTYPING OF BRUCHIDS RESISTANCE IN A BEAN ANDEAN DIVERSITY PANEL -CASE *ZABROTES SUBFASCIATUS*

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INTRODUCTION

Storage insects are relevant pest of grains and in beans two species are the most common in the tropics, *Zabrotes subfasciatus* (Mexican bean weevil-MBW) and *Acanthoscelides obtectus* (common bean weevil). Although the host use for larvae is similar in both species, bean genotypes with resistance to one species are not necessarily resistant to the other one. Bean resistance to MBW is based in different types of arcelin, a lectin involved in antinutrient effect on the larvae, reducing their development and causing mortality (Cardona et al., 1990). However, lines resistant to *Zabrotes* (RAZ), have not been widely used in the Alliance Bioversity and CIAT bean breeding pipelines due to their undesirable performance in other agronomic traits (e.g. low yield). An Andean elite nursery (VEF2023) has been developed for high yield and tolerances to biotic and abiotic factors, and the objective of this work was to test the response of their seeds to the MBW and through these results, develop an automatized method of phenotyping based in image analysis.

MATERIALS AND METHODS

Fifteen seeds from each of 480 accessions were infested with three pairs of newly emerged MBW adults reared in massive colonies under controlled conditions (maximum 24 hours old). For the infestation, the seeds were placed into 50 mL tubes with the cap loose. After 30 days these insects were removed and after 60 days the insect's life cycle was interrupted storing the tubes at -2°C by one day. The evaluation was conducted in three distinct temporal blocks. Pictures were taken of emerged adults and two sides of the seeds. From the total, 625 pictures were analyzed using CVAT (Computer Vision Annotation Tool) and 17.276 annotations of the emergence holes and the adults were generated for developing an automatized counting tool (Fig.1).

Labels were exported in Ultralytics YOLO Detection 1.0 format and uploaded to the Roboflow platform along with the images. Images were split into 80% training, 10% validation, and 10% test sets. Preprocessing and data augmentation techniques were applied to balance both data and labels. Several object detection models were trained. The best performance was achieved by RF-DETR (Nano), a Detection Transformer (DETR) architecture optimized for real-time tasks. This model combines high accuracy and speed and does not require Non-Maximum Suppression (NMS), which removes duplicate detections of the same object. To compare counting efficiency, 50 samples (comprising seeds and bruchids) were processed manually and via the automated model.

The number of seed holes was analyzed using a Generalized Linear Mixed Model (GLMM) with a Tweedie distribution, appropriate for data with many zeros and positive continuous values. The model included Genotype as a fixed effect and Block as a random effect. Adjusted means (model-predicted means) were calculated for each genotype to account for block effects.

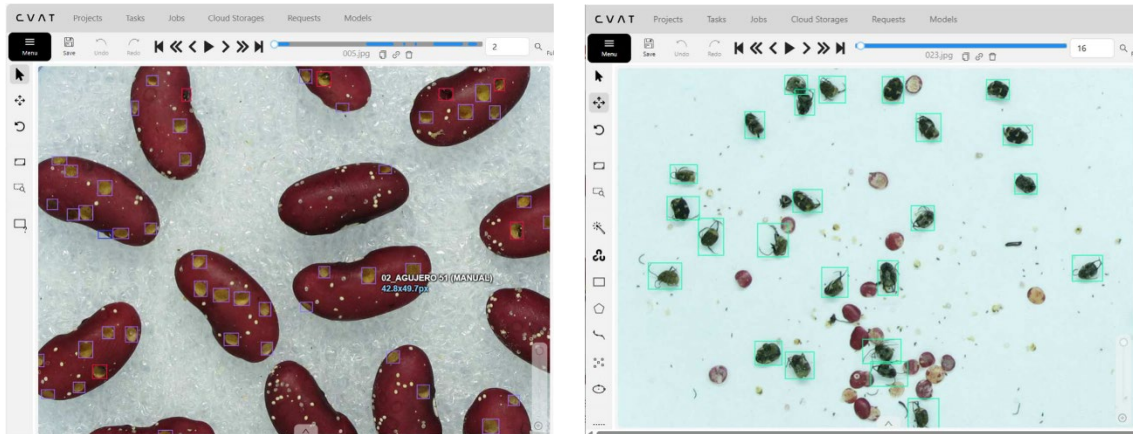


Figure 1. Annotations of holes in seeds previously infested (left) and of adults (right) to separate them of the hole lids broken when the adults emerge.

RESULTS AND DISCUSSION

Model performance was assessed using standard detection metrics. Key performance indicators such as mAP@50 (82.0%), Precision (89.3%), and Recall (77.1%) were obtained. These results indicate a strong balance between accuracy and sensitivity, with the model reliably identifying most objects (Precision) while maintaining a low rate of false detections (Recall).

In terms of speed efficiency, the direct counting per sample spent 139.03 seconds/sample while the photo capturing and the automatized counting required 76.53 seconds/sample.

Twenty lines had between 0.2 and 1 holes per seed (the resistant check RAZ124 had 0.19 holes per seed, while the susceptible check Calima had an average of 4.4 holes per seed), and their backgrounds included: *P. vulgaris* Andean Elite x Elite , *P. vulgaris* Andean x Mesoamerican, crosses with Colombian lines, and Interspecific lines from crosses between *P. vulgaris*, *P. acutifolius* and *P. montanus*.

These potential sources of resistance are valuable for breeding schemes and given their divergent origins, new resistance mechanisms can be involved.

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PINPOINTING CANDIDATE GENES IN A QUANTITATIVE TRAIT LOCUS ASSOCIATED WITH RESISTANCE TO BACTERIAL BROWN SPOT IN ADZUKI BEANS

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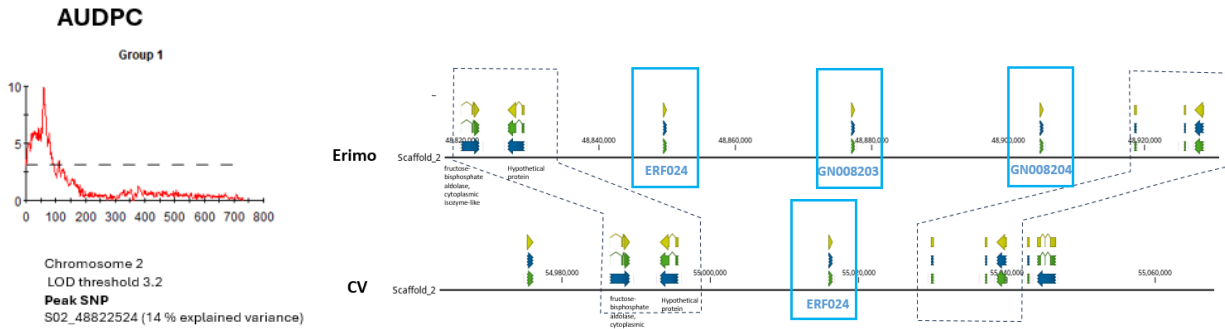
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INTRODUCTION: Canada is the second-largest exporter of adzuki beans [*Vigna angularis* (Willd.) Ohwi & Ohashi], generating US \$32 million from exports of dried adzuki beans in 2024 (Tridge, 2024). Adzuki bean was described as the most profitable bean in Ontario in 2023 (Zandbergen, 2024). *Pseudomonas syringae* pv. *syringae* causes bacterial brown spot in beans. Yield losses from bacterial brown spot in adzuki beans range from benign to entire crop losses (Wally, 2019). Bacterial brown spot is the second biggest threat to adzuki bean cultivation after white mold (King, 2019). Cultural, physical, and chemical control measures have not been effective in managing bacterial brown spot. The most effective control measure is cultivating resistant varieties (OMAF, 2023). No commercial adzuki variety grown in Ontario shows resistance to bacterial brown spot (OMAF, 2023). Furthermore, there has been no publication describing the interactions between the pathogen and the adzuki host or mechanisms that confer resistance or susceptibility to the disease. Elucidating the genetic basis for resistance to bacterial brown spot in adzuki beans will accelerate breeding of disease-resistant, elite varieties. Quantitative trait loci (QTL) regions associated with traits often comprise 100s of candidate genes. Fine mapping QTL regions will involve innovative strategies (Jaganathan *et al.*, 2020). This research exploited knowledge of plant-pathogen molecular interactions by matching unique virulence factors present in a *P. syringae* pv. *syringae* strain to host target genes within a QTL region to identify candidate genes involved with resistance to bacterial brown spot in adzuki bean.

MATERIALS AND METHODS: Pss27, Me2, Me3, and Li6 were the *P. syringae* strains used in this study. Pss27 (*P. syringae* pv. *syringae*) was obtained from AAFC, Harrow Research Centre, Ontario, Canada, courtesy of O Wally. Me2, Me3, and Li6 were isolated in this study. Me2, Me3 (*P. syringae* pv. *aceris*), and Li6 (*P. syringae* pv. *dysoxylis*) were isolated from adzuki seed lots (courtesy Hensall Coop) collected from Meaford and Lincoln, Ontario, respectively. Comparative genomics was carried out among the strains to identify unique virulence factors. Pathogenicity screening was conducted by computing the area under the disease progress curve (AUDPC) after scoring two adzuki bean varieties, Erimo and a Chinese variety (CV), for symptoms following inoculation with Pss27, Me2, Me3, or Li6 under controlled conditions. Pss27 was then used to phenotype 106 F₆ recombinant inbred lines (RILs) from a cross between Erimo and CV for their reaction to inoculation with the bacterial brown spot pathogen. The RILs were genotyped by genotype-by-sequencing (GBS). Single-nucleotide polymorphisms (SNPs) were called from the GBS reads, and a linkage map with eleven linkage groups was generated using JoinMap5. Using the AUDPC data for the RILs, a QTL associated with resistance to bacterial brown was identified

on the linkage map. The QTL regions in the annotated Erimo and CV genomes were scanned for host genes that interact with the unique virulence factors present in Pss27.

RESULTS AND DISCUSSION: In pathogenicity tests, Erimo was partially resistant to Pss27 inoculation and CV was susceptible ($p < 0.001$). Ten (ahhI, ahlR, ppkA, avrRpm1, hopAB1, hopAF1, hopAP1, hopH1, hopL1, sypA) and four (hcp1, acrB, rmlA, rmlD) unique virulence factors were identified in Pss27 and Me2, respectively. Of the ten unique virulence factors in Pss27, hopAB1 and hopL1, both effectors, had cognate target genes within the QTL region associated with resistance to bacterial brown spot. The QTL region on chromosome 2 (Fig. 1A) was approximately 6 Mbp in size and comprised about 200 candidate genes. hopAB1 and hopL1 had four and three host targets within the QTL, respectively. Of all the host target genes present within the QTL, only Ethylene-Responsive Transcription Factor (ERF024) showed polymorphisms between Erimo and CV. ERF024 had two extra copies in tandem present in Erimo (Fig. 1B). ERF024 was the closest target gene to the peak SNP marker in the QTL. ERF024 was located 20 kbp downstream of the peak marker. Copy number variation has been associated with



disease resistance in plants (Dolatabadian *et al.*, 2017).

A

B

Fig. 1 A and B: **A**, QTL associated with bacterial brown spot resistance in adzuki RILs identified on Chromosome 2. **B**, ERF024 gene tandem duplication/copy number variation. ERF024 has a single copy in CV. ERF024, GN008203, and GN008204 have 100 % sequence similarity in Erimo.

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GENOMIC INSIGHTS INTO IRON AND ZINC BIOFORTIFICATION IN COMMON BEAN: LEVERAGING CROP WILD RELATIVES AND INTROGRESSION MAPPING

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INTRODUCTION

Iron (Fe) and zinc (Zn) deficiencies affect over two billion people worldwide (WHO, 2025) and remain a major public health concern in regions where common bean (*Phaseolus vulgaris* L.) is a dietary staple. Seed Fe and Zn concentrations in common bean range from 34–96 ppm and 21–59 ppm, respectively (Islam et al., 2002; Beebe et al., 2002; Cichy et al., 2022). However, genomic-assisted improvement has been limited by small allelic effects and genotype by environment interactions (Cichy et al., 2022). Crop wild relatives such as *P. parvifolius* and *P. acutifolius*, which evolved in iron-poor, alkaline soils, represent valuable sources of adaptive alleles. This study aimed to (i) evaluate an interspecific recombinant inbred population incorporating wild alleles, (ii) identify QTL for seed Fe and Zn, and (iii) characterize introgression regions associated with biofortification traits.

MATERIALS AND METHODS

An interspecific VAP9 × SEN118 (VxS) population of 412 recombinant inbred lines (RILs) was developed to incorporate alleles from domesticated and wild gene pools. VAP9 is a pre-breeding line with elevated seed iron (88 ppm) and zinc (37.7 ppm), while SEN118 is an elite, drought-tolerant, high-yielding genotype. Field trials were conducted at the Alliance Bioversity–CIAT research station in Palmira, Colombia, during the 2023A and 2023C seasons under irrigation using an alpha-lattice design with three replicates. Traits measured included days to flowering (DF), 100-seed weight (100SdW), grain yield (kg ha⁻¹), seed iron (SdFe), and seed zinc (SdZn), with mineral concentrations quantified by energy-dispersive X-ray fluorescence (EDXRF).

GBS libraries were prepared using ApeKI (Elshire et al., 2011) and sequenced on the Illumina HiSeq X platform. Reads were processed with Stacks and Trimmomatic, aligned with BWA to the G19833 and UI-111 reference genomes, and variants were called using NGSEP ($Q > 40$; $DP > 3$) with filters for bi-allelic SNPs, heterozygosity $\leq 10\%$, and minor allele frequency $\geq 5\%$. To minimize reference bias, QTL mapping was conducted using three assemblies: G19833, UI-111, and a de novo VAP9 assembly. Linkage maps were constructed in ICI Mapping using Kosambi's function, and QTL were detected with QTL IciMapping v4.2 (ICIM-ADD; 10 cM window, 0.5 cM step, 1,000 permutations). Introgression was evaluated by aligning assemblies with AnchorWave and estimating Dsuite D' statistics using the 95th percentile as the significance threshold.

RESULTS

The VAP9 × SEN118 (VxS) population showed wide phenotypic variation for seed mineral concentration and agronomic traits across the 2023A and 2023C seasons. VAP9 consistently exhibited higher seed iron (SdFe) and zinc (SdZn) than SEN118, while SEN118 outperformed VAP9 for 100-seed weight and grain yield. Transgressive segregation was observed for both

mineral and agronomic traits, and overall yield was greater in 2023C than 2023A, indicating seasonal effects.

Using three reference genomes (G19833, UI-111, and VAP9), 60 QTL were identified, including 12 for SdFe and 6 for SdZn. The 12 SdFe QTL were distributed across four chromosomes and showed positive additive effects, largely contributed by VAP9 alleles. The largest effect QTL explained 15.5% of phenotypic variance. Several iron QTL co-located with yield or seed weight QTL of opposite allelic effect, suggesting linkage drag. SdFe QTL on linkage groups 3 and 10 were not reported in the meta-analysis of Izquierdo et al. (2018), indicating novel genomic regions for iron accumulation.

Six SdZn QTL were detected with generally small but positive additive effects. None co-located with yield QTL, suggesting fewer trade-offs for zinc improvement. A major introgression block at the distal end of chromosome 04 co-located with iron and yield QTL, indicating that favorable iron alleles likely originated from *P. parvifolius* but may be linked to reduced yield. Overall, the VxS population reveals beneficial interspecific alleles for mineral enhancement alongside regions constrained by linkage with agronomic traits.

CONCLUSIONS

This interspecific population revealed heritable variation for seed Fe and Zn and identified genomic regions associated with biofortification. Multi-reference QTL mapping improved detection of both shared and genome-specific loci. The Pv04 introgression represents a key target for fine mapping to reduce linkage drag. Zinc QTL unlinked to yield provide immediate breeding opportunities toward biofortification targets of ≥ 90 ppm Fe and ≥ 50 ppm Zn.

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A FRAMEWORK FOR GENOMIC SELECTION IN DRY BEAN BREEDING: FROM GBS TO SNP CHIP DEVELOPMENT

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INTRODUCTION: Genomic selection (GS) has the potential to accelerate genetic gain in dry bean (*Phaseolus vulgaris* L.) breeding by enabling earlier and more accurate selection decisions, thereby saving time and resources. Despite its potential, implementing a scalable framework requires optimized tools tailored to specific breeding programs. This study aimed to develop a GS pipeline specifically tailored to the North Dakota State University (NDSU) dry bean breeding program by selecting trait-based single-nucleotide polymorphisms (SNPs) for genotyping chip development.

MATERIALS AND METHODS: For marker optimization, a training population of 427 advanced breeding lines, encompassing eight market classes (Pinto and Slow-dark Pinto, Great Northern, Small Red, Pink, Black, Navy, and Kidney bean) from both gene pools (Middle American and Andean) was evaluated (2020-2023) for eight traits. Agronomic traits, canning appearance, and disease-resistance traits were included (Figure 1). Genotyping was initially performed using genotyping-by-sequencing (GBS), generating approximately 400,000 SNPs. After quality filtering, 109,000 high-confidence markers were retained. Cross-validation genomic predictions (GP) for the traits of interest were estimated in the training population using Ridge Regression Best Linear Unbiased Prediction (rrBLUP). To optimize marker density for chip design, genome-wide association studies (GWAS) and GS-based additive effects were used to identify 4,440 significant SNPs. This set of markers was refined by selecting the top 600 most significant SNPs for each trait. An additional 298 SNPs were included based on previously reported genomic regions associated with other important traits (Figure 1). For chip validation, two independent populations were used for cross-validation GS analyses. The first population consisted of 142 advanced breeding lines and 50 lines from the USDA *Phaseolus* germplasm collection (USDA, 2024), evaluated for their response to soybean cyst nematode (SCN - female index). The second population included 217 advanced breeding lines from the NDSU dry bean breeding program and was used to estimate protein content.

Table 1. Marker distribution across the genome after marker optimization and quality control

Chromosome	SNPs	%
1	288	7%
2	277	7%
3	411	11%
4	154	4%
5	387	10%
6	291	8%
7	338	9%
8	620	16%
9	250	6%
10	173	4%
11	678	18%
Total	3867	100%

RESULTS AND DISCUSSION: The initial evaluation of the GP model using the complete dataset resulted in moderate to high prediction accuracies, ranging from 0.33 to 0.92 across traits, where days to maturity obtained the lowest prediction accuracy, and 100-seed weight got the highest prediction accuracy. After marker optimization and quality control, a custom SNP chip containing 3,867 markers was designed, distributed across the genome (Table 1). SNPs were distributed in all the traits, including in the designing process (Figure 1), where a total of 10 SNPs

were shared across four traits, 29 SNPs were shared among three traits, and 178 SNPs were shared between two traits. The first validation population tested for SCN resistance had a prediction accuracy of 0.80. In contrast, the second population achieved a prediction accuracy of 0.53 for protein content on cross-validation results

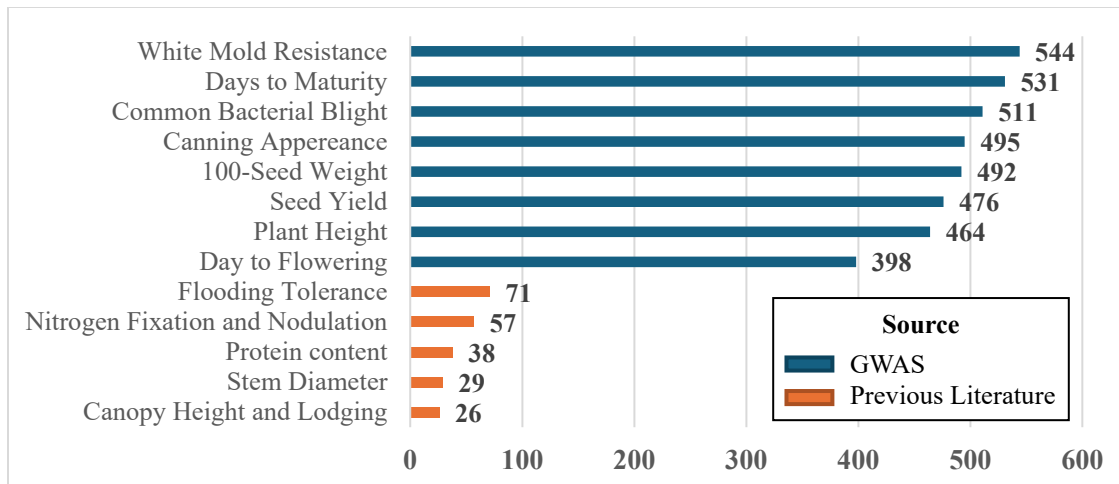


Figure 1. Distribution of SNPs by trait in the chip after marker optimization and quality control. 5.6% of the total SNPs were found in common across at least two traits.

These results highlight that marker optimization significantly enhances GP accuracy. The development of the 3.8K SNP chip provides a cost-effective and scalable tool for the NDSU Dry Bean breeding pipeline. This study establishes a robust framework for integrating genomic tools into dry bean breeding. By transitioning from high-density GBS data to a specialized SNP chip, the program can achieve reliable prediction accuracy across diverse traits. This approach facilitates more efficient selection cycles and demonstrates the practical application of genomic selection in public breeding programs.

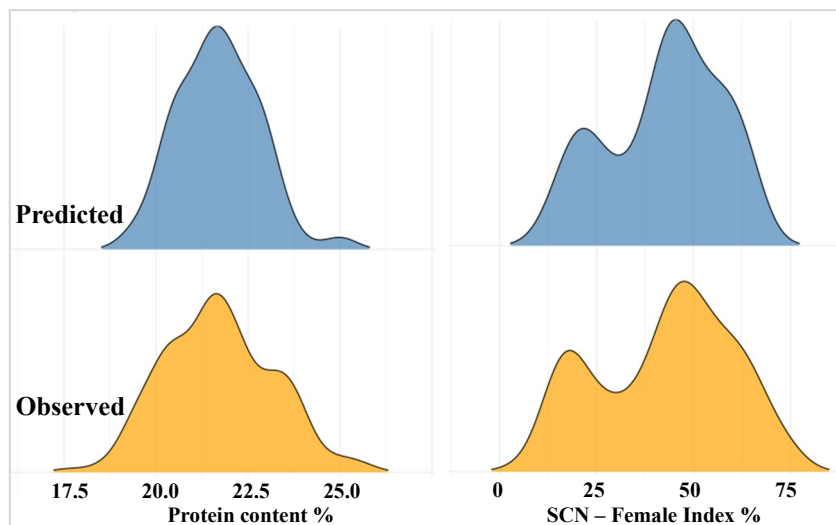


Figure 2. Observed vs predicted phenotype for protein content (%) and the reaction to SCN (%) in two independent populations.

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DEVELOPING PROTEIN-RICH DRY BEANS (*Phaseolus vulgaris* L.) THROUGH GENOMIC PREDICTION

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INTRODUCTION: Dry beans are recognized as a nutritious food source and an important source of plant-based protein (Parker, et al., 2022). However, combining key agronomic, seed quality, and nutritional traits into a single dry bean cultivar remains a challenge in breeding programs. Genomic prediction enables the assessment of multiple important traits within breeding lines prior to field testing, potentially reducing the time and resources required for selection (Saldares et al., 2024). The objectives of this research were to (1) create a catalog of protein content for dry bean germplasm within the North Dakota State University (NDSU) Dry Bean Breeding Program and (2) assess the effectiveness of various genomic prediction models for accuracy of predicting protein content and assess how to integrate genomic prediction into our breeding pipeline.

MATERIALS AND METHODS: This study evaluated protein content of 520 breeding lines and check cultivars within the NDSU Dry Bean Breeding Program grown in Hatton, North Dakota in 2024. Protein concentration (%) was measured using near-infrared spectroscopy (NIR). Mean protein content was calculated for each market class. Differences among market classes were evaluated using a mixed linear model and Tukey' HSD test ($P < 0.05$). Genotyping was conducted using an in-house trait-based SNP chip containing approximately 4K markers. After quality filtering for minor allele frequency (MAF) > 0.01 and heterozygosity < 0.2 , 470 genotypes and 2,164 SNP markers were retained. Genomic prediction models were implemented using an in-house platform. Seventeen genomic prediction models were evaluated under cross-validation, including Bayesian alphabet models, genomic best linear unbiased prediction (GBLUP) models, machine learning models, and deep learning models.

Table 1. Protein concentration and market class comparisons for dry bean germplasm evaluated in Hatton, ND (2024).

Market Class	Sample No.	Mean Protein %	Protein Range	Group
Navy	122	22.7	19.4 - 27.6	A
Pinto	12	22.7	20.2 - 24.2	AB
Slow-Darkening Pinto	101	22.5	18.0 - 26.3	A
Great Northern	25	22.3	20.2 - 24.6	AB
Black	191	21.7	18.4 - 26.0	B
Small Red	7	21.5	17.6 - 23.6	AB
Pink	12	21.1	19.9 - 23.2	B
Total	520	22.1	17.6 - 27.6	

RESULTS AND DISCUSSION: Across all evaluated lines, the overall mean protein concentration was 22.1% (Table 1). Among the evaluated genomic prediction

models, the machine learning model random forest (RF) showed the highest predictive ability with an R^2 value of 0.56. To evaluate potential implementation within breeding pipelines, model performance was assessed based on its ability to classify genotypes with the lowest and highest 20% of protein values (Figure 1). The RF model predicted low-protein genotypes with an accuracy of 36.23% and high-protein genotypes with an accuracy of 32.29%. Using genomic prediction models to remove low-protein genotypes could eliminate approximately 36% of undesired lines early in the breeding process. In contrast, selecting high-protein genotypes would identify approximately 32% of superior genotypes, while potentially missing a large portion of high protein lines that are not captured by the model predictions. This indicates that

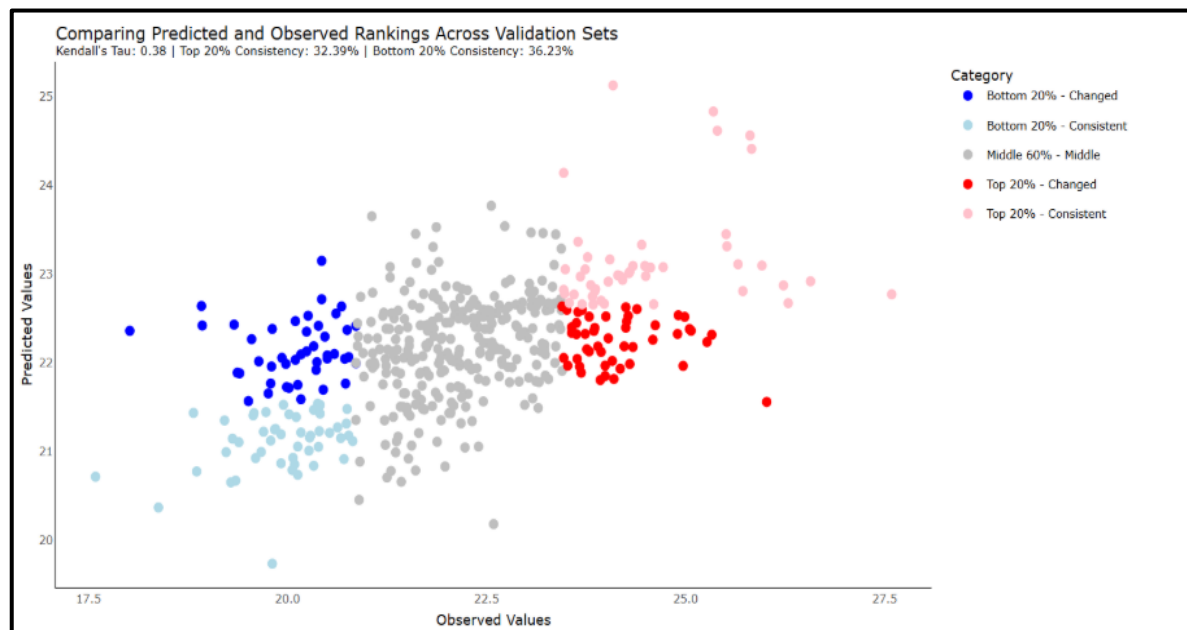


Figure 1. Comparison of prediction rankings used to evaluate genomic prediction performance for selection decisions in protein. Points represent individual genotypes and are grouped based on consistency of classification.

genomic prediction models appear more effective for early-stage negative selection and removal of low-protein genotypes rather than for reliably predicting superior high-protein genotypes.

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GENETIC MAPPING, PROXIMAL SENSING, AND CROP MODELING OF NUTRITIONAL AND AGRONOMIC TRAITS IN A COWPEA MAGIC POPULATION ACROSS THREE CALIFORNIAN ENVIRONMENTS

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INTRODUCTION:

Cowpea (*Vigna unguiculata*) is an important crop in the U.S., including in California where ~8,000 acres are grown annually. Cowpea produces mineral- and protein-rich grains supporting global food and nutritional security. Due to cowpea's architecture, with pods and flowers visible from top-down views, cowpea breeding is well-suited to benefit from proximal remote sensing. Sensing can provide predictions of yield and/or its components, as well as reproductive and canopy dynamics, which in turn can serve as inputs to genetic mapping and crop modeling efforts aimed at parsing the genetic and physiological bases of these traits.

METHODS:

In this study, a cowpea MAGIC population was grown for two years in three Californian environments: two in the Central Valley (differing primarily in temperature) and one in the Coachella Valley (Figure 1). Agronomic traits were scored via traditional (groundtruth) assessments, while grain nutritional composition was assessed using near-infrared spectroscopy (NIRS), including the development of a custom calibration.

The Central Valley environments were sensed weekly including thermal and RGB deployed via drone and rover. Reproductive traits, including visible flower and pod counts, were estimated from rover-based RGB. Additionally, a reproductive dynamics study combined manual weekly scoring of flower and pod traits with smartphone sensing to predict yield and peak flowering time (date when the greatest number of flowers were open). A machine learning pipeline leveraging sensor images and synthetic images from a 3D crop model was also developed to predict stomatal traits. Genetic mapping was performed on groundtruth nutritional and agronomic traits, rover- and drone-based predictions of reproductive and canopy traits, and modeled stomatal conductance.

RESULTS:

Significant genomic regions were identified for several traits with varying stability across environments tested. Our results showcase three key advantages that the integration of sensing and modeling present to molecular breeding of cowpea: 1) overlapping significant regions between sensed and manually scored trait analogs demonstrate potential of sensing as a scalable proxy for manual scoring; 2) sensing-enabled crop models provide access to physiological traits not

previously measurable at population scale; and 3) spatiotemporal resolution of trait assessment is enhanced through repeated sensing campaigns. Our findings illustrate the potential of combining sensing, crop modeling, and genomics to accelerate molecular breeding of cowpea, among other leguminous and/or partially occluded crops.

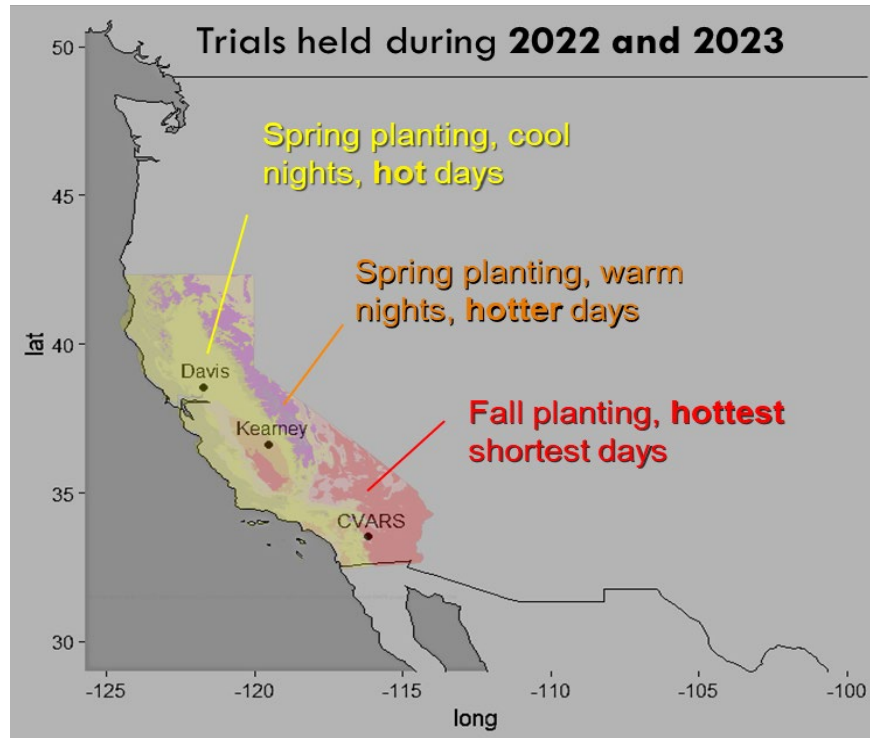


Figure 1. Locations and description of cowpea field trial environment in California.

HIGH-THROUGHPUT PHENOTYPING AND DEEP LEARNING FOR POD-BASED YIELD PREDICTION AND RUST SCREENING IN DRY BEANS

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INTRODUCTION

Developing dry bean (*Phaseolus vulgaris* L.) cultivars with high yield potential and disease resistance is a primary goal of the NDSU breeding program. Because yield is typically evaluated after harvest in advanced generations, early selections are often done without direct yield data. To improve early selection, we are testing a rover-based high-throughput phenotyping (HTP) platform using side-view imagery and a YOLOv11 model to detect and quantify pods as a proxy for yield. Improving disease resistance remains a key objective of the breeding program. Although common bean rust (*Uromyces appendiculatus*) is not the main disease threat in North Dakota, significant losses can occur under favorable conditions. Rust is traditionally evaluated visually; however, we are also testing a greenhouse imaging platform paired with image segmentation and deep learning to improve disease screening efficiency and accuracy.

MATERIALS AND METHODS

The first study was conducted during the 2024 growing season in NDSU field trials in Hatton, ND, where a rover-based platform collected side-view videos of advanced yield trial plots in different market classes. Approximately 80,000 images were used to train a deep learning model for pod detection, with data split into training and test sets at a 90:10 ratio. Model performance was assessed using MS COCO metrics, including precision, recall, and mean average precision (mAP). Platform and model details are described in Mathew et al. (2023) and the BIC 2025 Annual Report. The second study used a greenhouse-based imaging platform to capture images of 362 genotypes, including preliminary and advanced yield trial lines, germplasm lines, and cultivars. Genotypes were grown in two replications and inoculated with urediniospores of *Uromyces appendiculatus* race 20-3 following the protocol described by Erfatpour et al. (2025). Disease severity was assessed via RGB imaging and conventional 1-9 visual scoring (Schoonhoven and Pastor-Corrales, 1987). Images were segmented to remove background, and a color ratio was applied to distinguish healthy from diseased tissue. Image-derived disease area values were compared with visual scores using correlation analysis, and genome-wide association studies (GWAS) were conducted using both visual ratings and image-based estimates.

RESULTS AND DISCUSSIONS:

The YOLOv11 model achieved a mAP@50 of 92%, indicating that the detections were generally reliable when the overlap with the ground truth was at least 50%. However, the mAP@50:95 was 78%, indicating reduced accuracy at higher overlap thresholds, which suggests some localization errors. The recall was 83%, meaning the model correctly identified 83% of all objects present in the image. High precision and recall values demonstrate the model's strong ability to accurately detect pods. The trained model was used to count the number of pods per plot, and these counts served as a proxy for yield estimation. Correlation analysis showed no strong evidence of a linear relationship between yield estimated by the camera and yield measured by the combine in this

dataset. Among market classes, slow darkening pinto had the highest correlation ($R = 0.13$), although the relationship remained weak. The low correlation may be due to image exposure issues, especially strong shadows that likely decreased the model's ability to detect all pods within a row. Additionally, the platform was designed to collect data from single-row plots, which may not fully capture yield variation in two-row plots. An updated platform that considers two-row plots will be evaluated in future studies. For the greenhouse platform, a low correlation was observed between image-derived disease estimates and visual scores, indicating that the current imaging method to quantify the disease area is not yet reliable. Genome-wide association studies (GWAS) conducted with conventional visual scores identified known rust resistance loci on Pv11 (Ur-11) and Pv4 (Ur-5), supporting the reliability of visual phenotyping. The signal on chromosome 11 overlapped with previously reported regions, while the signal on chromosome 4 requires further validation. In contrast, GWAS using image-derived disease estimates showed weaker genetic signals and a low correlation with visual scores, highlighting the need for further improvement of the model and imaging process. A deep learning model is currently being trained to enhance disease detection accuracy.

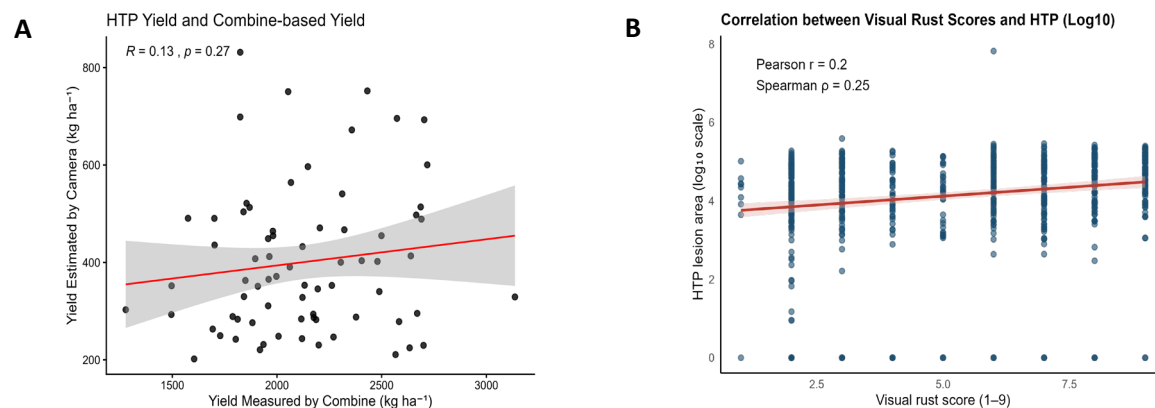


Figure 1. A) Relationship between camera-estimated and combine-measured yield, showing a weak and non-significant association. B) Relationship between image-derived disease area and visual rust score, indicating a weak association.

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EVALUATION OF MULTIPLE BOTRYTIS SPECIES CAUSING CHOCOLATE SPOT ON FABA BEAN (*VICIA FABAE*) IN THE MID-ATLANTIC AND FUNGICIDE MANAGEMENT OPTIONS

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INTRODUCTION: Faba beans are an emerging rotational crop in the Mid-Atlantic region of the United States. They are valued for their human health benefits as they are high in protein compared to other legumes and can be planted as an alternative winter crop in the region (Raman, et al., 2024). There are several cultivars for fresh-market, dry, or canned bean uses in various sizes. However, production is often challenged by fungal diseases. Of which, chocolate spot is the most economically important fungal disease, causing high annual yield losses (Sundheim, 1973). This disease can also decrease plant value because of low-quality or unusable pods and seeds. Chocolate spot, caused primarily by *Botrytis cinerea*, *B. fabae*, and *B. fabiopsis*, is largely a foliar disease characterized by small rust-brown circular lesions that expand and coalesce, forming a papery, brown lesion with red margins (Deverall, et al., 1961). Advanced infections may develop concentric rings and cause defoliation or stem and pod lesions. Management of chocolate spot includes a combination of cultural and chemical controls; however, production in the US is limited by a lack of current, research-based management recommendations. This study aims to investigate which species of *Botrytis* cause chocolate spot in the Mid-Atlantic and which available fungicides are effective in managing chocolate spot.

MATERIALS & METHODS: To investigate *Botrytis* species associated with chocolate spot in the Mid-Atlantic, symptomatic faba bean leaves from five field locations across Virginia were sampled in spring 2025. Symptomatic leaves were isolated onto antibiotic potato dextrose agar, incubated at room temperature until fungal growth was observed, and then transferred to potato dextrose agar. DNA was extracted from these isolates using the Quick-DNA Miniprep kit (Zymo Research, Irvine, CA, USA) and amplified using four primer sets from the glyceraldehyde-3-phosphate dehydrogenase (G3PDH), Heat-shock Protein 60 (HSP60), DNA-dependent RNA polymerase subunit II (RPB2) (Staats, et al., 2005), and the necrosis and ethylene-inducing protein (NEP1) (Staats, et al., 2007) regions. PCR amplicons were Sanger sequenced by Psomagen (Cambridge, MA). Resulting sequences were analyzed in Geneious Prime (Geneious Auckland, New Zealand). A multilocus sequence analysis using three housekeeping genes (G3PDH, HSP60, RPB2) was performed, and a Bayesian phylogenetic tree was created using *Monilina fructigena* as the outgroup. Another Bayesian tree was created using the NEP1 region with *B. cinerea* as the outgroup.

A fungicide efficacy trial was completed in spring 2025 in Painter, VA. Felix faba beans were planted on 13 March into a bare ground, overhead irrigated cropping system. Plots were 2.4m by 9.1m with rows spaced 19.1cm apart and a barrier plot of the same size between treatments. The sixteen fungicide treatments and an untreated control trial were arranged in a randomized complete block design with four replications. The trial relied on natural inoculum to cause disease. Disease incidence was visually assessed as the percentage of symptomatic leaves per plot on a 0-100% scale. Disease severity ratings were also taken as the percentage of foliage covered by diseased tissue on a 0-100% scale. Disease ratings were taken on 4, 23, and 30 May, 5 and 11 June. The final disease incidence and severity ratings and disease incidence and severity area under the

disease progress curve (AUDPC) values were analyzed using the SAS statistical program (JMP Pro 18.0.2, Cary, NC) as a generalized linear mixed model with block as a random effect.

RESULTS & DISCUSSION: Of the isolates collected, four morphologically identified isolates were initially selected for use in molecular analysis. In the multilocus sequence analysis (MSLA) of the three housekeeping genes (G3PDH, HSP60, RPB2), all isolates clustered closely with *B. fabiopsis* and *B. caroliniana* (Fig. 1A). The NEP1 Bayesian tree showed that the four isolates clustered closely with *B. caroliniana* (Fig. 1B). Li et al., (2012) noted that the three housekeeping genes alone could not distinguish *B. caroliniana* from *B. fabiopsis*. However, the two species only share 90% identity of the NEP1 region. The isolates in this study share over 98% identity with *B. caroliniana*. At the time of the study, no NEP1 reference sequence was available for *B. fabiopsis*. Because of this, the isolates in this study have a high likelihood of being *B. caroliniana*. Further confirmation will be completed once a *B. fabiopsis* NEP1 sequence is identified.

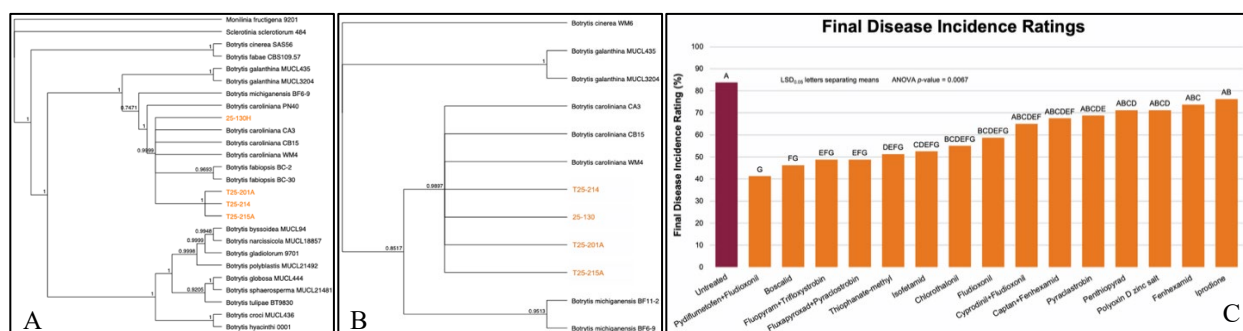


Figure 1. (A) Bayesian phylogenetic tree of the MSLA with concatenated sequences of G3PDH, HSP60, and RPB2. (B) Bayesian phylogenetic tree of the NEP1 gene. (C) Fungicide efficacy trial final disease incidence ratings.

In the field trial, disease pressure was widespread but low intensity, with the highest incidence and severity in the nontreated plots being 83% and 20%, respectively (Fig. 1C). In the final disease incidence rating, cyprodinil+fludioxonil, captan+fenhexamid, pyraclostrobin, penthiopyrad, polyoxin D zinc salt, fenhexamid, and iprodione did not differ from the nontreated control. Pydiflumetofen+fludioxonil had among the lowest final disease incidence, but did not differ from boscalid, fluopyram+trifloxystrobin, fluxapyroxad+pyraclostrobin, thiophanate-methyl, isfetamid, chlorothalonil, or fludioxonil. Pydiflumetofen+fludioxonil and boscalid are commercially available and registered for *Botrytis* management on faba bean as Miravis Prime and Endura, respectively. The final disease severity showed similar trends across products compared to the final disease incidence (*data not shown*). The trial will be repeated in spring 2026. Results from this efficacy trial are a good starting point for developing a fungicide disease management program.

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GENOME-WIDE ASSOCIATION STUDY TO IDENTIFY GENOMIC REGIONS ASSOCIATED WITH RESISTANCE TO SOYBEAN CYST NEMATODE HG TYPE 2.5.7 IN DRY BEANS

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INTRODUCTION

Soybean cyst nematode (SCN; *Heterodera glycines*) is an emerging threat to dry bean (*Phaseolus vulgaris* L.) production in the United States. Micro-plot evaluations of SCN effects on dry bean growth revealed significant seed yield reductions of 30-56% depending on initial SCN egg densities, market class, and environmental conditions (Poromarto et al. 2010). In North Dakota, increasing prevalence of virulent SCN populations has been reported, particularly HG type 2.5.7, now more prevalent in surveyed fields across the state (Chowdhury et al. 2021; Singh et al. 2025), posing a potential risk to dry bean production in the state. Although host resistance is an effective and environmentally sustainable management strategy, the genetic basis underlying resistance to HG type 2.5.7 in dry bean remains poorly understood (Poudyal et al. 2025). Therefore, a genome-wide association study (GWAS) was conducted on a diverse panel of dry bean genotypes tested against HG type 2.5.7 to identify genomic regions associated with resistance.

MATERIALS AND METHODS

A panel of 263 dry bean genotypes representing the Middle American and Andean gene pools, comprising six market classes (great northern, black, navy, slow-darkening pinto, light red kidney, and dark red kidney), was evaluated. Phenotypic data from two independent greenhouse experiments were analyzed using mixed linear models to generate best linear unbiased predictions (BLUPs), which were used for GWAS analysis. Genomic DNA was extracted from leaf tissues and genotyped using the NDSU 3.8K Bean GBS Panel (Figueroa-Cerna et al. 2025). After quality control filtering, 2,019 single-nucleotide polymorphism (SNP) markers distributed across the 11 dry bean chromosomes were retained for the analysis. GWAS was conducted in GAPIT using multiple models, including GLM, MLM, SUPER, FarmCPU, and BLINK. Model performance was evaluated based on control of population structure and relatedness, as assessed by quantile-quantile (QQ) plots. The BLINK model was selected for final reporting because it showed the best balance between statistical power and control of false positives, with minimal *P*-value inflation and improved resolution of marker-trait associations (MTAs) compared to other tested models.

RESULTS AND DISCUSSION

Phenotypic evaluation identified 29 (11%) dry bean genotypes exhibiting moderate resistance reaction to HG type 2.5.7 (Fig. 1). The Manhattan plot exhibited clear peaks on Pv02 and Pv07 (Fig. 2), corresponding to two significant MTAs identified by GWAS analysis for resistance to HG type 2.5.7. The MTA on Pv02 (represented by SNP marker: *S02_50534194*), explained 57.88% of the phenotypic variance, suggesting the presence of a major-effect resistance locus. The MTA on Pv07 (*S07_37564475*), explained 1.84% of the variance, indicating a minor-effect locus contributing to quantitative resistance. The similar MTA on Pv02 has also been reported recently

for HG type 1.2.5.7 (Poudyal et al. 2026; unpublished). These MTAs identified in this study point to genomic regions that may underlie resistance to HG type 2.5.7 in dry beans and provide a foundation for candidate gene discovery. This study provides a basis for developing high-throughput markers to support marker-assisted and genomic selection to expedite the breeding of dry bean cultivars with improved resistance to SCN.

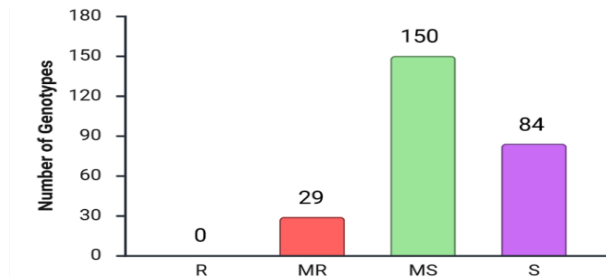


Fig. 1. Number of dry bean genotypes categorized as resistant (R), moderately resistant (MR), moderately susceptible (MS), and susceptible (S) to HG type 2.5.7 based on female index (FI) values ($R \leq 10\%$, $MR = 10-30\%$,

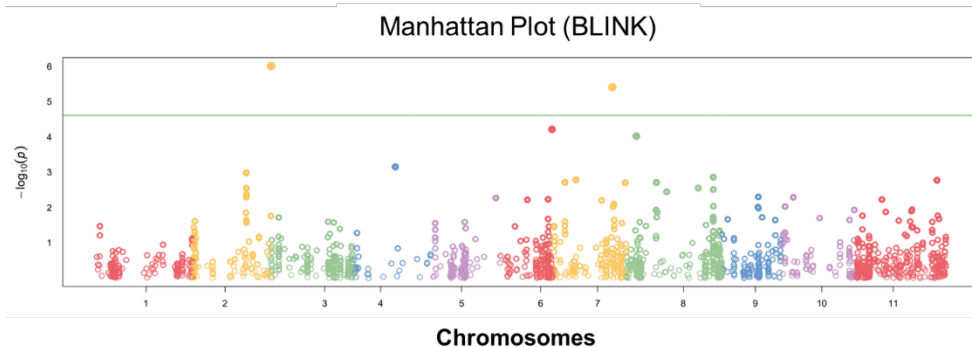


Fig. 2. Manhattan plot showing SNP associations across 11 dry bean chromosomes for resistance to HG type 2.5.7 using the BLINK model.

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VALIDATION OF MOLECULAR MARKERS FOR APHANOMYCES ROOT ROT RESISTANCE IN COMMON BEAN (*Phaseolus vulgaris* L.)

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a globally significant legume that serves as a source of cultural, dietary, and economic importance. Roughly 30 million tons of dry beans were harvested from 33.7 million hectares across the globe in 2024, making it the third most widely grown legume after soybean and peanut (FAOSTAT, 2026). Various types of disease resistance have been bred into common bean, including for viruses, foliar pathogens, and abiotic stresses. However, common bean remains vulnerable to soilborne pathogens, particularly those within the root rot complex. Among those, *Aphanomyces euteiches* is an oomycete agent of root rot in legumes, causing yield loss or complete crop failure. Known sources of resistance are typically patented or otherwise protected, leaving breeders and growers unable to utilize it in their own breeding programs. In addition, *Aphanomyces euteiches* is a particularly difficult pathogen to isolate and culture when compared to other members within the bean root rot complex. This research seeks to determine the genetic basis for *Aphanomyces euteiches* resistance in bean, and ultimately, develop efficient molecular tools for breeding *Aphanomyces* root rot resistance in common bean and facilitate the improvement of germplasm.

MATERIALS AND METHODS

An F₅ recombinant inbred line (RIL) population of 294 lines was developed from the cross of two bean lines, a pinto bean resistant to *Aphanomyces* (EX1845), and a susceptible great northern line (Matterhorn). These materials were subject to *Aphanomyces euteiches* disease screening, where 9-day old plants were inoculated with a liquid culture containing the infectious agent (zoospores) of an *Aphanomyces* isolate collected in Wisconsin. Ten days after inoculation, plants were scored



Figure 1. Common bean roots displaying susceptibility to *Aphanomyces euteiches* (left) and resistance (right). Note the discoloration in the roots and hypocotyl of the roots on the left, while the roots on the right appear healthy.

from a scale of 1-9 (highly resistant to highly susceptible), based on root and hypocotyl appearance, an example of which is displayed in Figure 1. The disease scoring was paired with Genotype-by-Sequencing (GBS), with SNPs called using the TASSEL pipeline (Bradbury et al, 2007) and common bean reference genome *Phaseolus vulgaris* v2.1. After filtering, the F₅ RIL population had 23,331 markers. Genetic mapping was conducted in R/GAPIT (Wang et al, 2021), utilizing a Mixed Linear Model. After QTL mapping a candidate R gene was sequenced via Oxford Nanopore sequencing. Three SNPs co-segregating between resistant

and susceptible lines were used to develop PCR Allelic Competitive Extension (PACE) markers (Figure 2).

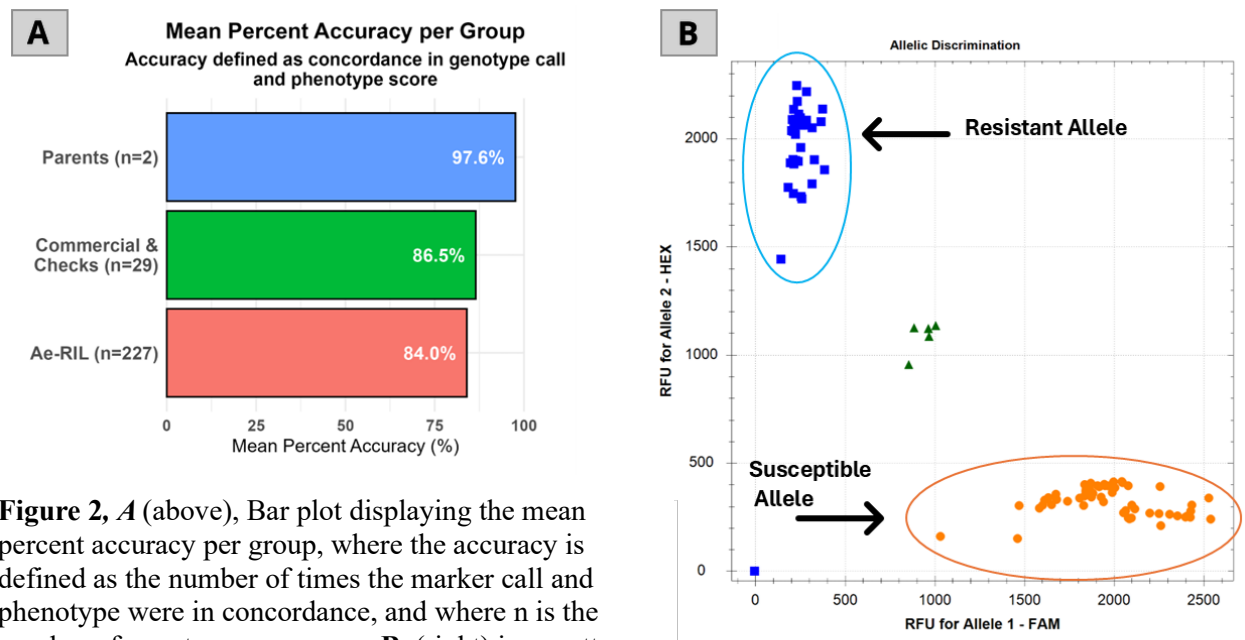


Figure 2, A (above), Bar plot displaying the mean percent accuracy per group, where the accuracy is defined as the number of times the marker call and phenotype were in concordance, and where n is the number of genotypes per group. **B.** (right) is a scatter plot displaying the allelic discrimination of the PACE assay, where 3 distinct genotypes are called (homozygous for the resistant allele, heterozygous, or homozygous for the susceptible allele) dependent on the amount and ratio of the HEX and FAM fluorescence measured.

RESULTS AND DISCUSSION

Genetic mapping resulted in the discovery of a major QTL on chromosome 10 for *Aphanomyces euteiches* disease resistance in common bean. Utilizing sequencing data, three markers were developed, and then tested across the Ae-RIL population and unrelated commercial materials. PACE assay validations combined with phenotyping determined one marker showed strong predictive potential for resistance across diverse genetic backgrounds and market classes (Figure 2A); displaying reliable accuracy in determining if a common bean genotype is resistant or susceptible to *Aphanomyces euteiches* (Figure 2B). Further refinement via fine mapping is in progress, as well as additional experiments to explore functional gene analysis. Utilizing the knowledge from this marker and validations, more accurate markers will be designed to improve the efficiency and accuracy of this tool for breeding.

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MARKER-ASSISTED BACKCROSSING TO INTRODUCE THE NON-DARKENING TRAIT INTO CRANBERRY BEAN (*PHASEOLUS VULGARIS*) VARIETIES

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INTRODUCTION:

Seed coat darkening is an undesirable post-harvest quality trait of several market classes of dry beans (*Phaseolus vulgaris* L.). It is determined by crop genetics and exacerbated by environmental conditions, such as high temperatures, humidity, and excessive light exposure. This trait reduces market acceptance, as darkened seeds are often perceived as old and slow to cook, leading to economic losses for producers. The current research was designed to introduce the non-darkening trait, controlled by a homozygous recessive condition for the *j* gene on chromosome 10 in *P. vulgaris*, into high-yielding, regular-darkening cranberry bean varieties, OAC Navabi and OAC Firestripe, without compromising their qualities.

The non-darkening variety Wit-rood was crossed with OAC Navabi and OAC Firestripe to introduce the recessive *j* allele. The resulting F₁s were backcrossed with the elite parents to establish non-darkening OAC Navabi and OAC Firestripe backcross (BC) breeding populations. The BC seedlings were screened with a Kompetitive Allele Specific PCR (KASP) marker to identify *Jj* individuals, which were used for additional backcrossing with the elite parents and finally selfed to obtain individuals that were homozygous for the recessive *j* allele. Backcross and selfed progeny were also screened with a BARCBean12K bead chip to determine their levels of homozygosity for recurrent parent alleles at almost 1,000 sites throughout the bean genomes. These results demonstrate that marker-assisted backcrossing, combining foreground selection for the *j* allele with background selection for RPG recovery, is effective for developing non-darkening cranberry bean lines while retaining the genetic background of elite cultivars.

MATERIALS AND METHODS:

Genotypes of backcrossed 3(BC3) were screened with the KASP marker; developed from the SNP marker (G/-)(Erfatpour and Pauls, 2020) and the background markers; assayed with the BARCBean 12K BeadChip (Song et al., 2015) to identify individuals with the non-darkening recessive *j* allele of the Phvul.010G130600 gene and determine the extent of recurrent parent allele recovery, respectively in the recurrent and selfed progeny. Non-darkening homozygous individuals (*jj*) in the selfed progeny were selfed again and their field performance was tested at the Elora Research Station with their backcross parental lines in a RCBD with 78 X 3 = 234 plots.

RESULTS:

The KASP marker was effective in identifying heterozygous *Jj* individuals in the backcross families and homozygous *jj* individuals in the selfed progeny (Figure 1). The SNP-chip markers that were polymorphic markers between the parents (Firestripe vs Wit-rood; Navabi vs Witrood) were used to evaluate the extent of recurrent parent genome (RPG) recovery in the backcrossing generations. For OAC Firestripe the homozygosity for the recurrent parent alleles went from 38% in BC1 to 90% in BC4 (Figure 2). For OAC Navabi the homozygosity for the recurrent parent alleles went from 56% in BC1 to 94% in BC4 (Figure 3). Polymorphic markers between the parents were used to evaluate the plants in subsequent generations. Background analysis revealed that the extent of RPG recovery ranged from 38% to 90% in OAC Firestripe and 56% to 94% in OAC Navabi from BC1 to BC4-selfed.

CONCLUSIONS:

Marker-assisted backcrossing is an effective strategy to recover recurrent parent genome with background selection and integrating foreground selection for the *j* allele for developing non-darkening cranberry bean lines while preserving the genetic background of elite cultivars.

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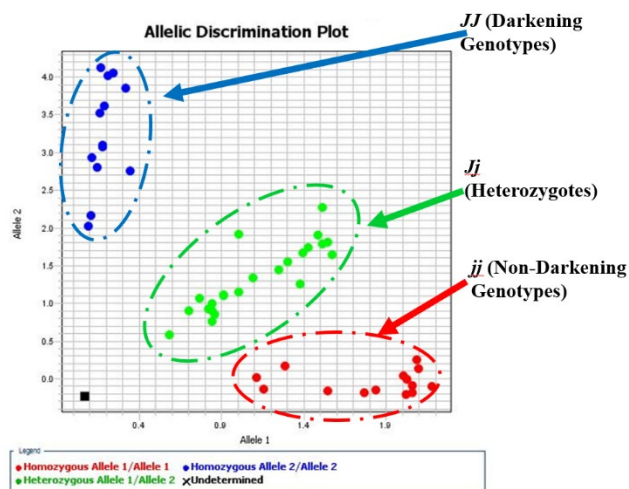


Figure 1. KASP marker identification of BC3-Selfed individuals homozygous for *j*.

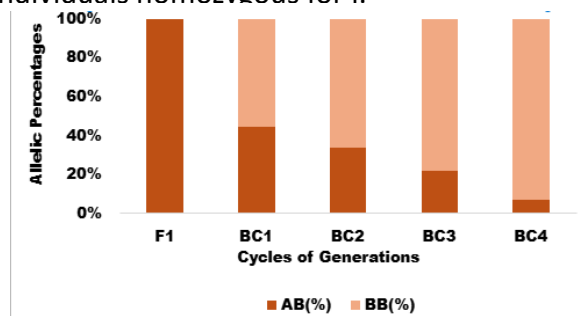


Figure 2. Recovery of background markers across generation of OAC Firestripe.

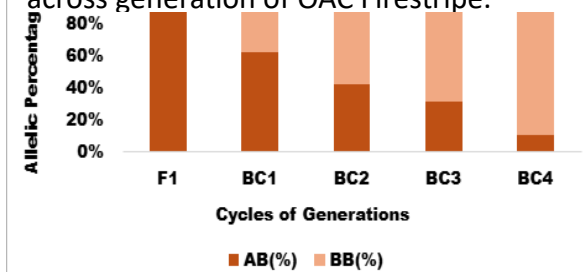


Figure 3. Recovery of background markers across generation of OAC Navabi.

REACTION OF COMMON BEAN CULTIVARS AND BREEDING LINES TO ROOT ROT CAUSED BY *FUSARIUM OXYSPORUM* F. SP. *PHASEOLI*

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is a legume of great socioeconomic importance, especially in developing countries, where it constitutes one of the main sources of plant protein. However, common bean yield is often limited by various biotic and abiotic factors, where diseases caused by soil pathogens are particularly significant. Among them, Fusarium wilt, caused by the fungus *Fusarium oxysporum* f. sp. *Phaseoli* (Figure 1), is one of the most severe diseases that may lead total yield loss. The evaluation of resistant genotypes is essential for effective management and production sustainability.



Figure 1. Common bean plants showing stem symptoms caused by *Fusarium oxysporum* infection (left) and a healthy plant (right).

MATERIAL AND METHODS

This study aims to evaluate the reaction of common bean cultivars and breeding lines of the carioca and black commercial groups to Fusarium wilt. The experiment was conducted in a greenhouse, evaluating 39 genotypes from the black group, and 30 from the carioca group. A completely randomized design was employed, with four replications and plots consisting of a single pot containing one plant each. The materials were artificially inoculated with a suspension of 10^6 conidia/mL 14 days after emergence. Assessments were carried out 33 days after inoculation using

the disease severity index developed by the International Center for Tropical Agriculture (CIAT). Disease severity data was converted by square root of $(x + 0.5)$, and statistical analysis was performed by Genes software.

RESULTS AND DISCUSSION

Analysis of variance revealed a significant effect of genotypes, and the heritability estimates (h^2). Among the 69 materials evaluated, only three cultivars showed susceptibility to the disease (Figure 2): IAC Alvorada and IAPAR 81 (carioca group), and BRS Supremo (black group), while the remaining genotypes demonstrated resistance or moderate resistance to *Fusarium* wilt. The genetic parameters, index B (0.744) and h^2 (67.3%), indicated good responses for selecting resistant genotypes.



Figure 2. Symptoms of the disease in susceptible genotypes: chlorosis, premature defoliation of lower leaves, extensive necrosis in vascular tissue, and wilting.

CONCLUSION

The genotypes may be recommended for cultivation in areas infested with the pathogen, as well as used as parents in breeding programs aimed at developing *Fusarium* wilt-resistant varieties.

ACKNOWLEDGEMENTS

This research was financially supported by the Rural Development Institute of Paraná – IAPAR-EMATER (IDR-Paraná).

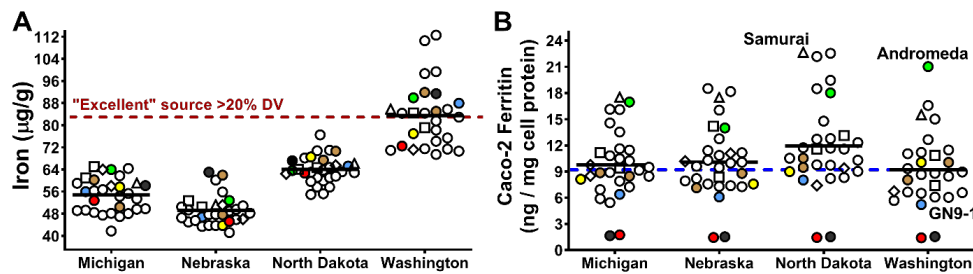
IRON NUTRITION FROM GREAT NORTHERN BEANS: THE ABSENCE OF FLAVONOIDS AND EFFECTS OF CANNING

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INTRODUCTION: Depending on the market class and variety, dry beans (*P. vulgaris*) are a good source of iron (Fe), capable of providing 10-15% of the Daily Value (DV) with each ½ cup serving. Public awareness of iron deficiency is increasing as anemia in the US is on the rise, however, the consumption of dry beans and other pulses remains low. Promoting beans as an excellent source of dietary Fe can be misleading, as many of the dark colored market classes have seed coat flavonoids that can dramatically Fe absorption. Great northern beans are generally white and have no Fe uptake-inhibiting flavonoids. Therefore, a collection of Great Northern beans was assembled to evaluate the market classes' potential as a source of bioavailable dietary iron.

MATERIAL & METHODS: The Great Northern Collection (GNC) consists of 20 great northern dry bean varieties. This study also includes 10 non-great northern field checks, representative of other market classes (w. kidney, navy, yellow, slow-darkening pinto, black, and red) produced and processed under the same conditions. The GNC was grown at research sites in Michigan, Nebraska, North Dakota, and Washington. Cooked beans were stored at -80°C until freeze drying and milling into a fine powder using an analytical hammer mill. Iron



concentrations were measured using ICP-AES. A phytate/total phosphorus kit (K-PHYT;

Figure 2: Dot plots depicting the (A) iron concentrations and (B) iron bioavailability of 30 dry bean entries from the GNC. Each dot represents the mean value of two field replicates grown over one field season at each production site. Hyphenated lines indicate target values for improved iron concentrations (A; red) and iron bioavailability (B; blue) in soaked and cooked beans. Green and blue dots highlight great northern beans with high (Andromeda) and low (GN9-1) iron bioavailability across all locations. Field controls: Δ Otebo (cv. Samurai); □ white kidney; ◇ navy; yellow – Mayocoba; brown – pinto (slow-darkening); red - small red (cv. Merlot) and black (cv. Eclipse) are represented as colored dots on each graph.

Megazyme® International, Bray, Ireland) was used to measure phytate. Iron bioavailability was measured according to the established methods described in Glahn, 2022 *JoVE*, 182; e63859.

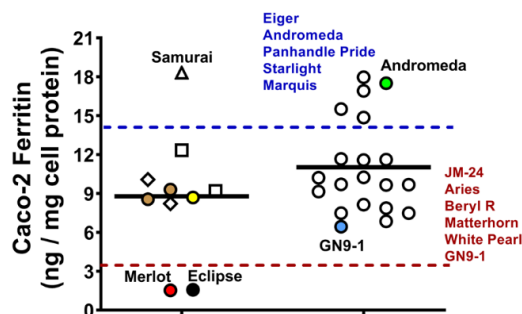


Figure 2: Dot plots depicting iron bioavailability of 30 dry bean entries from the Great Northern Collection and field controls. Each dot represents the mean value of two field replicates grown over one season for all locations. Green and blue dots represent great northern beans with high and low iron bioavailability (Andromeda and GN9-1) across locations.

RESULTS: Iron concentrations ranged from 42-113 $\mu\text{g/g}$ across all locations, with significant differences among locations, suggesting a high GxE interaction (**Figure 1A**). Beans produced in Nebraska (soil pH 8) had the lowest iron concentrations, while the highest iron was measured beans from Washington. Despite the large differences in iron concentrations, the patterns of iron bioavailability were similar across the locations (**Figure 1B**). Five great northern varieties (Andromeda, Eiger, Panhandle Pride, Starlight, Marquis) exhibited consistently high Fe bioavailability across all locations. Many of the great northrens had more bioavailable iron than the commercial white kidney bean (*cv.* Snowden), as well as slow-darkening pintos (*cv.* ND Palomino and USDA-Diamondback), which are used as reference standards for improved iron bioavailability (**Figure 1B**). Several great northern varieties (GN9-1, White Pearl, BerylR, JM-24, Matterhorn) had iron bioavailability scores lower than the white kidney standard but still higher than the red (*cv.* Merlot) and black bean (*cv.* Eclipse) field checks (**Figure 1B**). The high iron concentrations of the GNC from Washington did not result in more bioavailable iron. Washington beans also had 15-20% more phytate (an Fe bioavailability inhibitor) relative to the other locations. There was a significant ($r = -0.314$, $P = 0.002$) relationship between the phytate and iron bioavailability of the GNC across locations.

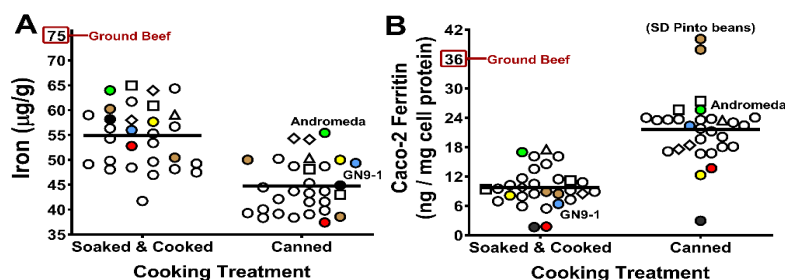


Figure 3: Dot plots depicting iron concentrations (A) and iron bioavailability (B) of 30 dry bean entries from the Great Northern Collection that were produced in Michigan and either cooked or canned. Each dot represents the mean value of two field replicates grown over one season at each production. Green and blue dots represent great northern beans with high and low iron bioavailability (Andromeda and GN9-1) across locations.

CONCLUSIONS: Genotypic differences exist in iron bioavailability of great northern beans, with some varieties demonstrating superior and stable iron bioavailability across all locations, independent of their iron concentrations. Many of the GNC represent excellent Fe bioavailability. Canning of the bean varieties lowered Fe concentration but increased Fe bioavailability in all samples except the black bean. This is the first study to examine canning and show a beneficial effect on Fe bioavailability, a significant piece of information for dietitians and nutritional scientist.

BREEDING POPPING BEANS FOR TEMPERATE U.S. PRODUCTION

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INTRODUCTION Nuña or popping beans are a form of dry bean that is cooked without hydration. When dry seeds are heated for only a few minutes, the beans will ‘puff’ and soften, rendering them ready to eat. Various methods may be used to pop them, including hot oil, hot sand and microwaving, with the key being a rapid and even transfer of heat into the seed. Nuña beans arose in the Andes of Peru and Bolivia in a genetic background that is adapted to short days, cool temperatures and intense sunlight. Attempts to grow these beans at higher latitudes outdoors fail because the lines will not flower until September, when day length approaches 12 hours, and no warm season remains to mature the crop. The OSU program has worked with nuña beans for the past 30 years with breeding efforts to transfer the popping trait into a North American adapted genetic background. The effort was inspired by publication of ‘Lost Crops of the Incas’ (National Research Council, 1989), and several public breeding programs initiated breeding efforts that were subsequently delayed in 2000 for 12 years because of two utility patents (US6,040,503 and US6,419,976). When these patents were abandoned, breeding efforts resumed. We recently released two popping bean cultivars (Myers et al., 2025) that perform well in many bean growing areas of the U.S. Below, we describe what we have learned during the last 30 years working with nuña beans. We will use the term popping bean to distinguish derived cultivars from traditional nuña beans.

MATERIALS AND METHODS The newly released cultivars were derived from the 1996 cross ‘Pava’ nuña x ‘5-593’ using the pedigree breeding method. Selection for determinate growth habit and early flowering and maturity was imposed in the field in the F₂ generation. A portion of the seed from single F₂ plants was popped to select those with popping ability. The population was advanced in subsequent generations to the F₅ as single plants, with continued selection for desirable field traits and for popping ability. Beginning in the F₆ generation, plants were bulked by family for testing in replicated plots in Oregon. Breeding lines were subsequently sent to Washington, Wyoming and Michigan for testing. Proximate analysis of breeding lines was carried out at WSU and disease testing was performed at University of Idaho.

RESULTS AND DISCUSSION Research was initially carried along as an adjunct to regional dry bean breeding programs, but in 2024, the USDA-NIFA-SCRI grant “POPBEANS SREP: Protein-Rich Wholesome Popping Beans to Enhance Agricultural Production, Nutrition, and Sustainability” was funded, which provided additional support to characterize breeding lines and support their release as cultivars. Below are some of the lessons learned.

The popping trait is complex and includes not only factors that affect seed composition and cellular structure but also traits that affect heat transfer such as seed shape. While bean fragments will pop, popping percentage is highest when the testa is intact. For unknown reasons, the best popping lines in the breeding population have dark-colored testas. In the OSU breeding program, all of lines with the best popping percentage came from a single F₄ family out of about 1,450 single plant families screened, demonstrating that without the availability of molecular markers, large numbers of lines must be evaluated to identify those with the best combination of favorable alleles. In terms of composition, the popping bean lines fall within the range of conventional dry beans with 34% carbohydrates, 22% protein, 2.8% lipids and 4.2% ash, but at 18% are lower in total dietary fiber (24-27% is considered the range for dry beans). This difference should be investigated to determine whether it is associated with popping ability.

Dry bean seeds must be cooked to eliminate antinutritional factors, such as phytohemagglutinins, and this is traditionally performed through hydrated cooking methods. It takes 12 minutes at 100°C to render phytohemagglutinins biologically inactive and even longer at high altitudes where nuñas have traditionally been used. We evaluated popping beans for their levels of phytohemagglutinins and whether the rather rapid popping process eliminates the toxic effects. Popping beans have similar quantities of phytohemagglutinins to conventional dry beans in raw seeds, but the phytohemagglutinins are rendered biologically inactive in fully popped beans but may be present in trace amounts in seeds that have been heated but failed to pop.

At present, there are no markets for popping beans and no products. The challenge of bringing this new form of bean to consumers will require solutions to various technical production problems as well as an education program for consumers. Where we have had stakeholders taste popping beans, the response has been overwhelmingly positive. Some of the technical issues include 1) incomplete popping, which requires methods for removal of unpopped seeds, 2) maximizing seed expansion and complete popping of the seed, 3) determining optimum method, time and temperature for popping, 4) determining optimum harvest methods to achieve best seed moisture (approximately 8.5%) for popping and 5) optimizing the harvest process prevent seed damage that might decrease popping percentage.

Going forward, we may begin to see popping beans consumed as high protein snack foods and used in the development of dehydrated products that require less energy to process, as well as novel uses as a healthy ingredient in foods.

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INTRODUCING A WEB APP FOR DRY BEAN STAND COUNTING

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INTRODUCTION

Accurate stand counting is a critical agronomic trait for cultivar development and crop management, helping growers detect planting issues and interpret yield variability. Traditional manual counting is time-consuming, labor-intensive, and prone to error. While Unoccupied Aerial Systems (UAS) and RGB imagery offer an affordable alternative, traditional rule-based pipelines often struggle in dense stands where canopies overlap, leading to significant undercounting. This research addresses these gaps by developing a complete workflow that benchmarks traditional thresholding against the newest YOLOv12 detection and instance segmentation models. The study specifically evaluates a multi-class approach designed to resolve overlapping plant clusters in dry bean breeding trials.

MATERIALS AND METHODS

The study utilized multi-year RGB data collected between 2021 and 2025 from dry bean trials at the Saginaw Valley Research and Extension Center (SVREC) in Michigan. Data acquisition and processing involved collecting imagery using DJI Phantom 4 Pro v2 and Mavic 3 Multispectral drones at sub-centimeter Ground Sampling Distances ranging from 0.6 to 0.7 cm. To manage this extensive data, a custom ArcPy script was developed to unify multi-year ArcGIS exports into a single, YOLO-compatible dataset consisting of 113,349 total image chips. Counting methodologies were split into two primary approaches: a thresholding-based baseline and deep learning models. The baseline consisted of a deterministic workflow using the Visible Atmospherically Resistant Index (VARI) combined with geometric operations, such as negative buffering and splitting, to approximate individual plant footprints. For the deep learning approach, YOLOv12 models were tested under two scenarios: Scenario 1 utilized a single "plant" class to establish a simple baseline, while Scenario 2 employed three distinct classes for single, double, and triple-plant clusters to specifically teach the model how to differentiate and count overlapping targets. Finally, for deployment, the best-performing model was integrated into a lightweight Flask web application. This tool allows non-technical users to upload orthomosaic imagery and receive georeferenced outputs, including GeoJSON, CSV files, and shapefiles containing plant detection data.

PRELIMINARY RESULTS

The evaluation across 15 independent test locations demonstrated a clear hierarchy in performance:

Method	MAE (Plants)	RMSE (Plants)	R ²
Thresholding	26.2	35.1	0.922
YOLOv12 Detection	71.3	96.4	0.408
YOLOv12 Segmentation	16.7	21.1	0.972

Key Findings:

The evaluation revealed a clear hierarchy in performance, with segmentation superiority being the most prominent finding: the YOLOv12 segmentation model, leveraging pixel-level supervision and a multi-class structure to resolve overlapping clusters, achieved the highest accuracy ($R^2 = 0.972$) with minimal bias. In contrast, a significant detection failure was observed in the detection-only model, which suffered from severe systematic underestimation because it tended to merge overlapping plants into single bounding boxes. The operational window for this technology is closely tied to crop phenology, with accuracy peaking during the Canopy Expansion stage at 94.5% (16 Days After Planting); however, detection failure occurred after 40 Days After Planting due to total canopy closure obscuring individual plant centers. Despite these temporal limitations, the segmentation model demonstrated strong environmental robustness, generalizing effectively across diverse soil textures, weathered surfaces, and heavy residue conditions encountered over four distinct growing seasons.

NEXT STEPS

While the current methodology provides a robust foundation for precision phenotyping, future research will aim to broaden environmental robustness by incorporating Near-Infrared (NIR) bands to reduce the system's sensitivity to variations in soil color, shadows, and lighting contrasts. Efforts will also be directed toward computational optimization, exploring methods to reduce the current dependency on high-end GPU resources and centimeter-level Ground Sampling Distance (GSD) to facilitate the integration of fixed-wing or satellite data.

SELECTION OF LIMA BEAN (*PHASEOLUS LUNATUS*) GENOTYPES FOR TOLERANCE TO DROUGHT STRESS

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INTRODUCTION:

Lima bean (*Phaseolus lunatus*) is a legume of great agricultural and nutritional importance in different world regions. One of the major problems for its production is intermittent or terminal drought that it could be increasing for climate change in the next years. This research has the main goal to select lima bean genotypes that have good agronomic and yield performance under drought stress conditions that could be an alternative to food production in growing regions with water deficit and high temperatures. In the Experimental Research Center of the Universidad Nacional de Colombia at Candelaria (CEUNP), 104 lima bean genotypes from CIAT germplasm bank were planted under drought environment, irrigation was cut-off before genotypes flowering and it not was irrigated again until experiment was harvested. All genotypes showed tolerance to drought stress at vegetative stage however there are differences among genotypes at reproductive stage. Almost half of genotypes produced seeds under drought stress. Ten genotypes showed outstanding seed production and agronomic performance under drought stress.

OBJECTIVE

To identify and select *P. lunatus* genotypes showing high tolerance to drought

MATERIAL AND METHODS

In February 24 of 2025, in the Experimental Center of the Universidad Nacional de Colombia at Candelaria (Valle del Cauca) were planted the selected 104 germplasm accessions of *P. lunatus*, one genotype of *P. vulgaris* (AFR298), and one of *P. acutifolius* (G40001) into three screenhouses with plastic roof for evicting precipitation go inside. Genotypes were given for Alianza Bioversity and CIAT at Palmira, Colombia. Twenty seeds of the each one of the 104 germplasm accessions were planted in soil (udic Haplustert fine clay) rows of 3.0 m and they were planted under two water content environments. One environment under normal irrigation (drip irrigation -12.5 ml water/ m during 15 minutes, 3 times a week by 6 months) and the other under terminal drought condition. The drip irrigation was stopped in the drought environment before plants start to flowering on April 1 of 2025. Soil water content, morphological and phenological plant data were taken.

RESULTS AND DISCUSSION

All 104 *P. lunatus* genotypes produced vegetative biomass at drought conditions and they did not present wilting thought that not had irrigation before flowering. Under normal irrigation environment all genotypes produced more vegetative biomass than under drought environment. Seed production only was obtained in 43 genotypes under drought conditions. However, the seed production was better under drought conditions as showed in Table 1. One possible explanation for this unexpectable result is that the tested *P. lunatus* delayed flowering when have enough water and prefer to maintain vegetative growing. Many of them, under normal irrigation, started to flowering in the last two months when the drought essay was being harvested. The best performance eleven genotypes showed in Table 1 will be tested in an yield trail in 2026.

Table 1. Origin, growth habit, seed weight and seed color of Phaseolus lunatus genotypes selected for drought tolerance in Candelaria, Cauca Valley, Colombia

ID	Growth Habit	Country Origin	Region	Location	Altitude (m. a.s.l)	Seed color	Weight_100 seeds (g)	Seed weight (kg) Irrigated Essay	Seed weight (kg) Drought Stress Essay
G25014	Cl. Ind.2	Brazil	Goiás	Ipameri	739	Red	0.40	0.93	2.05
G25288	Cl. Ind.	Mexico	Chiapas	Tuxtla Gutierrez	535	White - Black	0.60	N.S	1.43
G25514	Cl. Ind.	Colombia	Cordoba	Pueblo Nuevo	67.5	Red	0.49	0.40	1.61
G25541	Cl. Ind.	Argentina	Tucuman	San Miguel De Tucuman	401	White	0.54	0.58	1.08
G25542	Cl. Ind.	Argentina	Corrientes	Goya	46	White	0.51	0.54	1.27
G25581	Cl. Ind.	Bolivia	Santa Cruz	Cordillera	750	White -Red	0.87	0.46	1.07
G25599	Cl. Ind.	Guatemala	Zacapa	Zacapa	229	Black	0.55	0.15	1.99
G26001	Cl. Ind.	Brazil	Piauí	Oeiras	200	Beige	0.74	0.95	1.64
G26438	Cl. Ind.	Costa Rica	Cartago	Turrialba	750	Brown-Black	0.55	0.39	1.20
G27429	Cl. Ind.	Colombia	Cordoba	Sahagun	60	Red	0.47	0.76	2.63
G27622	Cl. Ind.	Chile	Region IX Malleco	Purén	190	White	0.48	0.21	1.15

¹ID = Genotype Identification; ²CL. Ind =Climbing Indeterminate

HEAT STRESS IN BEANS: REPRODUCTIVE RESILIENCE AND SINK STRENGTH AS KEYS TO YIELD STABILITY

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INTRODUCTION

High night temperatures are an increasingly frequent constraint for common bean (*Phaseolus vulgaris* L.) production in tropical regions. Elevated minimum temperatures disrupt reproductive development, causing flower and pod abortion, reduced seed number per pod, poor grain filling, and ultimately yield losses (Soltani et al., 2019; Vargas et al., 2021). Previous physiological studies show that heat stress primarily alters source–sink relationships during the reproductive stage, reducing assimilate partitioning efficiency and pod harvest index. Thus, strengthening sink activity is central to maintaining yield stability under elevated night temperatures. This study integrates field validation, greenhouse screening, and image-based phenotyping to: (i) identify physiological traits linked to reproductive resilience, (ii) quantify sink strength under heat stress, and (iii) evaluate the contribution of interspecific introgression (*P. vulgaris* × *P. acutifolius*) to yield stability.

MATERIALS AND METHODS

A total of 150 elite and historical *P. vulgaris* lines (Mesoamerican and Andean gene pools) and one interspecific RIL population (*P. vulgaris* × *P. acutifolius*) were evaluated. Field trials were conducted in Espinal, Colombia, characterized by mean night temperatures ≥ 22 °C (natural heat-stress environment). Complementary greenhouse experiments were performed in Palmira under controlled heat-stress conditions (mean night temperatures ≥ 22 °C), with a non-stress reference (~ 19 °C minimum temperature). Measured variables included: Seed number per pod, Pod harvest index, Digital seed area and Grain yield (kg ha^{-1}). A custom in-house Phenobox platform was used to standardize image capture and automate seed quality assessment through controlled illumination and machine-learning analysis, enabling high-throughput phenotyping. Seed metrics were obtained using the OpenCV library in Python.

RESULTS AND DISCUSSION

Consistent with previous findings, heat stress significantly reduced pod set, seed number per pod, and grain filling. In the interspecific RIL population, reductions in seed number per pod were significant ($p < 0.05$), confirming reproductive sensitivity as a key driver of yield loss under elevated night temperatures. Nevertheless, clear genotypic variation was observed, with some *P. vulgaris* lines maintaining partial tolerance through higher pod harvest index and grain filling efficiency. Field data under natural heat stress showed that interspecific lines outperformed heat-adapted *P. vulgaris*, yielding 1750 kg ha^{-1} versus 1436 kg ha^{-1} , representing an approximate 22% advantage. This suggests that introgression from *P. acutifolius* enhances reproductive resilience, sink strength, and buffering capacity under heat stress, as reflected by a broader and higher yield distribution.

Digital seed area analysis revealed compensatory responses, where reduced seed number was partially offset by increased seed area under heat stress (Figure 1), indicating altered photoassimilates allocation. Genotypes with stronger sink strength (higher pod harvest index and stable grain filling) showed improved yield stability. Image-based phenotyping discriminated tolerant and susceptible lines, facilitating rapid selection. High night temperature affects reproductive development and photoassimilates partitioning. Combined field and greenhouse results confirm that the reproductive phase is the most heat-sensitive stage in common bean, sink strength is central to yield stability, and interspecific introgression (*P. vulgaris* × *P. acutifolius*) confers a measurable (~22%) field-level yield advantage under heat stress

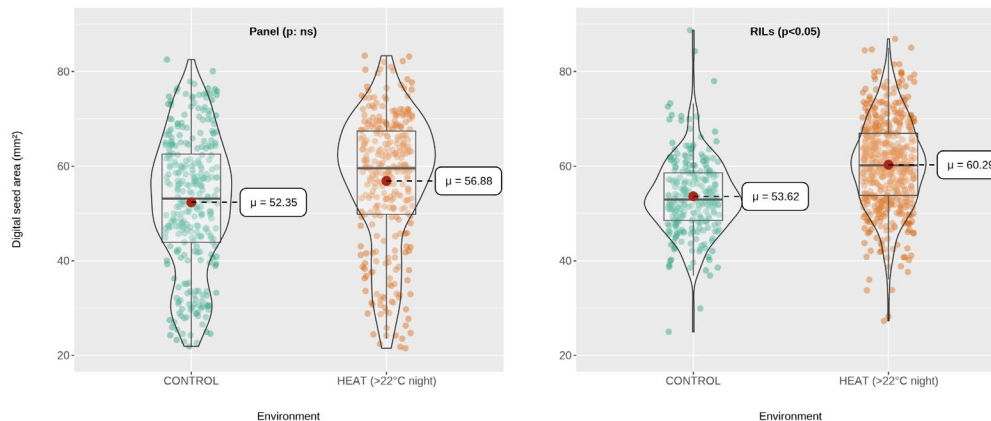


Figure 1. Digital seed area under control and heat-stress conditions. Left: Panel 150; Right: interspecific RIL population. Under heat, seed area increased, suggesting compensatory grain filling due to lower seed number, reflecting differences in assimilate allocation efficiency among genotypes.

CONCLUSIONS

High night temperatures significantly reduce seed number and grain filling in common beans. Yield stability under heat stress is strongly associated with sink strength and reproductive resilience. Interspecific lines showed a yield advantage over the best *P. vulgaris* per se under natural heat stress conditions. Image-based phenotyping provides an efficient tool for rapid screening of heat-tolerant germplasm. These findings support the strategic integration of physiological screening, digital phenotyping, and interspecific introgression to accelerate breeding for climate resilience in *Phaseolus*.

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GENOME-WIDE SELECTION FOR DROUGHT TOLERANCE IN MESOAMERICAN BEAN GENOTYPES

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INTRODUCTION

Water deficit (WD) is one of the main factors reducing the productivity of common bean (*Phaseolus vulgaris* L.), and the development of drought-tolerant cultivars represents a strategy for ensuring food security. This study aimed to evaluate agromorphological traits and identify genomic regions through genotyping-by-sequencing (GBS) for a genome-wide association study (GWAS) in a Mesoamerican common bean diversity panel, composed by 146 genotypes (G) under WD conditions.

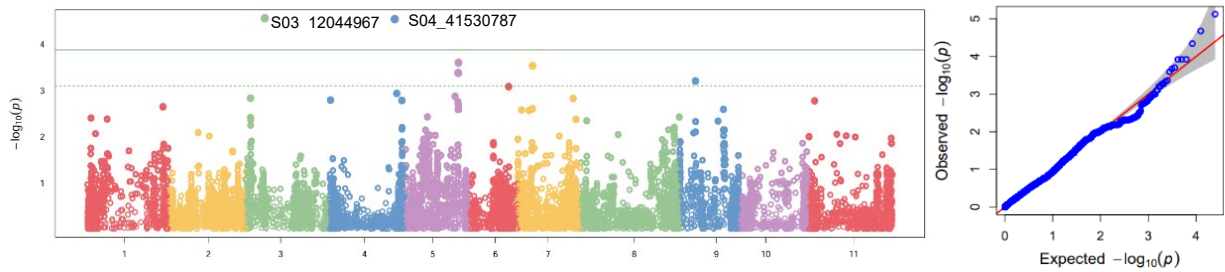
MATERIAL AND METHODS

The experiment was carried out under protected cultivation at the Experimental Station of IDR-Paraná, Londrina, Paraná State, Brazil, during the 2022 and 2023 fall-winter cropping seasons. The experiment was arranged in a randomized block design with two replications, in two environments (E): water deficit (WD), and well-watered (WW). The genotypes (G) BAT 477 (drought-tolerant), IPR Sabiá, and BRS Pontal (both drought-sensitive) were used as controls. The variables agromorphologicals evaluated were: total number of pods per plant, number of grains per plant, pod length, pod thickness, number of locules per pod, number of grains per pod, grains per locule ratio, total mass of grains per plant (g), and grain yield (kg ha⁻¹). The agromorphological traits were subjected to individual and joint analysis of variance. For GWAS, genotyping was performed using GBS, obtaining 25,011 single nucleotide polymorphisms (SNPs) with minor allele frequency (MAF) >0.05. Linkage disequilibrium was calculated using the kinship matrix for each individual chromosome, and the search for favorable alleles and candidate genes was performed using Gene Ontology. Quantitative trait nucleotides (QTNs) were identified using GLM, FarmCPU, and BLINK models, based on the *Phaseolus vulgaris* reference genome available in Phytozome v13. All analyses were performed using R[®] and Genes[®] software.

RESULTS AND DISCUSSION

ANOVA showed significant GxE interaction effects for all traits, and the phenotyping identified greater genetic diversity among the accesses under WD conditions. The genotyping identified 23 QTNs, as well as 462 genes associated with the traits evaluated under WD conditions. Seven significant QTNs S04_42040243, S04_43611052, S01_44975422, S04_45983322, S07_38826091, S08_60928027 and S01_45647418, were identified in the three models studied. Figure 1 shows the Manhattan plot of the variable number of pods per plant with the SNPs that passed the models studied.

Figure 1. Manhattan plot for the number pod per plant variable indicating the SNPs identified in the GWAS study of the genetic diversity panel of Mesoamerican bean genotypes, in Londrina, Paraná State, Brazil.



Among the identified genes stand out for their roles in mitigating reactive oxygen species (ROS), maintaining photosynthesis through thermal shock proteins (TSPs), and abscisic acid (ABA) signaling. Other genes are involved in the activation of ethylene response transcription factors (ERFs), reducing drought stress effects. Table 1 shows the candidate genes for drought tolerance with their molecular functions.

Table 1. Genes identified in the GWAS study and their functions.

Gene	Function
<i>Phvul.010G019100</i>	Mitigating reactive oxygen species (ROS), maintaining photosynthesis through thermal shock proteins (TSPs), and abscisic acid (ABA) signaling.
<i>Phvul.010G019600</i>	
<i>Phvul.009G137900</i>	Activation of ethylene response transcription factors (ERFs),
<i>Phvul.010G092300</i>	

Molecular techniques combined with phenotyping enabled the identification of genes regulating metabolic pathways related to drought tolerance.

CONCLUSIONS

In the future, following the validation of these genes, they will be associated with molecular markers and applied in the selection of drought-tolerant genotypes.

ACKNOWLEDGEMENTS

This research was financially supported by Capes and Rural Development Institute of Paraná State– IAPAR-EMATER (IDR-Paraná) associated with State University of Londrina (UEL).

FOUR NEW LIMA BEAN RIL POPULATIONS FOR EXPLORING AGRONOMIC AND SEED APPEARANCE TRAITS

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Lima bean (*Phaseolus lunatus* L.) is an important part of agricultural systems in certain regions of the United States with potential for increased production as a resilient crop, tolerant of heat and drought. Four lima bean RIL populations have been phenotyped in multiple environments/years for traits related to phenology, agronomic performance, plant architecture, growth habit and seed appearance. The populations were recently characterized using genotyping by sequencing.

DE17221 (PI 256417 x PI 534918) is derived from a cross between a photoperiod sensitive vining genotype and a bush, photoperiod insensitive genotype. This population includes lines with diverse seed size, color, pattern and shape. One parent of the population is highly heat tolerant and the other has multiple disease resistance traits.

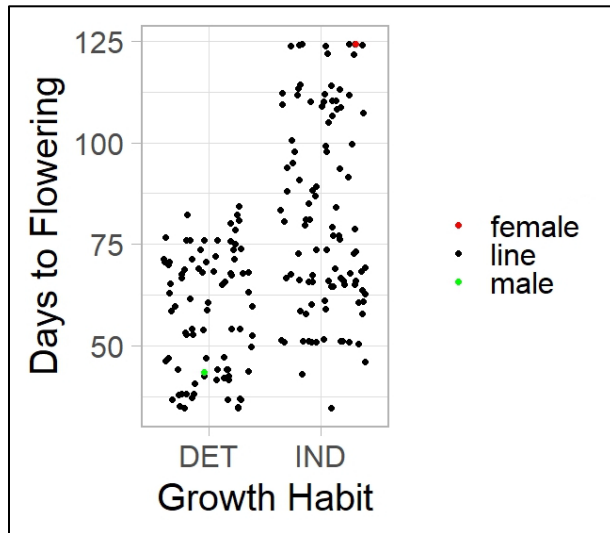


Figure 1. Days to flowering for determinate vs indeterminate lines in the DE17221 population.

In Delaware, DE17221 has been grown in a plasticulture system and indeterminate lines in the population have been trellised. Approximately half of the population has a determinate growth habit. Lines that are both determinate and photoperiod sensitive have been noted. In summer field conditions in Delaware the photoperiod sensitive determinate lines grow large plants that develop floral structures at the ends of all stems when a certain daylength is reached. The daylength requirement varies between photoperiod sensitive lines. Vining photoperiod sensitive lines were the latest to flower (Figure 1). Seed colors, patterns, shapes and sizes in DE17221 are diverse, but have not yet been fully characterized.

The parents of the other three populations are all photoperiod insensitive with determinate growth habits to facilitate phenotyping in the field. Each of the determinate growth habit populations has one green seeded parent with the goal of better understanding the inheritance and expression of this trait which is important for succulent lima beans produced in the Mid-Atlantic region.

DE21101 (PI 534918 x 'C-elite Select') contains lines with different seed coat colors, heat tolerance, phenology and plant size.

DE21102 (PI 549509 x 'C-elite Select') contains lines with different seed coat colors and patterns, different levels of heat tolerance and erect vs decumbent plant architecture.

DE20201 (DE1306583 x DE0802101A) contains lines with different levels of resistance to southern root-knot nematode (*Meloidogyne incognita*), different seed coat colors and patterns, and different phenology.

In 2024 Delaware Trials, lines in DE20201 had a narrower range of yield and harvest index values compared to the other two populations. DE21101 and DE21102 have a wider range in plant height than DE2020. Differences in other plant architecture traits are also present in the bush RIL populations, including branch angle, stem rigidity and pod location.

Seed size range is similar in all three bush RIL populations and is not wide ranging. This is expected since all parents are small-seeded types. Patterns of seed coat color frequency are different in each population (Table 1) which will allow for mapping of loci important for green seed color.

Table 1. Seed Color and Pattern Frequency in the Bush RIL populations

	DE20201	DE21101	DE21102
♀			
♂			
Frequency of Primary Seed Coat Colors			
Green	0.28	0.17	0.24
Light Green	0.09	0.27	0.29
White	0.13	0.08	0.06
Buff	0.23	0.14	0.41
Magenta	0.18	0.06	
Dark Magenta	0.09	0.15	
Pink		0.12	
Frequency of Seed Coat Patterns			
Self	0.76	0.74	0.56
Pattern	0.23	0.25	0.44
Heterozygous	0.01	0.01	

RIL population development, phenotyping and genotyping were supported by the Specialty Crop Research Initiative project titled: Development of Genomic Resources to Improve Lima Bean Breeding for Consumer Quality and Agronomic Traits.

ASSESSING THE ROLE OF POLLEN RELEASE AND STIGMA EXSERTION IN LIMA BEAN YIELD

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INTRODUCTION: Understanding the reproductive biology of lima beans (*Phaseolus lunatus*) is critical for improving yield potential, particularly under heat stress conditions. High nighttime temperatures during the flowering stage can disrupt floral development and reduce yield (Ernest and Wissner, 2024). One observed effect of heat stress is stigma exsertion, where the stigma extends beyond the anthers. Current research on stigma exsertion has focused on this trait in cultivated tomato and rice (Zhou et al., 2021; Vallejo et al., 2003). Traits such as pollen release and stigma exsertion influence pollination success, seed set, and ultimately yield.

MATERIALS AND METHODS: A panel of 149 diverse *Phaseolus lunatus* genotypes were evaluated in a greenhouse under cool (average) and heat-stress conditions using a randomized complete block design. The cool treatment was conducted in Spring 2025, with average temperatures of 28 °C during the day and 19 °C at night. The heat-stress treatment was conducted in Summer 2025 with average day and night temperatures of 33 °C and 27 °C respectively. Elevated nighttime temperatures were maintained using supplemental heating. Flowers were collected on the day of anthesis, with three flowers sampled in triplicate per genotype. Stigmas were extracted and placed in 0.5 mL microcentrifuge tubes containing 200 µL distilled water and 100 µL of 2% acetocarmine stain. For pollen imaging, 60 µL of 0.1% Tween 20 was added to disperse pollen, and 60 µL of the solution was mounted on microscope slides. Pollen counts were obtained using a deep learning-based object detection model. A total of 250 images were annotated in Roboflow to train and test a YOLOv11-X model, which achieved a mean average precision of 0.924. Mature pods were harvested at full desiccation and evaluated for seed number and seed weight, with empty pods recorded. Results were analyzed through linear mixed models and ANOVAs conducted in R (v4.4.1).

RESULTS AND DISCUSSION: Heat stress significantly reduced reproductive performance in lima bean, with overall yield (Figure 1) and the number of seeds filled per pod declining under elevated temperatures ($p < 0.001$). The magnitude of yield reduction was genotype specific, and Mesoamerican genotypes exhibited significantly smaller reductions in pod filling and higher yield under heat stress compared to Andean genotypes (Figure 2) ($p < 0.001$), indicating greater reproductive heat tolerance in Mesoamerican genotypes. Heat stress reduced pollen production across genotypes ($p = 0.016$), but pollen count under heat stress was not associated with gene pool or stigma exsertion, suggesting that pollen quantity alone does not explain yield differences. Increased stigma exsertion under heat stress was independently associated with reduced seed yield ($p = 0.017$). This effect did not differ between gene pools indicating similar sensitivity to stigma exsertion across genetic backgrounds (Figure 3). Together, these findings indicate that reproductive failure under heat stress is multifactorial: while reduced pollen production and increased stigma exsertion contribute to yield decline, additional factors such as pollen viability, reduced pollen tube growth, ovule abortion, and post-fertilization processes likely play critical roles in genotype-specific heat tolerance.

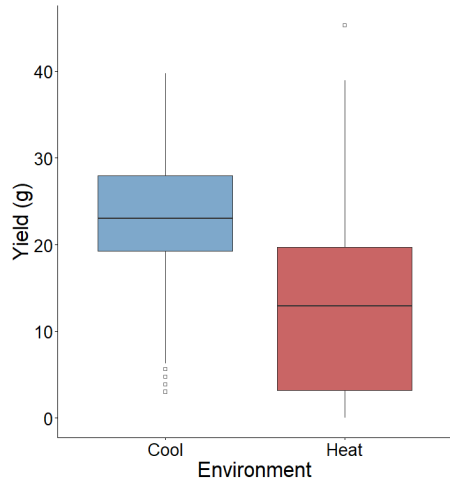


Figure 1. The average seed yield between cool and heat environments.

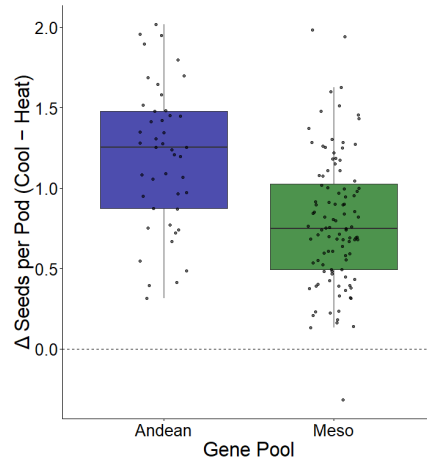


Figure 2. Distribution of heat-induced changes in seeds per pod ($\Delta = \text{Cool} - \text{Heat}$) by gene pool. Larger values indicate fewer seeds per pod under heat stress.

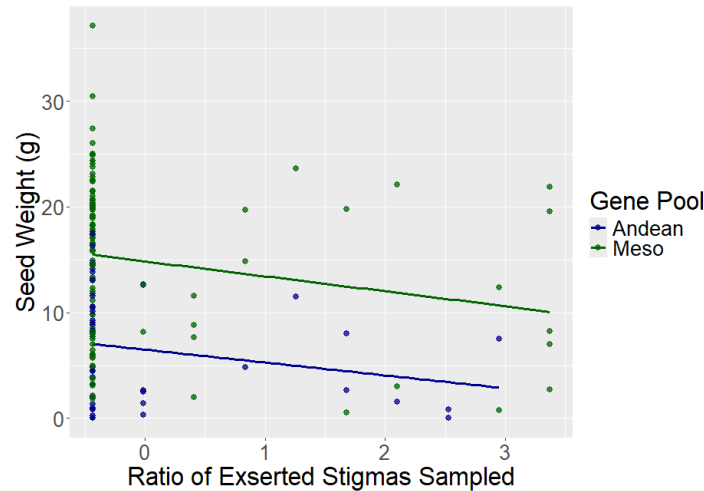


Figure 3. Seed weight vs the ratio of exerted stigmas out of all 9 stigmas sampled colored by gene pool with regression lines.

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PRESENCE OF NEW BEAN ANTHRACNOSE RACES IN NORTHERN SPAIN

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INTRODUCTION: *Colletotrichum lindemuthianum* (Sacc. & Magnus) Scribn. causes bean anthracnose, one of the most destructive diseases of *Phaseolus vulgaris* L. worldwide. Anthracnose resistance is generally considered race-specific. Numerous races and race-specific genes (*Co*-) have been identified. The most frequent pathogenic variant in northern Spain is race 38 (Ferreira et al., 2008), for which the *Co*-2 gene from cv. Cornell49-242 confers total resistance. Severe anthracnose attacks were observed in northern Spain in 2024, affecting the Fabada market class. These attacks were observed even in the A2806 breeding line, in which the *Co*-2 resistance cluster was introgressed from Cornell49-242 (*Co*-2^C). The aim of this work was to, i) identify the *C. lindemuthianum* races infecting Fabada market class in 2024, and i) assess their virulence on a diversity panel of bean lines.

MATERIALS AND METHODS: In 2024, naturally infected pods and seeds from Fabada bean crops were collected in Asturias (Northern Spain). Monosporic *C. lindemuthianum* isolates were obtained on PDA medium. The ITS region was amplified (primers ITS1/ITS4; White et al., 1990) for each isolate and sequenced using the Sanger method. **Resistance test:** Evaluations were performed under controlled conditions (Pastor-Corrales 1991). Resistance tests included 8-10 seedlings per line. Seedlings were evaluated after 7-9 days using a 1-to-9 scale (van Schoonhoven and Pastor-Corrales, 1991). Severity values of 1-3 were considered resistant, 4-6 were considered intermediate, and more than 7 were considered susceptible. **Race identification:** The 12 differential cultivars were used for race identification (Pastor-Corrales 1991). Each isolate was tested twice. **Virulence assessment:** A diversity panel of 450 *P. vulgaris* lines from America and Europe was tested (INCREASE panel). Additionally, a set of Fabada breeding lines developed by SERIDA (Ferreira et al. 2017), each with a different combination of known *Co*-resistant genes, was also evaluated: Andecha, A2806 (*Co*-2^C), A4804 (*Co*-2^C), X2776 (*Co*-2^C), X4562 (*Co*-2^C), A1220 (*Co*-9^{A493}, introgressed from the line A493), and A1258 (*Co*-2^{A252}, introgressed from the line A252).

RESULTS AND DISCUSSION: The obtained monosporic isolates CL232, CL233, and CL234 exhibited typical characteristics of *C. lindemuthianum*. CL232 and CL234 ITS sequences were aligned with *C. lindemuthianum* accession AJ301946.1 (e-value=0; query cover 100%), and CL233 was aligned with *C. lindemuthianum* accession PP545307.1 (e-value=0; query cover 100%). For race identification, the differential cultivars showed the same response to isolates CL232 and CL234, being Michelite and Perry Marrow susceptible, so they were classified as race 5. Isolate CL233 was classified as race 37, showing Michelite, Perry Marrow and Kaboon a susceptible response (although Kaboon showed more of an intermediate response).

Virulence assessment in a set of Fabada breeding lines. Both isolates produced severe symptoms in the Andecha cultivar and intermediate symptoms in lines carrying the *Co*-2^C gene obtained from Cornell49-242 (A2806, A4804, X2776, and X4562). In contrast, the A1220 line carrying *Co*-9^{A493} did not exhibit symptoms against CL232 and CL233. Both isolates produce a

different response in the line A1258 carrying the *Co-2*^{A252}; this gene protects against isolate CL233 but not against isolate CL232.

Virulence assessment in the INCREASE Diversity Panel. CL232 (race 5) and CL233 (race 37) revealed a high virulence on the INCREASE panel (Fig 1); 78% of the lines were susceptible to CL232 and 74% to CL233.

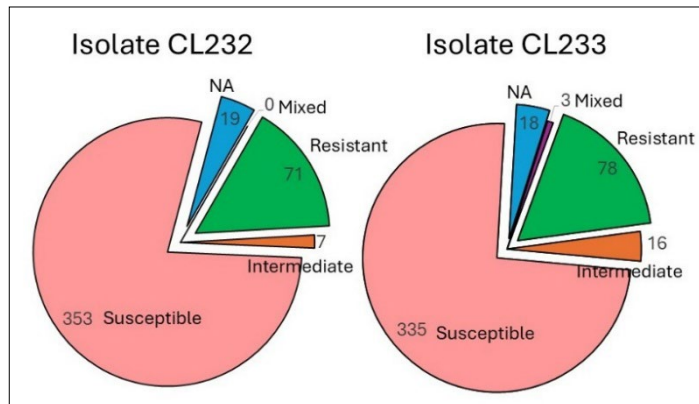


Fig 1. Response of 450 bean accessions from the INCREASE diversity panel to the two isolates CL232 and CL233 classified as anthracnose races 5 and 37, respectively.

CONCLUSIONS

- This is the first report of the anthracnose races 5 and 37 in Northern Spain.
- Races 5 and 37 show high virulence in the INCREASE panel, a set of lines that gathers a wide diversity.
- The *Co-9*^{A493} resistance gene from A493 protects against both races.
- The *Co-2*^C resistance gene from Cornell49-242 did not provide protection against isolate CL232 (race 5).
- The donor lines of the *Co-2* gene, Cornell49-242 and A252, showed a different resistant pattern, and only the gene derived from A252 protected against isolate CL233 (race 37).

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ACKNOWLEDGEMENTS

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POPULATION DYNAMICS OF *MEGALUROTHRIPS USITATUS* IN COMMON BEAN IN GUATEMALA

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INTRODUCTION: Since 2020, the twice-banded bean thrips (*Megalurothrips usitatus* Bagnall), a species with a preference for legumes, has been reported in several countries across the Americas (Cabrera & De Jensen, 2023; Cabrera et al., 2021; Cambero Campos et al., 2023; Elizondo et al., 2021; Orozco, 2022; Soto-Adames, 2020). Its presence in Guatemala was confirmed as early as 2021 in the locations of Zacapa, Petén, Chimaltenango, and Baja Verapaz, where it was found damaging both dry and snap beans (*Phaseolus vulgaris* L.) crops (Racancoj et al., 2023). This study aimed to characterize the behavior of *M. usitatus* and its impact on common beans.

MATERIALS AND METHODS: During the second semester of 2023 (August to December) in the central highlands of Guatemala (1,800 meters above sea level), an observational plot of 320 square meters was established with the cultivar ICTA Superchiva (a Bush-Type variety). A descriptive and quantitative study was conducted. The infestation by *M. usitatus* occurred under natural conditions. Weekly counts of adult and nymphal populations of *M. usitatus* were carried out, evaluating the stem, the upper and lower surfaces of the trifoliate leaves, and the growth points. During the reproductive phase at 44 days after planting (DAP), 30 flowers and pods were evaluated weekly. To assess the damage in the pods, a damage scale was developed, where 1 = healthy pod, 9 = severely damaged pod, verifying the scars, malformation, and the pod bronzing, characteristic damage of *M. usitatus* (Figure 1). Also, as part of this study the seed quality was assessed.



Figure 1: Diagrammatic scale for *M.usitatus* damage on common bean pods.

RESULTS AND DISCUSSION: The population level of *M. usitatus* varied according to the phenological stage of the crop. As flowering stage approached, the number of thrips increased drastically, following a decrease in thrips as the flowering stage ended. Colonization by *M. usitatus* began 10 DAP, with nymphal populations peaking at 31 and 66 DAP. At flowering, the highest adult density was recorded at 74 DAP, with 27 individuals per flower (Figure 2). Nymphal feeding

caused pod deformities and scarring of the pericarp. Pod damage incidence reached 60 %, of which 45 % corresponded to severe damage. Infestation by *M. usitatus* resulted in a 28 % reduction in seed yield; the seed from healthy pods had a greater weight (26 g), compared to the grains from the severely damaged pods (14 g). The pest also decreases the commercial seed quality. Increasing pod damage was associated with reduced seed weight and shorter cooking times, leading to uneven cooking. These findings indicate that *M. usitatus* is a significant threat to common bean production in Guatemala, where the infestation of *M. usitatus* increased during the reproductive, and the nymphs were the primary cause of the pod damage.

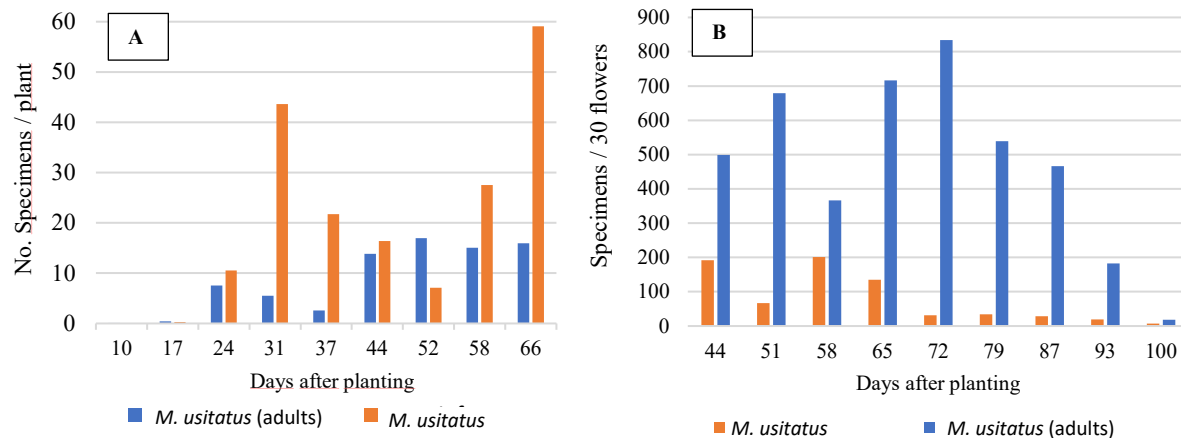


Figure 2: A. Population dynamics of *M. usitatus* on ICTA Superchiva's plants. B. Population dynamics of *M. usitatus* on ICTA Superchiva's flowers.

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IDENTIFYING GENOMIC DIVERSITY AMONGST NORTH AMERICAN *SCLEROTINIA SCLEROTIORUM* ISOLATES: A STEPPINGSTONE TOWARDS IMPROVED WHITE MOLD SCREENING

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INTRODUCTION: For several years, improving white mold tolerance has been ranked as the top research priority by bean growers in Michigan (Bales, 2024). Improving bean varieties is challenging because white mold tolerance is highly quantitative and *Sclerotinia sclerotiorum* (Lib.) de Bary (Ss), isolates vary in their aggressivity towards common bean. Our objective is to better understand genomic diversity of white mold isolates collected from geographically distant locations using whole genome sequence data in order to identify an appropriate panel of Ss isolates for comprehensive white mold screening.

MATERIAL & METHODS: Isolates were collected from eight Canadian provinces and four American States spanning over 2700 miles. Whole genome sequencing of 264 Ss isolates was performed on an Illumina NovaSeq6000 machine. Reads were trimmed with Fastp, mapped to the reference genome using BWA-mem2 and used to generate distance matrices for neighbor-joining phylogenies visualized in SplitsTree. Variants were called with GATK; SNPeff predicted variant effects and a genetic relatedness matrix was used to identify clonal isolates. After filtering and LD pruning, population structure of a diverse subset (n=97) was assessed with ADMIXTURE (Figure 1). GO enrichment was performed using InterProScan and clusterProfiler in R.

Thus far, 151 of the sequenced isolates have been screened with the Seedling Straw Test (Arkwazee & Myers, 2017) on three bean genotypes including a susceptible check (Beryl), a partially tolerant middle American line (USPT-WM-12) and a partially tolerant Andean line (G122). Associations between genetic clade and aggressivity phenotype were assessed using a mixed linear model. Once phenotyping of all nonclonal isolates is complete, we will conduct a multi-trait GWAS to identify loci in each Ss subpopulation associated with aggressivity.

RESULTS & DISCUSSION: Aggressivity differed significantly among Ss clades. K5 isolates were more aggressive ($\Delta+0.71$ SST) and K2 isolates were less aggressive ($\Delta-0.42$ SST) compared to clades K1, K3, K4, and K6 (Figure 2). As expected, a strong isolate-by-genotype interaction was observed (Figure 3). Province of origin showed borderline effects, and host species effects were negligible; these will be re-evaluated once phenotyping is complete.

Two GO terms for DNA/Nucleic acid binding were highly enriched (GO:0003677 and GO:0003677) across all isolate clades. Given that DNA/Nucleic acid binding is tightly linked to regulation, this will be investigated further as Ss phenotypic data is collected. GO analysis of high impact mutations revealed lineage-specific functional signatures. For example, K2 isolates (less aggressive) harbor unique mutations consistent with reduced adaptive capacity.

CONCLUSIONS: A relationship has been observed between ADMIXTURE population structure and observed variation in pathogen aggressivity. SST differences are driven by isolate level differences more than clade, province or host species. Breeding for white mold resistance may be more effective if multiple, diverse isolates are used to screen material. This panel should include an isolate from K1, K2 and K5.

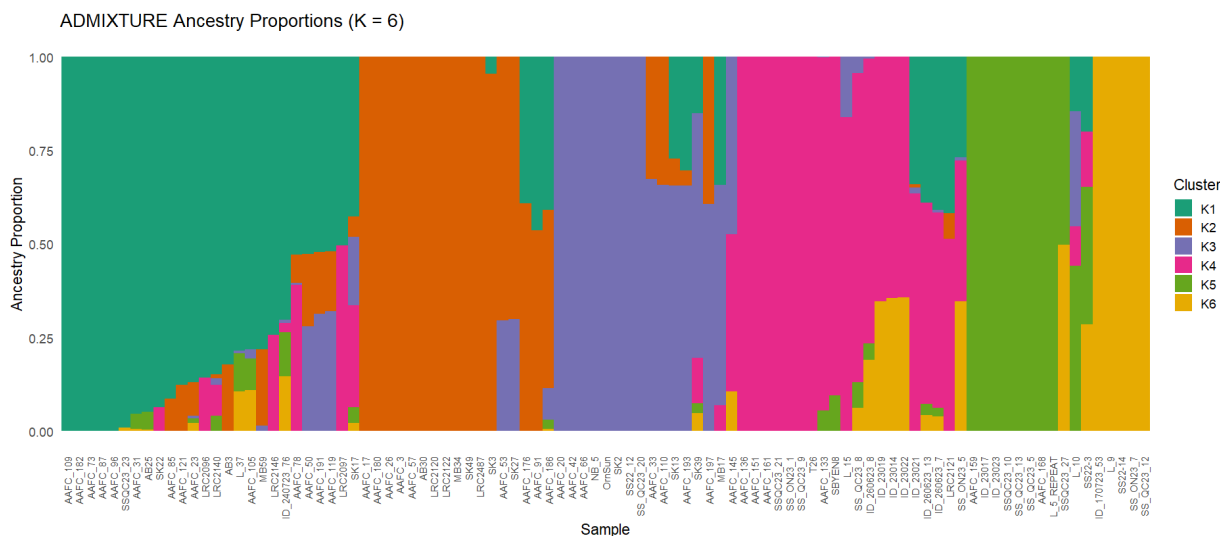


Figure 1. ADMIXTURE analysis with $K=6$ subpopulations. K5 isolates, predominantly from Quebec and Ontario, were significantly more aggressive ($\Delta+0.71$ SST) than K1, K3, K4 and K6 while K2 was significantly less aggressive ($\Delta-0.42$ SST).

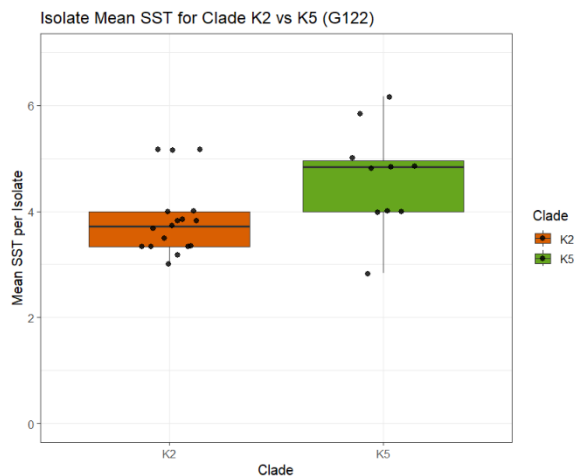


Figure 2. Variation in mean aggressivity of isolates from K2 and K5

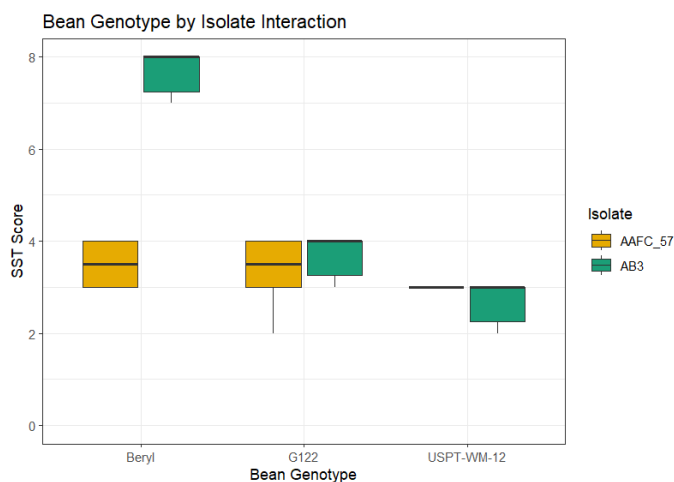


Figure 3. *Ss* isolate by bean genotype interaction observed from SST scores

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PREDICTION OF WHITE MOLD SEVERITY AND YIELD UNDER DISEASE PRESSURE IN DRY BEANS FROM UAS DATA

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White mold caused by *Sclerotinia sclerotiorum* is a major yield-limiting disease in dry beans, and white mold resistance is a goal in dry bean breeding. The typical method of phenotyping white mold is visual rating. These ratings are not fully objective or replicable. Yield under white mold pressure is also an important measure of white mold tolerance. Machine learning approaches were explored to develop UAS imaging-based models for white mold phenotyping.

The image dataset consists of RGB and MS images taken by UAS flights over the MSU white mold nursery. UAS flights were conducted weekly from flowering to plant maturity in 2021-2024). Images were compiled into orthomosaics using Pix4D Mapper.

MATERIALS AND METHODS

The VIs used for random forest modelling were ExG, ExR, NDVI, gNDVI, and NDRE. Each was extracted using QGIS. The dataset also included the maximum and minimum values of each VI across the season and the change in each VI across imaging dates. Outliers with z-scores greater than 3 were removed from the data. Reverse feature elimination was used to identify unneeded features for removal, but all features were shown to contribute. A 75-25 train test split was performed. A preliminary version of the white mold random forest model was trained on 75% of the VI dataset with the field white mold ratings as a ground truth dataset, using ten-fold cross validation and a random forest of 800 trees implemented in the R caret package. The RMSE of the model was evaluated on unseen data.

Models were also trained for yield under white mold pressure using the same VI dataset. The yield values calculated at harvest were used as a ground truth dataset. Data processing and random forest parameters were the same as the white mold model.

To explore deep learning to identify white mold, a yolo12x deep learning classification model was trained on an orthomosaic with zones manually annotated as soil, living plants, or stems bleached by white mold. Over 1,000 zones in each category were manually annotated in a shapefile in QGIS. Python was then used to convert this data into the yolo format.

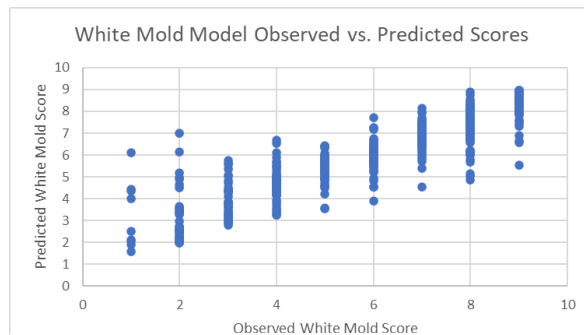


Figure 4. Observed vs. Predicted Values from the

RESULTS/DISCUSSION

The preliminary white mold random forest model has an RMSE on unseen data of 0.924 white mold points and explains 58.58% of the variation. When predicted scores were rounded to discrete point values, this model had an accuracy of 58.65%. When scores were grouped into low (0-3), medium (4-6), and high (7-9) white mold scores, accuracy was 87.5%.

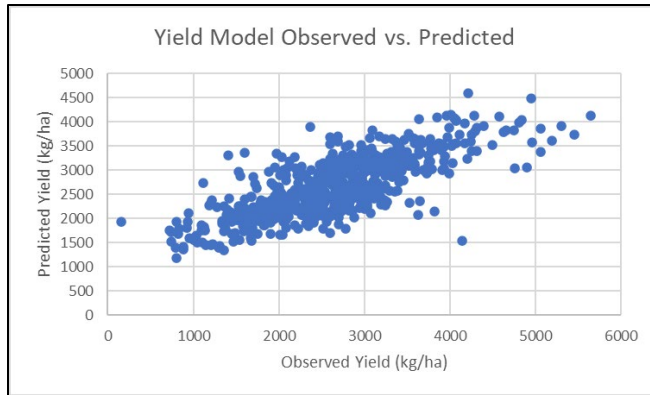


Figure 5. Observed vs. Predicted Values from the Yield Model

The preliminary yield model explained 58.04% of the variation with an RMSE of 564.91 kg/ha. While this may seem like a large RMSE value, the standard deviation is 916.78 kg/ha.

The preliminary deep learning classification model achieved a 99.6% classification accuracy on the orthomosaic it was trained on. Creating a generalizable deep learning model for white mold damage identification will require an annotated dataset spanning multiple years.

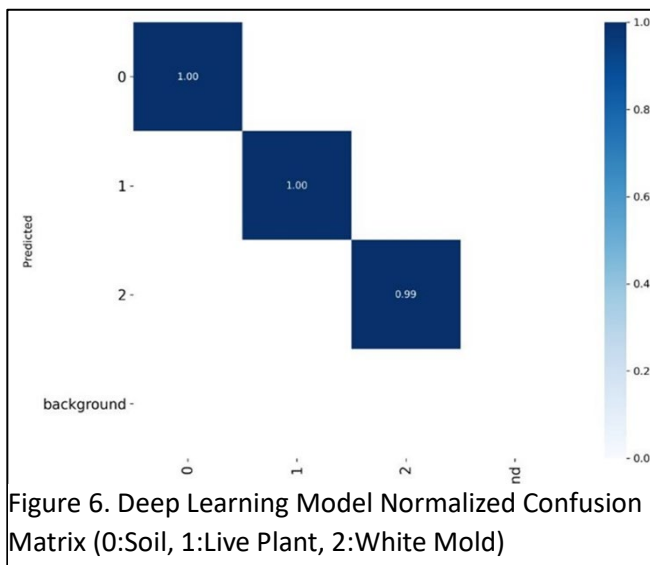


Figure 6. Deep Learning Model Normalized Confusion Matrix (0:Soil, 1:Live Plant, 2:White Mold)

IDENTIFYING EARLY ROOT TRAITS FOR IMPROVED FUSARIUM ROOT ROT RESISTANCE IN FIELD GROWN *PHASEOLUS VULGARIS*

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INTRODUCTION

Fusarium root rot (FRR), caused by pathogenic strains of *Fusarium solani*, is a major global limitation to common bean (*Phaseolus vulgaris*) production. The disease produces reddish-brown lesions that begin at the hypocotyl and extend into the taproot, leading to significant root necrosis and reduced plant growth. Root tissues have been shown to exhibit greater developmental plasticity than shoots and early root architecture may play an important role in how plants respond to infection. In previous greenhouse studies, FRR-susceptible lines showed a shorter length of the apical unbranched zone (L_{AUZ}) and more clustered first order root distribution compared to resistant lines in the same population. These findings suggest that specific early root traits may contribute to disease resistance. Although these traits correlated strongly with resistance under greenhouse conditions, it was necessary to validate whether they also contribute to FRR resistance in an agricultural field setting. To evaluate whether these relationships hold under field conditions, a complementary field experiment was conducted using the same bean lines.

METHODS & MATERIALS

Two parental (Cal 96 and MLB49-89A) and four recombinant inbred lines (CM222, CM299, CM517, and CM521) of *Phaseolus vulgaris* were evaluated in a field experiment conducted at the MSU Plant Pathology Farm. The lines were cultivated under two conditions: plots under native disease pressure (no additional inoculum) or plots with increased disease pressure (inoculated). The inoculated plots were infected by tilling sorghum seed treated with *F. brasiliense* into the soil along side the *P. vulgaris* seeds. Seedlings were collected at four-, six-, eight- and ten-days post planting. Roots were washed then scanned and the root architecture traits were quantified using ImageJ and RhizoVision Explorer. In total, 46 root architectural traits across 755 seedlings are being evaluated to determine whether the phenotypic indicators identified in controlled greenhouse conditions reliably predict FRR resistance under field environments. Disease scoring was conducted for all sampled seedlings. Disease severity was assessed using a 1–9 scale, where 1 indicated healthy tissue with no lesions and 9 indicated complete necrosis and death of the plant.

RESULTS & DISCUSSION

Previous experiments showed that resistant lines displayed a shorter L_{AUZ}, more uniform basal root spacing, and a shorter distance between the final basal root and first lateral root compared to susceptible lines. To better capture early root phenotypes associated with resistance, the field experiment was designed to sample seedlings at developmental stages corresponding pre- and post-symptom development. When comparing disease scores across Days 8 and 10, susceptible lines displayed both a higher incidence of symptomatic plants and increased disease severity by Day 10 (Fig. 1A), consistent with previous data.

Principal component analysis (PCA) of all measured root traits illustrates early seedling root architecture plasticity. Day 4 seedlings cluster tightly, indicating minimal architectural

divergence at this earliest stage (Fig. 1b); day 6 seedlings show a similar pattern, although with slightly greater variation; and by days 8 and 10 the points broaden substantially along PC1 and 2, reflecting increased variability in root system development. Most of the variation in this experiment can be explained by overall root system size traits such as total root length, surface area, volume, and perimeter. Together, these patterns indicate that developmental stage is the primary source of root trait variation during early seedling establishment. Future analyses of this dataset will evaluate whether early-stage architectural traits, particularly L_{AUZ} length and basal root positioning, serve as robust predictors of FRR resistance across growth conditions.

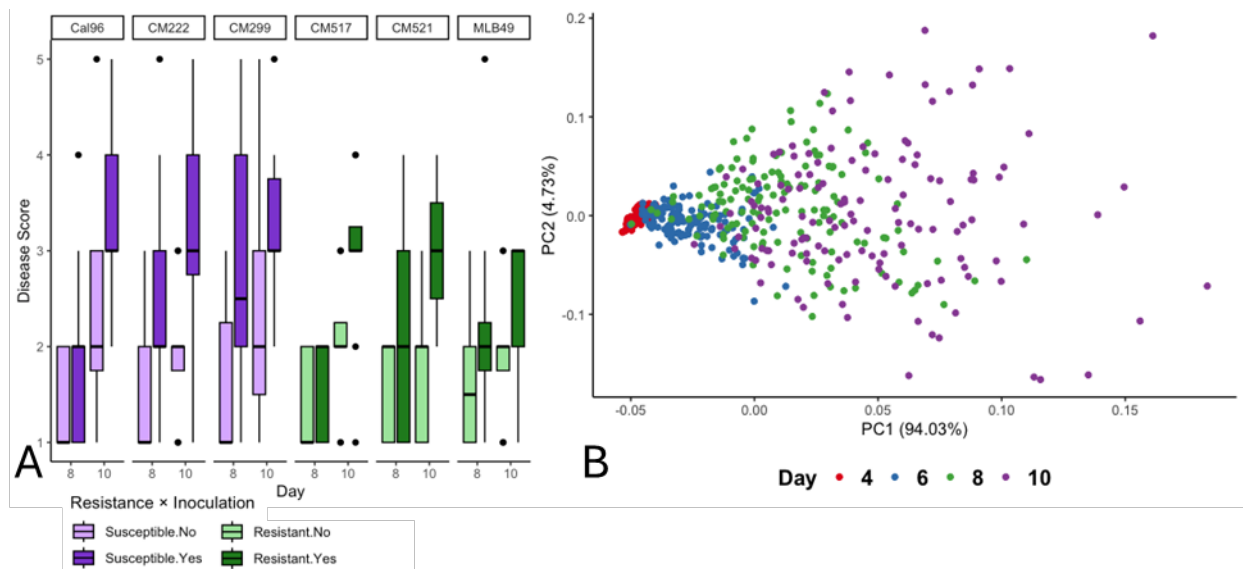


Figure 1. (A) Box plots showing range of disease scores at 8 and 10 days post planting between susceptible (purple, left) and resistant (green, right) lines. Native disease pressure is indicated with lighter shading while increased disease pressure (inoculated) is indicated with darker shading. **(B)** Principal component analysis (PCA) illustrating variation in early seedling root architecture across developmental timepoints and inoculation treatments.

ACKNOWLEDGEMENTS

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DISEASES RESISTANCE, ADAPTABILITY AND STABILITY OF COMMON BEAN LINES IN MULTI-ENVIRONMENT TRIALS IN PARANÁ, BRAZIL

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INTRODUCTION

Brazil is one of the world's largest producers and consumers of common bean (*Phaseolus vulgaris* L.), a crop of major importance for food security. However, bean production is strongly constrained by diseases, pests, and pronounced agro-climatic variability, underscoring the need for breeding programs focused on the development of high-yielding, stable, and disease-resistant cultivars. Among available management strategies, the deployment of cultivars carrying broad-spectrum resistance genes remains the most effective, economical, and environmentally sustainable approach to disease control (Gonçalves-Vidigal et al., 2020). In this context, the present study evaluated the agronomic performance of common bean lines across multiple environments in the State of Paraná, Brazil, with the objective of identifying genotypes exhibiting high yield stability, adaptability, and resistance to major diseases. The evaluated lines were screened for resistance to anthracnose, angular leaf spot, bacterial blight, and curtobacterium wilt, providing a comprehensive assessment of their potential for cultivar recommendation in diverse production conditions.

MATERIAL AND METHODS

In this study, six common bean lines along with three control cultivars were evaluated for anthracnose (*Colletotrichum lindemuthianum*), angular leaf spot (*Pseudocercospora griseola*), bacterial blight (*Xanthomonas axonopodis* pv. *Phaseoli*) and curtobacterium wilt (*Curtobacterium flaccumfaciens*). The experiments were conducted in six municipalities in the State of Paraná, Brazil: Guarapuava, Ponta Grossa, Santa Tereza do Oeste, Pato Branco, Maringá, and Campo Mourão (2021 only)-during the 2020, 2021, and 2022 agricultural years. Disease symptoms were evaluated using the severity scale proposed by Van Schoonhoven and Pastor-Corrales (1987), which ranges from 1 to 9, where 1 to 3 are considered 'resistant', 4 to 6 'intermediate' and 7 to 9 susceptible. The evaluation of adaptability, and stability across these environments followed methodologies established by Eberhart and Russell (1966), Lin and Binns (1988), modified by Carneiro (1998), Annicchiarico (1992), and WAASB (Olivoto et al., 2019), allowing a comprehensive analysis of genotype-by-environment (GxE) interaction

RESULTS

The LP 09-180 line demonstrated consistent anthracnose tolerance across different locations and years, particularly when the fungus incidence was high (Table 1). Angular leaf spot, had a low incidence in the evaluated lines, indicating good tolerance under field conditions. The CHC 04-233-2, CHP 12-355-02, LEC 03-16, and LEP 01-16 lines demonstrated tolerant behavior to common bacterial blight in various environments, reinforcing their adaptability and resistance to environmental conditions conducive to pathogen development. Conversely, the LP 08-186 and LP 09-180 strains varied in their response to common bacterial blight, ranging from moderately tolerant to susceptible in different environments, which may be attributed to genotype-environment (GxE) interactions.

Table 1. Evaluation of bean lines and cultivars for bacterial blight (BB), curtobacterium wilt (CW), anthracnose (ANT) and angular leaf spot (ALS), in different cities of Paraná, Brazil during dry and wet seasons of the years of 2020, 2021 and 2022

Lines/Cultivar	Guarapuava.wet.2020				Guarapuava.dry.2022				Campo Mourão.wet.2021			
	BB	CW	ANT	ALS	BB	CW	ANT	ALS	BB	CW	ANT	ALS
BRS Esteio	I	I	R	R	R	S	R	R	R	R	R	R
CHC 04-233-2	I	I	R	R	R	I	R	R	R	R	R	R
CHP 12-355-02	I	I	R	R	R	I	R	R	R	S	R	R
IPR Sabiá	I	I	R	R	R	I	R	R	R	R	R	R
IPR Urutau	I	I	R	R	R	S	R	R	R	R	R	R
LEC 03-16	I	R	R	R	R	I	R	R	I	R	R	R
LEP 01-16	I	I	R	R	R	I	R	R	I	R	R	R
LP 08-186	S	I	R	R	R	S	R	R	R	S	R	R
LP 09-180	S	I	R	R	R	I	R	R	R	S	R	R
Pérola	I	I	R	R	R	I	R	R	I	R	R	R
Lines/Cultivar	Maringá.wet.2020				Maringá.wet.2021				Maringá.wet.2022			
	BB	CW	ANT	ALS	BB	CW	ANT	ALS	BB	CW	ANT	ALS
BRS Esteio	R	I	R	R	I	R	R	R	I	I	R	I
CHC 04-233-2	R	I	R	R	R	R	R	R	I	I	R	I
CHP 12-355-02	R	I	R	R	I	R	R	R	I	I	R	R
IPR Sabiá	R	I	R	R	I	R	R	R	I	R	R	I
IPR Urutau	R	I	R	R	R	R	R	R	I	I	R	I
LEC 03-16	R	I	R	R	R	R	R	R	I	I	R	I
LEP 01-16	R	I	R	R	R	S	R	R	I	S	R	I
LP 08-186	R	S	R	R	R	S	R	R	I	S	R	R
LP 09-180	R	S	R	R	I	R	R	R	I	I	R	I
Pérola	R	S	R	R	I	R	R	R	I	I	R	I
Lines/Cultivar	Pato Branco.dry.2022				Ponta Grossa.wet.2021				Ponta Grossa.dry.2022			
	BB	CW	ANT	ALS	BB	CW	ANT	ALS	BB	CW	ANT	ALS
BRS Esteio	R	I	R	R	R	I	R	R	I	S	I	R
CHC 04-233-2	R	I	R	R	R	R	R	R	I	I	I	R
CHP 12-355-02	R	I	R	R	R	R	R	R	I	S	I	R
IPR Sabiá	R	I	R	R	R	R	R	R	R	I	I	R
IPR Urutau	R	I	R	R	R	R	R	R	R	R	R	R
LEC 03-16	R	I	R	R	R	R	R	R	R	I	I	R
LEP 01-16	R	I	R	R	R	R	R	R	I	S	I	R
LP 08-186	R	I	R	R	R	I	R	R	R	I	I	R
LP 09-180	R	I	R	R	R	R	R	R	I	I	R	R
Pérola	R	I	R	R	R	R	R	R	I	I	R	R
Lines/Cultivar	Santa Tereza.wet.2020				Santa Tereza.wet.2021				Santa Tereza.dry.2021			
	BB	CW	ANT	ALS	BB	CW	ANT	ALS	BB	CW	ANT	ALS
BRS Esteio	R	I	R	R	R	I	R	R	R	I	R	R
CHC 04-233-2	R	R	R	R	R	R	R	R	R	R	R	R
CHP 12-355-02	R	R	R	R	R	I	R	R	R	I	R	R
IPR Sabiá	R	I	R	R	R	R	R	R	R	R	R	R
IPR Urutau	I	I	R	R	R	R	R	R	R	I	R	R
LEC 03-16	R	R	R	R	R	I	R	R	R	I	R	R
LEP 01-16	R	I	R	R	R	I	R	R	R	I	R	R
LP 08-186	R	I	R	R	R	I	R	R	R	R	R	R
LP 09-180	R	R	R	R	R	I	R	R	R	I	R	R
Pérola	R	R	R	R	I	I	R	R	R	R	R	R

R: Resistant, I: Intermediate; S: Susceptible.

CONCLUSION: Common bean lineages responded differently to the diseases in different environments and years. Lines such as CHC 04-233-2 and LEC 03-16 stood out for their good performance, showing resistance in several regions, suggesting superior tolerance under conditions favorable to the pathogen. The results underscore the importance of selecting lines that integrate agronomic efficiency and

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FINE MAPPING OF THE ANTHRACNOSE RESISTANCE GENE *CO-PA* IN THE ANDEAN COMMON BEAN CULTIVAR PALOMA

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INTRODUCTION

Anthracnose caused by *Colletotrichum lindemuthianum*, is one of the most significant diseases affecting common bean crops, with potential production losses of up to 100%. This disease can occur during all three growing seasons of beans, leading to reduced productivity and grain quality under favorable conditions (Chiorato et al., 2006). The high genetic variability of the pathogen challenge anthracnose control, requiring an integrated management that includes the use of healthy seeds, crop rotation and resistant cultivars. Identifying new sources of broad-spectrum resistance is crucial for common bean breeding programs. In this context, the Andean cultivar Paloma is notable for its differentiated resistance to *C. lindemuthianum*, exhibiting resistance to Andean races 23, 31, and 55, as well as Mesoamerican races 65, 73, 1545, 2047, and 3481. The resistance gene (*Co-Pa*) in the Paloma cultivar was mapped by Lima Castro et al. (2017), on chromosome *Pv01*, located between markers SS82 and SS83 at 50,155,987 bp and 50,546,985 bp, respectively, spanning a region of 390.9 Kb. The present study aims to fine-map the anthracnose resistance gene region in the Paloma cultivar by identifying molecular markers linked to the gene and identifying candidate genes in the reference genome.

MATERIAL AND METHODS

The experiments were conducted in a greenhouse at Nupagri, Universidade Estadual de Maringá, using 100 F_{2:3} families derived from the Paloma × AB136 cross to evaluate resistance to anthracnose caused by *Colletotrichum lindemuthianum* race 3481. Plants were inoculated with a spore suspension (1.2×10^6 conidia mL⁻¹) and maintained under high humidity (>95%) and controlled temperature (20 ± 2 °C) for three days, followed by an additional seven days at 22 °C. Disease severity was visually assessed using a 1–9 scale, with scores from 1 to 3 classified as resistant (Pastor-Corrales, 1995). Segregation analysis was performed using the chi-square test to evaluate conformity with the expected Mendelian ratio of 1:2:1. Genotyping was conducted at the USDA-ARS (United States) using DNA extracted from trifoliolate leaves of F₂ plants and parental lines. SNP markers from the Illumina BeadChip BARCBean6K_3 were employed, and KASP markers were subsequently applied for fine mapping.

A genetic linkage map was constructed using JoinMap 4.0 with the Kosambi mapping function and a minimum LOD threshold of 3.0. Candidate genes within the mapped interval were identified based on the *Phaseolus vulgaris* v1.0 reference genome, and their molecular functions were predicted through comparison with homologous proteins in *Arabidopsis thaliana* using BLASTp, with functional annotation retrieved from TAIR.

RESULTS AND DISCUSSION

A study on the inheritance of resistance was conducted using 109 F_{2:3} families derived from the cross between Paloma (resistant) and AB136 (susceptible). The results revealed a segregation ratio of 1RR:2RS:1SS ($\chi^2 = 0.743$; $p = 0.68$), indicating that resistance to *Colletotrichum*

lindemuthianum race 3481 in Paloma is controlled by a single dominant gene. Initially, the resistance gene, *Co-Pa*, was mapped to a 390 kb region on chromosome Pv01, between markers SS82 and SS83. However, fine mapping using 100 F₂ plants narrowed this interval to 54 kb, flanked by markers SS97 and SS90 (Figure 1A). This refined region places *Co-Pa* in a genomic position distinct from previously identified resistance genes on chromosome Pv01 (Figure 1B), including *Co-1*, *Co-1⁴*, *Co-x*, *Co-AC*, *Co-I^x*, and *CoPv01^{CDRK}/PhgPv01^{CDRK}* (Lima Castro et al., 2017; Gilio et al., 2020; Gonçalves-Vidigal et al., 2020; Lima et al., 2023). Among the six genes identified within the 54 kb interval, *Phvul.001G245300*, which encodes a leucine-rich repeat protein kinase (LRR kinase), emerged as the most promising candidate for *Co-Pa*, given its well-established role in plant defense responses. These findings provide valuable insights for breeding programs aimed at developing common bean cultivars with enhanced resistance to anthracnose.

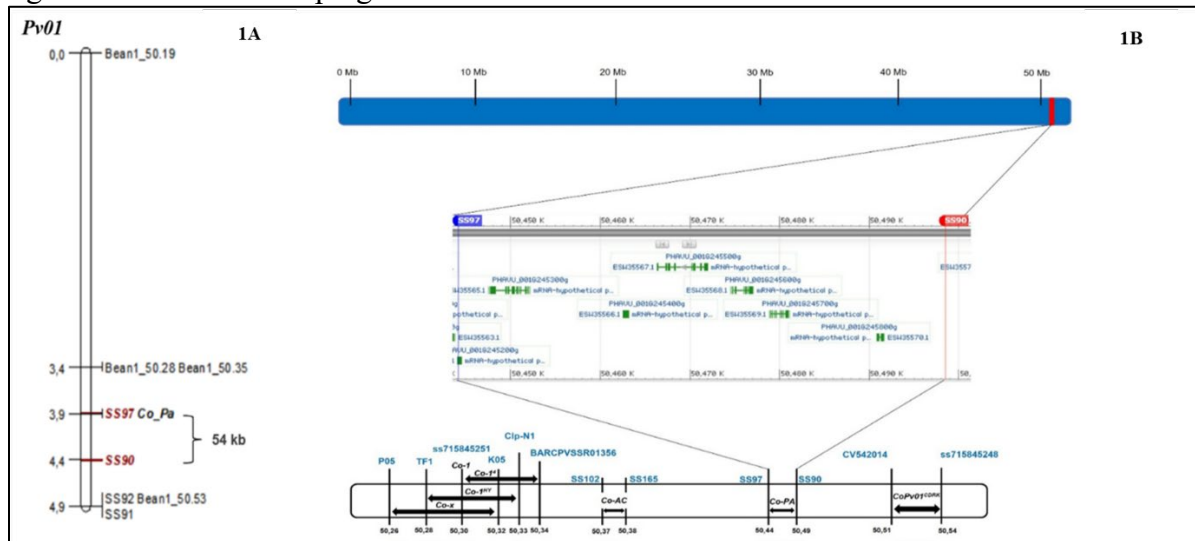


Figure 1. Genetic map of chromosome Pv01 of *Phaseolus vulgaris* built using 100 F₂ plants from the Paloma × AB136 cross, showing the *Co-Pa* gene for anthracnose resistance flanked by markers SS97 and SS90. (A) Genome browser view of the *Co-Pa* gene region in the reference genome v1.0 (<https://www.ncbi.nlm.nih.gov>). (B) Physical positions of *Co-loci* located at the end of chromosome Pv01.

CONCLUSION

In conclusion, the *Co-Pa* gene was delimited to a 54 kb genomic region flanked by the markers SS97 and SS90. Within this interval, *Phvul.001G245300*, which encodes a leucine-rich repeat protein kinase (LRR kinase), emerges as the most promising candidate gene associated with anthracnose resistance. Although further gene expression and functional validation studies are required, these results represent an important step toward elucidating the molecular basis of resistance and provide valuable resources for marker-assisted selection and genetic improvement of common bean.

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THE PAN-GS CONSORTIUM: LEVERAGING COLLECTIVE BREEDING PROGRAM DATA FOR DURABLE GENOMIC SELECTION MODEL

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INTRODUCTION

Genomic selection (GS) offers a powerful approach for improving complex quantitative traits such as yield in common bean (*Phaseolus vulgaris* L.). However, the successful implementation of GS requires large training populations with sufficient genetic diversity and strong genetic relatedness to the breeding population. Individual breeding programs often struggle to meet these requirements independently. Previous research has demonstrated that larger and more genetically diverse training populations yield greater prediction accuracy and genetic gain (Merrick et al., 2022; Plavšín et al., 2021), and that models trained on larger datasets exhibit slower decay in predictive performance over time. The Pan-GS Consortium was established to address these challenges by combining phenotypic and genomic data from multiple common bean breeding programs. The primary objectives are to: (1) create a robust, durable, and universally applicable GS model; (2) identify unique and redundant alleles within and among breeding programs; and (3) provide an open-source, web-based interface that enables any breeding program to calculate genomic estimated breeding values (GEBVs) and identify superior lines for crossing. This report summarizes the progress made thus far and next steps.

MATERIALS AND METHODS

A combined phenotypic dataset was assembled from 14 dry bean breeding programs. This dataset consisted of 3,763 breeding lines and 280 check lines across 33 locations in Canada, the United States, Puerto Rico, Colombia, France, and Uganda. Pedigree information was used to identify sibling lines within the same family. To eliminate genetic redundancy with the training population, the highest yielding sibling from each family was identified based on the highest BLUP score calculated using the ASReml-R package. The final training population size was 1,284 breeding lines as well as 245 checks lines, of which 42 of these checks were shared across at least two breeding programs. Genomic DNA was extracted from selected breeding and check lines, and these lines were genotyped using the BARCBean12K SNP Chip. Population structure was assessed through principal component analysis, and genetic relationships among breeding programs were characterized using kinship coefficients and genetic distance matrices. Hierarchical clustering of SNP data was performed to identify subpopulation structure and allelic diversity patterns across programs.

RESULTS

Whilst the Pan-GS training population consisted of slightly more entries originating from the Meso-American gene pool (895 entries) than the Andean gene pool (507 entries), the major market classes are well represented with similar number of entries for each class. Substantial phenotypic

variation for yield was observed across the 1,419 genotypes. A clear distinction was observed between temperate and tropical germplasm, with temperate genotypes from USA and Canada exhibiting broader variability and significantly higher mean yields compared to tropical genotypes from Colombia, Uganda, and Puerto Rico (Figure 1). The first two principal components distinctly separated the Andean and Mesoamerican gene pools, consistent with their independent domestication history (Figure 2).

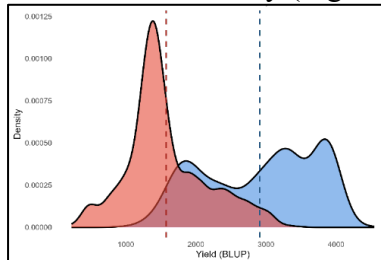
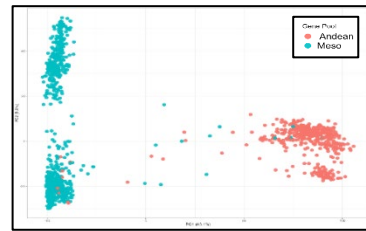


Figure 1: Yield Distribution of Temperate and Tropical lines in the Pan-GS Training Population

SNP-based hierarchical clustering revealed 3-4 major genetic groups within temperate germplasm, indicating that programs share common ancestry while maintaining unique allelic combinations. Importantly, programs exhibited complementary diversity patterns. Haplotypes were preserved in others, presenting opportunities for targeted introgression guided by GS (Figure 3B). Kinship and genetic distance analyses confirmed minimal shared ancestry between temperate and tropical germplasm, while temperate programs showed higher kinship values and lower genetic distances consistent with shared founder genotypes (Figure 3A). Tropical programs maintained greater between-program differentiation, suggesting potential for strategic crosses to capture complementary diversity.

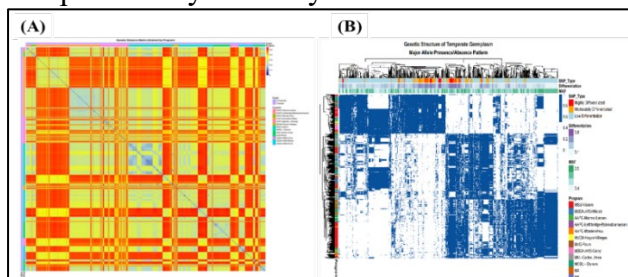


Figure 3: Population Structure of the Pan-GS Consortium: Genetic Distance Matrix (A) and (B) Major Allele Presence/Absence Pattern

NEXT STEPS: Immediate priorities include: (1) training and comparing predictive models using various approaches on the complete training population and subsets stratified by gene pool, market class, and geographic origin; (2) evaluating cross-validation strategies to assess prediction accuracy within and across breeding programs; (3) developing and validating a web-based interface for GEBV calculation; (4) Exploring the complementary diversity patterns identified among programs as an opportunity for guided germplasm exchange, particularly to introduce novel allelic diversity into the narrower Andean gene pool.

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EXPLORING THE GENETIC CONTROL OF SEED COAT COLOR IN A RIL POPULATION DERIVED FROM A RED X RED CROSS

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INTRODUCTION: Seed coat color in common beans (*Phaseolus vulgaris* L.) results from the accumulation of pigments, mainly phenolic compounds. These compounds provide health benefits to humans (Tapia et al., 2024), confer agronomic advantages related to disease resistance, and strongly influence market acceptance due of the wide phenotypic diversity of seed coat colors (García-Fernández et al., 2021). Classical inheritance studies have described a complex network of major genes controlling color (*C complex* and genes *P*, *C*, *V*, *R*, *Prp*, *G*, and *B*, among others) and distribution (*C complex*, *Z*, *T*, *Bip*, and *Fib*) in different market classes of bean types (Bassett, 2007). Objective: To investigate the genetic control of red seed coat color in the ABM RIL population and contribute to the understanding of the network of genes controlling this trait.

MATERIALS AND METHODS. Plant material: A recombinant inbred line population derived from AB136 × MDRK (ABM) with 109 recombinant lines (F_{6:7}) was used. The parents have red seed color but differ in the phenolic profile of the seed coat (Campa et al., 2023). **Phenotyping:** The recombinant lines were grouped into classes according to seed coat color, considering the parental phenotype. **Genotyping:** Genotyping by Sequencing (GBS) was performed to genotype the ABM population based on the methodology described by Elshire et al. (2011) and Schröder et al. (2016). SNP calling was performed using the G19833 v2 genome (NCBI accession GCA_000499845.2). **Map construction:** A genetic linkage map was constructed using the OneMap 3.0.0 package (Margarido et al., 2007) and visualized with Linkage Mapview version 2.1.2 (Ouellette et al., 2018). **Genetic analysis:** The goodness of fit between the observed and expected segregation ratios was tested using chi-square (χ^2) tests ($\alpha \leq 0.05$). Gene mapping for seed coat color was performed using contingency tests to assess the associations between seed coat color and SNP markers included in the genetic map. Significant associations were determined using the Bonferroni correction ($\alpha = 0.05$).

RESULTS AND DISCUSSION.

Phenotypic segregation. Qualitative evaluation of the seed coat color revealed three main phenotypic classes (Fig.1): red (parental), pink, and dark purple. Variations in color intensity were also observed in each phenotypic class. The overall segregation fitted a 2:1:1 ratio ($\chi^2 = 0.39$, $p = 0.82$), suggesting the involvement of two independent genes, where the presence of at least one parental genotype results in red color (AB136: A₁A₁B₁B₁; MDRK A₂A₂B₂B₂), the recombinant genotype A₁A₁B₂B₂ results in dark purple color, and the recombinant genotype A₂A₂B₁B₁ leads to a pink color.

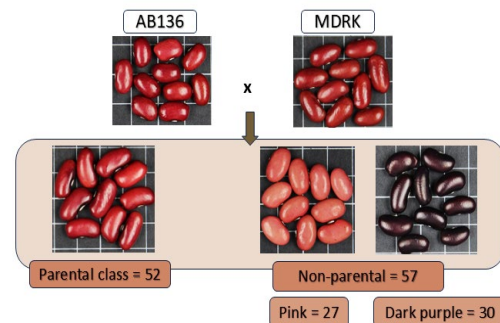


Fig. 1. Phenotypic classes identified in ABM RIL population and segregation observed

Genetic map development. Genotyping generated 352,875 SNPs, which were filtered based on the proportion of missing data, heterozygous genotypes, and distorted segregation. In total, 9,789 SNPs were used to construct a genetic linkage map. The final version of the ABM linkage map contained 796 SNPs distributed across 11 bean chromosomes. The number of markers per chromosome ranged from 14 (Pv10) to 106 (Pv02), with an average distance of 1.5 cM between loci. The total length of the ABM map was 1,143 cM.

Mapping. Based on contingency analysis, three regions were significantly associated with seed coat color (Fig. 2):

* Region A (47.48–49.64 Mb) on Pv02 overlaps with candidate genes involved in polyphenol synthesis and associated with black seed coat color (*Phvul.002G314000*, *Phvul.002G314100*, *Phvul.002G315400*, and *Phvul.002G317400*) (Campa et al. 2023). Additionally, the ‘greenish-brown factor’ (*B*) gene, located near the telomere of Pv02, regulates the production of anthocyanin precursors in the seed coat color pathway (Beninger et al., 2000).

* Region B (37.04–41.73 Mb) of Pv02 considers as hypothesized to regulate color intensity.

* Region C (1.82–3.84 Mb) on Pv08 corresponds to the position of the *C complex*, a cluster of genes involved in determining seed coat color and its distribution (García-Fernández et al., 2021).

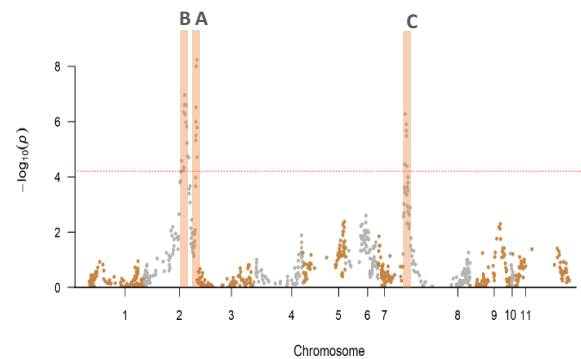


Fig. 2. Significant associations between seed coat color (red, pink, and black) and the 796 SNPs mapped in the ABM genetic map.

CONCLUSIONS

- Results suggested that red seed coat color in the ABM population is primarily controlled by two major *loci* located on the Pv02 (Region A) and Pv08 (Region C), likely corresponding to the *B* gene and the *C complex* respectively.
- The function of the second locus located on Pv02 (Region B) should be investigated. One hypothesis is that plays a key role in regulating seed coat color intensity.
- The different genetic control for red seed color observed in the ABM population agrees with the different phenolic profiles reported for the parent AB136 and MDRK.

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IDENTIFICATION OF ANTHRACNOSE RESISTANCE LOCI INTROGRESSED FROM *P. coccineus* INTO *P. vulgaris* COMBINING BSA AND WGS

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INTRODUCTION: Runner beans (*P. coccineus*, Pc) is a species closely related to common bean (*P. vulgaris*, Pv) in evolutionary terms. Pc shows high resistance to many common stresses in Pv such as, anthracnose, angular leaf spot, and oidium, among others, as well as other characteristics related to its roots (Schwemberet al., 2017). Bean anthracnose has a worldwide distribution, but it is particularly problematic in temperate regions like north Spain (Ferreira et al., 2008). This disease is race-specific, with numerous pathogenic variants described (Padder et al. 2017). In Asturias, several races have been identified with race 38 being the most frequent (Ferreira et al., 2008). Lines (HYB) derived from the interspecific cross $Pv \times (Pv \times Pc)$ were developed at SERIDA using the single-seed descent method. The lines used in the program were MDRK (Pv), which is susceptible to anthracnose race 38, and V215 (Pc), which is resistant to this race. The goal of this study was to investigate the inheritance of resistance to race 38 identified in the HYB028 line and to identify the genomic regions responsible for this resistance through a combination of Bulk Segregant Analysis (BSA) and Whole-Genome Sequencing (WGS).

MATERIALS AND METHODS. Plant material. A segregating population was developed from the cross MIDAS x HYB28. MIDAS is a snap bean susceptible to race 38, and HYB028, is an interspecific line with resistance to anthracnose race 38 derived from Pc. Single crosses were performed and advanced by self-crossing until $F_{2:3}$, with a total of 85 families. **Phenotyping.** The response to race 38 was evaluated under controlled conditions using a standardized method (Pastor-Corrales et al., 1995). At least, sixteen F_3 seedlings descendant of each F_2 plant were evaluated. Seedlings were evaluated after 7–9 days using a 1-to-9 scale, where 1 indicated no visible symptoms and 9 indicated severely diseased or dead plants. Families were classified as resistant (all F_3 plants had scores <3), susceptible (all F_3 plants had scores >4), or heterozygous (presence of resistant and susceptible F_3 plants). **Genetic analysis.** The goodness of fit of the observed to expected ratios was tested using chi-square tests (χ^2), with $\alpha \leq 0.05$. BSA was used to locate the regions involved in resistance. Two bulks with 10 F_2 plants each were established: a resistant bulk (R28) and a susceptible bulk (S28). The two bulks, parents MIDAS and HYB028 as well as Pc accession (V215) were genotyped by WGS (BMKGENE, GmbH, Münster, Germany). Sequencing reads were aligned using the bean genome G19833 v2 (NCBI accession number GCA_000499845.2). **QTL-seq analysis.** The QTLseq v 0.7.5.2 R package (Mansfeld and Grumet, 2017) was used to compute the Δ SNP index. Genomic regions surpassing the confidence interval at 95% (CI95) were considered associated with the resistance.

RESULTS AND DISCUSSION. The observed segregation in the $F_{2:3}$ population (MIDAS $\times$ HYB028) was 21 resistant, 40 heterozygous, and 24 susceptible families, which fitted the expected ratio for one major gene ($\chi^2 1:2:1 = 0.21$, $p = 0.78$). The $F_{2:3}$ families with the heterozygous genotype

showed segregation that conformed to a 3 resistant:1 susceptible ratio, indicating the dominant nature of this resistance. WGS analysis of the genotypes V215, Midas, HYB28, bulk R28, and bulk S28 yielded 5,766,560 SNPs. After filtering by missing values or physically close positions (50bp), 5,432,040 SNPs were retained for analysis. BSA revealed two statistically significant regions using the Δ SNP index (Fig 1): region 1 at the end of chromosome Pv07 and region 2 at the beginning of chromosome Pv11 (Table 1). Surpassing the CI95 and the positive Δ SNP index indicate that the region involved in the resistance comes from the resistant parent Pc. PCR-based markers and linkage analysis are underway to verify which of the two candidate regions is involved and whether the observed response fits the hypothesis of a major gene.

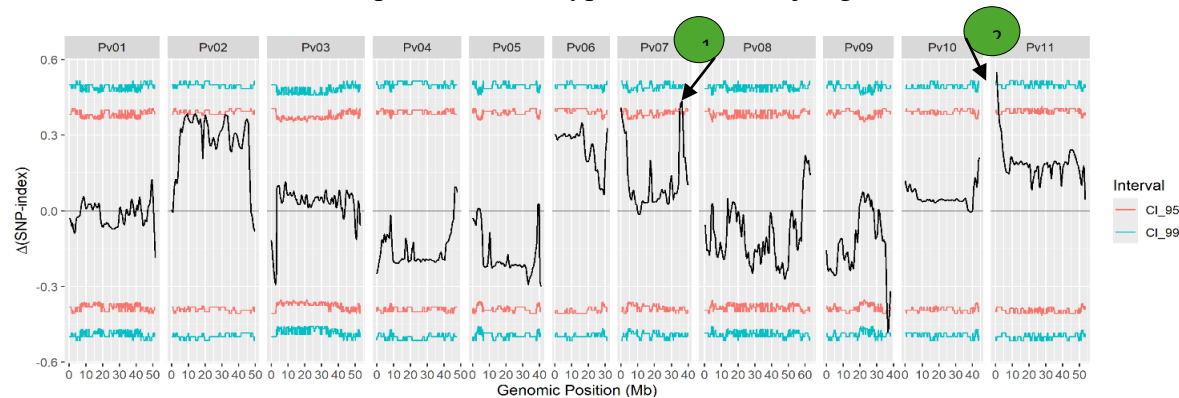


Fig 1. Distribution of the Δ SNP index across the 11 bean chromosomes considering two confidence intervals (CI95 and CI99) provided by the QTLseqR package. Candidate regions involved in resistance are indicated.

Table 1. Position in the bean genome of the significant regions associated to resistance to race 38 using the Δ SNP index and the QTLseqR package.

CHROM	Start	End	Num. SNPs	Peak Δ SNP	avg Δ SNP
Pv07	35009891	368384343	6595	0.44	0.42
Pv11	8452	1988219	4611	0.58	0.48

CONCLUSIONS.

This study exemplifies the potential use of the secondary gene pool of *Phaseolus* spp. in common bean breeding. This also demonstrates that the combination of BSA and WGS can be a rapid and cost-effective approach for identifying genomic regions associated with complex traits.

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UNDERSTANDING HEAT TOLERANCE IN *PHASEOLUS VULGARIS* THROUGH COMPARATIVE GENOMICS

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INTRODUCTION: Common bean (*Phaseolus vulgaris* L., 2n=2x=22) is known for its agricultural, economic, and nutritional benefits with both fresh (snap beans) and dry beans (e.g., pinto, kidney, black, navy) grown worldwide. However, dry bean production can be severely impacted by abiotic stressors including heat with elevated nighttime temperatures directly impacting plant reproduction and yield. In this project, we aim to understand the basis of heat tolerance in common bean on the molecular level by employing comparative genomic strategies using contrasting heat sensitive and heat tolerant cultivars. Indeterminate Jamaica Red (IJR) is heat tolerant and has been used as a donor of heat tolerance to TARS-HT-1 (HT-1), TARS-HT-2 (HT-2), AAR2 and AAR3¹ and is a key parent of a recombinant inbred line population² that revealed quantitative trait loci associated with heat tolerance. In contrast, Ica Quimbaya (IQ) and Montcalm are heat sensitive.

RESULTS AND DISCUSSION: Using Oxford Nanopore Technologies (ONT) long read genomic sequencing, we generated chromosome scale genome assemblies for five cultivars with known importance to heat tolerance (Table 1). Reads were assembled using HiFiasm³ and scaffolded into chromosomes using Ragtag⁴. The final genome assemblies were highly contiguous ranging in size from 536 Mb to 591 Mb (Table 1). We also generated chromosome-scale assemblies of TARS-HT-1 and TARS-HT-2 using previously generated ONT genomic contigs⁵ with Ragtag⁴.

Assessment of genic representation in all seven assemblies revealed >99% complete Benchmarking Universal Single Copy Orthologs (BUSCO)⁶ suggestive of high-quality genome assemblies.

Genotype	Total length (bp)	Number of scaffolds	Largest scaffold (bp)	Scaffold N50 (bp)
IJR	564,964,479	77	63,993,889	53,435,030
IQ	586,675,925	217	63,460,045	51,575,336
Montcalm	591,882,828	143	63,092,499	51,041,419
AAR2	566,843,379	65	62,966,324	54,790,602
AAR3	567,230,917	44	63,064,142	54,296,024
HT-1	538,950,940	47	62,442,880	50,174,156
HT-2	536,553,977	43	62,814,423	51,906,282

All seven genomes were annotated for protein coding genes as described previously⁷. Using the comparative genomics tool GENESPACE⁸ and the G19833 reference genome⁹, 23,067 syntelogs were present across all eight common bean genome assemblies consistent with the high degree of collinearity between the genomes (Figure 1). Efforts are in progress to identify genes

within quantitative trait loci associated with heat stress tolerance and genes differentially expressed under heat stress in reproductive tissues to identify genetic mechanisms for heat stress tolerance.

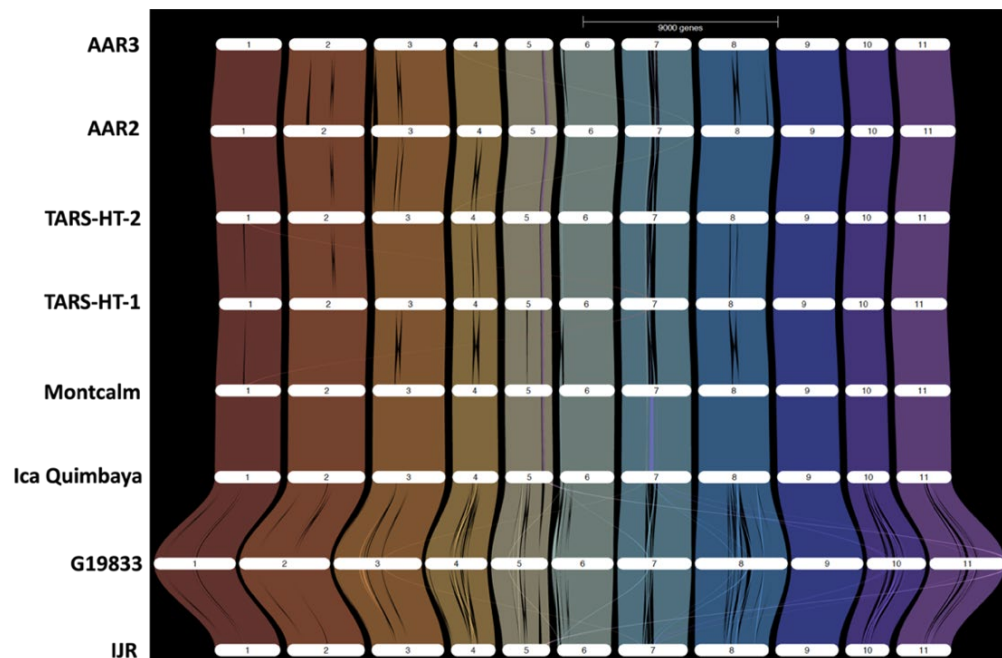


Figure 1. Riparian plot of eight common bean genomes, including the common bean reference genome G19833⁹, generated using GENESPACE⁸.

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TOWARD A NAVY BEAN PANGENOME FOR DISSECTING COMMON BACTERIAL BLIGHT RESISTANCE AND TEPARY BEAN INTROGRESSIONS

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INTRODUCTION: Common bacterial blight (CBB) of dry beans is attributed to two distinct species, *Xanthomonas phaseoli* pv. *phaseoli* and *X. citri* pv. *fuscans* (1). CBB can cause yield losses of up to 40% and reduces marketable yield through seed lesions and discoloration (2). Resistance to CBB has been historically incorporated into dry bean breeding programs at the University of Guelph and Agriculture and Agri-Food Canada (AAFC), Harrow, Ontario through interspecific hybridizations with tepary bean (*Phaseolus acutifolius* A. Gray) accessions PI 440795 (3, 4, 5) and PI 319443 (6). Resistance derived from PI 440795 was introgressed into *P. vulgaris* at the University of Guelph by an interspecific cross and a backcross to create the resistant breeding line MB 7, which was to develop several resistant cultivars, such as OAC Rex (7), Rexeter (8) and several others (9). Resistance from PI 319443 was introgressed into the breeding line XAN 159 (10, 11) at CIAT (Centro Internacional de Agricultura Tropical), Cali, Colombia and subsequently incorporated into the derivatives HR45 (6) and HR67 (12) at AAFC, Harrow. This resistance is primarily conditioned by two major quantitative trait loci (QTL). One QTL is located on linkage group B6 (chromosome Pv06) and is associated with the sequence-characterized amplified region (SCAR) marker BC420 (12, 13). The second QTL is located on linkage group B8 (chromosome Pv08) and is associated with the SCAR marker SU91 in the *P. vulgaris* genome (13, 14). The combined breeding programs at the University of Guelph and AAFC developed CBB resistant navy bean cultivars Apex (15), and Mist (16) and several other market classes (9). These cultivars exhibit improved resistance to CBB, yet the extent of *P. acutifolius* genome integration and the potential contribution of additional resistance or agronomically beneficial alleles remain unclear. Molecular marker-based estimates (17) and more recent genomic studies indicate that the actual retained tepary introgression is typically limited to small, highly localized regions often restricted to genomic areas associated with stress tolerance (18). The availability of third-generation sequencing platforms, such as Oxford Nanopore Technologies (19), has made whole-genome sequencing (WGS) more affordable, enabling comprehensive characterization of introgression through advanced bioinformatic approaches such as pangenomics. The objectives of the current work were to: (i) validate the previously reported Niemann-Pick-associated locus (now annotated as a patched family protein) for CBB resistance across multiple genetic backgrounds using the pangenome, (ii) quantify the genomic contribution of *P. acutifolius* accession PI 440795 to the University of Guelph navy bean CBB-resistant cultivars through pangenome-based comparative analyses, and (iii) identify novel candidate genes and allelic variations that may contribute not only to disease resistance but also to enhanced resilience to biotic and abiotic stress.

MATERIALS AND METHODS: A panel of eleven navy bean genotypes, including four CBB-resistant introgression lines (OAC Rex, Rexeter, Apex, and Mist) and seven susceptible cultivars, including Ex Rico 23 (20), OAC Laser (21), OAC Gryphon (22), AC Compass (23), AC Cruiser (24), T9905 (CFIA registration no. 5740), and Envoy (CFIA registration no. 3605), together with

the tepary bean PI 440795, were selected for whole-genome analysis. High-molecular-weight DNA was extracted from young leaf tissue and sequenced using the Oxford Nanopore PromethION 24 platform. *De novo* genome assemblies have been generated, scaffolded to chromosome scale, and evaluated for quality and structural integrity. Ongoing and subsequent analyses will include repeat identification and masking, *ab initio* and evidence-based gene prediction, structural and functional annotation, and construction of a chromosome-scale pangenome for comparative genomic analyses.

RESULTS: Long-read WGS generated high-coverage datasets for the navy bean panel and the tepary bean PI 440795. *De novo* assembly of PI 440795 produced a total assembly size of 677.9 Mb, closely matching the 661.9 Mb reference genome length, with strong contiguity (NG50 = 10.2 Mb; largest contig = 31.5 Mb). Genome fraction was ~65%, and GC content (35.8%) aligned with the reference. Across the eleven navy bean genotypes, assemblies likewise showed high continuity, with genome sizes near the ~555 Mb reference, large contigs (up to 101 Mb), strong N50 values (28-47 Mb), and genome fractions of ~89-92%, reflecting robust long-read performance suitable for comparative genomics. This study is ongoing, and downstream analyses will provide comprehensive characterization of structural variation, gene presence/absence diversity, and introgressed regions derived from *P. acutifolius*, particularly those associated with CBB resistance.

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USE OF MOLECULAR MARKERS TO FIX THE *bc-3* GENE IN ANDEAN LARGE-SEEDED CLIMBING BEANS

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the most important grain legumes for food and nutritional security in Latin America and Sub-Saharan Africa. It provides protein, fiber, carbohydrates, vitamins, and essential micronutrients to millions of people. However, bean productivity is severely constrained by viral diseases that can cause yield losses ranging from 20% to 100%. The *bc-3* resistance gene, originally derived from *Phaseolus vulgaris* cv. “MDRK,” provides broad-spectrum resistance to BCMV and bean common mosaic necrosis virus (BCMNV). Introgression and fixation of this gene into elite Andean climbing bean backgrounds is a critical step toward achieving durable virus resistance and safeguarding seed quality and market value.

MATERIALS AND METHODS

A three-way cross breeding strategy was applied to combine resistance to BCMV, yield, and grain quality traits. Crosses were performed between elite Andean climbing bean lines (MAC's) and donor sources carrying the *bc-3* gene. In early segregating generations (F₂), marker-assisted selection with Tm shift marker techniques (Miklas et al., 2006; Raatz & Beebe, 2015) was implemented to identify individuals carrying the *bc-3* gene even in the absence of viral pressure. The primers used were: ***bc3a*_Forward 1:** gcgggcagggcggcGAATTCCTGGACCTTCTGGTt, ***bc3a*_Forward 2:** gcgggcAGAATTCCTGGACCTTCTGGTa, ***bc3a*_Reverse 1:** TATATGGGTCGGATGGAAGT. A spatial model was used during statistical analysis to correct for row and column effects, thereby minimizing environmental variation and improving selection accuracy.

RESULTS

Marker-assisted selection successfully identified the presence of the *bc-3* gene in early generations, enabling rapid advancement of resistant lines. The use of MAS in the conventional breeding program significantly shortened the breeding cycle, reducing costs and increasing efficiency in the recovery of desired traits. Lines fixed for the *bc-3* gene demonstrated yield potential up to 4 tons per hectare (Figure #1), surpassing the commercial check (MAC 44) by 20–40%, while maintaining large-seeded Andean grain types preferred by markets (Figure #1). The spatial analysis model effectively reduced field variability, improving the reliability of yield estimates, and facilitating the identification of superior genotypes.

Genotype	Market Class	YIELD (ton/ha)	PHI
MAC 44	Red Mottled	2.7	0.70
1	Red Mottled	3.7	0.79
34	Red Mottled	4.6	0.75
37	Sugar	5.3	0.77
54	Sugar	3.2	0.73
19	Red	3.8	0.81
21	Red	4.6	0.75

Figure #3: Yield and PHI range of Large-Seed Andean for mottled, red and sugar market class. MAC 44 Commercial check. Tto (Genotype in PYT).

DISCUSSION

The successful introgression and fixation of the *bc-3* gene into Andean climbing beans demonstrates the effectiveness of combining traditional breeding with Tm shift marker techniques. Moreover, the integration of marker-assisted selection (Miklas et al., 2006; Raatz & Beebe, 2015) allows breeders to make genetic gains even in the absence of viral infection, reducing the risk of exposure and supporting sustainable breeding practices.

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GENOME-WIDE ASSOCIATION MAPPING OF ANTHRACNOSE RESISTANCE AND RELATED TRAITS IN ONTARIO DRY BEANS

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INTRODUCTION: Anthracnose is a plant disease caused by *Colletotrichum lindemuthianum*, which is known to cause significant yield loss in dry beans (Conner et al. 2020). It is an aggressive, seed-borne disease that thrives in humid, high-precipitation environments and can persist in infected plant residues left in the field, allowing the pathogen to spread to subsequent crops (Conner et al. 2020). In Ontario, race 73 is the most prevalent race of anthracnose (Conner et al. 2020). Small-seeded dry beans such as navy and black beans hold great importance in Ontario because they are the highest produced and exported dry beans out of the province (Hesami and Yoosefzadeh-Najafabadi 2025). Though anthracnose infections were dormant due to the development of strong resistant cultivars, there was a surge of infections in Ontario in the year 2024 due to a high-pressure environment for the fungus (Dry Bean Seasonal Summary - Field Crop News 2024). This presented a new challenge for breeders to address, that is, a need to build cultivars of dry beans with stronger resistance to anthracnose in high-pressure environments. Therefore, this study aims to address this issue by employing a GWAS to develop molecular markers associated with resistance against race 73. The findings of this project may be significant in helping growers maximize yield and productivity, it can also contribute to the growing feed insecurity problem because new cultivars with greater resistance will be less susceptible to the yield losses that this fungus can cause (Hesami and Yoosefzadeh-Najafabadi 2025).

METHODS: A population of 207 genotypes consisting of anthracnose differential lines and commercial, preliminary and advanced breeding lines from the core germplasm of the dry bean breeding and computational biology program at the University of Guelph were planted in two fields, in Woodstock and Elora in southern Ontario, in two replications and in a RCBD experimental design in the year 2025. Young trifoliolate leaves were collected for each genotype in four folds and freeze-dried, then stored at -80°C for extra protection. The field was then inoculated with anthracnose after flowering important agronomic traits (disease progression from a scale of 0 to 9 (a rating of 0 corresponds to no visible infection symptoms and a rating of 9 corresponds to severe visible disease symptoms on most plants in a given plot), height at maturity (cm), maturity (days after planting), yield (kg/ha), and harvestability on a scale from 1 to 5 where 1 represents plots that are easy to harvest by machine and 5 represents plots difficult to harvest by machine) were measured. This will be repeated for the year 2026 to provide robust data for the GWAS analysis. In the future, DNA will be extracted from the previously collected leaves and then sequenced. Analysis, which will be conducted using the collected data, includes population structure and kinship analysis, bioinformatics analysis of the SNP data via different conventional and machine learning based GWAS, and fine-mapping analysis.

RESULTS: Yield was significantly higher at Woodstock with an average yield of 5037.65 kg/ha in comparison to Elora with an average yield of 3435.84 kg/ha (Figure 1 A; Figure 2A, C). On average, Elora had higher harvestability ratings, with a mode rating of 5, than at Woodstock, with a mode rating of 1 (figure 1C). This is an indication that plots in Elora would be difficult to harvest by machine. Plots in Woodstock show a greater height distribution (26-90 cm) compared to Elora (29-80 cm) (Figure 1 D), the average height in Elora was 47.6 cm and 58.1 cm in Woodstock. As noted by Cordoba-Novoa and Hoyos-Villegas in 2025, there is strong evidence that plant architecture can have effect on yield stating dry bean plants that have an upright architecture, a stem that is thicker and prevents lodging, such as ones that would have a lower harvestability score, can have a positive impact on yield. The maturity on average was higher in Elora (Figure 1B; 2 B, D), with an average of 95 days after planting, compared to Woodstock, where the average harvestability was 81 days after planting. Cordoba-Novoa and Hoyos-Villegas, 2025, suggest that short maturity can be a positive trait for high yield in Mesoamerican dry beans, including navy and black beans. Disease severity ratings report that most plots in both Woodstock and Elora have a low disease severity ranking of 0 (Figure 1 E and F), with Elora having more occurrences of higher ratings which may be another factor driving the low yield in comparison to Woodstock (Conner et al. 2020). The lower disease severity rankings can be attributed to 2025 being a low-pressure environment for anthracnose during the growing season in Ontario due to low precipitation and environmental moisture (Canada, n.d.).

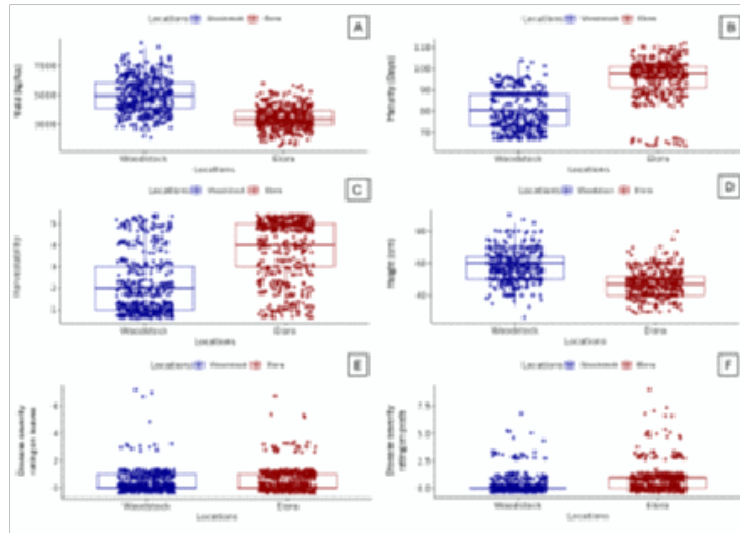


Figure 8. Box plots displaying field data collected from Woodstock and Elora for yield (A), harvestability (B), maturity (C), height (D), and anthracnose disease severity ratings for

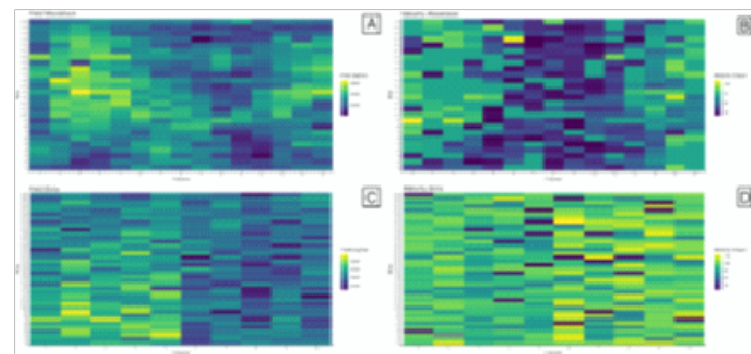


Figure 7. Heat maps for yield and maturity in Woodstock (A and C. respectively) and Elora (B and D. respectively).

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THIRTY-FIVE YEARS OF GENETIC GAIN IN DRY BEAN BREEDING: EVIDENCE FROM MULTI-ENVIRONMENT TRIALS IN NORTH DAKOTA AND MINNESOTA

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INTRODUCTION

Plant breeding programs rely on multi-environment trials (METs) to evaluate genotypes across diverse spatiotemporal scales, identifying lines with superior performance and stability. Long-term MET datasets offer a robust framework for quantifying genetic progress and evaluating the impact of breeding strategies over time. In the United States, dry bean production is concentrated in the Upper Midwest, specifically North Dakota and Minnesota, which serve as critical hubs for domestic and export markets.

Dry bean (*Phaseolus vulgaris* L.) productivity is highly susceptible to environmental variability due to its short growing season (65–100 days), which limits its physiological capacity to compensate for stress (Kelly, 2010). Consequently, NDSU breeding efforts have prioritized enhancing yield potential alongside resistance to biotic and abiotic constraints, such as drought and white mold. This study utilizes 35 years of MET data to estimate the annual genetic gain in seed yield (SY) across five major dry bean market classes, providing a retrospective analysis of breeding effectiveness in the North Dakota–Minnesota region.

MATERIALS AND METHODS

Historical performance data spanning 1987–2022 were synthesized from NDSU Advanced Yield Trials and Variety Trials. These trials were conducted across nine locations (six ND counties and three MN counties) within the Red River Basin. The consolidated dataset comprises over 70,000 plot records, transitioned from legacy handwritten field books (1987–2009) to digital databases (2010–2022) using Agrobase (Agronomix, 2008).

Five market classes were analyzed: Pinto, Navy, Black, Kidney, and Great Northern. All trials utilized a randomized complete block design (RCBD) with three to four replications. To account for unbalanced data and environmental heterogeneity, Best Linear Unbiased Estimates (BLUEs) were calculated using a mixed linear model: Location and block were treated as random effects, while genotype and year were treated as fixed effects.

RESULT AND DISCUSSION:

Analysis of the 35-year period revealed a mean seed yield gain of 0.0584 cwt per acre per year (equivalent to 5.84 lbs/acre/year) across all evaluated market classes (Fig 1). This positive trend underscores the long-term success of selection pressure for high-yielding, adapted germplasm.

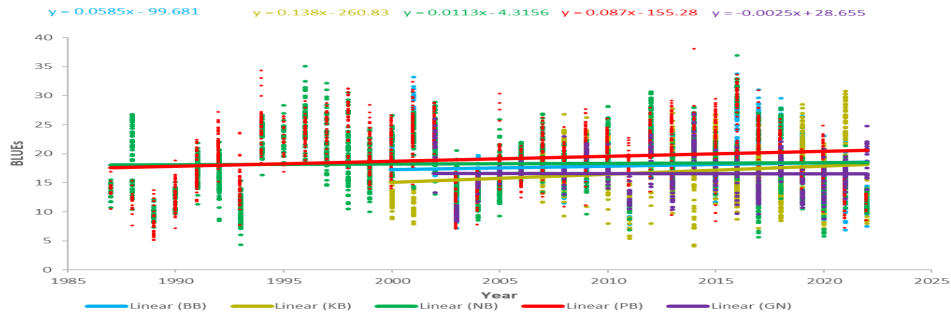


Figure 1: Linear model showing total BLUEs results based on each MC for 35 years

Significant variation in genetic gain was observed among the five market classes (Table 1). The Kidney bean class demonstrated the highest rate of improvement at 13.8 lbs/acre/year. Pinto and Black beans followed with robust gains of 8.67 and 5.9 lbs/acre/year, respectively. Navy beans showed a more modest increase of 1.13 lbs/acre/year. Conversely, the Great Northern market class was the only group to show a marginal yield decline (-0.25 lbs/acre/year), suggesting that this class may require refreshed genetic diversity or revised selection criteria to overcome yield plateaus in the region.

Table 1. Annual seed yield gain and statistical parameters by market class (1987–2022)

Market Class	cwt/acre	lbs/acre/year	R ²	SE
Black (BB)	0.059	5.9	0.005	2.161
Navy (NB)	0.0113	1.13	0.000	2.459
Kidney (KB)	0.138	13.8	0.022	2.271
Pinto (PB)	0.0867	8.67	0.025	2.412
Great Northern (GN)	-0.0025	-0.25	0.000	2.399

The difference in gains between classes (e.g., Kidney vs. Navy) likely reflects differences in the genetic base of the starting germplasm, the intensity of selection, and the complexity of combining yield with specific market-class quality requirements.

CONCLUSION:

The analysis of 35 years of MET data provides clear evidence of sustained genetic progress in the NDSU dry bean breeding program. With four of the five major market classes showing positive yield trajectories, the results validate the effectiveness of the program’s selection methodologies. These findings highlight that NDSU breeders have successfully increased yield potential without sacrificing environmental adaptability. Furthermore, the stagnation observed in the Great Northern class identifies a specific area for future breeding priority. This retrospective study serves as a benchmark to guide future strategies, ensuring that genetic gains are sustained to meet the evolving demands of both regional producers and global consumers.

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GENETIC DIVERSITY OF ANDEAN COMMON BEAN CULTIVARS AND BREEDING LINES REVEALED BY MORPHOAGRONOMIC TRAITS

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INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is a legume widely cultivated, and constitutes one of the main sources of food for human consumption, with high nutritional value and significant socio-economic importance. Andean beans stand out for their diversity of grain colors, shapes, and sizes. In this context, genetic diversity studies are essential to understand the relationships among accessions adapted to specific edaphoclimatic conditions as well as to guide plant breeding strategies. This study aimed to evaluate the genetic diversity of Andean common bean cultivars and breeding lines through morphological and agronomic descriptors.

MATERIAL AND METHODS

The experiment was conducted during the 2024/25 rainy season at the Experimental Station of IDR-Paraná, in Londrina, Paraná State, Brazil. A randomized block design with three replications was used with plots consisting of four 4-m rows spaced 0.5 m apart. 13 breeding lines and 7 cultivars (BRS-Embaixador, IPR-Cardeal, BRS-Ártico, IPR-Garça, IAC-2157, BRSFS-311, and IAC-2153) were evaluated. Characterization was carried out using 66 traits, of which 23 were quantitative, and 43 qualitative. Quantitative traits were subjected to analysis of variance (ANOVA, $p \leq 0.05$) using Genes software. Subsequently, all traits were analyzed for genetic dissimilarity using Ward's distance, and principal component analysis (PCA) was performed using Genes and R software.

RESULTS AND DISCUSSION

ANOVA indicated a significant effect for 18 out of the 23 traits, highlighting the genetic variability among the breeding lines and the cultivars, confirming the potential of the genotypes for use in breeding programs. Three groups were identified in the genetic dissimilarity analysis (Figure 1). The first group consisted of genotypes that demonstrated the highest values for pod length, width, and thickness; number of locules and seeds per pod; total number of seeds; seed length and average yield of 2,990.72 kg ha⁻¹. The second group presented the longest total growth cycles and the highest values for first pod insertion height, number of nodes, and total number of pods per plant. However, it showed the lowest yield with an average of 2,314.47 kg ha⁻¹. Lastly, the third group demonstrated the highest values for plant height, seed thickness and width.

The principal component analysis (PCA) complemented the genetic dissimilarity analysis (Figure 2). Genotypes of the Cranberry group were associated with higher values of yield, central leaflet size, height of first pod insertion, and number of seeds per pod, reinforcing the superior performance observed for this group. In turn, genotypes of the White group were clustered in a region characterized by higher values of plant height, number of nodes, and apical pod beak length.

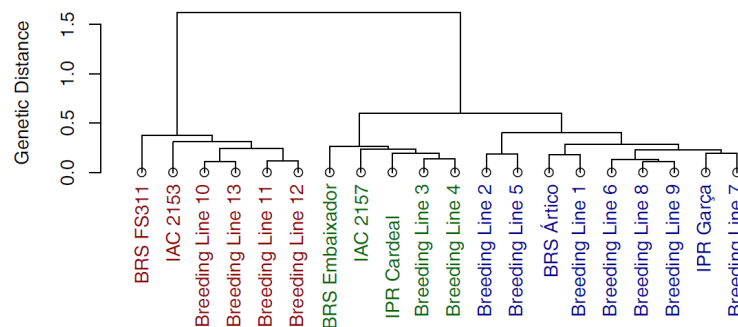


Figure 1. Ward's hierarchical clustering of 20 common bean genotypes evaluated during the 2024/25 rainy season at the IDR-Paraná Experimental Station, in Londrina, Paraná, Brazil.

These results demonstrate that the morphoagronomic descriptors were efficient in discriminating the evaluated genotypes, meeting the distinctness requirements established by the National Plant Variety Protection Service (SNPC), Ministry of Agriculture and Livestock (MAPA), Brazil, and providing consistent support for the selection and protection of new cultivars of the special group.

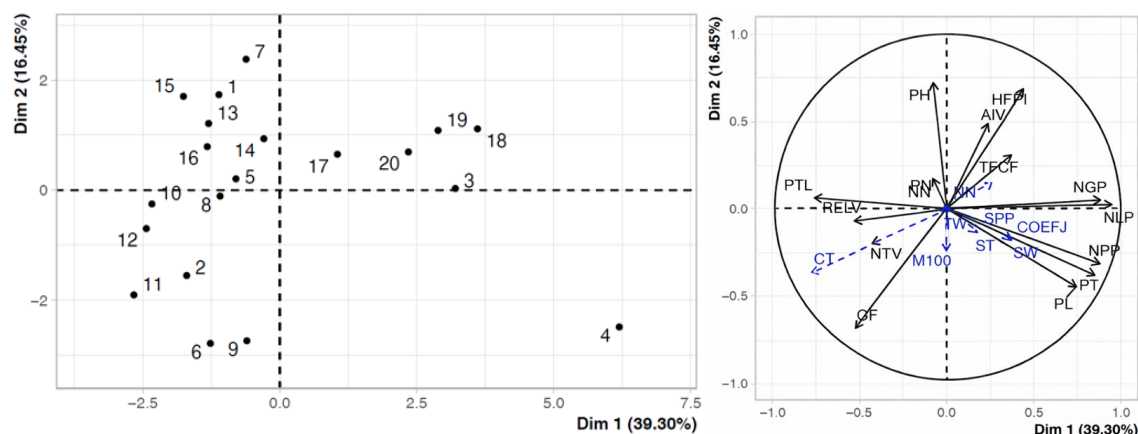


Figure 2. Principal component analysis of 20 common bean genotypes evaluated during the 2024/25 rainy season at the IDR-Paraná Experimental Station, in Londrina, Paraná, Brazil.

PH: Plant height (cm); **PL:** Pod length without beak (cm); **PW:** Pod width (mm); **PT:** Pod thickness (mm); **PTL:** Pod tip length (mm); **HFPI:** Height of first pod insertion (cm); **NN:** Number of nodes; **NLP:** Number of locules per pod; **NGP:** Number of grains per pod; **NPP:** Total number of pods per plant; **SPP:** Total number of seeds per plant; **ST:** Seed thickness (mm); **SW:** Seed width (mm); **SL:** Seed length (mm); **T/W:** thickness/width; **GMP:** total grains mass per plant (gm); **M100** – 100 grains mass (gm); **COEFJ** – J coefficient (length/width); **COEFH** – H coefficient (thickness/width).

CONCLUSION

Morphoagronomic traits enabled the distinction of common bean cultivars and breeding lines and revealed significant genetic diversity among the evaluated genotypes, highlighting their potential as parents in breeding programs aimed at developing high-yielding cultivars with broad adaptation to diverse edaphoclimatic conditions.

ACKNOWLEDGEMENTS

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REBUILDING CONFIDENCE IN BEAN INOCULANTS: IDENTIFYING CROP SPECIFIC RHIZOBIA IN COMMON BEAN VARIETIES FOR SUSTAINABLE NITROGEN FIXATION

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a relatively inefficient biological nitrogen fixer compared with other pulse crops, typically meeting less than 40% of its nitrogen demand through biological nitrogen fixation (BNF) (Peoples et al., 2009). In Canada, where approximately 150,000 ha of dry beans are grown annually, inconsistent performance of commercial *Rhizobium* inoculants has reduced farmer confidence and increased reliance on synthetic nitrogen fertilizers (STC; AAFC). Excess nitrogen application leads to low nitrogen use efficiency and significant environmental losses, contributing to greenhouse gas emissions and soil and water degradation (Canfield et al., 2010). Improving BNF in common bean requires identifying responsive genotypes and crop-specific *Rhizobium* strains adapted to Canadian soils to support sustainable bean production and breeding efforts.

MATERIALS AND METHODS

In this study, common bean genotypes and *Rhizobium* strains were evaluated under nitrogen-sufficient and nitrogen-deficient conditions to determine their true contribution to biological nitrogen fixation (BNF). Responsive genotype–inoculant combinations were selected for further testing under reduced nitrogen levels to identify elite genotypes and genomic regions associated with enhanced BNF for future breeding efforts. A total of 177 common bean genotypes, including elite cultivars, breeding lines, and landraces, were assessed in symbiosis with two *Rhizobium* strains isolated from Canadian soils as part of a large sampling effort developed under the BENEFIT project (<https://www.queensu.ca/microbes-for-agriculture/>). The two strains evaluated were Rh 258 (*Rhizobium croatiense*) and Rh 71 (*Rhizobium* sp.). Experiments were conducted in a controlled growth chamber using a two-way completely randomized design, consisting of two inoculated treatments (Rh 258 and Rh 71) along with nitrogen-sufficient (N+) and nitrogen-deficient (N–) controls, with temporal replication. Phenotyping was performed at the R1 growth stage and included nodulation traits, shoot and root biomass, leaf chlorophyll content measured by NDVI, and biologically fixed nitrogen estimated using the nitrogen balance method (Unkovich et al., 2008).

RESULTS AND DISCUSSION

For this report, results are presented from two replicates and are limited to nodule count, nodule weight, shoot fresh weight, root fresh weight, and NDVI as a measure of leaf greenness. Shoot and root biomass were strongly positively correlated across all treatments ($r = 0.62$), with similar relationships observed under Rh 71 ($r = 0.57$) and Rh 258 ($r = 0.58$), indicating stable biomass allocation regardless of inoculant. In contrast, root weight and nodule count were weakly

negatively correlated overall but shifted to positive under inoculation, particularly with Rh258 ($r = 0.30$), highlighting the importance of effective *Rhizobium*–host compatibility for nodulation. Nodule count and nodule weight were moderately correlated overall ($r = 0.56$), with a stronger association under Rh7 1 ($r = 0.65$) than Rh 258 ($r = 0.51$), indicating inoculant-dependent differences in nodule development.

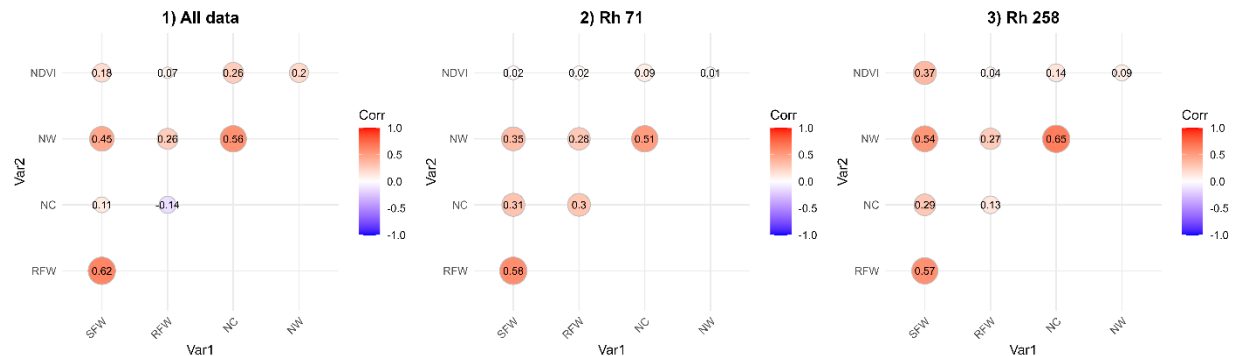


Figure 9: Correlations among NDVI (leaf greenness), nodule count (NC), nodule weight (NW), and shoot and root fresh weight (SFW & RFW) across all treatments and under *Rhizobium* strains 71 and

Top-performing genotypes across nodule count, nodule weight, NDVI, and shoot and root fresh weight included Agassiz, BelMiNeb_RMR_3, Higuera-E, CDC Minto, and Othello, which were consistently selected under both *Rhizobium* strains (Rh 258 and Rh 71). Additional genotypes were identified specifically under Rh 258 (WeiHING, OAC Inferno, HR185, BelMiNeb-RMR-7, and CDC Camino) and Rh 71 (SantaFe, MedicineHat, Eclipse, ND Falcon, and CDC Sol). These genotypes span release periods from the 1990s to the 2010s and represent diverse market classes, including Pinto, Great Northern, Yellow, Black, and Light Red Kidney types. Overall, older varieties and landraces showed greater responsiveness to rhizobial inoculation than more recently developed commercial cultivars and breeding lines.

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EVALUATING A BREEDING PANEL OF HISTORICAL COMMON BEAN (*PHASEOLUS VULGARIS*) LINES FOR EFFECTS OF INDIRECT SELECTION

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INTRODUCTION: Historically, common bean breeding has focused on curating a strong upright plant architecture better suited to direct harvesting than the vining and climbing growth habit of wild bean. This has resulted in greater phenotypic diversity of growth habits in domesticated populations compared to wild populations. While wild beans are indeterminate and maintain a climbing growth habit (Type IV), domesticated beans can range from indeterminate and prostrate (Type III), indeterminate and upright (Type II), to determinate and upright (Type I). Breeding for an ideotype of upright plant architecture has led to thicker stem widths to support upright plants and shorter plant lengths.¹ These breeding efforts have led to observed changes in aboveground structure and nutritional composition.^{2,3} However, possible changes to the below ground root architecture remain largely unknown. This study focuses on phenotyping the root architecture of historically relevant cultivars and comparing them to wild beans and landraces to understand possible effects of indirect selection in domestication and breeding.

MATERIALS & METHODS: Sixteen (16) lines, comprised of two wild bean accessions (PI535428, W624135), three landraces (Common Red Mexican, Black Turtle Soup, Robust), and eleven cultivars across three market classes (navy, black, and small reds) were grown in a randomized complete block design at the Montcalm Research Center during 2020 and 2021. Growth habits, maturity patterns, stem width, and plant length were recorded. Plants were sampled for leaf and seed mineral nutrition. Root systems of sampled plants were excavated using ‘shovelomics’ methods and scanned with a Nikon camera to produce images. A supervised machine learning model in RootPainter was used to identify root tissue from each image. The resulting black and white images distinguishing root tissue were used in RhizoVision, a program that skeletonizes and quantifies multiple root traits such as total root length, convex area, solidity, and average root diameter.^{4,5} Resulting values for root traits were used for statistical analysis in R.

RESULTS: Based on the year of cultivar release, stem width increased over time and plant length decreased over time, reflecting changes resulting from breeding efforts for plant architecture. Principal component analysis of 12 root traits showed that data separated distinctly by the year plants were grown, possibly due to management and environmental differences. Because of this, data separated by year was also analyzed and plotted. Across both years, basal root angle, lateral root number, and plant length contributed to variation in wild bean accessions, with basal root angle contributing the most. In plots of both years of data and with data only from 2020, basal root angle was positively associated with nodulation percentage; however, when 2021 data was plotted, lateral root number was positively associated with basal root angle. Additionally, basal root angle was consistently negatively associated with traits such as average root diameter, total root length, and basal root width. To further investigate traits contributing to variation, a t-test for basal root angle and nodulation percentage between pairs of wild accessions and domesticated beans of three market classes was completed. Nodulation percentage had a significant p-value compared to wild

accessions for only three cultivars: Sanilac, Alpena, and Domino. However, basal root angle had a significant p-value between the wild accessions and several cultivars as well as each landrace.

CONCLUSIONS: This study reveals evidence of indirect selection shown by different root traits contributing to variation, such as basal root angle and nodule percentage to wild accessions and average diameter or basal root width to domesticated lines. This is additionally supported by significantly different basal root angles between wild accessions and several lines tested. These results and continued research into differences between landraces and wild accessions as well as differences within market classes will illuminate how breeding decisions impact whole plants and how those impacts may differ across classified market classes.

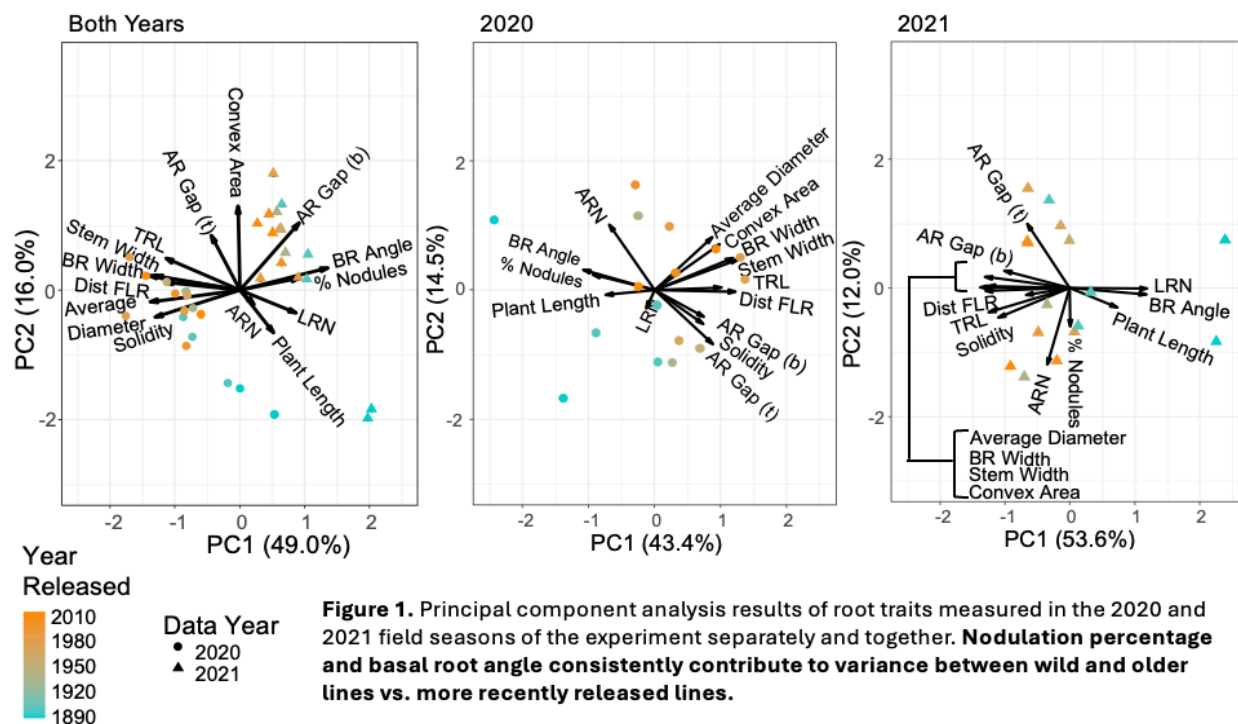


Figure 10 Principal component analysis results of root traits measured in the 2020 and 2021 field seasons of the experiment separately and together. Nodulation percentage and basal root angle consistently contribute to variance between wild and older lines vs. more recently released lines. Abbreviations: Adventitious Root (top/bottom) (AR (t/b)), Total Root Length (TRL), Lateral Root Number (LRN), Basal Root (BR), Adventitious Root Number (ARN), Distance from Lateral

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DEEP LEARNING AND COMPUTER VISION FOR HIGH-THROUGHPUT PHENOTYPING OF CANNING QUALITY TRAITS IN DRY BEANS

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INTRODUCTION

Canning color retention is a key quality trait in dry bean breeding, influencing consumer acceptance and commercial value. Current phenotyping methodologies rely on two major approaches for evaluating canning color in dry beans: 1). Visual rating, and 2). instrumental colorimetry using Hunter Labscan XE colorimeter and Minolta Chroma meter (Mendoza et al., 2014). Visual rating is a traditional method to assess canning color, where a group of trained panelists visually rate canned bean samples and the average of their score is used as the final rating. Visual rating is prone to subjectivity, perception bias and inconsistency across sessions. The instrumental colorimetry methods are point-based and generally only record measurements of a few square centimeters of the actual sample size. This limitation of providing limited spatial information makes them unrepresentative, especially for heterogeneous samples. To overcome the canning quality phenotyping bottleneck, this study aimed to develop an open-source, high-throughput image-based phenotyping pipeline tailored for canning quality trait evaluation in dry bean breeding programs. Using digital images of canned bean samples from Michigan State University's dry bean breeding program, this workflow integrates standardized image acquisition of canned bean samples with statistical, computer vision, and deep learning tools to deliver a streamlined pipeline that processes the images for bean detection, segmentation, pixel level color extraction in the CIE L*a*b* space and delivers an objective score metric.

MATERIALS AND METHODS

A total of 525 black dry bean genotypes from Preliminary and Advanced Yield Trials conducted by the Michigan State University Dry Bean breeding program were used to develop and evaluate the phenotyping pipeline. We used YOLOv8n model within a transfer learning framework, fine-tuned on a custom dataset consisting of 1,170 training images and 299 validation images. The YOLOv8n model detects each canned sample and output its bounding box coordinates. These bounding box coordinates and a set of five-points were given as a prompt to SAM to guide the segmentation process. Both the bounding box coordinates and the set of five-point prompts were provided to SAM as inputs for each sample. SAM processed these inputs to produce a binary segmentation mask separating the sample from surrounding tray surfaces and background elements at the pixel level. After segmentation, CIE L*a*b* values were extracted from each pixel within the segmented mask using a scikit-image library in python. The L*, a*, and b* values were then averaged across all pixels to produce a single L*a*b* value for each sample. In this study, we developed a numerical and objective term the “D-score,” which quantifies the Euclidean distance (CIE76) between each calibrated CIE L*a*b* (LAB) values and the ideal color reference in LAB space.

RESULTS

The model demonstrated notable proficiency in object detection and showed consistent convergence, with box, classification and distribution focal loss steadily decreasing with

increasing epochs. For segmentation, the Segment Anything Model (SAM) v1 configured with the Vision Transformer–Huge (ViT-H) architecture, delivered accurate instance-level segmentation. A comprehensive comparison of discrimination power and measurement precision between D-score and visual rating revealed consistent superiority of the image-derived metric across all evaluated parameters. D-score demonstrated significantly higher discriminating power, with an F-statistic of 10.01 compared to 8.24 for visual rating, representing a 21.48% improvement. The eta-squared (η^2) values further confirmed this advantage, with D-score explaining 90.3% of the total phenotypic variance compared to 78.9% for visual rating, a 14.5% improvement in variance explained by genotypic differences. The mean coefficient of variation was 11.63% for D-score compared to 15.85% for visual rating, indicating 26.6% better measurement consistency. The separation index, which integrates both discrimination and precision into a single metric, was 4.91 for D-score compared to 3.78 for visual rating, a 29.8% improvement. The scatter plot relating visual rating to D-score (Figure 1) demonstrates the enhanced resolution of the image-based approach in detecting subtle phenotypic differences that visual assessment cannot reliably capture.

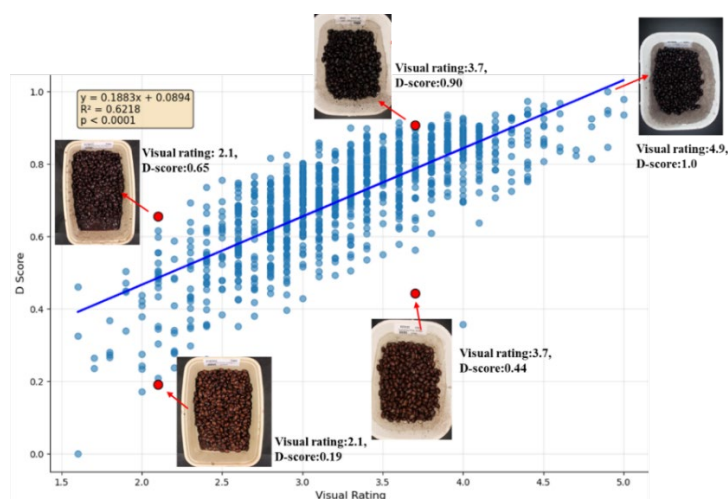


Figure 1: Relationship between visual rating and D_Score for dry bean canning color. Each point represents a genotype mean across environments, with example genotypes are highlighted in red to illustrate cases where visual ratings assigned similar scores, but D_Score captured substantial differences in color intensity and uniformity.

CONCLUSION AND NEXT STEPS

In this study, we developed a novel objective metric for dry bean canning color evaluation which can significantly decrease cost, reduce subjectivity and bias in the analysis. The canning color evaluation using proposed workflow can enhance the selection accuracy of breeding materials and consequently increase the rate of genetic gain. The workflow will be expanded to the other high-throughput objects, instance segmentation such as texture, seed size, seed shape and canning appearance.

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NOTICE OF NAMING AND RELEASE OF AD 1, A HIGH YIELDING AND DISEASE RESISTANT AZUFRADO COMMON BEAN CULTIVAR

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INTRODUCTION. The Valle del Guadiana Experiment Station of the Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP; National Research Institute for Forestry, Agriculture and Livestock) announces the naming and release of AD 1, a new azufrado (sulfur, yellow) improved common bean cultivar. This new common bean variety has a determinate erect growth habit (type I; CIAT, 1984) and is considered a well-adapted and high yielding cultivar for irrigated and high-rainfall areas (> 450 mm) in the Highlands of México. At this region AD 1 was considered as disease-resistant (CIAT, 1987), especially to anthracnose [*Colletotrichum lindemuthianum* (Sacc. & Magnus) Lambs. Scrib.] and rust [*Uromyces appendiculatus* (Pers.) Unger. var. *appendiculatus*]. AD 1 was tested as the common bean improved line AZ16010 in Durango and Aguascalientes, originated from a triple modified cross (AGS466/AZR87//NAVAR74//NAVARB/CAN101) made in 2011 at the Valle del Guadiana Experiment Station in Durango, México. The cross was developed to improve the drought susceptibility and low disease resistance registered in azufrado cultivars (Higuera and Adufrado Pimono 78) when are sown in the Highlands of México.

Ags466 (Aguascalientes 466) is a mid-season bayo (yellow) common bean cultivar with indeterminate (type III) growth habit adapted to the Highlands of México, also showing wide adaptation, phenological plasticity and drought resistance. Despite the seed shape observed in Ags466, the seed coat color is similar to that registered in the azufrado type cultivars, also showing disease resistance specially to anthracnose and rust. Adufrado Regional 87 (AZR87) possesses the typical seed shape, color and size of the azufrado cultivars mainly cultivated in Sinaloa, México. NAVAR74 and NAVARB are selected lines collected in Sinaloa and Nayarit, both showing typical seed color, shape and size of the azufrado and peruano cultivars. Canario 101 is an early season cultivar with determinate growth habit and stems ending in reproductive organs (flower buds, flowers, pods and seeds) and large seeds with rectangular-cylindrical shape. It was considered as a gene source for early maturity and high seed size (37-46 g/100 seeds). The crossing plan included increments for drought tolerance, disease resistance and higher seed size, maintaining an erect canopy of the plants, and to strength the slow darkening capability of the seeds.

In 2012, the F₁ plants ((AGS466/AZR87//NAVAR74//NAVARB/CAN101)-1) were bulk advanced under field conditions in the State of Durango, located in the Semi-arid Highlands of México. In 2013, the F₂ population was sown directly in the field at CEVAG-Durango experiment station and individual F_{2:3} plants were selected considering the plant vigor, pod load, disease resistance and grain quality (seed size and color). Multiple plants were selected, including [((AGS466/AZR87//NAVAR74//NAVARB/CAN101)-1)-42]. During 2014 and 2015, the outstanding F_{3:4} plant [(((AGS466/AZR87//NAVAR74//NAVARB/CAN101))-1)-42-1)] was

selected in the observation nursery considering its phenological adaptation, disease resistance, yield (pod load) and seed commercial quality.

In 2016, uniform traits were observed in the selected population, and the improved line was coded as (AZ16010) that was extensively tested under irrigated conditions in the State of Durango and Aguascalientes (trials were conducted at locations above an elevation of 1,800 m). AZ16010 was selected for its favorable agronomic traits, yield performance, and seed quality under 18 environments studied from 2014 to 2025. In all the experimental and commercial plots established under irrigated conditions, AZ16010 recorded high yields averaging 1,985 kg/ha, ranging from 640 kg/ha to 3,184 kg/ha. During 2025, AZ16010 was registered as AD 1 and grown in semi-commercial plots (1 ha) established under irrigated conditions at INIFAP's experiment station in Durango, reaching an average yield of 3,184 kg/ha. The seed size of AD 1 averaged 42 g/100 seeds, and the highest value was registered in 2025 reaching 46 g/100 seeds. Cultivar used as control (Azufrado Higuera) showed low performance, disease susceptibility and low to nil yield. AD 1 has intermediate growth cycle (matures 104 days after sowing), is photoperiod neutral and produces large seeds (42 g/100 seeds) with sulfur color (dense yellow) and slow darkening seed coat, which extend the shelf life of the grains. Farmers stated that require common bean varieties such as AD 1 to increase production diversity, improve grain quality, and promoting the commercialization process of common beans produced in north-central México. The breeder and foundation seed classes are produced and maintained by the INIFAP's Valle del Guadiana Experiment Station in Durango, México. For further information and request of small free seed samples for experimental purposes, please contact: Dr. Rigoberto Rosales-Serna. Carretera Durango-El Mezquital km 4.5. Durango, Dgo., México. C. P. 34170. Tel. (52) 5538718700, 01 (800) 088-22-22. Ext. 82714.

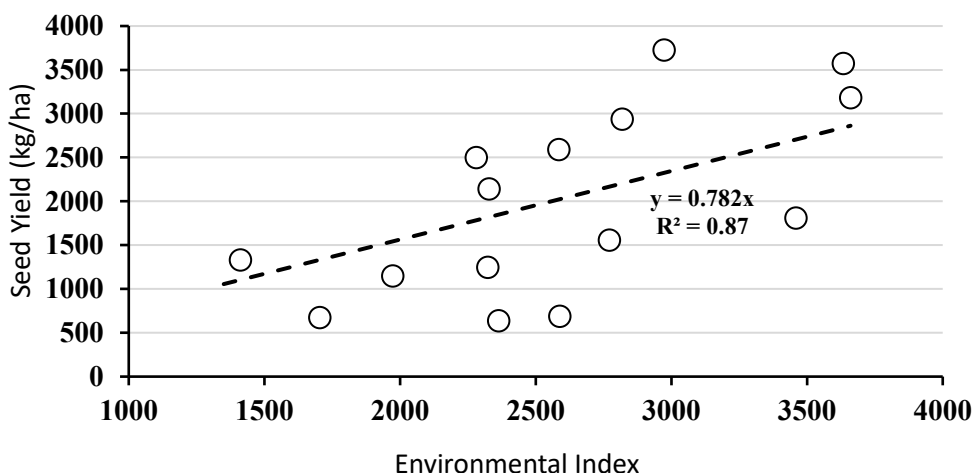


Figure 1. Seed yield for the common bean variety AD 1 sown in 18 irrigated environments (2014-2025) in Durango and Aguascalientes, México.

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COMMON BEAN PRODUCTIVE PREFERENCES IN THE STATE OF DURANGO MÉXICO

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INTRODUCTION. Pinto Saltillo common bean (*Phaseolus vulgaris* L.) cultivar is the most used cultivar in commercial plantings established in the Semi-arid Highlands of México. This cultivar is used by farmers to produce food and forage (vegetative residues), generating economic resources throughout the year. Pinto Saltillo has improved the farmers income obtaining high seed yield and an increased negotiation time period because the extended shelf life of the grain, showing slow darkening seed coats. Pinto Saltillo showed a high adoption level and persistence of use in commercial plantings in north-central México, mainly in the states of Durango and Chihuahua (Ávila *et al.*, 2011). Actually, Pinto Saltillo acceptance has expanded to eleven states in the Highlands and Dry Tropics of northern and central México. Negro San Luis and in a lesser extent Negro Querétaro are another important common bean cultivars sown in wide areas due to its prolonged shelf life and preference in the markets of Central and Southern México, helping to farmers during the marketing process. The bayo and pinto commercial classes, including several common bean cultivars (Bayo Blanco, Bayo Rata and Bayo Criollo, as well as Pinto Nacional, Pinto Burro, Pinto Mantequilla, and Pinto Español) are preferred by old farmers and consumers due to its traditional taste. Federal Government of México implemented in Durango and other states, the Program of Escuelas de Campo (ECA) para Productores (Field Schools for Farmers: FSF), including technical support and on-site training for the production of common bean and other crops. Free selection of crops and cultivars is permitted to the members of the FSF to improve food supply and to increase the family income. The objective of this work was to analyze the preference of common bean cultivars in the FSF implemented in the state of Durango located in the Semiarid Highlands of north-central México.

MATERIALS AND METHODS. Seed samples (500 g) were obtained in several ECA implemented in Durango by the Federal Government of México. Common bean and the other crop cultivars used in each FSF were free selected by local members without external influence. Selected species and cultivars were sown in 2025 in each FSF implemented at different municipalities of Durango in north-central México. Under irrigated conditions the plantings were performed in the period from June 24th to July 10th while under rainfed conditions the sowings were performed from July 10th to August 05th, due to rain irregularity. During the harvest season (October-November, 2025) random FSF were visited and small samples of common bean cultivars were donated by FSF members before they start the commercialization process. Samples were identified and separated by cultivar with the help of common bean experts at INIFAP-CEVAG experiment station in Durango, México. Descriptive statistic was used; cultivar frequency was calculated and histogram constructed by using the Excel computer program.

RESULTS AND DISCUSSION. Pinto Saltillo was the preferent common bean cultivar sown in Durango (54%), followed by Negro San Luis (also known as Negro Bola) and Negro Querétaro (Figure 1). Landrace cultivars known as Pinto Español and Bayo Mexicano were collected in a

FSF isolated (Simón Bolívar-San Juan de Guadalupe) from the main common bean producing area, known as ‘Los Llanos’ region. Since 2005, an upward trend for the total area planted with Pinto Saltillo has expanded in Durango despite an overall decline in common bean acreage, which fell from 347,000 to 150,000 hectares under rainfed conditions (SIAP, 2026) and dropped by 63% under irrigation. This shift is driven by a preference for forage and industrial crops—including corn (*Zea mays*), oats (*Avena sativa*), alfalfa (*Medicago sativa*), sorghum (*Sorghum bicolor*), pine (*Pinus greggii*), and maguey cenizo (*Agave durangensis*). Consequently, bean cultivation has been displaced to marginal areas with poor soils and low rainfall, negatively impacting productivity and seed size. Pinto Saltillo’s persistence in Durango has improved seed yield, grain quality, and commercialization. Key attributes such as slow darkening and shorter cooking times fueled its expansion across Mexico, establishing a distinct "Pinto Saltillo" market class to differentiate it from rapid-darkening varieties like Pinto Nacional and Pinto Villa. Additionally, Negro San Luis remains a viable alternative due to its long shelf life and profitability during production deficits in central and southern Mexico.

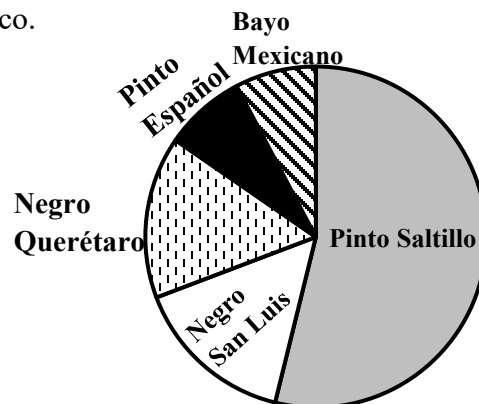


Figure 1. Cultivar preference for common bean grain production in Durango, México.

During the period from 2021 to 2023, 78% of the planted area and 81% of the common beans produced in the state of Durango were obtained with Pinto Saltillo variety. Common beans need to be considered as an important component to recover degraded soils, also achieving ecological sustainability in agricultural production carried out in Durango. Expansion of cultivated area planted under irrigation is recommended to increase yield and stability of common bean production in Durango.

CONCLUSIONS. The persistence (2005 to 2025) of use for Pinto Saltillo common bean variety in Durango and other common bean-producing states of México exceeded the expectations. Characteristics associated with preference of this common bean variety included disease tolerance, high seed yield, extended shelf life, and reduced cooking time. The productive, preference and commercial impact of this improved variety influenced government agricultural production and food market statistics, which included a new commercial category called “Pinto Saltillo”.

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YIELD RESPONSE OF COMMON BEAN BRED LINES SELECTED IN THE BREEDING PROGRAM DEVELOPED IN DURANGO, MÉXICO

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INTRODUCTION. Important success has been obtained in the common bean breeding program established at Valle del Guadiana Experiment Station (INIFAP). Increased levels for common bean drought tolerance, disease resistance, seed yield and grain quality have been achieved during sixty-year period. Drought tolerance has been obtained by phenological plasticity and accelerated recovering after a drastic environmental event. Aggravated problems were observed due to environmental variations throughout the year and production areas (Rosales *et al.*, 2025). Modernization implemented in agriculture machinery also affected the genetic breeding objectives, due to that common bean plant morphology is related to efficiency during the weeding and harvest. Improved seed quality is also necessary due to market, consumer and health programs requirements. The objective was to evaluate eight improved lines showing outstanding response in yield trials established under diverse environmental conditions in the state of Durango, México.

MATERIALS AND METHODS: A group of eight improved common bean lines were planted in Durango on June 24th, 2025: pinto (PT, 1), flor de mayo (pink, FM, 3), opaque black (NGO, 3) and azufrado (sulfur, AZ, 1). Improved lines were compared to commercial controls (Negro San Luis, Pinto Saltillo, PID 1, PID 2 and AD 1). A Randomized Complete Block Design (RCBD) was used, with a sampling plot of two 5 m rows, 0.81 m apart (8.1 m²) and five replications. Fertilizer was applied in the dose of 35-50-00 (N-P₂O₅-K₂O). One drone application was also performed by mixing 3 L of UAN 32 (32-00-00) + 3 L Fertigro P (08-24-00). Weed control was achieved by mechanical weeding (2), one hand weeding, one broad leave herbicide application (Fomesafen), and two localized herbicide mix (Fluazifop-p-butyl, and clethodim) applications. Three insecticide applications were made (spinetoram and dimethoate) for the control of Mexican bean beetle (*Epilachna varivestis*) and pod weevil (*Trichapion* spp.). One irrigation was applied to avoid severe water stress in the common bean plants during the flowering stage (R₆). Register was performed for the days to first flower (DFF), disease response (CIAT, 1987), days to physiological maturity (DPM), yield, and the weight of 100 seeds. The cooking time was evaluated at the laboratory using the Mattson Method (Rosales *et al.*, 2025). The data was analyzed under a RCBD design with five replications for field traits and two replications for cooking time (SAS ver. 9.4).

RESULTS AND DISCUSSION: Average values for DFF and DPM were 48 and 107 days after sowing (DAS), with interval from 40 to 56 DAS and 92 to 115 DAS, respectively (Table 1). Results showed that a favorable environmental condition for common bean production was registered during 2025. Environmental conditions favored the full-season cultivars thus early maturity cultivars and improved lines (AD 1 and AZ17023) registered low yield related to water stress effects (R₆). No symptoms were registered for anthracnose (*Colletotrichum lindemuthianum*) and rust (*Uromyces appendiculatus* var. *appendiculatus*); while common bacterial blight

(*Xanthomonas campestris* = *axonopodis* var. *phaseoli*) showed moderate (4) to generalized (6) symptoms. Significant differences were observed for seed yield, seed weight and cooking time. The full-season cultivar Negro San Luis (4,095 kg/ha) and the opaque-black improved lines NGO14014 (3,974 kg/ha), NGO14013 (3,919 kg/ha) and PT220142 (3,860 kg/ha) showed high seed yield. High average for seed weight was observed for PT22042 (39.5 g/100 seeds), PID 1 (37.8 g/100 seeds), AD 1 (37.8 g/100 seeds) and FM14011 (37.3 g/100 seeds). The lines with opaque black grains represent an option in this market class where values close to 25 g/100 seeds are preferred.

Table 1. Mean values for traits evaluated in common bean bred lines and cultivars sown under irrigation in Durango, México. 2025.

Variety/Line	¹ DFF	A	R	B	DPM	Yield kg/ha	100SW (g)	Cooking Time (min)
N. San Luis	52	1	1	5	115	4,095 ^a	35.3 ^{bc}	70 ^{abcd}
² NGO14014	56	1	1	5	115	3,974 ^a	31.5 ^d	61 ^{bcd}
NGO14013	52	1	1	4	115	3,919 ^{ab}	28.6 ^e	72 ^{abcd}
PT22042	48	1	1	5	111	3,860 ^{abc}	39.5 ^a	64 ^{abcd}
Pinto Saltillo	46	1	1	5	104	3,459 ^{abcd}	35.1 ^{bc}	57 ^{cd}
FM14002	51	1	1	5	110	3,437 ^{abcd}	36.5 ^{bc}	93 ^{ab}
Pinto Villa	51	1	1	5	112	2,950 ^{bcde}	35.7 ^{bc}	89 ^{abc}
PID 1	42	1	1	6	104	2,920 ^{cde}	37.8 ^{ab}	96 ^a
FM14011	53	1	1	5	111	2,676 ^{de}	37.3 ^{ab}	84 ^{abc}
NGO16029	44	1	1	5	102	2,551 ^{de}	23.6 ^f	65 ^{abcd}
FM17001	44	1	1	6	104	2,265 ^e	33.9 ^{cd}	57 ^{cd}
AD 1	42	1	1	6	95	1,030 ^f	37.8 ^{ab}	46 ^d
AZ17023	40	1	1	6	92	353 ^f	32.0 ^d	58 ^{cd}
Mean	48	1	1	5	107	2,884	34.2	70

¹DFF= days to first flower, A = anthracnose, R = rust, B = Common Bacterial Blight, DPM = days to physiological maturity, 100SW = 100 seeds weight. ²NGO = small opaque black, PT = pinto, FM = flor de mayo and AZ = azufrado.

^{a-f}Different letters in the column denote significant differences based on Tukey ($p \leq 0.05$).

Higher values for cooking time were observed for PID 1 (96 min) and FM14002 (93 min). In contrast the AD 1 cultivar registered the lowest cooking time (46 min) and differences were related to genetic origin and environmental effects.

CONCLUSIONS: Outstanding improved lines and cultivars were selected, showing similar traits to the commercial varieties. The seeds of PT22042 were larger in size compared to Pinto Saltillo, which can improve the commercial value and marketing pinto common beans. The evaluated lines registered low cooking time considering values registered in some control cultivars. Advance has been obtained by the breeding program established in Durango, México, identifying highly productive lines in market classes preferred in México.

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PRODUCTIVE IMPORTANCE OF NATIVE AND IMPROVED CULTIVARS OF COMMON BEAN IN THE SEMIARID HIGHLANDS OF MÉXICO

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INTRODUCTION. The arid and semiarid lands of the “Comarca Lagunera” includes part of the states of Durango and Coahuila in north-central México. Agriculture activities are performed using well water, dam irrigation, and the use of temporal water currents. Common bean native, traditional bred and modern improved cultivars are cultivated in Los Llanos region and other productive areas of Durango, located in the Arid and Semiarid Highlands of México (Rosales *et al.*, 2025). Some native cultivars such as Negro San Luis and Flor de Mayo Media Oreja are appreciated by farmers due to its wide adaptation, seed availability and high yield potential. Similar traits were observed in cultivars developed in the early stages of genetic breeding program (traditional bred varieties), such as Río Grande and Negro Querétaro, exception was Pinto Nacional showing precocious maturity, drought tolerance and stress escape-avoidance traits. Modern cultivars such as Pinto Villa (1991), Pinto Saltillo (2001) and Pinto Centauro (2011) show different adaptation mechanisms to drought stress, including early maturity and phenological plasticity, also showing high seed quality. Productive balance needs to be done to evaluate genetic advances obtained in the breeding program developed at the Valle del Guadiana Experiment Station (INIFAP). A yield trial was implemented in Durango including common bean germplasm at different evolutive level: native (landrace), early breeding varieties and modern cultivars. The objective was to evaluate productive importance of native and improved cultivars of common bean in the Arid and Semiarid Highlands of México.

MATERIALS AND METHODS: A group of twelve common bean native and improved lines and cultivars with different commercial types of grain were planted from July 24th to July 28th 2025 at four locations of the semiarid and arid regions of the state of Durango. Cultivars in each site were selected according to farmer’s criteria in order to obtain grain for self-consumption and for sale at regional markets. Technical support was provided during production process mainly for fertilizer application at the doses 25-30-00 (N-P₂O₅-K₂O) under rainfed and 35-50-00 for irrigated conditions. Exception was Poanas, where agroecological management was applied using organic amendments. Weed control was reached by two mechanical weeding, complemented with one hand weeding. In Huarichic, one irrigation was applied to avoid severe water stress in the common bean plants. Data was taken for days to physiological maturity (DPM), seed yield and 100 seeds weight (P100S). Samples were taken using a sampling-plot of two 5 m long rows, 0.81 m apart (8.1 m²) and five replications. In each planting site, the obtained data was analyzed under a Completely Randomized Design (CRD) with three replications. The comparison of means was carried out with the Tukey test ($p \leq 0.05$) (SAS ver. 9.4).

RESULTS AND DISCUSSION: Values for DPM varied from 75 days after planting (DAP, for AD 1 at La Granja) to 100 DAP for Pinto Saltillo at Poanas, Dgo. Variations in maturity were related to values of annual mean temperature registered in Poanas (18 °C) compared to Ceballos, Dgo. (20 °C), thus reduction of biological cycle was observed in the arid region of Durango. High seed yield was observed in Huarichic, with an average of 866.0 kg/ha, and Pinto Centauro showed high seed yield (880.9 kg/ha), resulting similar to the control (Pinto Villa, 851.1 kg/ha). The PID

2 cultivar showed higher seed yield at La Granja (700.1 kg/ha) and Poanas (938.7 kg/ha). Other outstanding lines and cultivars were AD 1, NGO14013, NGO14014 and PID 1. Native (Negro San Luis and Flor de Mayo Media Oreja) and introduced cultivars (Pinto Americano) registered low seed yield, due to its full-season growth cycle, drought stress and poor adaptation under production system implemented in Ceballos, Dgo.

Highly significant differences were observed for the weight of 100 seeds only in La Granja, due to an increased number of cultivars and improved lines. The highest average weight was observed for PID 2 (33.3 – 36.3 g/100 seeds), which was statistically equal to the PID 1 used as a control (32.1-34.6 g/100 seeds), and AD 1 (32.5 g/100 seeds). The lines with opaque black grains (NGO) showed low values for grain weight, although this was related to preferences in this market class (25 g/100 seeds).

Table 1. Mean values for traits evaluated in common bean bred lines and cultivars sown in four locations of Durango, México. 2025.

Line/Variety	¹ DPM	Seed Yield (kg/ha)	P100 Seeds (g)
		La Granja, Simón Bolívar	
PID 2	90 ^a	700.1 ^a	33.3 ^a
AD 1	75 ^c	666.7 ^{ab}	32.5 ^a
NGO14013	85 ^b	647.1 ^{ab}	26.4 ^b
NGO14014	85 ^b	647.5 ^{ab}	27.0 ^b
NOD 1	90 ^a	586.8 ^b	27.0 ^b
PID 1	90 ^a	458.0 ^c	32.1 ^a
Negro San Luis	90 ^a	441.6 ^c	22.8 ^b
Mean	86	593.5	28.7
		Huarichic, Lerdo	
Pinto Centauro	85	880.9	31.2
Pinto Villa	85	851.1	30.5
Mean	85	866.0	30.9
		Ceballos, Mapimí	
Pinto Americano	90	458.2	27.0
Flor Mayo Media Oreja	90	333.2	26.4
Mean	90	395.7	26.7
		Poanas	
PID 2	95	938.7 ^a	36.3
PID 1	95	805.7 ^{ab}	34.6
Pinto Saltillo	100	745.3 ^c	33.1
Mean	97	829.9	34.7

¹DPM = Days to physiological maturity. ^{a-c}Different letters differs according to Tukey (p ≤ 0.05).

CONCLUSIONS: Outstanding improved lines and cultivars were identified in the arid and semiarid region of the state of Durango. PID 2, PID 1, AD 1 and lines NGO14013 and NGO14014 showed adaptation in drought-prone areas. INIFAP's common bean breeding program developed highly productive cultivars and improved lines in the most important common bean market classes consumed in Mexico.

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SEED PRODUCTION FOR PREFERENT COMMON BEAN CULTIVARS IN THE SEMIARID HIGHLANDS OF MÉXICO

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INTRODUCTION. Seed requirement of common bean native, traditional bred and modern improved cultivars was observed in Los Llanos and other productive areas of the state of Durango, in the Arid and Semiarid Highlands of north-central México. Some native cultivars such as Negro San Luis are appreciated by farmers due to its wide adaptation and high yield potential. Similar traits were observed in cultivars developed in the early stages of genetic breeding program (traditional bred varieties), such as Río Grande and Pinto Nacional. Seed of modern cultivars such as Pinto Saltillo are also required to improve quality of grain produced in north-central México. Seed productive potential start with yield obtained under favorable conditions of irrigation and high soil fertility. A yield trial was implemented in Durango including preferent common bean cultivars for farmers, representing different evolutive level: native (landrace), early breeding phase (traditional varieties) and modern cultivars. The objective was to evaluate seed productive importance of common bean native and improved cultivars in the arid and semiarid highlands of México.

MATERIALS AND METHODS: A group of ten common bean native and improved cultivars with different commercial grain type were planted on June 24th 2025 in Valle del Guadiana Experiment Station at Durango, México. Cultivars were selected according to farmer's demand for certified seed to improve yield and quality of common bean grain produced in Durango. A Randomized Complete Block Design (RCBD) was used, with a sampling plot of two 5 m rows, 0.81 m apart (8.1 m²) and eight replications. Fertilizer was applied using the dose 35-50-00 (N-P₂O₅-K₂O) (INIFAP, 2017). One drone application was also performed by mixing 3 L of UAN 32 (32-00-00) + 3 L Fertigro P (08-24-00). Weed control was achieved by two mechanical weeding, one hand weeding, one broad leave herbicide application (Fomesafen), and two localized herbicide mix (Fluazifop-p-butyl, and clethodim) applications for grass control. Three insecticide applications were made (one spinetoram and two dimethoate) for the control of Mexican bean beetle (*Epilachna varivestis*) and pod weevil (*Trichapion godmani*). One irrigation was applied to avoid severe water stress in the common bean plants during flowering stage (R₆). Data was collected for the number of days to first flower (DFF), disease response (CIAT, 1987), days to physiological maturity (DPM), yield, and the weight of 100 seeds. The data obtained was analyzed under a RCBD design with five replications. The comparison of means was carried out with the Tukey test ($p \leq 0.05$). The analysis of variance and mean comparison were performed with the SAS ver. 9.4 computer program.

RESULTS AND DISCUSSION: Values for DFF varied from 40 (Bayo Gordo) to 62 (Canario Magón) days after planting (DAP). The number of days to physiological maturity varied from 92 (Bayo Gordo) to 115 DAP for Canario Magón. Variations in maturity were related to values of

mean the number of days to first flower, and genetic origin of the cultivars. Early cultivars belong to Durango genetic race (Santana *et al.*, 2022). Most of the cultivars showed no symptoms for anthracnose (*Colletotrichum lindemuthianum*) and rust (*Uromyces appendiculatus* var. *appendiculatus*); while for common bacterial blight (*Xanthomonas campestris* = *axonopodis* var. *phaseoli*) moderate (4) to generalized (6) symptoms were registered. High seed yield average was observed in a group of cultivars including Pinto Saltillo, Río Grande and Negro San Luis. Native cultivars (Canario Magón and Vaquita Negro) registered low seed yield, due to its full-season growth cycle and poor adaptation under production systems implemented in Durango, Dgo. Highly significant differences were observed for the weight of 100 seeds, due to germplasm diversity including varieties from two genetic races (Durango and Jalisco). The highest average weight was observed in Ojo de Pato (duck eye) (52.6 g/100 seeds), which was statistically equal to Bayo Gordo (47.2 g/100 seeds) and Sangre de Toro (44.6 g/100 seeds). The Río Grande and Canario Magón grains showed low values for grain weight, although this was related to preference for market in these commercial classes (< 30.0 g/100 seeds).

Table 1. Mean values for traits evaluated in common bean native and bred cultivars sown for seed production under irrigated conditions in Durango, Dgo. 2025.

Línea/Variedad	DFF	A	R	B	¹ DPM	Seed Yield (kg/ha)	P100 Seeds (g)
Pinto Saltillo	46	1	1	5	102	3,458.6 ^a	35.1 ^c
Río Grande	56	1	1	4	114	3,302.7 ^a	26.5 ^e
Negro San Luis	53	1	1	5	114	3,051.7 ^a	32.8 ^c
Pinto Villa	42	1	1	6	96	2,949.9 ^a	35.7 ^c
Pinto Nacional	43	1	1	6	106	2,857.1 ^a	31.4 ^c
Sangre de Toro	51	1	1	5	107	2,609.6 ^b	44.6 ^b
Ojo de Pato	53	1	1	5	114	2,416.0 ^{bc}	52.6 ^a
Bayo Gordo	40	1	1	6	92	1,789.0 ^c	47.2 ^b
Canario Magón	62	2	1	5	115	1,299.3 ^c	24.5 ^e
Vaquita Negro	50	1	1	6	104	1,182.4 ^c	31.5 ^c
Mean					97	2,433.8	34.7

¹DPM = Days to physiological maturity. ^{a-c}Different letters differs according to Tukey (p ≤ 0.05).

CONCLUSIONS: Improved cultivars showed higher yield and possibilities for successful seed production under irrigated conditions in Durango, Dgo. Adequate agronomic management favored high seed weight related to an increased seedlings emergence capacity and vigor, as well as rapid seedling establishment. The best options for seed production in Durango were Pinto Saltillo and Negro San Luis; followed by Pinto Villa, Pinto Nacional and Río Grande.

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PROMISING GERMPLASM FROM AN INTERSPECIFIC DIVERSITY PANEL

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INTRODUCTION

Common bean, *Phaseolus vulgaris*, shows limited genetic diversity for tolerance to abiotic stress, such as heat, drought, and salinity, while tepary bean (*P. acutifolius*) is an important genetic reservoir of both abiotic and biotic stress tolerance. Previous efforts have resulted in interspecific-derived (*P.v./P.a.*) lines introgressing traits such as common bacterial blight (Singh and Muñoz, 1999), bruchid (Kusolwa and Myers, 2011) resistance and heat tolerance (Cruz et al., 2023) into common bean. The goal of this effort was to develop an interspecific *P.v./P.a.* diversity panel (IDP) with the G40001 (TDP001) tepary bean as the source of unique traits and to identify lines with superior performance.

MATERIALS AND METHODS

The interspecific cross of ICA Pijao, a Middle American common bean with black seed type, as the female parent and the cultivated white-seeded tepary Frijol Bayo (G40001), for which the tepary reference genome was developed, was completed at Michigan State University using embryo rescue (Soltani et al., 2020). The F₁ was backcrossed to ICA Pijao and the F₁ advanced to the F₂ at MSU. The F₂ progeny of this backcross were then crossed to a set of elite Middle American common bean varieties and breeding lines at ARS in Mayaguez, PR. The lines developed from these crosses were advanced, selected for adequate maturity and architecture, agronomic traits, and seed yield under a variety of conditions. Superior performers from these lines, as well as additional interspecific and check lines, were then selected to form the IDP, composed of 188 lines. These were advanced and bulked for field testing.

The IDP, and then subsets of superior performers, were evaluated in 6 field trials: in Isabela, PR under heat in 2023 (E1) and under combined heat, low fertility and root rot in 2023 (E2), and under drought (E3, E4) and “non-stress” (E5, E6) in Juana Diaz in 2024 and 2025, respectively. Seed yield was evaluated as kg ha⁻¹. The METAN-R program was used to calculate BLUPs, conduct an additive main effects and multiplicative interaction (AMMI) analysis, and produce the GGE biplot on yield in these multiple-year and environment trials.

RESULTS AND DISCUSSION

Performance was evaluated based on yield in the IDP under the non-stress and abiotic (heat and drought) and biotic (root rot) conditions in Isabela and Juana Diaz, Puerto Rico. In a combined analysis, one of the lines that showed superior performance was IDP111. IDP111 was developed from Int(F₂)-2 GC, an F₂ developed from the Ica Pijao/G40001/Ica Pijao backcross at Michigan State U., which was then crossed to ‘Beniquez’ and MCS 1325-41 at ARS-PR resulting in the pedigree Ica Pijao/G40001/Ica Pijao///Beniquez/4/MCS 1325-41. The line was then tested as a F₅ derived line and has a small dark red seed type.

The AMMI PC1 by yield biplot shows IDP111 (G23, Figure 1a) as the highest yielding line that performed particularly well under the non-stress, higher yielding environments E5 and E6, but also under stress. The GGE biplot (Figure 1b) shows the genotype and genotype-by-environment interaction for the 6 trials showing the mean yield across environments for IDP111 (G23). Genotypic performance grouped the lower yielding E3 (Drought) Juana Diaz environment with the Isabela environments (E1 and E2), while the Isabela trials were conducted in the higher temperature summer season and on a distinct oxisol (Isabela) versus mollisol (Juana Diaz) soil type.

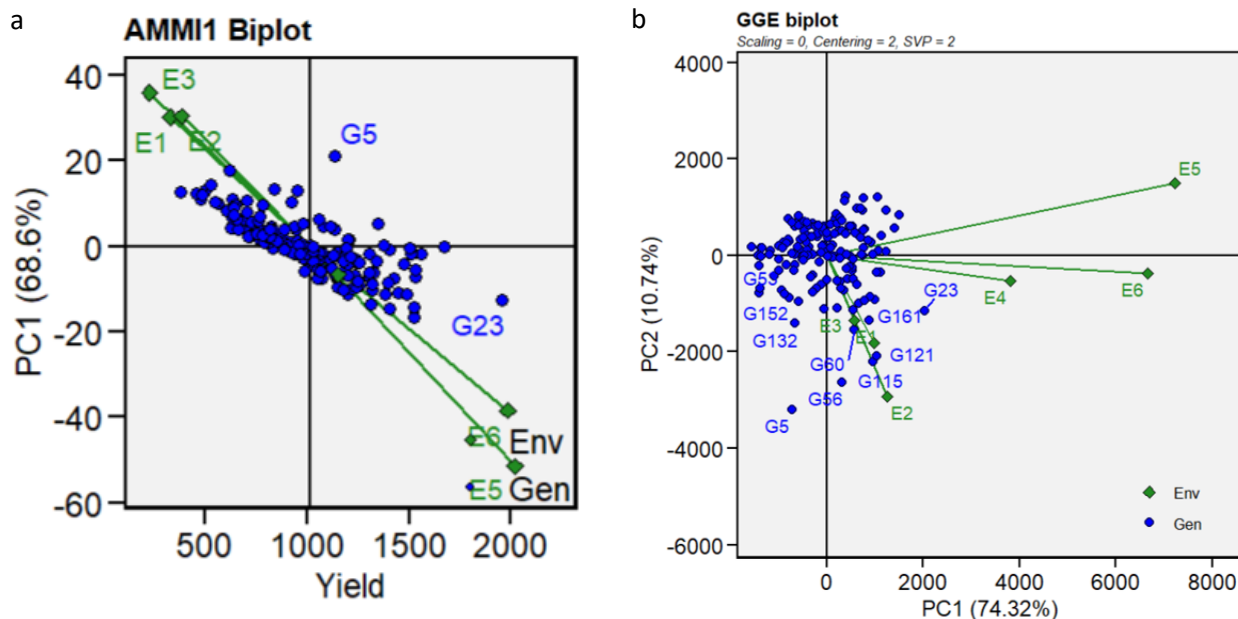


Figure 1. (a) AMMI analysis showing the biplot of yield (kg ha^{-1}) versus PC1 and the GGE biplot (b) showing the environment vectors (E) and the response of each line (G).

CONCLUSIONS

IDP111 is a high yielding interspecific-derived line from this study that may be useful for common bean improvement. Further genotyping and GWAS will be used to determine the genetics of elevated yield performance in the IDP under stress and non-stress conditions and the *P. acutifolius* or *P. vulgaris* source(s) of this and other traits.

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YIELD POTENTIAL OF CYCLE I LINES DERIVED FROM THE UFV BLACK COMMON BEAN RECURRENT SELECTION PROGRAM

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) stands as a global cornerstone of plant-based nutrition, underpinning food security for socio-economically marginalized populations (Uebersax et al., 2022). In Brazil, the crop is highly relevant, with black beans accounting for approximately 26% of the national production in the 2024/25 harvest, totaling around 811,000 tons (CONAB, 2026). Despite this, the national average yield, approximately 1,600 kg ha⁻¹, remains low compared to the crop's yield potential. Against this backdrop, plant breeding emerges as a pivotal approach for sustainable grain yield enhancement (Cordoba-Novoa et al., 2025). Recurrent selection, in particular, acts as a powerful driver, systematically concentrating favorable alleles within populations (Chagas et al., 2025). Therefore, this study aimed to select the top 10 superior black bean lines from the Recurrent Selection Program at the Federal University of Viçosa (SRFP-UFV) to constitute future Value for Cultivation and Use (VCU) trials in Minas Gerais.

MATERIALS AND METHODS

Forty-four black bean lines (VP1 to VP44) from Cycle 1 of the SRFP-UFV, along with five commercial cultivars used as checks (BRS FP403, Ouro Negro, IPR Uirapuru, BRS Esteio, and BRS Valente), were evaluated for grain yield (PROD - kg ha⁻¹). The experimental design was a 7x7 triple lattice. Plots consisted of two 2-meter rows spaced 0.5 m apart. The experiment was conducted in the municipality of Coimbra, MG (20° 49' 44'' S, 42° 45' 56'' W, elevation 713 m), during the 2025 dry season. Data were subjected to analysis of variance (ANOVA) using R software. Genotype and replication effects were considered fixed, while blocks within replications and residual effects were considered random. Additionally, the Least Significant Difference (LSD) was calculated, and the 10 lines with the highest agronomic potential were identified.

RESULTS AND DISCUSSION

The lines presented adjusted means for PROD ranging from 2,960 to 5,165 kg ha⁻¹, with the top 10 performing lines exceeding 4,664 kg ha⁻¹ (Fig. 1). Among the 10 selected lines, the cultivar BRS Valente ranked fourth, with a mean grain yield of 4,864 kg ha⁻¹. Notably, the 10 selected lines were statistically indistinguishable regarding grain yield (LSD = 1371.93). Among the top 10 lines,

two originated from cross 620 and another two from cross 621. Consequently, these results corroborate the efficiency of the UFV breeding program and indicate promising perspectives for increasing black bean productivity in Minas Gerais.

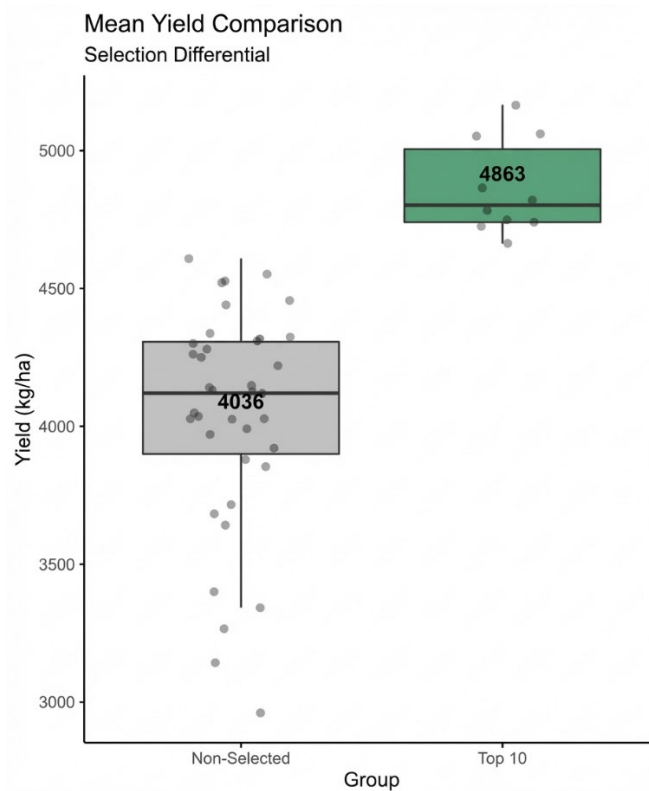


Figure 1. Grain yield kg ha^{-1} of non-selected genotypes and the ten superior black bean lines (Top 10), evaluated during the 2025 dry season in Coimbra, MG.

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POD QUALITY, YIELD AND DISEASE RESISTANCE OF NEW TROPICALLY ADAPTED VEGETABLE RUNNER BEAN LINES

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INTRODUCTION

Runner bean (*Phaseolus coccineus* L), also known as butter bean or scarlet runner bean, has shown considerable promise as a high value export crop. However, its productivity is severely constrained by high production costs due to lack of tropically adapted short-day vegetable varieties that do not require extended artificial lighting to stimulate flowering and pod formation, resistant to major diseases and with market preferred pod traits. Compared with common bean (*Phaseolus vulgaris* L.), runner bean has received relatively little research attention. As a result, there are very few runner bean improvement programs in the world, and virtually none in eastern Africa (Kimani et al, 2009). Consequently, all seed grown by exporting companies in Kenya is imported and expensive. The imported vegetable type varieties meet the consumers demand like taste, shape, tenderness, physical appearance, cooking and eating qualities which are lacking in local varieties produced for grain type for domestic consumption. The University of Nairobi has been developing new *short day* vegetable runner beans which are tropically adapted and can be grown without extended light (Kimani et al, 2019; Mulanya et al 2018 & 2019). The objective of this study was to evaluate new locally developed short-day vegetable runner bean lines for pod quality, pod yield and resistance to diseases.

MATERIALS AND METHODS

Fifty new vegetable runner bean, and one commercial variety were evaluated at Ol-Joro-Orok and Kabete Field Station during the long rain season (March-August). The materials originated from F₅ single plant selections, F₆ progeny rows and F₇ families previously selected at Ol Joro Orok and Kabete Research Stations. The plants were harvested on single plant. Based on pod characteristics, the plants with high pod quality (grade 1 and grade 11), high pod yield and disease resistance were selected. Data was collected on number of racemes, duration to flowering, reaction to diseases, pod length and diameter and pod yield, and analyzed using Genstat software version 14. Scoring for plant vigour and diseases was based on 1 to 9, where 1-3 is resistant/vigorous, 4-6 intermediate and 7 to 9 susceptible/ poor vigour. Ten pods per plot were randomly selected and evaluated for pod length, pod curvature, pod yield and disease resistance. The pods were graded according to fresh produce standard commercial classes (Sunripe, 2013). Pod yield was determined as the cumulative weight from all the harvests. The data was subjected to ANOVA and the means separated by least significant difference (LSD) at P=0.05.

RESULTS AND DISCUSSION

Results showed that there were significant differences among the test lines for pod yield, pod quality and disease resistance (Table 1). Most of the new lines were far better by about 16,000kg ha⁻¹ in pod yield than the commercial variety, White Emergo. e.g. KAB-RB13-1-105/2 (18,354kg ha⁻¹) and KAB-RB13-380-55 (17,163kg ha⁻¹) while White Emergo produced 896 kg ha⁻¹. White Emergo flowered poorly without extended light. At least thirty new lines had straight pods and met market pod length requirement of 18cm. Most of the new lines were resistant to angular leaf

spot, anthracnose, common bacterial blight and rust diseases while the commercial variety was susceptible to angular leaf spot and powdery mildew (Table 1). High pod yield, pod quality and disease resistance of these lines can contribute to increased productivity, reduction in production costs and enhance competitiveness of local products in regional and export markets.

Table 1. Pod yield, grade and disease scores of advanced short-day vegetable runner bean lines grown at two locations in Kenya.

Genotype	Pod traits				Genotype	Disease score*				
	Pod yield (kg ha ⁻¹)	Pods plant ⁻¹	Grade I (%)	Grade II (%)		ALS	ANT ^a	CBB	Powdery mildew	Rust
KAB-RB13-1-105/1	9705.9	10.8	33.9	66.1	KAB-RB13-1-105/1	1	1	1	1	1
KAB-RB13-1-105/2	18353.7	19.6	21.3	78.7	KAB-RB13-1-105/2	2	2	1	1	1
KAB-RB13-1-105/3	10114.1	4.7	93.9	6.1	KAB-RB13-1-105/3	2	1	1	2	1
KAB-RB13-129-121/2	8667.3	10.3	43.8	56.2	KAB-RB13-1-105/4	2	1	1	1	1
KAB-RB13-311-103/1	9027.2	10.9	21.6	78.4	KAB-RB13-129-121/1	1	2	1	1	1
KAB-RB13-331-66/2	9455.6	2.0	20.9	79.1	KAB-RB13-129-121/2	2	2	1	1	1
KAB-RB13-379-33	17162.8	1.3	27.8	72.2	KAB-RB13-138-38	1	2	1	1	1
KAB-RB13-46-22/2	7959.7	2.8	58.8	41.2	KAB-RB13-240-119	1	2	1	1	1
KAB-RB13-471-118/4	7960	7.3	44.0	56	KAB-RB13-294-24	1	1	1	1	1
SUB-RB13-133-80/1	7428.9	8.0	59.7	40.3	KAB-RB13-296-111/1	2	2	1	1	1
SUB-RB13-133-80/2	7763.8	6.4	81.5	18.5	KAB-RB13-296-111/2	1	1	1	1	1
SUB-RB13-234-13/1	8936.1	9.5	11.0	89	KAB-RB13-299-43/1	2	2	1	2	1
SUB-RB13-240-125/1	6664.1	7.3	9.2	90.8	KAB-RB13-299-43/2	1	1	1	1	1
Check					Check					
WHITE EMERGO	895.6	1.0	50	50	WHITE EMERGO	5	2	7	5	1
Mean	356.6	0.4	19.3	31.9	Mean	1.56	1.39	1.19	1.33	1
LSD _{0.05}	146.1	0.2	5.6	5.6	LSD _{0.05}	1.38	0.31	0.23	0.21	0
CV (%)	9.6	10.3	2.8	1.6	CV (%)	45	41.3	35.7	29.2	0

*ALS= angular leaf spot, ANTH-anthracnose, CBB-common bacterial blight

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BREEDING RUNNER BEAN FOR CANNING INDUSTRY IN EASTERN AFRICA

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INTRODUCTION

Canning bean industry in eastern Africa is constrained by inadequate supply of grain because available landraces are low yielding and susceptible to diseases. Demand for canned bean products exceeds supply due to preference for fast cooking off-shelf products, high cost of cooking fuel and population growth. Little has been done to develop improved runner bean varieties for the canning industry due to lack of investment in breeding runner bean and local capacity to assess canning characteristics during variety development. Several new, grain-type runner bean lines with superior agronomic traits were recently developed at the University of Nairobi (Kimani et al, 2019; Mulanya et al, 2018 & 2019). However, their potential for use by the processing industry is not known. The objective of this study was to evaluate the canning quality of the new breeding lines and identify those which meet industry canning criteria and acceptability to consumers.

MATERIALS AND METHODS

Forty-three F_{5.8} lines and the industry reference variety grown at Ol-Joro-Orok Research Station and Kabete Field Station were evaluated for canning quality. The beans were cleaned, soaked, blanched, canned in brine and incubated for seven days, and subsequently evaluated for canning quality attributes including hydration coefficient (HC), washed drained weight (WDWT) and percentage washed drained weight following a modification of procedures described by Khanal et al (2014) and Van der Mwerwe et al., (2006). Laboratory canning and sensory evaluations were conducted at the Pilot Food Processing plant, Department of Food Science, Technology and Nutrition, University of Nairobi. Industrial canning quality was determined by two collaborating food processing factories in Kenya. Physical properties (size, shape, uniformity) and visual appearance properties (splits, clumping and brine clarity) were determined subjectively using seven-point hedonic scale as described by Warsame and Kimani (2014). The data was subjected to analysis of variance, and the means separated by least significant difference (LSD) at P=0.05.

RESULTS AND DISCUSSION

Results showed significant ($P<0.05$) differences in all traits evaluated. The best performers at Kabete were KAB-RB13-327-92/1, KAB-RB13-326-207/1B and KAB-RB13-326-207/1B. However, the best performers at Ol-Joro-Orok were KAB-RB13-471-117/1, SUB-OL-RB13-275-248/3 and KAB-RB13-310-161/5 suggesting a genotype x environment interaction for canning traits. More than 30 lines met or exceeded industry canning standards for runner bean (Table 1). To our knowledge, these are the first grain type runner bean lines designed and bred in east, central, southern and west Africa. Utilization of the new lines can increase productivity, incomes of smallholder farmers, and ensure regular supply and diverse, high quality value-added products for the processing industry and consumers. Data generated provides a baseline for further breeding of runner beans for the canning industry.

Table 2. Summary of canning quality characteristics of the new runner bean lines developed and evaluated at two locations in Kenya.

Trait	Range/Locations		Industry reference variety	Lines $\geq$ reference
	Kabete	Ol-Joro-Orok		
Soakability 16 h (%)	55-155	70-125	115	27
Water uptake after blanching (%)	95-174	111-187	131	31
Hydration coefficient	1.7-2.7	2.1-2.6	2.3	25
Fresh weight to yield solids (g)	111-115	110-112	110	31
Brine pH	5.8-6.0	6.0-6.1	5.7	31
WDWT (g)	253-298	256-312	269	31
PWDWT (%)	59-69	57-73	58	31
Texture (N)	93.7-194	101.9-219	125	16 (31*)
Seed size (score)	3-7	5-7	4	30
Uniformity (score)	1-3	1-3	2	25
Seed shape (score)	1-4	1-5	2	22
Splits (score)	3-7	4-7	6	27
Clumping (score)	5-7	3-7	6	31

WDWT- washed drained weight; PWDWT-percent washed drained weight;

*texture: 31 lines better than 72N standard for beans, and 16 better than industry reference check variety used in Kenya.

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AGRONOMIC PERFORMANCE OF CARIOCA COMMON BEAN LINES FROM THE FIRST CYCLE OF RECURRENT SELECTION AT UFV FOR FUSARIUM WILT RESISTANCE

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) plays a pivotal role in global food security, serving as the primary protein source for developing nations (Ambrósio et al., 2024). Plant breeding is a crucial strategy to address the challenges posed by climate change, food security demands, and economic constraints associated with common bean cultivation (Cordoba-Novoa & Hoyos-Villegas, 2025). In this context, grain yield, upright plant architecture, commercial grain quality, and disease resistance, particularly to Fusarium wilt (*Fusarium oxysporum* f. sp. *phaseoli*), are among the traits of greatest interest in common bean breeding (Ciappina et al., 2026). To simultaneously improve these traits, recurrent selection based on progeny evaluation is a highly effective strategy (Carneiro et al., 2015). Notably, selection should initially prioritize agronomic traits, followed by pathogen resistance tests on advanced lines. This sequence is justified by the need for experimental replicates to mitigate false positives. The genotype-ideotype distance index is a robust strategy for simultaneous selection, using standardized and weighted variables to classify genotypes based on the mean Euclidean distance from a predefined ideotype (Carvalho et al., 2002). Thus, this study aimed to select Carioca bean lines from the first cycle of the Recurrent Selection Program for Fusarium wilt resistance at UFV (SRF-UFV), focusing on agronomic traits of interest to the production chain.

MATERIALS AND METHODS

A total of 393 lines (VC1 to VC393) from the first cycle of the SRF-UFV program and seven checks were evaluated during the 2024 winter crop season in Coimbra, MG (latitude: 20°49'44'' S, longitude 42°45'56''W, altitude 713 m). The experiment was arranged in a 20 × 20 triple lattice design, with plots consisting of one 2-meter row. The evaluated traits were grain yield (PROD, kg ha⁻¹), plant upright architecture (ARQ), and commercial grain quality (AG). AG and ARQ were evaluated using a 1-to-5 scale, where 1 indicates a favorable phenotype and 5 an unfavorable one. AG and ARQ were assessed using a 1 to 5 scale, where 1 represents a favorable phenotype and 5 an unfavorable one. Statistical analyses were performed using mixed models (REML/BLUP), with the significance of genetic variance tested by the Likelihood Ratio Test (LRT). The selection of the top 5 lines with the highest simultaneous potential for ARQ, AG, and PROD was performed using the genotype-ideotype distance index adapted from Carvalho et al. (2002), based on the BLUPs of the genotypic values of the lines

RESULTS AND DISCUSSION

The Likelihood Ratio Test (LRT) revealed a significant effect ($p < 0.01$) across the lines for all three evaluated traits. This statistical significance is more than a metric; it confirms the deep genetic variability between these lines, affirming that we have the necessary variability and potential for success through selection. Selective accuracy ranged from moderate to very high, with values of 0.63 (ARQ), 0.95 (AG), and 0.63 (PROD). Specifically, the high accuracy for commercial grain quality demonstrates a strong alignment between the predicted genotypic essence and the physical phenotypes we observe in the field. This alignment provides reliability to the selection process. The data suggest that selecting for a single trait in isolation is a narrow path. When we focused solely on maximizing yield (PROD), we often saw a decline in grain quality or a shift toward a prostrate architecture (ARQ) that pulls the plant away from its ideotype. In contrast, the genotype-ideotype distance index was effective for simultaneous trait selection. The five lines with the highest potential (Top 5) showed gains ranging from 0.39 to 2.81% (ARQ), 2.73 to 8.18% (AG), and 4.80 to 14.51% (PROD), highlighting the efficiency of recurrent selection in Carioca bean breeding. Therefore, the index proved to be a robust tool, selecting lines that combine favorable alleles for the three traits simultaneously. This approach proved far more effective for simultaneous selection, ensuring no single characteristic was sacrificed for another.

Table 1. BLUPs of genotypic values of the five best common bean lines regarding upright plant architecture (ARQ), commercial grain quality (AG), and grain yield (PROD) – Viçosa, MG.

Lines	ARQ	AG	PROD	Rank
VC292	2.29 (0.39) ¹	2.09 (5.46)	6039 (14.51)	1
VC246	2.23 (2.81)	2.17 (2.73)	5675 (7.61)	2
VC206	2.29 (0.39)	2.02 (8.18)	5814 (10.24)	3
VC205	2.23 (2.81)	2.09 (5.46)	5527 (4.80)	4
VC327	2.23 (2.81)	2.17 (2.73)	5611 (6.40)	5
BRSMG Madrepérولا	2.31	2.24	5274	117
Mean BLUP	2.33	2.22	5157	

¹ Values in parentheses refer to the estimated genetic gain (%) corrected according to dos Anjos et al. (2019).

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OPTIMIZATION OF THE EVALUATION TO SEED SIZE AND SHAPE OF COMMON BEAN LINES

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INTRODUCTION: The size and shape of common bean seeds (*Phaseolus vulgaris* L.) are important for the commercial acceptance of new cultivars. Evaluations of these traits have been carried out using calipers. However, this methodology requires long time, which makes it unfeasible to evaluate a large number of seeds and lines. The use of images may be a feasible alternative to assist in the evaluation of seed size and shape of lines seeds. Silva et al. (2024) have already showed that this methodology is precise and accurate for evaluating the color of the seed coat of common bean seeds. However, there is still no information about its effectiveness for evaluating the size and shape of common bean seeds. Therefore, the objective of this study was to validate the use of images to evaluate the size and shape of common bean seeds.

MATERIALS AND METHODS: A total of 32 common bean cultivars from the carioca commercial group, recommended between 1980 and 2015 by Brazilian research institutions, were evaluated for seed length, width, and J index (length-to-width ratio) using both digital calipers and image-based methods. These evaluations were conducted in an experiment designed in a randomized complete block design with three replications. From each plot, 15 seeds were randomly sampled and evaluated for length and width. Image acquisition (Figure 1) was performed using the GroundEye® equipment, model S800 (Silva et al., 2024), located at the Image Laboratory (LASUFLA) of the Seed Sector of the Department of Agriculture at UFLA. Images were captured in the RGB system and converted to CIE Lab, and then subjected to segmentation according to Otsu (1979). Thus, from the image containing only the seeds, it was possible to individualize them and obtain measurements of length, width, and J index. The evaluated methodologies were compared using the coefficient of variation, accuracy, least significant difference at the 5% and 1% levels by the Tukey test (1949), number of groups formed in the Scott–Knott clustering test (1974), and Pearson’s correlation coefficient among lines data obtained at the seed level, plot mean, and treatment mean.



Figure 1. GroundEye (S800) and image of an experimental plot containing 15 common bean seeds.

RESULTS AND DISCUSSION: The cultivar effect was significant for all evaluated traits, regardless of the measurement methodology used. Therefore, both methodologies were effective in identifying variability among cultivars for all traits. Estimates of the coefficients of variation for the traits length, width, and J index measured using digital calipers and image-based methods

ranged, respectively, from 2.21 to 2.39% and from 1.84 to 2.42% (Table 1). Estimates of accuracy for all traits assessed using both methodologies were equal to or greater than 0.91.

Table 1. Estimates of statistical parameters for the traits length, width, and J index (J) obtained using digital calipers and image-based method.

Parameters	Caliper			Image		
	Length	Width	J	Length	Width	J
Mean (mm)	9.62	6.55	1.47	8.94	5.98	1.50
Accuracy	0.96	0.92	0.93	0.98	0.94	0.91
CV (%)	2.18	2.39	2.21	1.84	2.20	2.42
LSD (5%)	0.68	0.51	0.11	0.53	0.43	0.12
LSD (1%)	0.77	0.57	0.12	0.60	0.48	0.13
NG	5	5	4	6	4	4

CV (%): Coefficient of Variation; LSD: Least significant difference by the Tukey test (1949) at 5% and 1% probability; NG: Number of groups according to the Scott–Knott test (1974).

The values of the least significant difference at the 5% and 1% levels by the Tukey test for image-based evaluations of seed length and width were lower than those obtained using digital calipers (Table 1). The number of groups observed in the mean clustering test Scott–Knott for each trait, in both methodologies, was similar. Estimates of the correlation coefficient between caliper-based and image evaluations for all traits were significant and equal to or greater than 0.78 (Table 2), therefore of high magnitude.

Table 2. Estimates of Pearson’s correlation coefficients between data obtained using calipers and image-based methods to length, width and J index.

Level	Length	Width	J
Seed	0.92*	0.83*	0.78*
Plot	0.96*	0.93*	0.89*
Treatment	0.98*	0.94*	0.93*

*: Significant at the 5% probability level by the *t* test.

The results showed that image-based evaluation of seed size and shape in common bean lines has high experimental precision and maintains a line ranking similar to that observed in caliper-based assessments. In addition, the use of this methodology allows better discrimination among lines by Tukey mean comparison test and groups lines in a manner similar to that obtained with caliper-based evaluations for seed size and shape. It is noteworthy that image-based assessment of common bean seeds allows the assessment of larger sample sizes and a greater number of genotypes in a shorter time. Therefore, the use of images makes the assessment of common bean seeds more efficient.

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TERMINAL DROUGHT TOLERANCE AND PRODUCTIVE EFFICIENCY OF TROPICAL-ADAPTED BLACK BEAN GENOTYPES

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INTRODUCTION. In the humid tropical region of southeastern Mexico, terminal drought is the main environmental factor reducing common bean yield in commercial plantings during the autumn–winter growing season. Terminal drought periods have been observed to occur more frequently and with greater intensity as a result of climate change (Chaves-Barrantes et al., 2018), potentially reducing grain yield by more than 60% and even causing total crop failure (López et al., 2011). The objectives of this study were to evaluate a group of black bean genotypes in order to identify those showing lower susceptibility to moisture stress and higher productive efficiency under both irrigated and terminal drought conditions, compared with the commonly used black bean cultivar Negro Jamapa in this region.

MATERIALS AND METHODS. During the 2024 winter–spring growing season, two field trials were established in Cotaxtla, Veracruz, Mexico, to evaluate 10 advanced lines developed by the INIFAP National Bean Program, the CIAT-103-25 line from the International Center for Tropical Agriculture (CIAT), and the cultivars Verdín, Rubí, Rincón Grande, and Negro Jamapa, the latter used as the regional check. The experimental design was a randomized complete block with three replications. One trial was conducted under full irrigation throughout the growing season, whereas in the other trial irrigation was suspended at the onset of flowering. Days to physiological maturity and grain yield (kg ha^{-1}) were recorded. Analyses of variance were performed separately for each moisture condition, mean comparisons were conducted using the least significant difference (LSD) test ($\alpha = 0.05$), and correlation analyses were performed. Drought response was assessed using the drought susceptibility index (DSI) (Fischer and Maurer, 1978) and the relative yield efficiency index (RYE) (Graham, 1984).

RESULTS AND DISCUSSION. Under both irrigated and terminal drought conditions, the number of days required for genotypes to reach physiological maturity was negatively and significantly correlated with grain yield ($y = -0.719^{**}$ and -0.557^{*} , respectively). Under both moisture regimes, Verdín was the earliest genotype to reach maturity (Table 1). The earliness of this genotype is highly desirable to avoid or minimize damage caused by terminal drought. In this study, a drought intensity index of 0.21 was observed, corresponding to an average yield reduction of 304.4 kg ha^{-1} due to terminal water stress. The lines Papaloapan/SEN 46-7-10, CIAT-103-25, Jamapa Plus/XRAV-187-3-4-4, Papaloapan/SEN 46-2-6, and the cultivar Rubí showed the lowest susceptibility to terminal drought, with DSI values < 0.90 , whereas the lines Jamapa Plus/XRAV-187-3-4-1, Negro Citlali/XRAV-187-3-1-6, Papaloapan/SEN 46-7-7, and the cultivar Negro Jamapa were the most susceptible, with DSI values > 1.0 (Table 1). Among the genotypes showing greater tolerance to terminal drought, CIAT-103-25 and Jamapa Plus/XRAV-187-3-4-4, together with Verdín, exhibited the highest RYE values, indicating high yield under both moisture conditions (Graham, 1984).

Table 1. Effect of terminal drought stress on days to physiological maturity (PM) and grain yield (Y) of black bean genotypes evaluated under irrigated and terminal drought conditions (TD), as well as the estimated drought susceptibility (DSI_i) and relative yield efficiency (RYE_i) indices.

Genotype	PM (d)		Y (kg ha ⁻¹)		DSI _i	RYE _i
	Irrigated	TD	Irrigated	TD		
Papaloapan/SEN 46-2-6	77.7cde	73.3ab	1480.0abc	1198.3ab	0.89	1.10
Papaloapan/SEN 46-3-2	74.7fgh	73.3ab	1581.7ab	1215.0ab	1.09	1.19
Papaloapan/SEN 46-7-7	82.3a	73.7a	1033.3de	768.3cd	1.20	0.49
Papaloapan/SEN 46-7-10	79.0bcd	72.7abcd	1106.67cde	1000.0bcd	0.45	0.69
Papaloapan/SEN 46-7-12	80.7ab	74.0a	838.3e	645.0d	1.08	0.34
Ngo Citlali/XRAV-187-3-1-5	75.7efg	73.3ab	1538.3ab	1211.7ab	1.00	1.16
Ngo Citlali/XRAV-187-3-1-6	76.0efg	73.7a	1486.7ab	1088.3abc	1.26	1.00
Ngo Citlali/XRAV-187-3-1-8	74.3fgh	70.0e	1570.0ab	1260.0ab	0.93	1.23
Rincón Grande	80.0abc	71.3cde	1430.0abc	1093.3abc	1.10	0.97
Jam Plus/XRAV-187-3-4-1	80.7ab	73.7a	1450.0abc	1040.0abcd	1.33	0.94
Jam Plus/XRAV-187-3-4-4	76.0efg	71.3cde	1601.7ab	1300.0ab	0.88	1.29
CIAT-103-25	79.3bc	73.0abc	1630.0ab	1343.3ab	0.83	1.36
Negro Jamapa (TR)	76.7def	71.0de	1380.0bcd	1020.0abcd	1.22	0.87
Verdín	72.3h	68.0f	1781.7a	1418.3a	0.96	1.57
Rubí	73.7gh	71.7bcde	1546.7ab	1286.7ab	0.79	1.23
Promedio [§]	77.3	72.3	1430.3a	1125.9b	1.00	1.02
DMS (0.05)	2.54	1.97	379.9	406.7		

[§]Mean of the variable under irrigated and terminal drought (TD) conditions. *Genotypes with different letters within each column for days to physiological maturity and grain yield are statistically different according to the least significant difference (LSD, 0.05) test.

CONCLUSIONS. Papaloapan/SEN 46-7-10, CIAT-103-25, Jamapa Plus/XRAV-187-3-4-4, Papaloapan/SEN 46-2-6, and Rubí were the most tolerant genotypes to terminal drought, whereas Jamapa Plus/XRAV-187-3-4-1, Negro Citlali/XRAV-187-3-1-6, Papaloapan/SEN 46-7-7, and Negro Jamapa were the most susceptible. CIAT-103-25 and Jamapa Plus/XRAV-187-3-4-4, together with Verdín, also showed the highest yield efficiency under both full irrigation and terminal drought conditions, greatly outperforming the Negro Jamapa cultivar.

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SPATIAL DISTRIBUTION AND NICHE SUITABILITY OF COMMON BEAN POD WEEVIL IN NORTH-CENTRAL MÉXICO

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INTRODUCTION. Common bean (*Phaseolus vulgaris* L.) is the most important cash crop in the states of Durango and Zacatecas, and to a lesser extent in Chihuahua, located in north-central México. Two pests that have been repeatedly observed in northern México are the Mexican bean beetle (*Epilachna varivestis* Mulsant) and the common bean pod weevil (*Trichapion godmani* Sharp). An increasing trend has been observed in pod weevil populations, especially in common bean cultivated in the Guadiana, Canatlán, and Nombre de Dios Valleys in Durango. Other states of the Semiarid Highlands of México are included in models of insect-plant coevolution, which will be used to explain interactions among pests, native populations, intermediate forms, and modern varieties of leguminous plant species (*Phaseolus* spp.). It was found that plants developed a variety of defense mechanisms, and insects evolved adaptations to acquire insecticide resistance and survive interactions with other insect species considered parasitoids. The objective was to identify niche suitability and spatial distribution of the common bean pod weevil in north-central México.

MATERIALS AND METHODS. Historical records (1992) and 2025 field sampling in Durango, Chihuahua, and Zacatecas were analyzed to establish occurrence points for *Trichapion godmani*. Sampling (Durango, 2025) followed the 1992 protocol, collecting 30 mature pods per site to determine the proportions of damage. Data was cleaned using the *tidyverse* package in R v4.5.1 (R Core Team, 2024), resulting in 64 unique geo-referenced records. A distribution map was generated in QGIS v3.28 (2023) to evaluate spatial adjustment at the national level. Seven bioclimatic variables from WorldClim v2.1 at 30 arc-seconds resolution (Fick & Hijmans, 2017) were incorporated. To avoid multicollinearity and redundancy, a Principal Component Analysis (PCA) and a bivariate Pearson correlation ($|r| < 0.7$) were conducted. Final variables included: BIO4 (Temperature seasonality), BIO5 (Max temperature of the warmest month), BIO6 (Min temperature of the coldest month), BIO7 (Temperature annual range), BIO15 (Precipitation seasonality), BIO16 (Precipitation of wettest quarter), and BIO17 (Precipitation of driest quarter). Ecological Niche Modeling (ENM) was performed using MaxEnt v3.4.3k (Phillips *et al.*, 2006) for continental México and then regionalized for Chihuahua, Durango, and Zacatecas. Model calibration and evaluation were executed via the *ENMevaluate* package in R, selecting configurations with the lowest Corrected Akaike Information Criterion (AICc). A total of 100 replicates produced final suitability maps (scale 0–1) under current conditions. Model performance was validated using Area Under the Curve (AUC) from ROC analysis, Jackknife tests, and optimization of regularization multipliers (RM) and feature class (FC) combinations based on the lowest AICc values.

RESULTS AND DISCUSSION. The model demonstrated high predictive performance (training AUC = 0.91; test AUC = 0.83), indicating strong discriminative capacity for studies on *T. godmani* adaptation. The primary bioclimatic drivers were BIO4 (Temperature seasonality) with an average contribution of 31.5%, and BIO5 (Max temperature of the warmest month) with 20.6%. These results highlight the critical role of thermal variability and extreme temperatures in the species' ecology. The environmental suitability map (Figure 1) identified high-suitability areas across north-central México, particularly in Durango, Chihuahua, and Zacatecas. Notable concentrations were observed along the México-USA border (Valle de Juárez, Ascensión, and Janos, Chih.), the regions of Los Llanos de Durango and Los Llanos de Cabrera (northern Dgo.), and the municipalities of Mazapil and Valparaíso in Zacatecas. These contrasting spatial patterns confirm a robust environmental suitability for *T. godmani* throughout the study region.

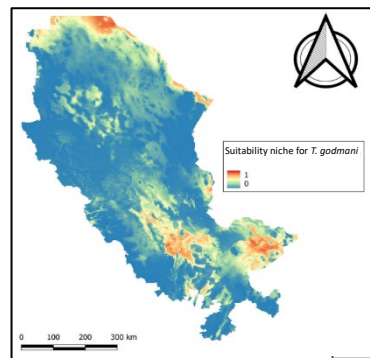


Figure 1. Potential ecological niche for *Trichapion godmani* in north-central México.

CONCLUSIONS. The response curves indicate that the potential for *Trichapion godmani* presence varies depending on the temperature and precipitation gradients considered in the model. In particular, extreme temperature and climate variability were observed to influence environmental suitability for *T. godmani*, consistent with the species' dependence on specific climatic conditions. The interaction of individual effects for climate variables and external factors needs to be considered. In 2025, significant and negative effects of agrochemical applications (grasshopper control) in the Los Llanos region were observed on *T. godmani*. Natural regulation through parasitism should also be included in models combining climatic predictions with other factors affecting *T. godmani* populations.

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DISTRIBUTION OF *Macrophomina phaseolina* INFECTING COMMON BEANS AND OTHER CROPS IN MEXICO

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The fungus *Macrophomina phaseolina* (Tassi) Goid. (charcoal rot) is a pathogen with a wide range of hosts and distribution in Mexico and worldwide, with significant occurrences in warm and dry areas. To understand *M. phaseolina*'s global distribution and host preferences, providing essential insights for developing effective strategies to manage its spread and mitigate crop losses (1).

Based on bibliographic reports and our collection data by *M. phaseolina* infecting crops in Mexico, the sites were georeferenced, the coordinates were standardized using the WGS84 reference system, and converted into a point vector layer (shapefile) using QGIS 3.40.15. Environmental variables included six official layers from the Geoportal of the National Commission for the Knowledge and Use of Biodiversity (CONABIO, <http://www.conabio.gob.mx/informacion/gis/>) and the National Institute of Statistics and Geography (INEGI; <https://www.inegi.org.mx/>). Cartographic standardization integrated raster and vector layers, and environmental values were extracted using QGIS. The geospatial matrix integrated geographic coordinates and environmental information, and was analyzed with Multiple Correspondence Analysis (Statistica 14.3).

The pathogen *M. phaseolina* was reported at 40 sites, distributed across 12 states of Mexico and infecting ten crop species and soils (Fig. 1). Two gradients of variation were identified, the first was ecological-productive, with agricultural systems with warm-humid conditions, higher altitude, and thick soils, cultivated with hibiscus (*Hibiscus sabdariffa*), eggplant (*Solanum melongena*), peanut (*Arachis hypogaea*), soybean (*Glycine max*), chili pepper (*Capsicum annuum*), and sugarcane (*Saccharum officinarum*), in the southern and central states of the country, as opposed to systems with drier and temperate climates, lower altitudes, and fine or medium soils, cultivated with chickpeas (*Cicer arietinum*), tomatillo (*Physalis ixocarpa*), sorghum (*Sorghum bicolor*), and beans (*Phaseolus vulgaris*) in the northern states of Mexico. The second gradient was edaphic-altitudinal, separating low-altitude environments with fine soils and warm conditions, cultivated with soybeans and sugarcane in the central, southern, eastern, and southeastern states, from higher-altitude environments with temperate climates and more restrictive soils, characteristic of the central and northern parts of the country (Fig. 2). Large scale studies links to *M. phaseolina* abundance to clay soils, pH, and cation exchange capacity (3). Moreover, some global models identify the temperature gradients, as the most determining factors for the distribution of *M. phaseolina* (2). The ability of *Macrophomina phaseolina* to infect across different agricultural ecosystems in Mexico evidences a dangerous versatility that is reinforced by the influence of climate on its distribution in Mexico. This information reflects the wide range of adaptation of *M.*

phaseolina and the potential damage it could cause to crops that are important. Therefore, it is necessary to generate local predictive models that integrate edaphic and climatic variables to anticipate the spread of the fungus.

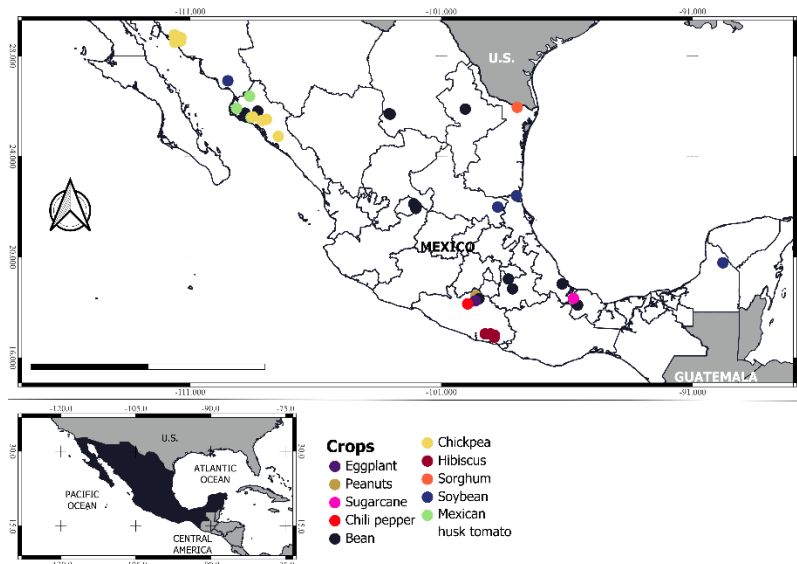
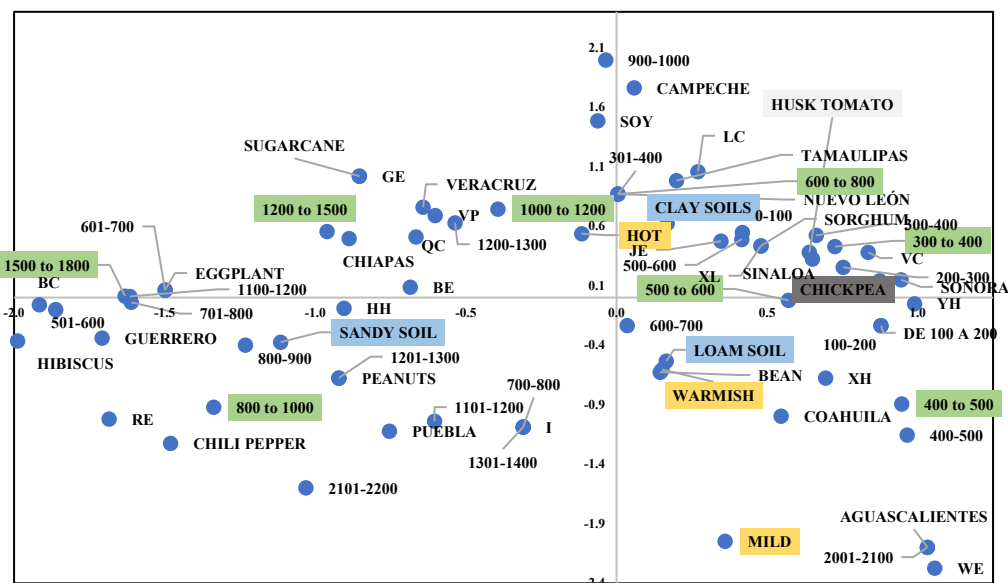


Figure. 1. Locations where the presence of *M. phaseolina* was reported in Mexico.



SCREENING OF POWDERY MILDEW (*Erysiphe vignae*) RESISTANCE IN A TEPARY BEAN DIVERSITY PANEL

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INTRODUCTION: Powdery mildew is a seasonal disease of legumes in Puerto Rico that occurs under conditions of moderate temperatures and high humidity. Tepary beans (*Phaseolus acutifolius*) are severely affected by this disease under field and screenhouse conditions. Symptoms initially appear on shaded lower leaves as pale-yellow spots that develop into white powdery lesions. These lesions enlarge and spread, covering the upper leaves with white powdery masses (Figure 1). Based on morphological characteristics of the anamorph (Figure 2), and PCR-based genetic markers including the internal transcribed spacer (ITS) region, isolates collected from experimental sites in Isabela and Juana Diaz were identified as *Erysiphe vignae* (GenBank Acc# PP911081 and PP911083) (Estevez de Jensen et al. 2024). At the Isabela (USDA/ARS) station, the response to powdery mildew in cultivated versus wild tepary beans have shown contrasting reactions with wild accessions being more resistant. From a field trial in Isabela, PR that evaluated a tepary diversity panel, a subset of 30 accessions were selected for screening under screenhouse conditions at two locations.

MATERIALS AND METHODS: In Mayagüez and Juana Diaz, PR, disease severity was evaluated in a subset of 30 different cultivated and wild tepary accessions and common beans (controls) from the Tepary Diversity Panel previously selected for extreme reactions in the field. These were planted under screenhouse conditions and humidity was augmented utilizing humidifiers. The humidity and temperature conditions during the experiment were: 78.9%, 27.3°C in Mayagüez and 76.5%, 27.7°C in Juana Diaz. In Mayagüez, plants were inoculated with 10⁷ conidia/ml using inoculum from infected leaves from Isabela; in Juana Diaz, it was natural infection. Disease severity was evaluated at 7, 14 days and 21-day intervals after disease onset, on a 1-9 scale, with 1= no disease, 9 = more than 90% of plant tissue diseased.

RESULTS AND DISCUSSION: For powdery mildew, symptoms began as small white spots that enlarged until they covered the entire leaf area of susceptible genotypes. The wild accessions TDP-96 (G40117A) and TDP-192 (G40213) showed no infection symptoms, with a severity score of 1. The common beans PR0443-151 and Beniquez also showed no symptoms or signs of the disease. In addition, the wild accessions TDP-203 (G40223), TDP-234 (G40253), and TDP-344 (PI 440811) showed resistance with severity values of 1.7, 2.3, and 2.3, respectively. The wild accessions that were susceptible to powdery mildew were TDP-62 (G40080), TDP-264 (G40288), TDP-44 (G40056), TDP-388 (G40121), and TDP-263 (G40287), with severity values of 6.8, 7.3, 7.3, 7.3, and 7.5, respectively. These results identified resistant tepary bean accessions that can serve as valuable sources of powdery mildew resistance for tepary and common bean improvement.

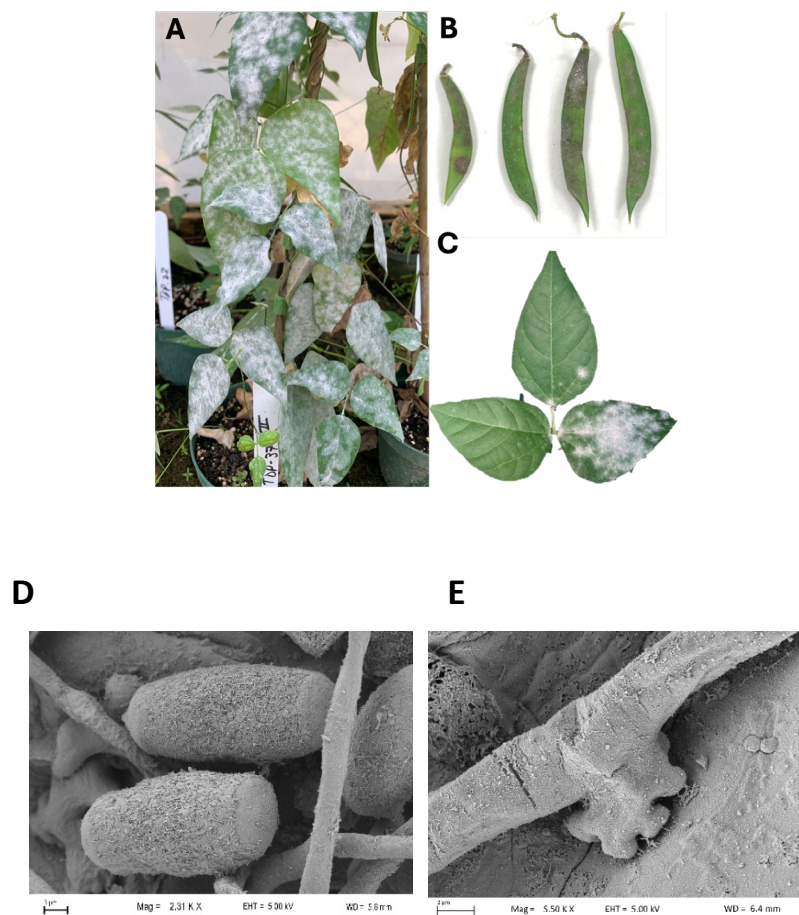


Figure 1. Symptoms of *Erysiphe vignae* on tepary bean on (A) whole plant); (B) pods; (C) leaf. *Erysiphe vignae* (D) conidia and (E) hyphal appressorium viewed under a scanning electron microscope.

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GENOME-WIDE ASSOCIATION STUDY OF WHITE MOLD RESISTANCE IN COMMON BEAN

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INTRODUCTION

White mold (WM) is a devastating disease of common bean (*Phaseolus vulgaris* L.) caused by the necrotrophic fungus *Sclerotinia sclerotiorum*. Under favorable conditions, WM can cause complete crop failure. Breeding for WM resistance is challenging because it is controlled by quantitative inheritance and involves intricate genetic mechanisms. The genetic resistance to WM is described as a combination of physiological resistance and disease avoidance. Avoidance traits help plants escape or limit disease development – for example, by reaching flowering before or after conditions are favorable for the pathogen or by creating a canopy microclimate that is less conducive to infection through altered growth habit and plant architecture. Major avoidance associated traits include canopy porosity, improved lodging resistance, fewer flowers, glabrous stems and leaves, and thicker cuticles. In contrast, physiological resistance involves defense pathways. The most sustainable approach to manage WM is breeding beans for host resistance to WM. A genome-wide association study (GWAS) was conducted to identify loci significantly associated with WM resistance using the genotypes from the Mesoamerican Diversity Panel (MDP).

MATERIALS AND METHODS

A total of 269 accessions in the MDP was phenotyped for reaction to WM in the greenhouse and field. The straw test was performed in the USDA-ARS greenhouses at Prosser, WA in six replications randomized in a complete block design in 2015 (Oraguzie, 2015) as described by Petzoldt and Dickson (1996). Reaction to WM disease in the field was measured at physiological maturity and was scored from 0 to 9 based on combined incidence and severity infection, where 0 = no diseased plants and 9 = 80 to 100% diseased plants and/or 60 to 100% infected tissue. Genotypic data were accessed from Moghaddam et al. 2016.

BLUP-adjusted means were used for the GWAS, and analyses were performed using GAPIT v3.5.0 in R v4.4.1. False positives due to population structure were controlled by using principal component analysis (PCA) and kinship parameters in the GWAS models. Kinship was calculated with the VanRaden method integrated into GAPIT. Mixed Linear Model (MLM), Fixed and random model Circulating Probability Unification (Farm -CPU), and Bayesian information and LD Iteratively Nested Keyway (BLINK) were compared based on the model adjustment in the QQ plots. The threshold for declaring a significant association was corrected for multiple testing using the False Discovery Rate (FDR) criterion with the Benjamini and Hochberg (1995) method.

Only significant SNPs that were consistent across FarmCPU and BLINK were selected for candidate gene analysis. Based on previous linkage disequilibrium (LD) studies in common bean diversity panels, a 100Kbp SNP -centered window was defined for each significant marker-trait association (Moghaddam et al. 2016). Genes within the defined windows were extracted using the *Phaseolus vulgaris* reference genome V2.1 (<https://phytozome-next.jgi.doe.gov/>).

RESULTS AND DISCUSSION

Four single nucleotide polymorphisms (SNPs) - S03_34048652 on chromosome Pv03; S04_1524379 and S04_29953085 on chromosome Pv04; and S08_22592413 on chromosome Pv08 - were significantly associated with WM resistance in both FarmCPU and BLINK models (Table 1). Of these, one SNP (S04_29953085) was identified by the seedling straw test, and three significant SNPs were identified by field data. The S04_1524379 (effect size = -0.39) was located within 11-37 Kb window containing three tandem leucine-rich repeat encoding genes. Similarly, the S08_22592413 (effect size = -0.35) was at a 1.5 -9.8 Kb window from two U-box E3 ubiquitin ligase genes. S08_22592413 falls within the previously reported WM8.3 QTL interval, while S03_34048652 is very close to the WM3.1 (Figure 1). These loci represent promising candidate markers for marker-assisted breeding program to improve WM resistance in common bean.

Table 1: Significant SNPs associated with White Mold (WM) response identified by FarmCPU and BLINK models in the Mesoamerican Diversity Panel.

SNP	Chromosome	Position	MAF	Effect	H&B.P.Value
S04_29953085	4	29953085	0.386	-0.16	1.1×10^{-3}
S08_22592413	8	22592413	0.390	-0.36	6.93×10^{-5}
S03_34048652	3	34048652	0.004	2.15	7.76×10^{-6}
S04_1524379	4	1524379	0.060	-0.39	7.17×10^{-5}

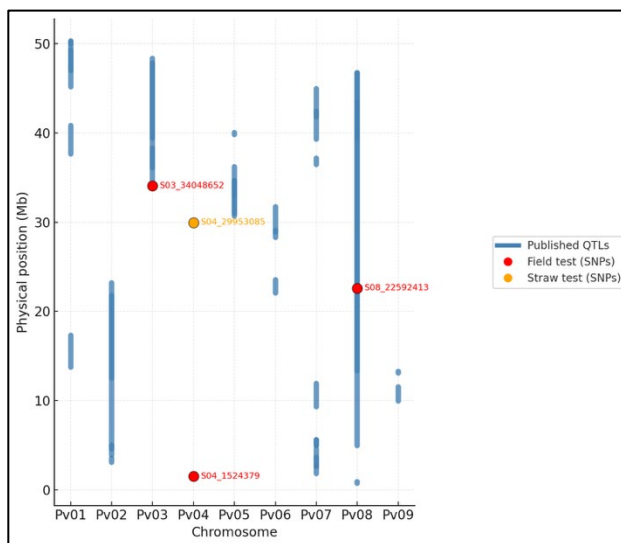


Figure 11: Genomic positions of significant SNPs relative to previously published white mold QTL in common bean. Blue vertical markers indicate the physical intervals/positions of published QTL across chromosomes Pv01-Pv09. Red points and orange points represent SNPs detected in the field and straw test respectively.

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REACTION OF COMMON BEAN LINES TO RACES 65 AND 89 OF *Colletotrichum lindemuthianum*

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INTRODUCTION

Anthrachnose, caused by the fungus *Colletotrichum lindemuthianum*, is one of the most severe and economically important diseases of common bean (*Phaseolus vulgaris* L.). The disease affects leaves, stems, and pods, resulting in dark spots and necrosis, compromising both plant development and grain quality. When not properly managed, it can cause losses 100% of productivity, especially in crops under conditions favorable to the pathogen (Singh and Schwartz, 2010). Knowledge about the resistance level of common bean cultivars/lines to this pathogen assists breeding programs from the selection of parents to the recommendation of new lines. The objective of this work was to assess the reaction of carioca-type common bean lines to different races of the pathogen.

MATERIALS AND METHODS

Twenty-four carioca bean lines (CXIV 31; CXIV 77; CXIV 150; CXV 35.3; CXV 35,23; MAXIII 3; MAXIV 15; CXIV 196; VC 44; VC 45; VC 46; VC 47; VC 48; VC 49; VC 50; VC 51; IAC 2051; IPR SABIÁ; DAMA; ANDC 9; BRSMG AMULETO; BRSMG ZAPE; BRS ESTILO; BRSMG UAI) and two controls (BRS Pérola and BRS Esplendor) were assessed for their reaction races 65 and 89 of *C. lindemuthianum* (Lv 134 - Race 65 and Lv 228 - Race 89). Two greenhouse experiments were conducted, one for each pathogen race, in a randomized block design (RBD) with three replications and six plants per plot of six plants. Tubes containing sterile bean pods were inoculated with each *C. lindemuthianum* isolate and incubated in a Bio-Oxygen Demand (BOD) incubator at 22°C for 10 days in the dark. Common bean seedlings at the V2 stage of each line were inoculated with a conidial suspension of the pathogen at a concentration of 1.2×10^6 conidia/mL and kept in a mist chamber with controlled temperature and humidity for 72 hours. After plants were transferred and maintained for eight days in greenhouse. Disease severity was assessed 10 days after inoculation using a diagrammatic scale of scores ranging from 1 to 9 (Schoonhoven and Pastor-Corrales, 1987) where score “1” indicates the absence of symptoms and score “9” indicates dead plants.

RESULTS AND DISCUSSION

The 24 assessed lines presented average severity scores ranged from 2.0 to 9 and from 2.1 to 9 for race 65 and 89, respectively. Common bean lines with disease severity scores between 1 and 3 were considered resistant, while strains with scores above 3 were classified as susceptible. Six lines presented resistance to race 65 (25%), three to race 89 (12.5%) and three for both races (Figure 1). The frequency distribution of severity scores of the lines inoculated with races 65 and 89 is presented in Figure 2. High frequency of lines inoculated with race 65 was observed with scores 2 and 9. However, high frequency of lines inoculated race 89 was observed with score 5 (Figure 2). The CXIV 150, MAXIV 15 and IPR SABIÁ common bean lines presented resistance to both races.

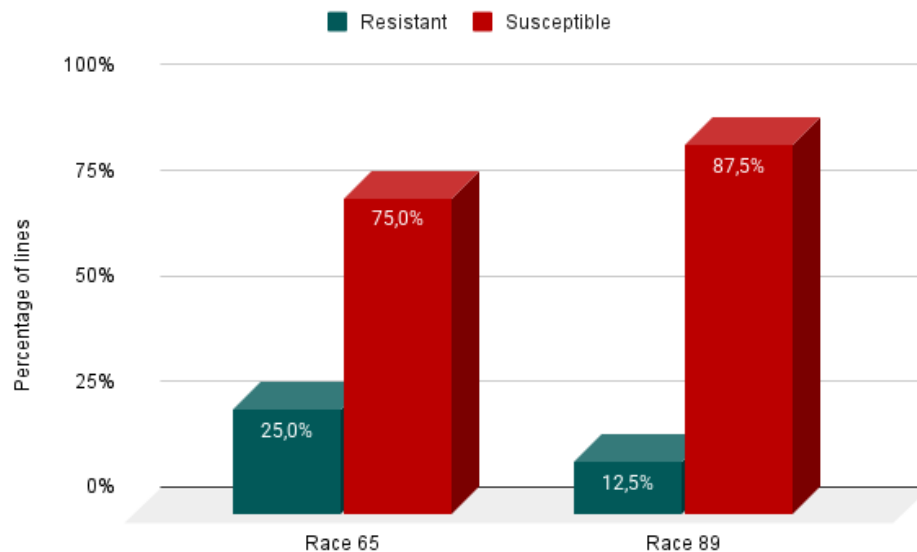


Figure 1. Percentage of resistant and susceptible lines of common bean to races 65 and 89 of *C. lindemuthianum*.

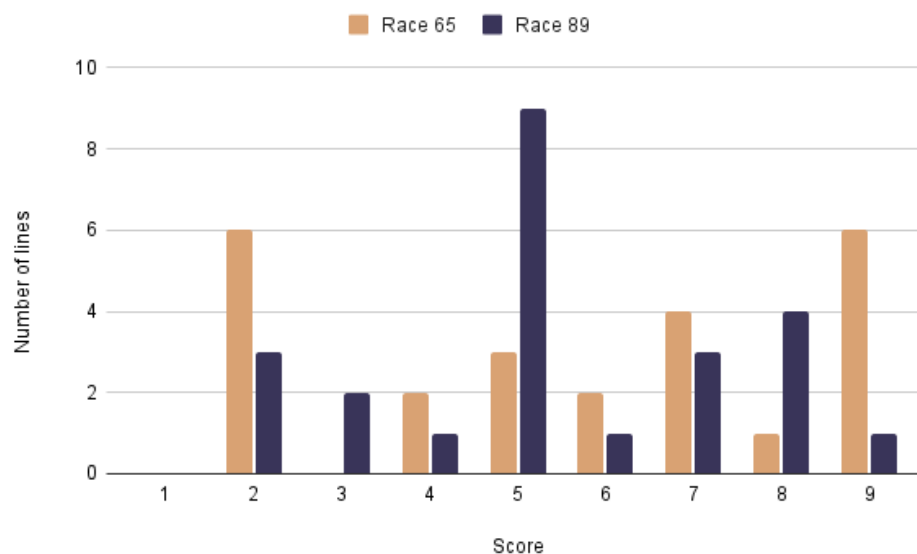


Figure 2. Frequency distribution of anthracnose severity scores (1-9) of common bean lines inoculated with races 65 and 89 of *C. lindemuthianum*.

ACKNOWLEDGEMENTS

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THE *UR-3* AND *UR-7* LOCI REVEAL CANDIDATE GENES FOR RUST RESISTANCE IN COMMON BEAN

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INTRODUCTION

Bean rust, caused by *Uromyces appendiculatus*, severely limits the productivity of common bean (*Phaseolus vulgaris* L.), an essential source of protein and micronutrients in human diets worldwide. Host plant resistance is critical and pyramiding resistance genes often facilitated by Marker-assisted selection (MAS), contributes to durable rust control. The *Ur-3*, *Ur-4*, *Ur-5*, *Ur-6*, *Ur-7*, and *Ur-11* genes have been widely used in common bean breeding programs aimed at developing rust-resistant cultivars (Hurtado et al., 2017; Park et al., 2003; Valentini et al., 2025). This study aimed to (i) resolve the genomic architecture of the *Ur-3* and *Ur-7* loci, (ii) identify candidate resistance genes, and (iii) develop gene-based markers to support MAS for durable bean rust resistance.

MATERIALS AND METHODS

An integrated genomic approach was applied, combining long-read genome assemblies, recombinant inbred line (RIL) populations, and genome-wide association analyses. High-quality long-read assemblies from multiple common bean genotypes, including USDA-Rattler, Aurora, and MEX 235 (Miklas et al., 2023; McClean et al., 2022), were used to resolve repetitive resistance gene clusters and capture structural variation absent from available *Phaseolus* reference genomes. SNP- and *k*-mer-based GWAS were conducted to identify genomic regions significantly associated with rust resistance phenotypes in the Durango Diversity Panel (DDP). Recombination patterns within RIL populations were used to narrow candidate intervals. Candidate gene-based markers for *Ur-3* and *Ur-7* were developed and performance was validated across dry bean accessions (Table1).

RESULTS AND DISCUSSION

SNP (Figure 1) and *k*-mer based GWAS and comparative genomic analyses revealed distinct genomic structures for *Ur-3* and *Ur-7* on chromosome Pv11. The *Ur-3* locus mapped to the distal end of Pv11 and exhibited extensive structural variation among assemblies, including gene copy number differences and rearrangements typical of NLR clusters. Within this region, a CC-NLR (CNL) gene (Pv11: 50,205,868–50,209,452 bp in the USDA-Rattler assembly), embedded within an NB-ARC-rich cluster, emerged as the *Ur-3* candidate gene. This gene was absent in rust-susceptible genotypes, supporting its role in resistance.

In contrast, *Ur-7* localized to a recombination-suppressed pericentromeric region of Pv11. Despite this limitation, integration of SNP and *k*-mer-based GWAS and RIL populations identified a single TIR-NLR (TNL) gene (Pv11: 36,604,755–36,611,252 bp in the UI 111 assembly) as the leading *Ur-7* candidate gene.

Marker validation across 177 dry bean accessions demonstrated that the newly developed *Ur-3* and *Ur-7* markers exhibited a 100% correlation with rust phenotypes observed in the DDP. The favorable *Ur-7* allele was detected in a subset of accessions with known broad-spectrum resistance,

while genotyping at *Ur-3* revealed cases where previously reported markers produced false positives.

This study highlights the importance of integrating long-read genomics with association analyses to resolve complex resistance loci. The distinct architectures of *Ur-3* and *Ur-7*, a distal NLR cluster versus a conserved pericentromeric locus, highlight the limitations of single-reference genome approaches in capturing the complete diversity of resistance genes. The identification of a CNL candidate for *Ur-3* and a TNL candidate for *Ur-7* is consistent with known NLR-mediated defense mechanisms and parallels rust resistance architectures described in other legumes. Importantly, the development of tightly linked, gene-based markers provide breeders with practical tools to pyramid resistance genes without labor-intensive greenhouse phenotyping, which is slow and difficult due to the biotrophic nature of *U. appendiculatus*.

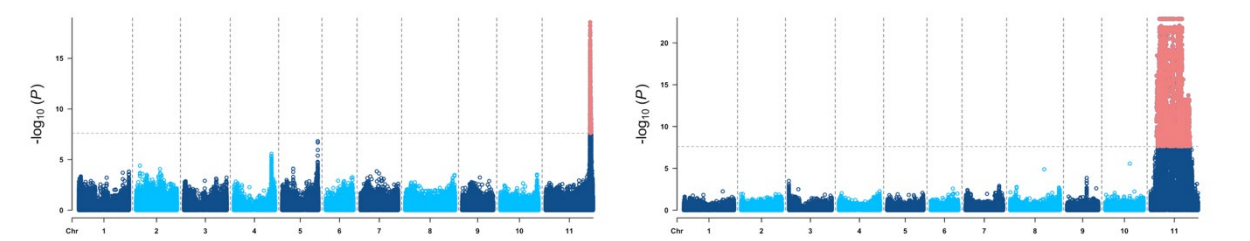


Figure 1. SNP-based GWAS identifying the rust resistance loci *Ur-3* (left), located at the distal end of Pv11, and *Ur-7* (right), located in a pericentromeric region of the same chromosome, using whole-genome sequencing data from the Durango Diversity Panel mapped to the UI 111 reference genome.

Table 1. Primers used to generate markers for *Ur-7* and *Ur-3* genes conditioning resistance to bean rust disease.

Id marker		Sequences	Gene	Ta (°C)	Location UI 111	Location Rattler v1
Ur-7_ Pv11_GeneR	Fa	gcgggcagggcggc-CGCTATTGAAGGGTCAGAAG	Ur-7	63	Pv11: 36,610,984	Pv11: 32,816,896
	R	TCTTTCACCCAATCAACGATCT				
	Fb	gcgggc-CGCTATTGAAGGGTCAGAAA				
Ur-3_ Pv11_GeneR	F	AGCGGTGTAAGAAAGAAGAGGGC	Ur-3	68	N/A	Pv11: 50,205,846 - 50,205,934
	R	GCTTCCAATTTCAGCTTTGTCCTATAT				

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INHERITANCE OF ASHY STEM BLIGHT RESISTANCE IN BLACK COMMON BEAN UPR-Mp-42

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INTRODUCTION

Ashy stem blight [causal agent: *Macrophomina phaseolina* (Tassi) Goidanich] is an important fungal disease of common bean (*Phaseolus vulgaris* L.) causing seed yield losses over 60%. The use of cultivars with physiological resistance is crucial for the disease management. Qualitative and quantitative resistance have been reported in the primary gene pool. Resistant genes/QTL were derived from Andean beans A 195, ‘Badillo’, ‘PC 50’, and PRA154 (Viteri and Linares, 2019; Viteri et al., 2024); and Middle American beans BAT 477 and XAN 176 (Méndez et al., 2017; Miklas et al., 1998; Olaya et al., 1996; Viteri et al., 2022). The objective of this research was to determine the inheritance of resistance derived from Andean bean breeding line UPR-Mp-42.

MATERIALS AND METHODS

Simple crosses and their reciprocals were conducted between black Middle American bean TARS-MST1 (susceptible) and black breeding line UPR-Mp-42 (partial resistant). Parents and F₁ plants were inoculated by the cut-stem method with the PRI24M *M. phaseolina* isolate at the V5 stage in a lateral branch close to the main stem in a greenhouse at Lajas Research Substation in 2024. Disease severity was evaluated at 35 days after inoculation using a 1-9 scale, where 1= no sign of infection and 9= the pathogen passed the second node above/below the point of inoculation (Viteri et al., 2024). Six F₂ (three for each TARS-MST1/UPR-Mp-42 and UPR-Mp-42/TARS-MST1 crosses) and 17 F₃ plants from both populations along with TARS-MST1 and UPR-Mp-42 were also inoculated and evaluated in the greenhouse using the described methodology in 2025.

RESULTS AND DISCUSSION

TARS-MST1 with a mean score of 8.1 was susceptible to PRI24M *M. phaseolina* isolate. UPR-Mp-42 had a partial resistance with a mean score of 4.4, as expected. F₁ hybrids from both populations were susceptible (scores > 7) to PRI24M isolate (Table 1). The TARS-MST1/UPR-Mp-42 and UPR-Mp-42/TARS-MST1 F₂ seeds segregated into 14 resistant (R) to 214 susceptible (S) and 10R to 207S, respectively in response to PRI24M ($\chi^2 = < 0.05$ and 1.00; $P > 0.30$). Thus, resistance in UPR-Mp-42 is controlled by two recessive complementary genes. A similar segregation pattern was reported by Viteri and Linares (2019) in genetic studies involving crosses between Andean common bean ‘PC 50’ and Middle American pinto ‘Othello’ to PRI16 isolate. F₃ seeds from three F₂ susceptible plants corroborated the 1R:15S segregation ratio in UPR-Mp-42/TARS-MST1 population (Table 1). Furthermore, F₃ seeds from six susceptible plants (with presumably alleles Aabb/aaBb) segregated into 56R to 131S, giving a good fit to 1R to 3S ratio ($\chi^2 = 2.44$; $P = 0.12$) in TARS-MST1/UPR-Mp-42 population. Also, F₃ seeds from four susceptible plants segregated into 1R to 3S ratio in UPR-Mp-42/TARS-MST1 population (Table 1). F₃ seeds from one susceptible plant with presumably alleles AAB_/AAbb/A_BB/aaBB were all susceptible

in TARS-MST1/UPR-Mp-42 population (Table 1). Conversely, F₃ seeds harvested from three resistant plants in both populations did not have resistant scores. Instead, 55R:55S and 23R:29S ratios were observed for TARS-MST1/UPR-Mp-42 and UPR-Mp-42/TARS-MST1 populations, respectively. The reasons are unknown and might be caused by excessive of susceptible gametes, interaction with other genes, and/or differences in the genetic background as reported in previous studies (Duncan et al., 2014; Viteri and Linares, 2019). The information provided in this study should help introgress and pyramid higher levels of ashy stem blight resistance into black common bean cultivars or other market classes.

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Table 1. Ashy stem blight response of common bean (*Phaseolus vulgaris* L.) TARS-MST1, UPR-Mp-42, and their F₁, F₂, and F₃ to PRI24M *Macrophomina phaseolina* (Tassi) Goidanich isolate evaluated at 35 days after inoculation in the greenhouse at Lajas Substation in 2024 and 2025.

Genotype	Nº plants	Range [†]	Mean	Ratio [‡]		χ^2	P
				Observed	Expected		
TARS-MST1	38	4-9	8.1	-	-	-	-
UPR-Mp-42	38	2-9	4.4	-	-	-	-
TARS-MST1/UPR-Mp-42							
F ₁	19	7-9	8.3	-	-	-	-
F ₂	228	3-9	6.8	14R:214S	1R:15S	<0.05	0.95
F ₃	187	3-9	6.0	56R:131S	1R:3S	2.44	0.12
F ₃	76	6-9	8.7	0R:76S	All S	0.00	1.00
UPR-Mp-42/TARS-MST-1							
F ₁	18	4-9	7.8	-	-	-	-
F ₂	217	3-9	7.7	10R:207S	1R:15S	1.00	0.32
F ₃	114	3-9	7.8	8R:106S	1R:15S	0.12	0.75
F ₃	141	3-9	5.5	45R:96S	1R:3S	3.60	0.06

[†] Ashy stem blight disease severity was scored on a 1 to 9 scale, where 1= no sign of infection and 9= the pathogen passed the second node above/below the point of inoculation (Viteri et al., 2024).

[‡] R, resistant; S, susceptible.

EVALUATION OF DRY BEAN BREEDING LINES FOR WHITE MOLD RESISTANCE IN THE GREENHOUSE AND FIELD USING MULTI-SITE SCREENING NURSERIES

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INTRODUCTION: Field and greenhouse evaluations were conducted in 2025 to determine white mold disease tolerance in dry bean breeding lines from three breeding programs. Evaluations were conducted at sites located in five US states (MI, NE, ND, OR, WA). Collectively, these testing sites are representative of the major bean production environments of North America. Multi-site screening is essential for robust evaluation under varied environmental conditions and *Sclerotinia sclerotiorum* pathogen populations that may differ across locations.

MATERIALS AND METHODS: Greenhouse evaluations were conducted at four locations with local isolates of *S. sclerotiorum* using the straw test method (Petzoldt & Dickson, 1996) that is intended to identify sources of physiological resistance in adapted and un-adapted bean germplasm. Twenty-one entries were evaluated, including G122 (partial resistance), USPT-WM12 (partial resistance), Bunsu (mostly field resistance), and Beryl (susceptible) that were included as checks. Field tests were conducted at four locations with sixteen entries. However, only ND developed sufficient disease pressure to collect meaningful disease severity and yield data. MI and OR had only minimal disease (Table 2). As in years past, this illustrates the necessity of multiple sites for generating data despite weather or other natural complications in field trials. Disease severity in field trials were rated using the CIAT scale, with 1=most resistant to 9=most susceptible.

RESULTS AND DISCUSSION: Greenhouse results indicated that six entries were not significantly different than G122 in regards to white mold tolerance (Table 1). These include a range of seed classes (DRK, LRK, pinto, and SDP) from three breeding programs. As previously observed in 2024, it was interesting to note all the most tolerant experimental pintos derive their resistance from interspecific introgression of *P. coccineus*, suggesting this breeding strategy has been effective at broadening the genetic base of white mold tolerance in *P. vulgaris*. However, the most susceptible entries were also pintos (EX2140-P and P2-098), which were no less susceptible than Beryl, and demonstrate that not all interspecific derived lines possessed equivalent tolerance. Field trial data for white mold disease ratings were collected in MI, ND, and OR but only ND had meaningful disease pressure as environmental conditions at the other locations were not conducive for sufficient disease development (Table 2). Focusing on the ND trial, checks ranked as expected, with G122 having the significantly lowest WM score. Among the experimental entries, EX2146-P, EX2141-P, P3-157, and P2-101 pintos all showed promising moderate scores of 4.2 to 4.9 (Table 2). Importantly, P2-101 had the lowest WM score (4.2) and also produced the highest yield (2988 lbs/acre) in the trial, suggesting it possesses a desirable combination of high yield and high disease tolerance. EX2146-P also demonstrated a similar combination of lower disease (4.9) with second best yield (2838 lbs/acre). This underscores both the success of introgressing improved disease tolerance from *P. coccineus* as well as the continued importance of selecting simultaneously for both high yield potential under intense white mold disease pressure rather than focusing solely on a low disease rating. Both of these entries would be valuable as parents in future crosses.

Table 1. Straw test results for twenty-one dry bean lines evaluated in the greenhouse at four locations.

Name	Breeder	Class	WA	ND	MI	OR	Mean	Group
EX2140-P	Kmiecik	PTO	7.8	7.8	5.5	7.3	7.3	A
P2-098	Miklas	PTO	6.8	8.1	5.9	6.3	6.8	A
Beryl	Check	Check	6.5	7.4	7.0	6.6	6.8	A
WMM-556	Osorno	SDP	7.0	6.3	5.5	3.9	5.8	B
ND172330	Osorno	BLK	6.5	7.3	5.1	3.3	5.7	BC
WMM-820	Osorno	SDP	6.3	6.0	5.2	4.4	5.6	BC
WMM-750	Osorno	SDP	5.8	4.1	6.1	5.3	5.3	BCD
NDF151006-2	Osorno	SR	6.5	5.1	4.3	4.5	5.3	BCD
EX2142-P	Kmiecik	PTO	5.5	3.5	4.7	6.7	5.2	BCDE
P3-157	Miklas	PTO	6.4	4.8	5.1	3.4	5.1	CDEF
Bunsi	Check	Check	6.2	3.9	5.1	4.6	5.1	CDEF
EX2145-P	Kmiecik	PTO	5.5	3.9	5.1	5.6	5.1	CDEF
P2-101	Miklas	PTO	5.6	6.3	4.3	3.6	5.1	CDEF
USPT-WM-12	Check	Check	4.6	4.4	5.4	5.5	4.9	DEFG
ND151660	Osorno	LTK	5.9	5.5	4.7	2.6	4.8	DEFGH
EX2146-P	Kmiecik	PTO	5.4	4.0	4.1	5.0	4.8	DEFGH
EX2141-P	Kmiecik	PTO	4.9	3.9	4.7	4.5	4.5	EFGH
G122	Check	Check	4.0	5.9	4.8	3.7	4.5	EFGH
ND222212	Osorno	SDP	4.9	3.8	4.5	4.0	4.4	FGH
P3-055	Miklas	PTO	4.5	4.5	5.2	2.9	4.3	GH
ND211214	Osorno	DRK	4.3	5.3	4.4	2.6	4.1	H
GRAND MEAN			5.8a	5.3b	5.1b	4.6c	5.3	
*WM Score rated on Petzoldt & Kickson scale: 1-3=Resistant, 4-6=intermediate, 7-9=susceptible.								
**Means followed by the same letter not significantly different at p≤0.05.								

Table 2. Yield and disease ratings for sixteen dry bean lines evaluated in the field at two locations for seed yield and white mold disease severity.

Combined Multi-State Yield Summary and Analysis						Multi-State White Mold Scores					
Name	ND*	Group	MI*	Mean**	Group	ND	Group	OR*	MI*	Mean*	Group*
Beryl	899.7	G	1806	1287.9	F	8.1	A	5.5	7.7	6.8	A
WMM-556	1986.2	F	3460	2617.8	BCD	7.7	AB	5.7	5.7	6.3	A
ND222212	2454.4	BCDE	3525	2913.2	AB	7.4	ABC	2.7	2.3	4.0	BC
EX2140-P	2341.1	CDEF	2332	2336.5	D	7.3	ABCD	4.2	1.3	4.5	B
NDF151006-2	2168.4	EF	2578	2344	D	6.7	BCDE	3.0	3.3	4.2	B
WMM-750	2617.3	ABCDE	2934	2775.7	ABC	6.3	CDE	3.7	2.7	4.3	B
WMM-820	2767.7	ABC	3426	3049.6	A	6.1	DEF	3.3	2.7	4.0	BC
Bunsi	962.7	G	1784	1314.6	F	5.9	EF	3.2	4.0	4.2	B
EX2145-P	2369.2	BCDEF	2950	2659.7	ABCD	5.7	EFG	3.3	2.0	3.8	BCD
ND151660	2295.8	DEF	920.9	1706.5	E	5.7	EFG	4.8	2.6	4.6	B
USPT-WM-12	2643	ABCD	2142	2428.4	CD	5.6	EFGH	3.3	3.0	4.0	BC
EX2146-P	2838.4	AB	2393	2647.3	BCD	4.9	FGHI	2.0	1.7	2.8	CD
EX2141-P	2515.3	ABCDE	2800	2657.8	BCD	4.5	GHI	3.7	3.5	3.9	BC
P3-157	2252	DEF	1477	1919.8	E	4.4	HI	3.5	1.3	3.3	BCD
P2-101	2988.2	A	2741	2882.3	AB	4.2	I	2.3	2.0	2.8	CD
G122	2284.1	DEF	2429	2346.3	D	2.8	J	2.0	3.0	2.5	D
Mean	2261.5		2481	2359.1		5.8a		3.5b	3.1b	4.1	
*Yield in Lbs/A @ 18%; Means followed by the same letter not significantly different at p≤0.05.											
**Multi-State Mean Yield presented above; note that only ND had meaningful disease pressure in 2025.											

GENETIC VARIABILITY OF GERMPLASM OF BEANS CULTIVATED IN OAXACA, MEXICO

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The study of beans (*Phaseolus* spp.) in their centers of domestication provides insights into their evolution and diversification and supplies information for formulating conservation and utilization strategies. Farmers mix seeds when sowing, seeking to mitigate seasonal changes during the crop cycle. The effect of these practices on the genetic structure of bean populations in the hands of farmers should be documented in native populations with potential value that are at risk of erosion or extinction (6). This study characterized the genetic structure of bean germplasm cultivated by farmers from different ethno-territorial regions of Oaxaca, Mexico.

The germplasm (71 common bean accessions) was collected in six regions of Oaxaca (Mixteca, Sierra Norte, Sierra Sur, Istmo, Valles Centrales, Cañada) and characterized with 14 genomic and genic microsatellite loci; Negro COMAPA and Negro Jamapa (*P. vulgaris*) and accessions 8180 and 8690 (*P. coccineus*) were included as controls. Genomic DNA was obtained using the Wizard® kit (Promega®; Madison, USA), following the manufacturer's recommendations. The 14 SSR markers (1, 4, 8) are located in genomic regions (BM 143, 154, 161, 170, 175, 181, 183, 184, 200, 211, 212) and in genic regions (PH7, PH10, Bmd1).

Genetic analysis identified 297 alleles; the highest number of alleles, effective alleles, and private alleles were observed in germplasm from the Mixteca region, and the highest heterozygosity was observed in populations from the Central Valleys and Sierra Sur regions. The highest proportion of variance was explained between populations, within populations, and to a lesser extent between regions of origin of the populations. Principal coordinate analysis identified three genetic groups: I. Mixteca-Isthmus, II. Sierra Norte-Mixteca, and III. Cañada-Sierra Sur-Valles Centrales (Fig. 1). Cluster analysis using a Bayesian approach determined an optimal value of $\Delta K = 3$, generating a population structure consisting of three genotype clusters (Table 1). The first genetic group consists mainly of populations from the Mixteca region. The second group consists of genotypes from the Sierra Norte and Mixteca, and the third group is dispersed and includes populations from the Cañada, Sierra Sur, and Valles Centrales. In previous studies, *P. vulgaris* beans from the northern Sierra of Oaxaca were separated from germplasm from other species (*P. dumosus* and *P. coccineus*) (7). Native bean populations form groups that do not reflect a single variety, but are influenced by morphological traits, geographical adaptation, uses and cultivation systems, and even sociocultural and economic factors (3). In this study, greater allelic diversity was observed in beans from the Mixteca region and greater heterozygosity in genotypes from the Valles Centrales and Sierra sur. While more than 20 alleles per locus were observed in Oaxacan beans, other studies report lower numbers, depending on the genetic status and origin of the germplasm analyzed (2, 5, 9).

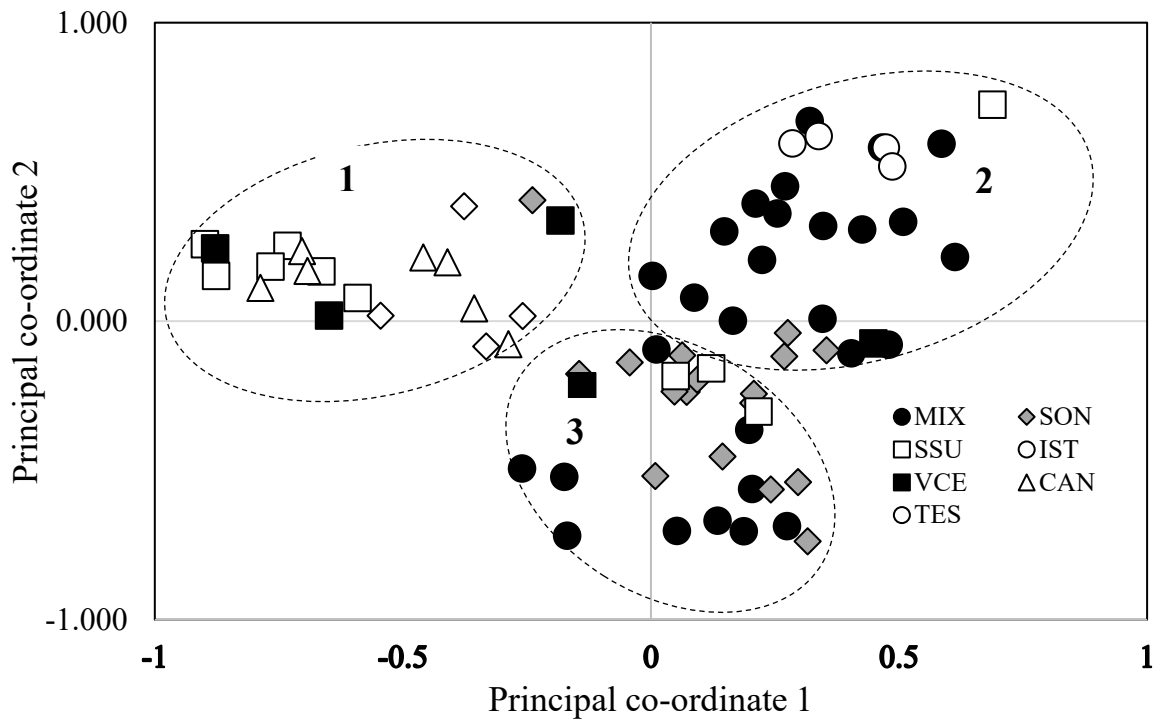


Figure 1. Dispersion of beans from Oaxaca, Mexico, based on principal coordinate analysis and SSR data (MIX = Mixteca, SON = Sierra Norte, SSU = Sierra Sur, IST = Istmo, VCE = Valles Centrales, CAN = Cañada, TES = Control).

Table 1. Germplasm of Oaxacan beans included in each genetic group of the Bayesian cluster analysis of SSR data.

Group	n	Cañada	Istmo	Mixteca	Sierra Norte	Sierra Sur	Valles Centrales	Controls
1	27	0	4	19	1	2	1	0
2	27	0	0	9	16	2	0	0
3	21	7	0	0	0	6	4	4
Total	75	7	4	28	17	10	5	4

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SNP DISCOVERY AND QTL MAPPING IN POPPING BEAN

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INTRODUCTION

Popping beans (*Phaseolus vulgaris* L.) are a class of common bean native to the highlands of South America. They belong to the Andean gene pool and when heated expand while creating a “pop” sound similar to popcorn (Zimmerer, 1986). The toasted, soft-texture beans have the potential of being a healthy snack. Identifying the genetic control of the popping trait is valuable in developing suitable cultivars for production in the United States. The objective of this study was to identify and characterize QTLs associated with the popping trait in a bi-parental population.

MATERIALS AND METHODS

PI 316019 (popping bean) was crossed with W6 33807 (black bean) and advanced via single seed descent to the F₄ generation in a greenhouse during winter (October 2023 to May 2024) with no supplemental light. The average temperature was 25±2 °C with humidity between 60 - 70%. After harvest, the seeds were cleaned for phenotyping. Three sets of ten seeds were toasted with sand in a cast iron skillet for 90 seconds. An infrared thermometer was used to measure the sand's temperature before popping ranging between 213 °C to 286 °C. Genotyping by sequencing was used to sequence leaf tissue from 142 F₄ lines to obtain SNP markers. Tassel version 5 was used for SNP calling, and linkage map construction was performed with Joinmap version 4.1. QTL analysis was performed using composite interval mapping and trait-marker associations were identified in WIN QTL-cartographer.

RESULTS AND DISCUSSION

A total of 1286 markers were mapped onto 11 linkage groups spanning 2247.1 cM. The average distance between markers was 0.59 cM/locus. Four QTLs detected by composite interval mapping explained 8.95-13.89 % of the phenotypic variation and combined explained 32.88%. A positive additive effect on chromosome 11 showed favorable allele contribution from PI 316019 for popping performance. A negative additive effect was found on chromosomes 2 and 3 indicating loci where the favorable allele was contributed by W6 33807. A similar pattern has been reported by Yuste-Lisbona et al. (2012) where the non-popping parent contributed favorable alleles at specific loci and through epistatic interactions. Yuste-Lisbona et al. (2012) also found QTLs for popping dimension index and expansion coefficient on chromosome 3.

Table 1: QTL effects detected for popping ability in an F₄ population of a cross between PI 316019 (popping bean) and W6 33807 (black bean).

Chr.	Marker	Pos.	LOD Score	Additive	Dominance	R ²	TR ²	S	QTL Name
2	112	91.3	3.87	-1.67	0	10.71	28.52	2.60	Pop-02-a
2	123	99.1	5.16	-1.63	0	13.89	31.71	2.50	Pop-02-b
3	118	77.0	4.60	-1.43	0	12.36	32.1	2.45	Pop-03-a
11	24	107.7	3.23	1.46	0	8.95	32.88	2.63	Pop-11-a

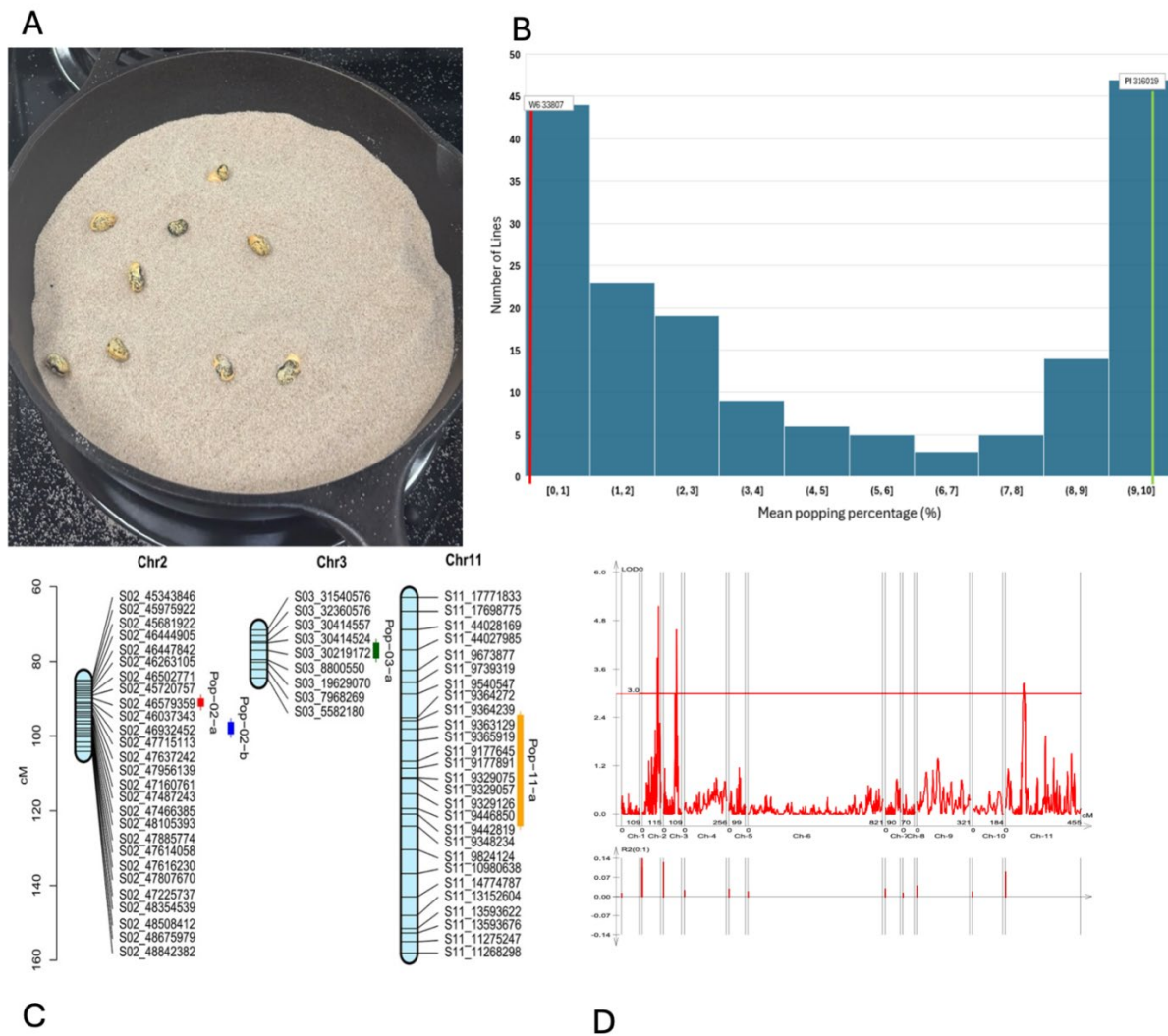


Figure 1: Popped beans in sand (A), Distribution of mean popping percentage across parents and F₄ population (B), Linkage groups with identified QTL positions (C), QTLs across all linkage groups (D)

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A PRACTICAL HAPLOTYPE GRAPH FOR TEPARY BEAN

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INTRODUCTION: With increasing numbers of genomic datasets, methods have been developed to identify and store genome diversity data for a species that utilizes a graph-based approach to identify and store sequence relationships, such as alleles (haplotypes) and structural variants. Currently, most pan-genome analyses are focused on genic content differences between accessions and have limited utility for users such as plant breeders and quantitative geneticists. To address these needs, the Practical Haplotype Graph (PHG) was developed and implemented for several crop species¹⁻⁴. To enable haplotype discovery and haplotype-based breeding for tepary bean, we constructed a PHG for tepary bean.

Table 1. Tepary genomes used as founders for the Practical Haplotype Graph.

TDP No.	Accession No.	Biological Status	Country	Importance
TDP001	G40001	Cultivated	Mexico	Reference genome; Parent of RIL population; Moghaddam et al. 2021 ⁵
N/A	W6 15578	Wild	Mexico	Reported in Moghaddam et al. 2021 ⁵
TDP013	G40022	Cultivated	USA	Parent of RIL population
TDP312	TARS-Tep 23	Improved	Puerto Rico, USA	Rust immunity, caused by <i>Uromyces appendiculatus</i>
TDP136	G40168	Wild	Mexico	Unique habit, terminal raceme (type 5)
TDP154	G40177E1	Wild	USA	Large seed; high nodulation capacity; resistant to common bacterial blight
TDP159	G40178	Wild	Mexico	Resistant to bean common mosaic necrosis virus (BCMNV) strain NL3
TDP176	G40199	Wild	Mexico	Resistant to common bean weevil (<i>Acanthoscelides obtectus</i>)

MATERIALS AND METHODS: Using Oxford Nanopore Technologies (ONT) genomic long read sequencing, we generated the genome sequence for six TDP accessions with key agronomic traits (Table 1). The G40001 (Frijol Bayo) genome and annotation was used as the reference for the PHG whereas the wild accession W6 15578⁵ and our six new ONT genome assemblies were used as additional ‘founder’ genomes. Consensus haplotypes at the G40001 reference loci were then determined using the PHG software (v2, https://github.com/maize-genetics/phg_v2).

RESULTS: Across the reference loci, consensus haplotypes in the Tepary Bean PHG v1 ranged from a single haplotype to eight haplotypes across all eight genomes (Table 2), reflecting loci that are highly conserved as well as diverged across the founder genomes. In general, haplotype diversity corresponded to gene density although regions of the genome with limited haplotype diversity were present (Figure 1).

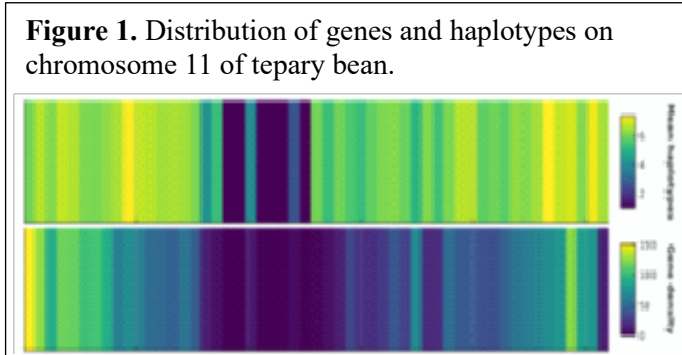


Table 2. Gene representation in PHG across founder genomes

No. of Founder Genomes in Reference Range	No. of Genes
1	81
2	116
3	28
4	95
5	140
6	266
7	1,034
8	30,094

SUMMARY: Using a combination of founder genome assemblies, we constructed v1 of a Tepary Bean PHG and determined the extent of haplotype diversity in tepary bean within these

accessions. We are currently expanding the founder genomes to capture haplotypes present across subpopulations that represent the overall diversity of tepary bean. We will then use whole genome shotgun sequence data from the Tepary Diversity Panel to impute haplotypes across the panel.

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THE COMPLEX *C* LOCUS: GENOMIC ORGANIZATION IN THE ANDEAN GENEPOOL

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INTRODUCTION

Seed coat color and pattern are defining traits of dry bean market classes worldwide and are strongly influenced by regional consumer preferences. Several genes controlling seed coat coloring and patterning have been cloned or genetically characterized, including *P* and *V*, with additional candidate genes proposed for *Bip*, *T*, and *Z* (Bassett, 2007; Parker et al., 2024; McClean et al., 2018, 2022, 2024). The complex *C* locus plays a central role in regulating mottling and striping patterns through interactions with other seed coat color genes. Historically, *C* has been described either as a multi-allelic locus or as a cluster of tightly linked genes located on chromosome Pv08 (McClean et al., 2002). Despite its importance, the genetic architecture underlying seed coat striping and mottling remains unresolved. In this study, we integrated next-generation sequencing with genetic mapping using recombinant inbred line (RIL) populations to identify candidate genes associated with these phenotypes, providing new insights into the molecular control of seed coat patterning in Andean common bean.

MATERIALS AND METHODS

Two genetic maps were developed using F_{5:7} RIL populations derived from the crosses ‘Rojo’ (*rk^d* / *c^u* / *B*; red kidney) × ‘CAL-143’ (*Rk* / *C^m* / *b*; red mottled), referred to as the RC population, and ‘G122’ (*RK* / *Cst* / *b*; cranberry) × ‘Montcalm’ (*rk^d* / *c^u* / *B*; dark red kidney), hereafter referred to as GM population. Both populations were genotyped using the BARCBear12K SNP BeadChip and genotyping-by-sequencing (GBS), with SNPs aligned to the *Phaseolus vulgaris* G19833 v2.1 reference genome. Phenotypic data for seed coat pattern (solid versus mottled or striped) from each RIL population were converted into binary classes and mapped using MapDisto v1.7.7 software. Furthermore, PACE markers were developed and genotyped in the GM RIL population.

To further investigate the structural variation underlying these phenotypes, parental lines Rojo and CAL-143 were sequenced using Nanopore long-read technology (>3 kb; ~6× coverage). Genome assemblies of Montcalm reported by McClean et al. (2022) were also aligned to the *P. vulgaris* G19833 (*Cst*; liborino) v2.1 reference genome. A dominant 268-bp insertion–deletion (indel) marker was subsequently developed and mapped in the RC RIL population; this marker amplified exclusively in CAL-143 and G122, which carries the *C^m* and *Cst* alleles, respectively.

RESULTS AND DISCUSSION

Seed coat pattern variation in both the RC and GM RIL populations mapped to the proximal region of chromosome Pv08. The solid (Rojo) versus mottled (CAL143) phenotype was located between 1.29 and 3.53 Mb, and an indel marker overlapping the first exon of Phvul.008G038400 co-segregated with the trait and mapped at 0 cM relative to the *C^m/c^u* locus. In the GM population, the striped (G122) versus solid (Montcalm) phenotype was refined to a narrower interval between 3.06 and 3.23 Mb.

Long-read sequencing revealed a 12.8-kb deletion spanning 3.18–3.19 Mb in the Rojo and Montcalm lines carrying the c^u allele. This deletion encompasses Phvul.008G038400, which encodes a MYB5 transcriptional repressor. Additionally, in genotypes carrying the C^m and c^u alleles, a premature stop codon was identified in Phvul.008G038200, and a likely transposase-mediated inversion was detected in Phvul.008G038600. This inverted segment was subsequently translocated upstream of the Phvul.008G038300 gene model (Figure 1).

The C locus delimited in common bean (RC and GM) shows homology to two genomic regions in soybean (*Glycine max*; Wm82.a6.v1 reference genome), located on chromosomes Gm09 (46,685,827–46,786,405 bp) and Gm18 (57,392,168–57,492,407 bp). Notably, Gm09 interval corresponds to the R locus in soybean, which is associated with black, brown, and striped seed coat patterns. Within this region, the gene model Glyma.09G235100 (formerly Glyma09g36990 [v109 a1_1.0] or Glyma09g36983 [v189 a1_1.1]) was identified as homologous to the *P. vulgaris* gene models Phvul.008G038200 and Phvul.008G038600 (BLASTp; p -value = 1.32×10^{-108}). The Glyma.09G235100 locus corresponds with the RM55- r^m allele, which is homozygous for a mutable allele (rm) that specifies black and brown striped seeds in soybean (Gillman et al., 2011; Zabala & Vodkin, 2014).

Together, these results provide a base for identifying candidate genes underlying other genes in the complex C locus, including R , Gy , and Pi , and for developing molecular markers associated with distinct seed coat color patterns controlled by the C locus. These findings also advance our understanding of whether the C locus represents a truly multi-allelic locus or a cluster of tightly linked genes, thereby offering new evidence to support and refine the complex C -locus hypothesis.

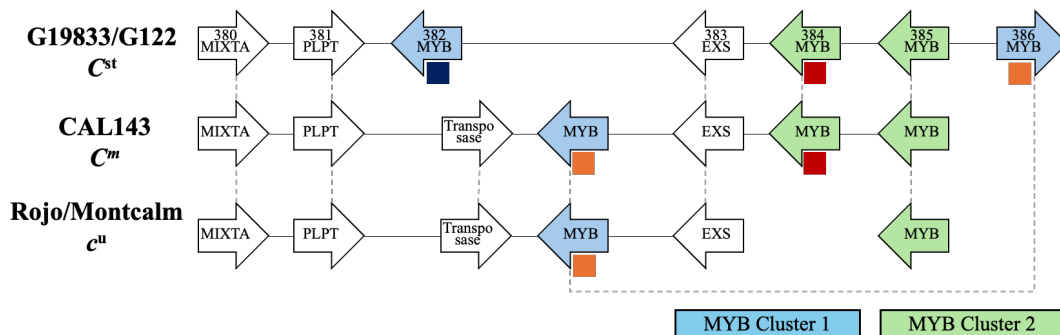


Figure 1. Structural organization of the complex C locus in Andean genotypes carrying the C^{st} , C^m , and c^u alleles. The candidate gene Phvul.008G038400 (gene 384; red square) is present in C^{st} and C^m genotypes. Phvul.008G038600 (gene 386; orange square) is transposed in C^m and c^u genotypes, likely via a transposase-mediated event. Phvul.008G038200 (gene 382; dark blue square) is detected only in C^{st} genotypes. Based on a UPGMA protein dendrogram (data not shown), MYB genes were grouped into cluster 1 (light blue) and cluster 2 (light green).

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APPLICATIONS OF YIELD AND SUITABILITY MODELS FOR COMMON BEAN IN THE MEXICAN TROPICS AND SUBTROPICS

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INTRODUCTION. Common bean (*Phaseolus vulgaris* L.) is a staple crop in the tropical and subtropical regions of Mexico, where production is predominantly rainfed and is frequently constrained by periods of terminal drought, high climatic variability, and soil limitations such as acidity and low fertility (Fadda et al., 2025). These adverse environmental conditions lead to low and unstable grain yields and pose a major challenge to sustainable bean production, a situation that has been exacerbated under current climate change scenarios. In this context, simulation and spatial modeling approaches have emerged as useful tools to analyze crop–environment interactions, estimate yield, and identify environmentally suitable areas for cultivation (Fadda et al., 2026). Therefore, the objective of this study was to assess which models have been applied in the tropical and subtropical regions of Mexico to estimate suitable areas and/or common bean yield, as well as to identify the main advantages and limitations of their use.

MATERIALS AND METHODS. A systematic review was conducted following the Reporting Standards for Systematic Evidence Syntheses (ROSES) protocol as a methodological framework. Bibliographic searches were performed in Scopus, Web of Science, and Google Scholar, covering studies published between 2000 and 2024 that applied quantitative modeling approaches to estimate yield and/or environmental suitability of common bean in tropical and subtropical regions of Mexico. The search strategy combined keywords related to the crop (“common bean”, “*Phaseolus vulgaris*”) and modeling approaches (“simulation model”, “crop model”, “ecological niche model”, “species distribution model”). The selected literature was analyzed and classified according to model type, environmental variables used, and spatial scale of application.

RESULTS AND DISCUSSION. The reviewed studies indicate a growing use of modeling approaches to estimate yield and identify suitable areas for common bean in the tropical and subtropical Mexico. Linear and statistical models were commonly applied and showed good predictive performance under rainfed and irrigated conditions, highlighting the importance of key edaphoclimatic variables such as temperature indices, soil moisture, and evapotranspiration for supporting planting decisions. Correlative modeling approaches were used to delineate agroclimatically suitable areas and to project changes in the potential distribution of common bean under climate change scenarios. These studies consistently reported reductions in suitable areas under unfavorable climatic conditions, particularly in regions characterized by fragile soils and heterogeneous landscapes. Mechanistic models were applied in fewer cases to explore the response of common bean to changes in precipitation and temperature, providing insights into potential impacts on yield and cultivated area. However, across all modeling approaches, the main limitations identified were the scarcity of high-resolution climatic and edaphic data and the limited availability of cultivar-specific parameters, which constrain model transferability and applicability at local scales.

Table 1. Modeling approaches applied to common bean in Mexico

Model	Purpose	Strengths	Limitations	Application
Linear models	Yield estimation	Simple; interpretable; low data demand	No physiological processes; limited extrapolation	Yield prediction and identification of key climatic and edaphic drivers
Correlative models (e.g. Maxent)	Environmental suitability	Works with few records; spatial projection	Sensitive to data quality; no management or genotype	Delineation of suitable areas and climate change projections
AquaCrop	Water–yield relationships	Efficient for water stress analysis; few parameters	Limited interaction among stressors	Yield response under water-limited tropical conditions
CLIMEX	Climatic suitability	Integrates thermal and moisture thresholds	No soil or management variables	Broad-scale climatic suitability assessment
ALMANAC	Crop growth simulation	Captures local variability	High parameterization	Applied in semi-arid regions; high potential in tropics

CONCLUSIONS. The models applied show strong potential to support common bean planting in the tropical and subtropical regions of Mexico. The identification of areas with environmental suitability provides a basis for determining the most appropriate sites for crop production and for assessing the yield potential of varieties adapted to the edaphoclimatic conditions of each region. Strengthening data availability and integrating emerging technologies will be essential to improve model accuracy and to support staple grain production in the face of climate change impacts.

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LARGE SCALE ENVIRONMENTAL GENOME-WIDE ASSOCIATION STUDY OF LANDRACES OF COMMON BEAN (*PHASEOLUS VULGARIS* L.): CURRENT PROGRESS

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INTRODUCTION. The common bean (*Phaseolus vulgaris* L.) is one of the most consumed legumes in the world and is a very important source of protein in Latin America and Africa. However, under climate change, beans will be under two pressures, as the area suitable for the crop will shrink and the nutritional quality of the harvest will be reduced (Hummel et al., 2018). As such, new sources of genetic variation are needed to adapt the crop to these new scenarios. Germplasm collections are important sources of genetic diversity, which makes the vital for current and future breeding efforts. Access and use of germplasm is limited because characterization data is limited and generating it at scale is expensive. This gap in knowledge can be addressed by using genomic and environmental data together in an environmental genome-wide association study (envGWAS), which permits the analysis of many genebank accessions. This work presents the preliminary results from multiple envGWAS with a combined total of 7,938 landraces of the common bean. The aim of this work is the identification of candidate alleles for heat and drought tolerance and the genebank accessions enriched for these significant markers.

MATERIALS AND METHODS. Genotyping. DNA was extracted from 11,465 common bean landrace accessions sourced from the Future Seeds germplasm bank of the Alliance Bioversity & CIAT. Sequencing and genotyping with DArTseq was done by SAGA (Mexico) and DArT P/L (Australia) in multiple batches and one global calling with all accessions included.

Climate data. The genotyped accessions had geographic coordinates available as part of their passport information (available at: <https://www.genesys-pgr.org/>). These georeferenced points were revised and curated using reverse geocoding and available documentation. From the initial list of 10,000 accessions, climate data was extracted from 8,175. The environmental variables extracted included: average maximum temperature, average minimum temperature, precipitation, vapor pressure deficit, aridity index and soil pH.

ENVGWAS. Codominant (SNP) and dominant markers (SilicoDArT) were initially used to assign landraces to three genetic groups: The Andean or Mesoamerican gene pools, the result of the domestication of the crop, and the admixed group, which exhibits intermediate ancestry coefficients (Figure 1). To reduce the effect of this genetic structure, the envGWAS was run with each genetic group separately. FarmCPU (Liu et al., 2016), LFMM2 (Frichot & François, 2015) and MatrxQTL (Shabalin, 2012) were used to fit the genomic and environmental data. The first two models were used with SNPs and all three with SilicoDArTs. Marker-trait associations (MTAs) were considered significant if found in all models tested.

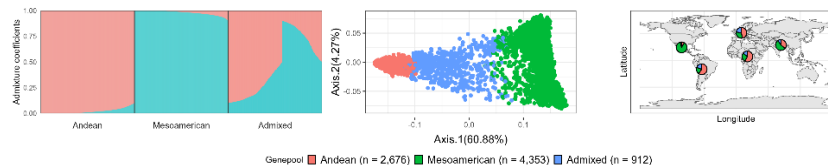


Figure 1. A. Estimated admixture coefficients. B. Principal Coordinate Analysis (PCoA). C. Assignment of accessions to gene pools across continents. Numbers in round brackets indicate sample size.

RESULTS AND DISCUSSION. Significant MTAs were found across all genetic groups, markers, and chromosomes of the common bean genome (Figure 2). Most associations were found in the Andean dataset, followed by the Mesoamerican and the Admixed. A functional annotation of these variants indicates that 10 of them have effects on the translated protein, 9 of them cause missense changes in the sequence, while one variant causes the gain of a stop codon. Identification of relevant candidate genes for adaptation to heat and drought and their putative function is underway, as well as the selection of accessions enriched for the MTAs identified.

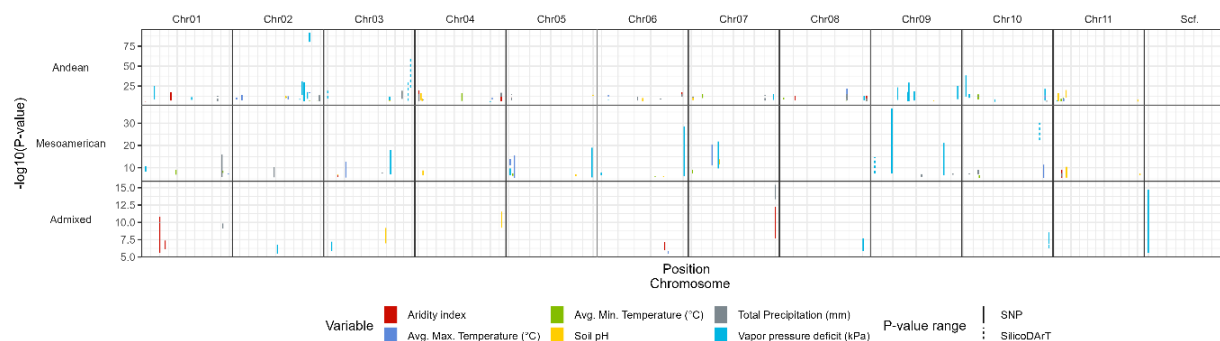


Figure 2. Summary of envGWAS results. Manhattan plot showing the location of significant associations from multiple GWAS models, environmental variables and genetic markers. Length of bars indicates range of p-values across models. Scf: Scaffold

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PHENOMICS-DRIVEN EARLY DETECTION AND BREEDING FOR ANTHRACNOSE RESISTANCE IN ONTARIO DRY BEANS

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INTRODUCTION: Dry beans (*Phaseolus vulgaris* L.) are a globally important legume, valued at \$30 billion USD from 27 million metric tonnes produced in 2020, and a rich source of protein, essential nutrients, and fiber (Messina, 2014; FAO, 2023). Anthracnose, caused by the seed-borne fungus *Colletotrichum lindemuthianum*, is a major threat in Ontario, causing severe yield and quality losses (Zuiderveen et al., 2016; Sharma et al., 2007). Conventional visual scoring is time-consuming, labor-intensive, subjective, and poorly predictive of field performance, particularly at early growth stages (Sharma et al., 2007; Simons et al., 2022). In addition, early detection before visible symptoms is critical, as conventional assessments identify infection only after lesions appear, by which point physiological disruption limits screening efficiency (Mahlein, 2016; Bock et al., 2008; Simons et al., 2022). High throughput phenomics (HTP), especially hyperspectral imaging, provides objective, rapid, and non-destructive methods for improving disease resistance screening (Furbank & Tester, 2011). HTP also enables rapid evaluation of large populations, improving early-generation selection and accuracy for complex traits like disease resistance. Hyperspectral imaging shows strong potential for early disease detection by capturing pathogen-induced physiological changes before symptoms appear (Mahlein et al., 2019). Therefore, this study aims to develop early anthracnose detection tools (particularly against race 73) and integrate phenomics into Ontario breeding pipelines. The specific objectives are to: (1) assess causes of resistance breakdown (new races vs. reduced efficacy against race 73); (2) develop high-throughput spectral imaging for early detection in breeding populations; (3) identify phenotypic markers to improve resistance selection; and (4) integrate phenomics tools into pipelines for high-yielding, anthracnose-resistant cultivars.

METHODS: Controlled-environment experiments were conducted in growth chambers prior to planting (2025 season), using a completely randomized design (CRD) with four replicates and two treatments (inoculated and non-inoculated). Six cultivars with contrasting anthracnose responses were tested: resistant (Rogue and Spades), intermediate (Argosy and Storm), and susceptible (Lighthouse and Zorro). Uniform temperature, humidity, and photoperiod conditions were maintained to minimize environmental variability and isolate disease-related physiological responses. The spatial arrangement included controls, inoculated treatments, differential lines, and replications. Inoculated plants received spore suspensions (1.2×10^6 spores/ml) of race 73 at the

last vegetative growth stage for consistent infection pressure (Dufresne et al., 2000; Padder et al., 2017). Non-inoculated plants served as controls. Early infection establishment was confirmed using confocal microscopy (Figure 1), to visualize pathogen structures and progression before symptoms.

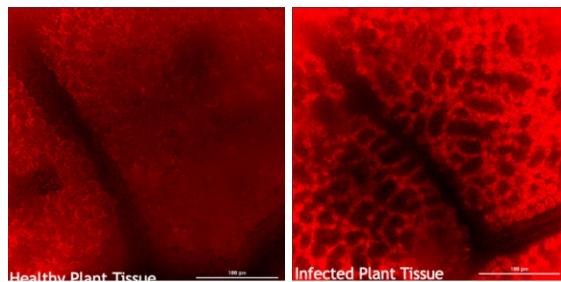


Figure 1. Lighthouse control showing signs of infection using confocal microscopy.



Hyperspectral imaging captured early physiological changes using a Specim IQ camera (400-1100 nm) from top and side views under halogen illumination, chosen for its broad spectrum resembling natural light. Reflectance patterns were analyzed to identify disease-sensitive wavelengths and indices associated with early anthracnose infection, building on established principles of spectral disease detection (Mahlein, 2016; Mahlein et al., 2019). QGIS was used to generate spatial data points for disease scoring and reflectance extraction (Figure 2), using images from all six cultivars and differential lines, capturing temporal changes in physiological and morphological responses.

Figure 2. Example analyses focused on the susceptible cultivar Zorro (Treatment Side Rep 1). Image 1 bands assigned to default wavelengths (red = 598.60 nm, green = 548.44 nm, blue = 475.50 nm). Image 2 bands assigned as red = 696.61 nm, green = 548.44 nm, and blue = 699.60 nm were used to visualize potential early stress indicators, with the band combination designed to enhance detection of early physiological responses using two red bands and one green band, thereby highlighting structural and chlorophyll changes.

RESULTS: Pathogen surveys from 2024 Ontario fields confirmed race 73 as the dominant race (~80 % of isolates). Confocal microscopy (Figure 1) showed biotrophic hyphal growth inside epidermal cells 2–4 days post-inoculation in cultivars lines, progressing to necrotrophic secondary hyphae and lesions by day 6–8; healthy controls had no pathogen structures. Spectral analysis identified the band combination red = 696.61 nm, green = 548.44 nm, blue = 699.60 nm as optimal for visualizing pre-symptomatic stress in Zorro (Figure 2, Image 2), indicating anthocyanin accumulation and chlorophyll degradation as early markers. Field trials (2025, Elora/Woodstock) will validate these tools under natural conditions and support the development of durable resistance.

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PILOT PRODUCTION OF TYPE IV CLASSIC FLAT WHITES™ USING A LIVING TRELLIS SYSTEM

Ken Kmiecik

Honorary Researcher U.W.- Madison, Ken Kmiecik, LLC

Many desirable dry beans are in type IV plant types and have limited availability and production. The Classic Flat Whites™ are a medium large flat white type of bean suitable and adapted for braising and exhibit a high level of seed integrity during cooking. Cultivars/landraces that comprise the Classic Flat Whites™ include landraces and modern varieties such as: Alaric (Hubert Bannrot), Soisson Blanc (INRA), and Planchada (Spain).

The flat white beans grouped under the trademark Classic Flat Whites™ are white in color, medium/large sized having a seed weight of 55-75 grams/100 seeds (825-613 seeds/lb). The typical seed length of 10 seeds set end to end is between 170 and 190 mm, seed height between 9-10 mm, and seed width/thickness of 5-6 mm which reflects their flatness. Currently all varieties and landraces grouped as Classic Flat Whites™ are type IV climbers and genetically appear to group together.

In an effort to expand the use and availability of this type of bean there is breeding effort under way to address several agronomic constraints including: building a trellis, hand labor for harvest and a late maturity. Currently the high cost of production pushes retail cost up into the \$7 and \$12 a pound range. This cost restricts access to these beans for many general consumers and while breeding can address some of the agronomic constraints in the long term, it is also possible to consider alternative production strategies.

In dry bean production areas such as Idaho or Central Valley in California it is possible to produce some of these materials on the flat, especially with furrow irrigation. In an effort to expand potential production into North Central production areas such as: North Dakota, Minnesota, Michigan, and Wisconsin, the CFW (classic flat white) project began to look at use of a living trellis to keep beans off the ground, then combining beans & trellis crop together, and separating the two crops post-harvest. It is an old idea using modern tools and technology.

Since the inception of the project type IV climbing beans of various sorts have been successfully grown and combined on popcorns, grain sorghum, and sunflowers at an early research level while building Western seed stocks. Seed cleaning and processing post-harvest based on size, weight, and color has been used to successfully separate various seed crops from each other. Combinations of techniques used in seed cleaning and processing vary with the trellis crop and bean grown. The combination of a corn or sorghum crop with beans has limited herbicides available to conventional growers. Sunflowers as a trellis crop has added some herbicide options. By in large the greatest interest in this system has been from organic growers looking to enter niche markets, along with an interest in the high soil surface residues left after harvesting a trellis crop and beans together.

As of 2025 the CFW Project has certified Western grown seed for limited pilot productions. Working with several members of the Artisan Grain Collaborative (AGC) pilot productions will be done in Michigan (1 ac.), Ohio (5 ac.), and Wisconsin (10 ac.) Collection of data on plant

populations, yields of beans and trellis crops, along with management information will be collected and made available to interested parties.

LOW-COST, HIGH-THROUGHPUT METHOD FOR HYDROGEN CYANIDE DETECTION IN SUCCULENT LIMA BEAN SEEDS

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INTRODUCTION

Lima bean (*Phaseolus lunatus*) produces linamarin and lotaustralin, two cyanogenic glycosides that release hydrogen cyanide (HCN) upon hydrolysis by the β -glucosidase linamarase¹. These components come together when tissue is disrupted (e.g., by insect damage or mechanical injury), releasing gaseous HCN². Seed HCN levels vary widely among lima bean germplasm, from undetectable in most U.S. cultivars to over 2000 ppm in some wild accessions³. Although processing methods such as cooking, boiling, and fermentation effectively reduce cyanide content, acute cyanide intoxication occurs at doses as low as 0.5mg/kg body weight⁴, necessitating routine screening of breeding material. Analytical methods such as HPLC and gas chromatography provide precise quantification of HCN but are low-throughput, costly, and require specialized expertise. The picrate paper assay offers a rapid, low-cost alternative, but requires in-house preparation with picric acid, a hazardous compound, and the resulting strips have a limited shelf life^{5,6}. Here, we evaluate Cyanotesmo paper (Macherey-Nagel) as a commercially available alternative for detecting HCN in succulent lima bean seeds, requiring no hazardous reagents or in-house strip preparation.

MATERIALS AND METHODS

A freeze-thaw approach was used to promote controlled tissue disruption. Succulent beans were frozen at -80°C for at least 12 hours, then transferred into 3D-printed 50-well plates designed to accommodate large-seeded lima beans. Alternating wells were left empty to prevent cross-contamination from HCN diffusion. Each plate included one positive control, PI 535341 (wild lima bean with high seed HCN content), and one negative control, succulent cowpea (no HCN content). Commercial Cyanotesmo paper (Macherey-Nagel, Düren, Germany; detection limit: ≥ 0.2 mg/L cyanide) was placed above the wells without direct contact with the frozen samples, and wells were sealed with transparent packaging tape to contain released HCN. Sealed plates were incubated at 55°C for two hours to promote thawing and enzymatic hydrolysis, as linamarase activity is highest near this temperature⁷. Immediately after incubation, plates were scanned on a flatbed scanner alongside a color reference card to enable standardized image-based phenotyping⁸. The assay was also conducted using standard ice cube trays as an accessible alternative to the 3D printed plates.

RESULTS AND CONCLUSIONS

The positive control (PI 535341) consistently changed from pale green to blue across all three biological replicates, whereas the negative control (cowpea) showed no detectable response, indicating high assay specificity and reproducibility (Figure 1). The method also performed reliably in ice cube trays, successfully distinguishing positive and negative control samples. A separate test strip must be used per well and each well must be completely sealed to prevent lateral diffusion of HCN gas between adjacent samples. Because HCN release is proportional to tissue

mass, differences in seed size among accessions influence the total HCN produced per well. Cutting seeds to standardize tissue quantity would prematurely trigger hydrolysis, so semiquantitative comparisons require standardization by seed weight. This freeze–thaw Cyantesmo protocol provides a practical, low-cost method for screening lima bean germplasm for cyanogenic capacity. We are currently refining the 3D printed plate design to eliminate the need for empty spacer wells and applying this method to evaluate HCN levels across a diverse panel of lima bean accessions.

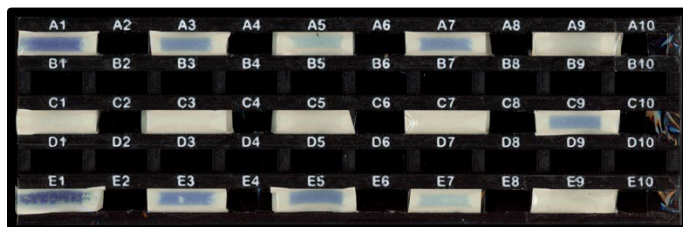


Figure 1. HCN detection using Cyantesmo paper in a 3D-printed 50-well plate after incubation at 55°C for 2 hours. Blue coloration indicates HCN release. The positive control (PI 535341, wild lima bean; well E1) produced a strong color change, while the negative control (cowpea; well E9) showed no response. Remaining wells contain experimental lima bean accessions with varying levels of color change.

ACKNOWLEDGEMENTS

We thank Dr. Emmalea Ernest for identifying PI 535341 as having high seed cyanide content, and Blake Wilson for designing and 3D-printing the 50-well plates for the assay.

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PHASEOLUS EXPLORATION AND COLLECTION IN THE SOUTHWESTERN USA

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INTRODUCTION

An international team was assembled in 2023 to explore and collect *Phaseolus* germplasm—primarily wild tepary bean (*P. acutifolius*) but also *P. filiformis* (Slim Jim bean). It has continued since then with annual missions, and when given the opportunity, collected other *Phaseolus* species. The geographic focus was New Mexico, an area underrepresented in germplasm collections. The primary objective was to secure genetic diversity of heat and drought tolerant wild relatives of common bean (*P. vulgaris*). Additional objectives were to increase our knowledge of the *Phaseolus* genus in the semi-arid, southwestern USA by obtaining herbarium vouchers, soil, and nodule samples from roots, and recording collection site characteristics.

MATERIALS AND METHODS

Specific regions were targeted based on the provenance of herbarium specimens, observations reported at the iNaturalist website (<https://www.inaturalist.org/>), and observations from scouting trips, with the soil moisture status of those areas as indicated by the U.S. Drought Monitor (<https://droughtmonitor.unl.edu/>) (Debouck et al. 2025). Emphasis shifted to eastern New Mexico and the Trans-Pecos region of far-west Texas (also underrepresented in seedbank collections) in 2025 because drought was less prevalent there.

RESULTS

The team encountered severe drought conditions in 2023 and 2024 but managed to identify sites which collectively contained all six native species (*P. acutifolius*, *P. angustissimus*, *P. filiformis*, *P. grayanus*, *P. maculatus* and *P. parvulus*) (Wootton and Standley, 1915; Freytag and Debouck, 2002).

Herbarium vouchers were obtained, and limited seed was secured, in 2023. The majority of herbaria and seed samples were obtained during 2024-2025. The team learned about microhabitats and nearby vegetation types of each taxon, which enabled it to find additional populations more readily. Populations were mostly found in protected areas of Upper Basin arroyos (primarily in the foothills) and in Mesquite/Scrub Oak Transition areas, while some were found in Madrean Forest Juniper/Pine habitats of Sky Island mountains (Figure 1).

The team has added a total of 35 new populations of wild tepary to the USDA collection at Pullman, WA from the 2023-2025 collections in New Mexico, the border area in Arizona, and the Trans-Pecos region of Texas. These collections are currently being regenerated. They will be accessioned and made available when sufficient seed has been generated.



Figure 1. Photographs of environments representing four distinct ecoregions of the Chihuahuan Desert (24a -Chihuahuan Basins and Playas, 24c - Low Mountains and Bajadas, 24d – Chihuahuan Montane Woodlands, and 24h – Lava Malpais) where wild tepary bean populations have been found during plant explorations in fall 2023-2025. Clockwise from top left Aden Lava Flow, NM; Sierra Vista Rec. Area, NM; Franklin Mountains, TX; Madera Canyon Trail, TX. Collection numbers, year, ecoregion, and elevation appear on the photo.

CONCLUSION

Multiple factors (e.g., extreme drought and record heat, "desperate" grazing, urban development, and forest fires) pose a cumulative threat for wild *Phaseolus* species in the Southwest. One or more of these factors may cause the soil seed bank to fail to recover sufficiently to ensure long-term survival of the populations. Engagement with public and private entities has enhanced the consideration of wild crop relatives in their management planning. Pilot projects of *in-situ* conservation in key areas, e.g. to examine questions related to the soil seed bank, will require additional outreach efforts. Support from the wider bean community is needed for evaluations of these accessions. Benefits they disclose will hopefully support further conservation actions.

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RESISTANCE GENE MAPPING AND TRANSCRIPTOMIC PROFILING OF COMMON BEAN IN RESPONSE TO THE INFECTION BY *COLLETOTRICHUM LINDEMUTHIANUM*

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INTRODUCTION

Bean anthracnose, caused by the fungus *Colletotrichum lindemuthianum*, leads to significant seed yield losses and is characterized by high genetic diversity, with numerous races reported worldwide (Nunes et al., 2021). The development of cultivars with durable resistance to *C. lindemuthianum* should therefore emphasize the pyramiding of resistance genes from both the Middle American and Andean gene pools. Beija Flor is an Andean common bean cultivar that exhibits broad-spectrum resistance to *C. lindemuthianum* and carries the *Co-Bf* resistance gene. Transcriptome sequencing (RNA-seq) has been applied to investigate genes associated with anthracnose resistance in common bean, providing valuable insights into host responses during the early stages of infection (Chang et al., 2024; Dambroz et al., 2025). In this study, we fine-mapped the *Co-Bf* gene and conducted RNA-seq analyses of Beija Flor and the susceptible cultivar Crioulo 159 to identify differentially expressed genes (DEGs) associated with anthracnose resistance.

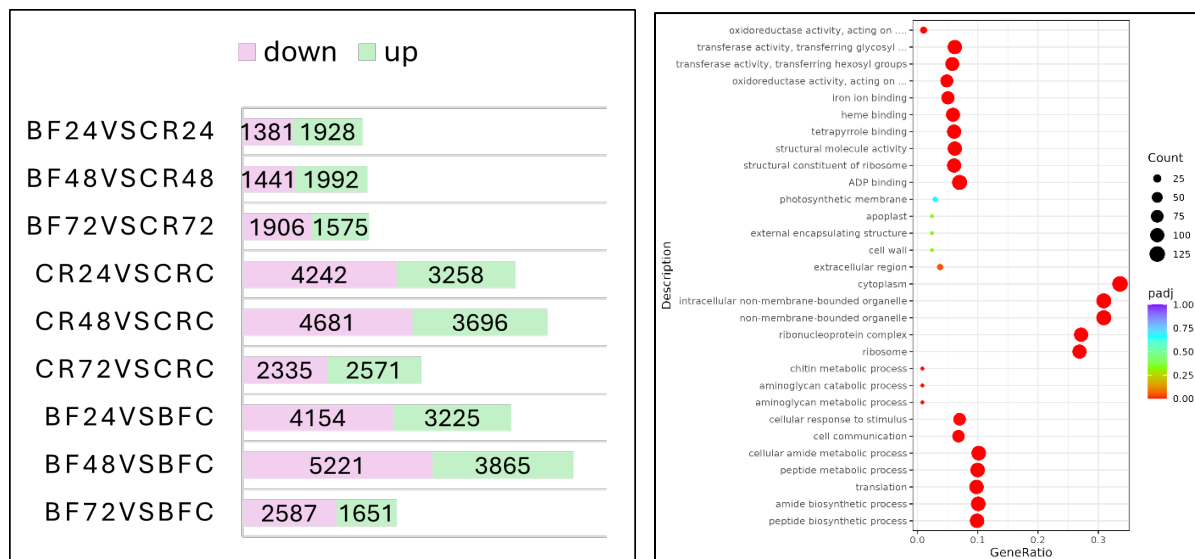
MATERIAL AND METHODS

Fine mapping of the *Co-Bf* gene from the Beija Flor cultivar was conducted using F₂ plants and F_{2:3} families derived from the Beija Flor (BF) × Crioulo 159 (CR) cross and genotyped with KASP markers. To further investigate genes associated with anthracnose resistance, RNA-seq analysis was performed using BF and CR cultivars. Fifteen plants per cultivar were grown, of which twelve were inoculated with race 453 of *C. lindemuthianum*, while three plants served as uninoculated controls. Inoculation was performed on the abaxial surface of primary leaves at 10 days after sowing, using a spore suspension of 1.2×10^6 spores mL⁻¹. Plants were incubated in a mist chamber at 20 ± 2 °C and >95% relative humidity in darkness for 48 h and then transferred to a greenhouse bench. Primary leaves were collected from three biological replicates per cultivar at 24, 48, and 72 h after inoculation (hai), as well as from control plants at 24 h. Samples were immediately frozen in liquid nitrogen and stored at -80 °C until further processing. Three additional inoculated plants per cultivar were maintained for anthracnose symptom evaluation. Total RNA was extracted from ground leaf tissue, mRNA was purified, and cDNA libraries were constructed for sequencing. Illumina sequencing was performed on the NovaSeq X Plus platform with 150 bp paired-end reads (>6 Gbp of raw data per sample) by Novogene (USA). Reads were mapped to the common bean reference genome using HISAT2 v2.0.5, gene expression levels were quantified as FPKM, Gene Ontology (GO) enrichment and KEGG pathway analyses of DEGs were performed using R software. Regulation patterns of significant DEGs were first analyzed across all comparisons. DEGs were classified into three groups: (i) DEGs showing concordant regulation between cultivars; (ii) DEGs exhibiting reciprocal regulation or cultivar-specific expression, potentially

associated with resistance mechanisms; and (iii) DEGs exhibiting reciprocal regulation or cultivar-specific expression, potentially associated with susceptibility mechanisms.

RESULTS AND DISCUSSION

The *Co-Bf* locus was mapped to a 30.2 kb genomic region on chromosome Pv04, within which three candidate genes were annotated, including *Phvul.004G005600.1*, which encodes a putative NBS-LRR resistance protein (Xavier et al., 2025). To identify DEGs potentially involved in the resistance response of common bean to anthracnose, RNA-seq analysis was performed. DEGs were identified using a threshold of fold change > 1 and $p < 0.05$. Initially, all DEGs were considered potential candidates associated with resistance or susceptibility (Fig. A). This list was subsequently refined based on expression patterns across contrasts. In total, 1,174 DEGs showed concordant regulation between BF and CR, likely associated with shared or basal responses; 2,830 DEGs exhibited reciprocal regulation or cultivar-specific expression, potentially linked to resistance mechanisms; and 1,307 DEGs were potentially associated with susceptibility mechanisms. Among these DEGs, 117 contained CC, kinase, LECM, LRR, LYSM, NBS, TIR, TM, and/or TRAN domains, or were classified as pathogenesis-related, disease resistance, or antifungal. The *Phvul.004G005600.1* gene showed upregulation with higher expression at 72 hai in BF compared to CR. In the same comparison, BFvsCR at 72 hai, revealed enrichment of GO terms associated with sustained activation of protein synthesis and redox homeostasis, indicating their importance in defense responses to *C. lindemuthianum* (Fig. B). Overall, resistance in BF appears to be a complex trait involving the coordinated action of multiple genes distributed across the genome, reflecting the complexity of host responses to this genetically diverse pathogen.



A) Number of differentially expressed genes in different combinations (Note: BFC- Beija Flor control; CRC- Crioulo 159 control); B) Number of DEGs categorized by Gene Ontology enrichment terms in the comparison between Beija Flor (R) and Crioulo 159 (S) at 72 hai.

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AGRONOMIC PERFORMANCE, NUTRITIONAL QUALITY AND COOKING TRAITS OF COMMON BEAN GENOTYPES GROWN UNDER TERMINAL DROUGHT CONDITIONS IN SOUTH-CENTRAL CHILE

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INTRODUCTION: Winter precipitation in Chile is projected to decline by more than 40% by the end of the century, contributing to a prolonged mega-drought characterized by reduced rainfall and Andean snowmelt. Under these conditions, drought stress is expected to affect both agronomic performance and grain quality of common bean (*Phaseolus vulgaris* L.), influencing yield components, bioactive compounds, and antioxidant capacity.

MATERIALS AND METHODS: The experiment was conducted at the Santa Rosa Experimental Station of the Instituto de Investigaciones Agropecuarias (INIA), located in Chillán, Chile, during the 2021/22 and 2022/23 seasons under Mediterranean climate conditions. The experimental design was a randomized complete block design (RCBD) with four replicates, including 20 common bean genotypes, comprising 15 lines from the University of Nebraska (USA) and 5 Chilean cultivars. Two water regimes were evaluated: under well-watered (ND) and terminal drought (DS) conditions, during the reproductive stage. The evaluated traits included grain yield (GY), number of grains per unit area (NGP), and hundred-grain weight (HGW). Grain quality parameters included crude protein content (PC), total phenolic content (TPC), antioxidant activity (DPPH), hydration capacity (HC), and cooking time (CT). Statistical analyses were performed using analysis of variance (ANOVA) under a general linear model (GLM). In addition, Pearson correlation analysis and heatmap visualization were conducted using RStudio software (v4.2.1).

RESULTS AND DISCUSSION: (DS) significantly reduced grain yield, with mean values declining from 3.891 kg ha⁻¹ under (ND) to approximately 3023 kg ha⁻¹, representing a 22.3% reduction. This decrease was primarily driven by a strong reduction in the number of grains per plant (−61.3%), confirming that reproductive processes are the most sensitive to water deficit. In contrast (HGW) showed a comparatively smaller reduction (≈10%), suggesting a partial compensation mechanism through assimilate remobilization during grain filling. The decline in harvest index (from 75% to ≈61%) further indicates a reduced efficiency in biomass partitioning toward reproductive organs under stress conditions.

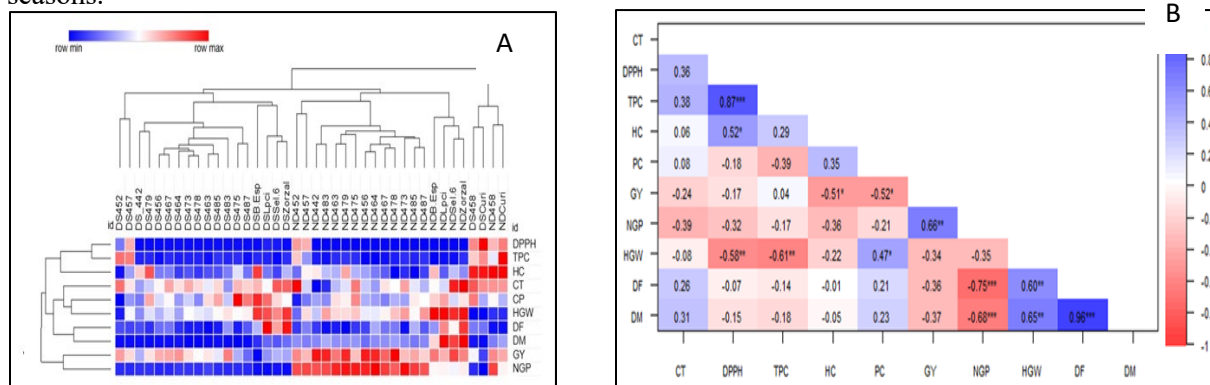
The differential genotypic response highlights the importance of physiological resilience mechanisms. Genotypes 452, 473, and 483 maintained yield stability (<11% reduction), suggesting improved source–sink balance and better stress tolerance, while Blanco Español, Curi, and Zorzal exhibited marked sensitivity (>50% reduction), likely associated with a stronger disruption of reproductive development and assimilate allocation under drought.

In grain quality (PC) remained stable or slightly increased under DS, the increase in (TPC) and (DPPH) across most genotypes suggest that drought stress induces the accumulation of phenolic compounds in several genotypes, likely as part of an antioxidant defense mechanism.

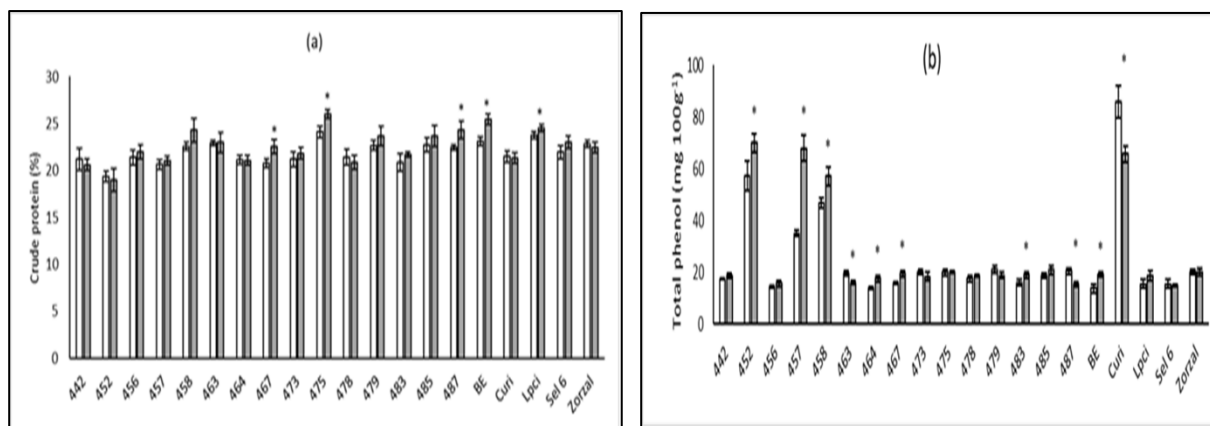
The observed increase in (HC) under DS conditions may be linked to potentially modifications in cell wall components or protein–starch interactions. In contrast (CT) showed a genotype-dependent response, with some genotypes exhibiting increased cooking time under DS. This variability suggests that ND during seed development can influence the physicochemical properties of seed coats and cotyledons, thereby altering cooking behavior.

CONCLUSIONS: Terminal drought significantly reduces common bean yield, however it can simultaneously promote the accumulation of bioactive compounds. While most genotypes maintained stable protein content under stress conditions, several exhibited increased total phenolic content and antioxidant capacity, suggesting an adaptive biochemical response associated with oxidative stress mitigation.

Figures 1. Heatmap and cluster (A) analysis ND and DS during two seasons and (B) Pearson correlation analysis among traits evaluated in twenty bean genotypes under Drought Stress (DS) during two seasons.



Figures 2. (a) Crude Protein Content (PC) and (b) Total Phenolic Content (PCT).



Error bars represent the standard error of the mean. Means followed by asterisks indicate significant differences between ND and DS for the same genotype, as determined by the independent samples t-test ($p \leq 0.05$).

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Tay, K.; Zapata, N.; Urrea, C.A.; Elazab, A.; Garriga, M.; León, L. Screening Terminal Drought Tolerance in Dry Bean Genotypes and Commercial Bean Cultivars in Chile. *Agronomy* 2025, 15, 1499. <https://doi.org/10.3390/agronomy15071499>

SUBJECT MATTER INDEX – BIC 2026

Abiotic Stress, Heat, Drought	47,49,51,77,117,157
Anthracnose	57,69,75,83,127,147, 155
Bruchids, Seed Storage	17,119
Common Bacterial Blight	15,79
Genetics, Genomics, Breeding	1,7,9,21,23,25,71,73,77,85,87,91,105,137,139,141,145
Genomic Selection	23,25,51,71
Germplasm, Diversity, Wild Relatives	3,7,9,17,21,61,87,105,135,145, 153
Interspecific Populations	11,75,79,105
Machine Learning, Phenotyping	17,27,29,45,63,93,147
Markers and Mapping	15,21,27,35,37,69,75,81,83,137
Nematodes	33
Nitrogen Fixation, Rhizobia	5, 89
Nutrition, Quality	21,25,27,41,43,53,151
Root Traits, Architecture	3,35,39,65
Rust	29,129
Seed Traits, Yield	1,9,27,43,53,67,73,85,95,97,99,101,103,107,109,115,143
White Mold, Sclerotinia	61,63,125,133
Yield and Stability	49,67,85,95,99,107,143

BIC FINANCIAL STATEMENT – 2025

BALANCE AS OF January 1, 2025 (US Bank)	\$ 20,048.44
INCOME	
2025 Membership Dues	\$465.70
BIC meeting sponsorships	\$17,850.00
Funds transfer from Paypal	\$9,333.55
BIC meeting net profit (after split with NAPIA)	\$5,904.49
Bank Interest	\$0
TOTAL INCOME	\$33,553.74
EXPENSES	
Labor charges	\$650.00
Postage, Copy Charges and Office Supplies	\$56.00
Pdf & Book editing and publishing fees	\$685.00
BIC Student travel awards (2025 meeting)	\$19,650.00
PayPal Fees	\$156.15
Bank Fees	\$136.00
TOTAL EXPENSE	\$21,333.15
BALANCE AS OF December 31, 2025	\$ 32,269.03