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TABLE OF CONTENTS

	Page
LIX Annual Report of the Bean Improvement Cooperative	i
BIC Committee Membership - 1957 to 2016	ii
BIC Genetics Committee Minutes	iii
2015 BIC Award Recipients	v
In Memory of M. Wayne Adams	ix
In Memory of James Ronald Baggett	x
In Memory of Hubert Bannerot	xi
In Memory of Merion Margaret Liebenberg.	xii
In Memory of Ronald Shellenberger	xiii
Letter to the BIC: Sclerotinia sclerotiorum isolates available for research	xiv
Review Paper: Major Loci Controlling Resistance to Angular Leaf Spot – Souza, T.L.P et al..	xv

RESEARCH PAPERS FOR 2016

ORAL REPORTS

HIGH DENSITY SNP GENOTYPING OF LINES WITH DIFFERENT STORAGE PROTEIN COMPOSITION REVEALS SITES OF INTERSPECIFIC INTROGRESSION AND MARKERS ASSOCIATED WITH PHASEOLIN OR LECTIN DEFICIENCY Diapari, M1, Pandurangan, S, Song, Q, Cregan, PB, Miklas, P, Marsolais, F,	1
INSIGHTS FROM SYNTENY ANALYSIS BETWEEN BEAN AND SOYBEAN Pauls KP, Reinprecht Y, Perry G, Martin JM, Munholland S, Crosby W, Siddiqua M, Qi Y, Castro ED, Xie W, and Smith T	3
CURRENT BEAN GERMLASM COLLECTIONS AND ACTIVITIES IN SPAIN De Ron AM, De la Rosa L, Marcos T, Lázaro A, Casañas F, Casquero PA, Ferreira JJ and Ruiz de Galarreta J	5
NUCLEOTIDE POLYMORPHISMS OF TWO NOVEL DREB GENES IN WILD MESOAMERICAN COMMON BEAN ACCESSIONS ARE STRUCTURED ACCORDING TO ENVIRONMENTAL VARIABLES Enéas Ricardo Konzen ¹ , Jorge Carlos Berny ² , Andrea Ariani ² , Gustavo Henrique Recchia ¹ , Paul Gepts, Siu Mui Tsai ¹	7
INVESTIGATING THE ROLE OF CANDIDATE GENES IN DROUGHT TOLERANCE OF COMMON BEAN GENOTYPES Konzen E.R.; Recchia G.H.; Pereira, A.C.V.Z.; Biazuzo, M. M. A.; Berny J.C.; Caldas D.G.G., Gepts P.; Tsai S.M.	9
SOYBEAN CYST NEMATODE - A THREAT TO DRY BEAN PRODUCTION Berlin D. Nelson Jr.	11
TOWARDS AN UNDERSTANDING OF INTERACTIONS BETWEEN BACTERIAL VIRULENCE FACTORS AND GENES IN BEAN RESISTANCE QTL FOR BREEDING BEANS WITH DURABLE COMMON BACTERIAL BLIGHT RESISTANCE Weilong Xie, Tom Smith, Gregory Perry, and K. Peter Pauls.	13
DEVELOPMENT OF A BLACK BEAN LINE THAT COMBINES BRUCHID AND MULTIPLE VIRUS RESISTANCE Beaver J.S., González, A., Trukhina, Y., and Porch T.G.	15
MAPPING THE <i>Co-1</i> LOCUS CONDITIONING ANTHRACNOSE RESISTANCE IN COMMON BEAN Grady Zuiderveen, Bilal Padder, Kelvin Kamfwa, and James D. Kelly.	17
EFFECT OF SEED-TO-SEEDLING TRANSMISSION OF COLLECTOTRICHUM INDEMUTHIANUM IN DRY EDIBLE BEANS UNDER FIELD CONDITIONS Jessica M. Halvorson, Kristin Simons, Robin Lamppa, Robert L. Conner, and Julie S. Pasche.	19

MOLECULAR CHARACTERIZATION OF <i>BEAN COMMON MOSAIC VIRUS</i> ISOLATE OVERCOMING THE <i>BC-3</i> ALLELE IN COMMON BEAN Xue Feng, James R. Myers, and Alexander V. Karasev	21
BREEDING COMMON BEAN FOR RESISTANCE TO WHITE MOLD Shree P. Singh, Howard F. Schwartz, Henry Terán, Carlos Centeno and Kristen Otto.	23
COLOR RETENTION IN CANNED BLACK BEANS Karen A Cichy, and Fernando Mendoza	25
MAPPING THE NON-DARKENING TRAIT FROM WIT-ROOD IN A PINTO BEAN POPULATION USING SNP MARKERS Erfatpour M, and Pauls KP	27
DISSECTING PHENYLPROPANOID PATHWAY IN COMMON BEAN (<i>PHASEOLUS VULGARIS</i>) BY RNA-SEQ BASED TRANSCRIPTOME PROFILING Siddiqua M, Munholland S, Crosby WL, and Pauls KP	29
UNDERSTANDING AND IMPROVING FLAVOR IN SNAP BEANS: SCREENING THE USDA PHASEOLUS CORE COLLECTION FOR POD SUGAR AND FLAVOR COMPOUNDS James Nienhuis, Theodore Kisha and Paul Bethke.	31
BREEDING FOR A FAST COOKING BEAN: A STUDY OF GENOTYPES ACROSS ENVIRONMENTS TO DETERMINE STABILITY OF THE COOKING TIME TRAIT IN <i>PHASEOLUS VULGARIS</i> Berry, M, Wiesinger, J, Nchimbi-Msolla, S, Miklas, P, Porch, T, Fourie, D, and Cichy, K	33

POSTERS

PHYSIOLOGICAL RESPONSES OF TWO DROUGHT-TOLERANT COMMON BEAN CULTIVARS Androcioni, L.G.; Tomaz, J.P., Moda-Cirino, V.	35
MINERAL DISTRIBUTION IN THE SEED COAT, COTYLEDONS AND EMBRYONIC AXIS IN COMMON BEAN CULTIVARS FROM DIFFERENT CENTERS OF ORIGIN Buratto, J.S.; Sholz, M.B.S.; Moda-Cirino, V.	37
AN EFFICIENT CULTURE MEDIUM FOR INCREASING SPORULATION OF <i>PSEUDOCERCOSPORA GRISEOLA</i> Caixeta MP, Gonçalves-Vidigal MC, Valentini G, Calvi AC, Elias JCF	39
VIRULENCE AND GENETIC DIVERSITY OF <i>PSEUDOCERCOSPORA GRISEOLA</i> ISOLATES FROM PARANÁ STATE, BRAZIL Gonçalves-Vidigal MC, Caixeta MP, Valentini G, Coelho M and Gálvan MZ	41
A PROTEIN BINDING IS INVOLVED IN THE RESPONSE TO POWDERY MILDEW IN THE COMMON BEAN CULTIVAR PORRILLO SINTETICO Campa A, Ferreira JJ	43
PHENOLIC COMPOSITION AND BIOACCESSIBILITY AS AFFECTED BY PRESSURE COOKING AND IN VITRO GASTROINTESTINAL DIGESTION OF REGULAR- AND NON-DARKENING CRANBERRY BEANS (<i>PHASEOLUS VULGARIS L.</i>) Chen PX, Marcone MF, and Pauls KP, Tsao R	45
GENETIC PARAMETERS IN COMMON BEAN UNDER DROUGHT STRESS Elias JCF, Gonçalves-Vidigal MC Valentini G, Franzon RC, Martins VS, Lacanallo GF, Moda-Cirino V	47
CONSERVATION AND CHARACTERIZATION OF NATIVE <i>PHASEOLUS VULGARIS</i> GERMPLASM FROM NORTHWESTERN ARGENTINA Ferreira MJ, Ibarra L, Menéndez Sevillano MC, De Ron AM and Galván M.	49
GENOTYPE X ENVIRONMENT INTERACTION ANALYSIS BY MIXED MODELS IN BRAZILIAN COMMON BEAN INBRED LINES Franzon RC, Gonçalves-Vidigal MC, Caixeta MP, Vidigal Filho PS, Gilio TAS, Castro SAL	51

NEW ALLELE IN THE AND277, MICHIGAN DARK RED KIDNEY AND JALO EEP558 ANDEAN CULTIVARS LINKED TO THE G2303 MOLECULAR MARKER Gonçalves-Vidigal M, Gonçalves-Coimbra G, Lacanallo G, Sousa L, Martins VS, Coelho M and Vidigal Filho PS	53
GENETIC MAPPING OF THE ANTHRACNOSE RESISTANCE GENE CO-14 IN THE COMMON BEAN CULTIVAR PITANGA Gonçalves-Vidigal MC, Pacheco CMNA, Vidigal Filho PS, Lacanallo GF, Sousa LL, Martins VSR	55
THE VALIDATION OF QTLs FOR POD QUALITY TRAITS IN SNAP BEANS (<i>PHASEOLUS VULGARIS L.</i>) THROUGH ASSOCIATION MAPPING IN THE BEAN CAP POPULATION Mashitah Jusoh and James Nienhuis	57
EFFECT OF IRRIGATION AND PLANT CANOPY ARCHITECTURE ON WHITE MOLD DEVELOPMENT IN DRY BEAN Kazi A. Kader, Parthiba M. Balasubramanian and Syama Chatterton	59
INVESTIGATING PHENOTYPIC VARIABILITY AND SENSITIVITY IN VITRO TO THE FUNGICIDES OF PSEUDOCERCOSPORA GRISEOLA STRAINS Samira S. Librelon, Rafael Pereira, Elaine A. de Souza and Luanna de B. W. Gomes	61
PATHOGENIC VARIABILITY OF COLLETOTRICHUM LINDEMUTHIANUM IN THE STATE OF PERNAMBUCO, BRAZIL Martiniano-Souza MC, Gonçalves-Vidigal MC, Lacanallo GF, Costa AF, Dartibale GB, Paulino PPS	63
SOURCES OF RESISTANCE TO ANTHRACNOSE IN TRADITIONAL ACCESSIONS OF COMMON BEAN FROM PERNAMBUCO STATE, BRAZIL Martiniano-Souza MC, Gonçalves-Vidigal MC, Castro SAL, Costa AF, Dartibale GB, Franzon RC and Vidigal Filho PS	65
GENETIC ANALYSIS OF YIELD COMPONENTS IN <i>PHASEOLUS VULGARIS L.</i> UNDER DROUGHT STRESS Martorelli DT, Martins VSR, Gonçalves-Vidigal MC, Lacanallo GF, Moda-Cirino V, Castro SAL, Coimbra GK and Caixeta MP	67
INTERACTION OF COMMON BEAN WITH RHIZOCTONIA SOLANI AND TRICHODERMA SPP. Mayo S., Gutiérrez S., Lorenzana A., Campelo P., González-López, O., Rodríguez-González, A., Casquero P.A.	69
GENOTYPIC VARIATION FOR TOLERANCE TO LOW SOIL PHOSPHOROUS IN COMMON BEAN UNDER CONTROLLED GREENHOUSE CONDITIONS Eninka Mndolwa, Harold P Collins and Phillip Miklas	71
RECURRENT SELECTION TO DEVELOPMENT OF CARIOCA TYPE COMMON BEANS CULTIVARS AT IAPAR Moda-Cirino, V.; Buratto, J.S.; Fonseca Jr., N.S.	73
ESTABLISHING IN VITRO REGENERATION TECHNOLOGY FOR COMMON BEAN (<i>PHASEOLUS VULGARIS</i>) VARIETIES Nowak J., Marsolais F., Tian L.	75
AN <i>IN SILICO</i> ANALYSIS OF PHENYLPROPANOID PATHWAY GENE FAMILIES IN COMMON BEAN: CYTOCHROME P450 Yarmilla Reinprecht, Gregory E. Perry and K. Peter Pauls	77
GENETIC ANALYSIS OF SEED HARDNESS TRAIT IN A BLACK BEAN RECOMBINANT NBRED LINE (RIL) POPULATION Kulbir S. Sandhu and Anfu Hou	79
MODIFIED SCREENING METHOD REVEALS PARTIAL ANTHRACNOSE RESISTANCE TO RACE 73 IN 16 GENOTYPES OF THE MESOAMERICAN DIVERSITY PANEL OF DRY BEANS Stephan Schröder, Samira Mafi Moghaddam, Ali Soltani, Sujan Mamidi, Robin Lamppa, Julie S. Pasche, Juan M. Osorno	81

GENETIC MAPPING OF THE COMMON BEAN RECOMBINANT INBRED LINES CALIFORNIA DARK RED KIDNEY × YOLANO USING SSR AND STS MOLECULAR MARKERS Sousa LL, Gonçalves-Vidigal MC, Valentini G, Vidigal Filho PS, Gilio TAS and Gepts P.	83
CHARACTERIZATION OF THE ANTHRACNOSE RESISTANCE GENE PRESENT IN THE ANDEAN CULTIVAR PERLA Taboada G, Galván M, Castro SAL2 Lacanallo GF and Gonçalves-Vidigal MC.	85
RELATIONSHIP BETWEEN PHYSIOLOGICAL AND PHENOLOGICAL TRAITS WITH ROOT PULL-OFF FORCE OF COMMON BEAN Tomaz, J.P.; de Barros, L. M., de Oliveira, F. , Fonseca Jr, N. da S.	87
VERDIN, OPAQUE DRY BEAN CULTIVAR TOLERANT TO TROPICAL TERMINAL DROUGHT OF SOUTHEAST PRODUCTION AREAS OF MEXICO Oscar Hugo Tosquy-Valle, Ernesto López-Salinas, Francisco Javier Ibarra-Pérez, Bernardo Villar-Sánchez, José Raúl Rodríguez-Rodríguez, Jorge Alberto Acosta-Gallegos	89
IDENTIFICATION OF QTL FOR RESISTANCE TO WHITE MOLD IN DRY BEAN I9365-25 Renato Vasconcellos, Qijian Song and Phil Miklas	91
IDENTIFYING WATERLOGGING TOLERANT DRY BEAN (<i>PHASEOLUS VULGARIS L.</i>) GENOTYPES USING CHLOROPHYLL CONTENT Katelynn Walter, Ali Soltani, Carlos F. Velasquez, Edgar G. Escobar, Juan M. Osorno	93
DIVERSITY FOR SYMBIOTIC NITROGEN FIXATION AND RELATED TRAITS IN COMMON BEAN (<i>PHASEOLUS VULGARIS L.</i>) Jennifer L Wilker, A Navabi, SM Moghaddam, T Porch, P McClean and KP Pauls	95
REGULAR REPORTS	
IDENTIFICATION OF TROPICAL BLACK BEAN BREEDING LINES RESISTANT TO BCMV AND BCNMV USING MOLECULAR MARKERS José Luis Anaya-López, Francisco Javier Ibarra-Pérez, Ernesto López-Salinas, Oscar Hugo Tosquy-Valle and Jorge A. Acosta-Gallegos.	97
BIOLOGICAL AND MOLECULAR CHARACTERIZATION OF <i>BEAN COMMON MOSAIC VIRUS</i> ISOLATES FROM PATHOGENICITY GROUPS I AND V Xue Feng, James R. Myers, and Alexander V. Karasev	99
UNRAVELING THE BROAD AND COMPLEX RESISTANCE IN COMMON BEAN CULTIVAR MEXICO 235 TO <i>UROMYCES APPENDICULATUS</i> Oscar P. Hurtado-Gonzales, Thiago A. S. Gilio, Marcial A. Pastor-Corrales	101
RESISTANCE TO FUSARIUM WILT IN COMMON BEAN CULTIVARS AND LINES IN PRE-COMMERCIAL STAGE Helton Santos Pereira, Leonardo Cunha Melo, Thiago Lívio Pessoa Oliveira de Souza, Luís Cláudio de Faria, Adriane Wendland, Mariana Cruzick de Souza Magaldi	103
SCREENING ANDEAN DRY BEAN GERMPLASM FOR ROOT ROT RESISTANCE Chilvers, M.I., Jacobs, J.L., Byrne, A.M., Kelly, J.D.	105
PATHOGENICITY AND VIRULENCE OF RHIZOCTONIA SOLANI AND PYTHIUM SPP. ON DRY BEAN Jacobs J.L., Rossman D.R., Tippie J., Witte A. and Chilvers M.I.	107
SNP MAPPING OF QTL ASSOCIATED WITH RESISTANCE TO APHANOMYCES ROOT ROT IN SNAP BEAN Kasukurthi Joseph RV, Felix Navarro and James Nienhuis	109
IDENTIFYING GENOMIC REGIONS ASSOCIATED WITH HALO BLIGHT RESISTANCE WITHIN THE USDA CORE COLLECTION OF COMMON BEAN Kiran Ghising, Julie S. Pasche, Robin Lamppa, Stephan Schroder, Jose Vasquez-Guzman, Ali Soltani, Samira Mafi Moghaddam, Sujana Mamidi, Kevin McPhee, Philip E. McClean, and Juan M. Osorno	111

RACES OF PSEUDOMONAS SYRINGAE PV. PHASEOLICOLA FROM YELLOW BEANS GROWN IN SINALOA, MÉXICO Rosa Navarrete-Maya, Rubén Félix-Gastélum and Jorge A. Acosta-Gallegos	113
IDENTIFICATION OF COMMON BEAN RESISTANT SOURCES TO ANGULAR LEAF SPOT DISEASE IN A BRAZILIAN GERMPLASM COLLECTION P.F. Pádua; Q.L. Barcelos, E.A. Souza, A.F.B. Abreu	115
EFFECT OF CHEMICAL CONTROL OF ALS (<i>PSEUDOCERCOSPORA GRISEOLA</i>) ON SEED YIELD OF TROPICAL BLACK BEAN CULTIVARS IN VERACRUZ, MEXICO Oscar Hugo Tosquy-Valle, Ernesto López-Salinas, Francisco Javier Ibarra-Pérez y José Raúl Rodríguez-Rodríguez	117
CHARACTERIZATION OF THE RESISTANCE LOCUS TO ANGULAR LEAF SPOT IN THE COMMON BEAN ACCESS ‘JAPONÊS’ Lopes, E. M. G.; Machado, M. A. M.; Batista, M. S.; Campos, R. G. C.; Santos, J. M. C.; Carneiro, A. R. T.; Batista, F. E. R.; Rocha, F. S. and Sanglard, D. A.	119
REACTION OF COMMON BEAN LINES TO <i>PSEUDOCERCOSPORA GRISEOLA</i> IN DIFFERENT ENVIROMENTAL CONDITIONS Rafael Pereira, Elaine A. de Souza 1, Larissa C. Costa and Ângela F.B. Abreu	121
PRODUCTION OF ANTHRACNOSE INFECTED DRY BEAN SEED UNDER GREENHOUSE CONDITIONS Robin S. Lamppa, Jessica M. Halvorson and Julie S. Pasche	123
PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF COMMON BEAN GENOTYPES FOR RESISTANCE TO ANTHRACNOSE Vieira, A. F.; Souza, T. L. P. O.; Rocha, F. S. and Sanglard, D. A.	125
FURTHER CHARACTERIZATION OF THE BROAD-SPECTRUM ANTHRACNOSE RESISTANCE IN ANDEAN COMMON BEAN AMENDOIM CAVALO T.A.S. Gilio, D.S.Y. Nanami, M.C. Gonçalves-Vidigal, G. Valentini, Q. Song, and M.A. Pastor-Corrales	127
SCREENING PHASEOLUS LUNATUS FOR RESISTANCE TO SCLEROTINIA SCLEROTIURUM Rebecca Selleck, Kathyne Everts, Emmalea Garver Ernest	129
POPULATION STRUCTURE AND FUNGICIDE SENSITIVITY OF 366 SCLEROTINIA SCLEROTIURUM ISOLATES FROM DRY COMMON BEAN S. Everhart, B.S. Amaradasa, R. Jhala, R. Higgins, and J.R. Steadman	131
USE OF MUTI SITE SCREENING TO IDENTIFY AND VERIFY PARTIAL RESISTANCE TO WHITE MOLD IN COMMON BEAN IN 2015 R. Higgins and J.R. Steadman	133
EFFICIENCY OF PROGENY SELECTION IN COMMON BEAN FOR OXALIC ACID REACTION Juliana Andrade Dias, Monik Evelin Leite, Filipe Couto Alves, Paulo Roberto Carvalho Gonçalves, Danuza Araújo de Souza, João Bosco dos Santos	135
EFFECT OF OXALIC ACID ON COMMON BEAN PROGENIES DERIVED FROM RECURRENT SELECTION FOR WHITE MOLD RESISTANCE Diego Zanardo Gallan, Juliana Andrade Dias, Monik Evelin Leite, João Bosco dos Santos	137
WITHIN-ROW PLANT DENSITY FOR TYPE III COMMON BEAN GENOTYPE WITH PARTIAL RESISTANCE TO WHITE MOLD Lima, R.C.; Soares, B.A.; Teixeira, P.H.; Rodrigues, L.B.; Vieira, R.F.; Paula Júnior, T.J.; Santos, M.G.P.	139
PERFORMANCE OF LINES/CULTIVARS SELECTED FOR PARTIAL RESISTANCE TO WHITE MOLD IN THE FIELD Lima, R.C.; Souza, A.F.F.; Rodrigues, L.B.; Vieira, R.F.; Paula Júnior, T.J.; Santos, M.G.P; Carneiro, J.E.S.	141

PARTIAL RESISTANCE TO WHITE MOLD AMONG COMMON BEAN ELITE LINES Lima, R.C.; Teixeira, P.H.; Souza, A.F.F.; Lehner, M.S.; Vieira, R.F.; Paula Júnior, T.J.; Carneiro, J.E.S.	143
IDENTIFICATION OF GENOMIC REGIONS INTROGRESSED IN NEAR-ISOGENIC LINES OF THE MARKET CLASS FABADA USING MASSIVE GENOTYPING Juan José Ferreira, Ester Murube, Ana Campa	145
DEVELOPMENT AND RELEASE OF NEW BIOFORTIFIED BEAN VARIETIES IN EASTERN AFRICA Paul Kimani, P. Mamiro, M. Ugen, and A. Musoni	147
CONTENT OF POLYPHENOLS AND ANTIOXIDANT CAPACITY OF DIFFERENT BEAN CULTIVARS AFTER AN ENZYMATIC EXTRACTION Mayra Denise Herrera, Raquel Karina Cruz Bravo, Edith Gisell Esparza Robles	149
USE OF COMMON BEAN FLOURS TO ENHANCE PHENOLIC CONTENT AND ANTIOXIDANT CAPACITY OF SOME BAKERY PRODUCTS Mayra Denise Herrera, Raquel Karina Cruz Bravo, and Edith Gisell Esparza Robles.	151
CENTESIMAL COMPOSITION OF CREOLE ACCESSIONS OF COMMON BEANS CULTIVATED IN NORTH OF MINAS GERAIS STATE, BRAZIL Guilherme. E. P. X.; Soares, F. J.; Santana. S. C.; Machado, M. A. M.; Batista, F. E. R.; Rocha, F. S. and Sanglard, D. A.	153
GENETIC VARIABILITY OF BEAN GRAINS CREOLE FOR WATER ABSORPTION Guilherme. E. P. X.; Santana. S. C.; Soares, F. J.; Machado, M. A. M.; Batista, F. E. R.; Rocha, F. S. and Sanglard, D. A.	155
PHYSICAL PROPERTIES OF CREOLE BEAN GRAINS Guilherme. E. P. X.; Santana. S. C.; Soares, F. J.; Machado, M. A. M.; Batista, F. E. R.; Rocha, F. S. and Sanglard, D. A.	157
GENETIC VARIABILITY ASSOCIATED TO PHYSIOLOGICAL QUALITY IN SEEDS OF COMMON BEAN GENOTYPES OF SPECIAL GRAIN M.B. de Oliveira, A.J. de Carvalho, A.M.S. de S. David, O.G. Brito, V.B. de Souza, J.E. de S. Carneiro, J. C. Figueiredo, L.V. de S. Cangussú, J.C.Medeiros, A.A.de Souza, J.V. S. Guerra, P. S. C. Batista, P.V. Santos Júnior	159
CHANGES IN TECHNOLOGICAL QUALITY OF CARIOCA BEANS Oliveira, D. P., Jesus, J. R., Carvalho, G. R., Silva, M. L. S., Pereira, J., Andrade, M. J. B.	161
COOKING TIME OF COMMON BEAN: GENETIC PARAMETERS AND SELECTION OF ELITE LINES S. M. Martins, H. S. Pereira, L. C. Melo, L. C. Faria, T. L. P. O. Souza, J. L. C. Díaz, M. C. S. Magaldi.	163
THE COMMON BEAN (<i>Phaseolus vulgaris</i> L.) DEMONSTRATION UNITY SYSTEM - SUDF - APPLICABILITY POTENTIAL FOR FAMILY FARMING Alexandre Terracciano Villela, Irajá Ferreira Antunes, Clause Fátima Brum Piana, João Gilberto Corrêa da Silva, Gilberto Antonio Peripolli Bevilaqua	165
FLOWERING, DISTRIBUTION OF DRY MATTER AND POD YIELD IN CLIMBING BEAN WITH PRUNING Escalante-Estrada José Alberto Salvador and MaríaTeresa Rodríguez-González	167
FERTILIZATION OF COMMON BEAN CV. BRSMG MADREPÉROLA WITH NPK ORGANOMINERAL FERTILIZER CONTAINING SOIL CONDITIONER Oliveira, D. P., Souza, H. C., Figueiredo, M. A., Nogueira, F. D., Andrade, M. J. B.	169
GRAIN YIELD COMPONENTS OF THE CULTIVAR BRSMG MADREPÉROLA AS A FUNCTION OF NITROGEN AND MOLYBDENUM FERTILIZATION AND INOCULATION WITH RHIZOBIUM SPP. Figueiredo, M. A., Oliveira, D. P., Soares, B. L., Martins, F. A. D., Morais, A. R., Moreira, F. M. S., Andrade, M. J. B.	171

INFLUENCE OF NITROGEN FERTILITY LEVEL ON GROWTH, GRAIN YIELD, AND YIELD COMPONENTS OF DIFFERENT DRY BEAN CULTIVARS Ali Alhasan, Annalisa Piccorelli, and Jim Heitholt	173
COMMON BEAN AND ORGANIC FERTILIZER USED AS COMPONENTS OF SUSTAINABLE AGROFORESTRY SYSTEMS IN DURANGO, MÉXICO Rigoberto Rosales-Serna, José Ángel Sigala Rodríguez, Luis Torres Uzarraga, Homero Sarmiento López	175
EFFECT OF DIFFERENT PHOSPHORUS LEVELS ON GROWTH AND YIELD COMPONENTS OF COMMON BEAN Amanda Thuany Navarro; José dos Santos Neto; Arthur Astuti Dantas; Renan Pupim Ignácio; Maria Brígida dos Santos Scholz; Vânia Moda-Cirino	177
EFFECTS OF SELENIUM APPLICATION ON YIELD AND SEED SIZE IN COMMON BEANS GROWN IN DURANGO, MÉXICO Marcos Cobaleda-Velasco, Ruth E. Alanis-Bañuelos, Miguel Ríos-Romero, Rigoberto Rosales-Serna, Sara Rodrigo, Ricardo Trejo Calzada, Rafael Jiménez Ocampo	179
COMMON BEAN PERFORMANCE EVALUATION (CULTIVAR IPR COLIBRI) IN DIFFERENT SULFUR LEVELS Silva, M. L. S.; Piccolo, M. C.; Trevisan, A. R.; Oliveira, D. P.	181
DEVELOPMENT AND REPRODUCTION of <i>heliiothis virescens</i> (LEPIDOPTERA: NOCTUIDAE) FED ON LEAVES AND FRESH PODS OF BEAN PLANTS Orcial Ceolin Bortolotto , Ana Paula de Queiroz , Eli Carlos de Oliveira , Adeney de Freitas Bueno, Ayres de Oliveira Menezes Jr	183
FEEDING OF <i>HELICOVERPA ARMIGERA</i> (HÜBNER) (LEPIDOPTERA: NOCTUIDAE) ON GENOTYPES OF <i>PHASEOLUS VULGARIS</i> L. L. Nogueira, Z.A. Ribeiro, M.M. Di Bello, M.M. Freitas1, B.H.S. Souza, A.L. Boiça Júnior	185
STRATEGIES FOR MANAGING THE WHITEFLY USING NEEM AND CHEMICAL CONTROL ON FIELD-PLANTED COMMON BEANS A.L. Boiça Júnior, B.H.S. Souza, Z.A. Ribeiro, W.I. Eduardo, L. Nogueira, I.R. Cedin	187
QTL MAPPING ASSOCIATED WITH MORPHOLOGICAL TRAITS OF BEAN SEEDLINGS AND RESPONSE TO LOW TEMPERATURE IN GERMINATION E Pérez-Vega, A Campa, S Mamidi, R Lee, Q Song, P McClean, J J Ferreira	189
DOCUMENTATION OF THE GERMPLASM ACTIVE BANK OF <i>Phaseolus lunatus</i> L. Antônia Maria de Cássia Batista de Sousa, Jessica Danielle Lustosa da Silva, Marilha Vieira de Brito, Regina Lucia Ferreira Gomes, Ângela Celis de Almeida Lopes	191
VALIDATION OF ELECTRICAL CONDUCTIVITY TEST FOR BUTTER BEAN SEEDS Rosa, JFS; Santos, MS; Borges, SS; Brandão Junior, DS; Rocha, FS and Sanglard, DA.	193
PROGENY TESTS FOR COMMON BEAN ISOLINES RESISTANT TO DISEASES WITH THE AID MOLECULAR MARKERS Sanglard, D. A.; Machado, M. A. M.; Batista, F.E.R.; Rocha, F. S.; Souza, T. L. P. O. and Barros, E. G.	195
PYRAMIDED LINES OF “CARIOCA” COMMON BEAN AND THEIR REACTION TO <i>Pseudocercospora griseola</i> Sanglard, D. A.; Machado, M. A. M.; Batista, F.E.R.; Rocha, F. S.; Souza, T. L. P. O. and Barros, E. G.	197
MARKER-ASSISTED SELECTION INTEGRATED TO THE EMBRAPA COMMON BEAN BREEDING PROGRAM Luana A. Rodrigues, Gesimária R. C. Coelho, Paula Arielle M. R. Valdisser, Rosana P. Vianello & Thiago Lívio P. O. Souza	199
THERMAL REQUIREMENTS OF THE MAIN ‘PINTO’ BEAN VARIETIES GROWN IN DURANGO, MEXICO Hilario Flores-Gallardo, Fabiola Zavala-Estrada, Héctor Flores-Magdaleno	201

INDICES OF NODULATION IN DRY BEAN CULTIVARS FOR DIRECT HARVESTING Gencho Milev and Dimitar Genchev	203
ADVANCES IN BREEDING STRESS TOLERANT, MARKET DEMANDED CANNING BEANS IN KENYA Kimani P. M. and A. Warsame	205
BREEDING RUNNER BEAN FOR GRAIN YIELD, DISEASES RESISTANCE AND SHORT-DAY ADAPTATION IN EASTERN AFRICA P.M. Kimani, M. M. Mulanya, S. Njau and R. D. Narla	207
GENETIC VARIABILITY IN LIMA BEAN ACCESSIONS OF THE GERMPLASM ACTIVE BANK Gabriel de Moraes Cunha Gonçalves, Vinícius Santos Freitas, Carlos Humberto Aires Matos Filho, Ângela Célis de Almeida Lopes, Regina Lucia Ferreira Gomes	209
VIRULENCE DIVERSITY OF <i>UROMYCES APPENDICUALTUS</i> IN THE HIGHLANDS OF GUATEMALA Plutarco Emanuel Morales Gonzales, Luis F. Aldana, and M.A. Pastor-Corrales	211
NEGATIVE IMPACT PROMOTED BY SALT STRESS IN COMMON BEAN SEEDLINGS J.R.S. Barbosa, M.A.M. Barbosa, G.D.M. Viana, T.S. Pereira, O.N. Silva, R.S. Okumura, E.M.S. Guedes, A.K.S. Lobato	213
ANTIOXIDANT AND ALPHA-AMYLASE ANALYSIS IN SNAP BEAN GENOTYPES USING THE REML/BLUP PROCEDURE Felipe Aranha de Andrade; Leandro S. A. Gonçalves; Oscar de Andrade Júnior; Dipayan Sarkar; Édison Miglioranza; Eli Carlos de Oliveira and Kalidas Shetty	215
EFFECT OF DEFOLIATION ON YIELD OF SNAP BEAN L.H.C. Almeida, E.C. Oliveira; F.F. Furlan; G.R. Gomes; A.P. Barbosa; G. H. Freiria ¹ ; E. Miglioranza	217
SNAP-BEAN GERMINATION RATES: A COMPARISON OF WHITE, PERSISTENT COLOR AND COLORED-SEEDED LINES Mustafa Al-Jadi, James Myers, Shinji Kawai, and L.J. Brewer	219
NUTRITIONAL QUALITY OF BUSH SNAP BEAN IN CONVENTIONAL AND ORGANIC PRODUCTION SYSTEMS Luiz Henrique Campos de Almeida ¹ ; Guilherme Renato Gomes; Gustavo Henrique Freiria; Felipe Favoretto Furlan; Vitor Rampazzo Favoretto; Douglas Mariani Zeffa; Eli Carlos de Oliveira; Lúcia Sadayo Assari Takahashi	221
PATH ANALYSIS OF YIELD AND ITS PRIMARY COMPONENTS IN SNAP BEAN Douglas Mariani Zeffa; Guilherme Renato Gomes; Gustavo H. Freiria; Vitor R. Favoretto; Luiz H. C. de Almeida; Felipe F. Furlan and Eli C. Oliveira	223
PATH ANALYSIS OF YIELD AND ITS PRIMARY COMPONENTS IN SNAP BEAN Douglas Mariani Zeffa; Guilherme Renato Gomes; Gustavo H. Freiria; Vitor R. Favoretto; Luiz H. C. de Almeida; Felipe F. Furlan and Eli C. Oliveira	225
DEVELOPMENT AND VALIDATION OF NEW SNAP BEAN VARIETIES FOR EASTERN AFRICA Paul Kimani, R. D. Narla, M. Ugen, C. Onyango, S. Kibet and A. Musoni	227
NUTRITIONAL CHARACTERIZATION OF SNAP BEAN GENOTYPES USING PRINCIPAL COMPONENT ANALYSIS Douglas Mariani Zeffa; Gustavo H. Freiria; Guilherme H. Gomes; Luiz H. Almeida; Felipe F. Furlan; Aline Moritz and Eli C. Oliveira	229
PHENOLOGY AND GROWTH OF CULTIVATED AND WILD <i>Phaseolus vulgaris</i> L. Marisol J. Flores-de la Cruz; A. García-Esteva; J. Kohashi-Shibata; J. R. García-Nava; Ma. C. Ybarra-Moncada and E. Uscanga-Mortera	231
TEPARY BEAN AS A DONOR OF ABIOTIC STRESS RESISTANCE GENES IN COMMON BEAN Jodi Souter, Christopher Todd, Timothy Porch & Kirstin Bett	233

YIELD COMPONENT RESPONSE TO WATER STRESS AMONG SIX DRY BEAN GENOTYPES Jim Heitholt and Annalisa Piccorelli	235
DEVELOPING A WATERPROOF DRY BEAN (<i>PHASEOLUS VULGARIS L.</i>): IDENTIFYING GENOTYPES AND GENOMIC REGIONS ASSOCIATED WITH WATERLOGGING TOLERANCE Ali Soltani, Samira Mafi Moghaddam, Katelynn Walter, Kiran Ghising, Jose Vasquez-Guzman, Stephan Schroder, Carlos F. Velasquez, Edgar G. Escobar, Rian Lee, Phillip McClean, and Juan M. Osorno	237
SUSTAINABLE SYSTEM FOR BEAN DRY PRODUCTION UNDER DRYLAND CONDITIONS Esteban S. Osuna-Ceja1, Miguel Á. Martínez-Gamiño, Mercedes Borja-Bravo, Carlos Rojas-Santillán y J. Saúl Padilla-Ramírez	239
WATER REGIME EFFECTS ON PHENOLOGY AND SEED YIELD OF COMMON BEAN IN DURANGO, MÉXICO Rigoberto Rosales-Serna, Hilario Flores-Gallardo, Juan Carlos López-González	241
WATER REQUIREMENTS OF ‘PINTO SALTILLO’ BEAN GROWN IN DURANGO, MEXICO Hilario Flores-Gallardo, Héctor Flores-Magdaleno, Rigoberto Rosales-Serna, Fabiola Zavala-Estrada	243
CONSEQUENCES RELATED TO WATER LIMITATION ON COMMON BEAN SEEDLINGS K.N.N. Coelho, E.S. Pereira, C.L.F.C. Souza, A.P. Martins Filho, T.R. Ferreira, R.S. Okumura, C.A.B. Andrade, A.K.S. Lobato	245
SEED YIELD PERFORMANCE AND REACTION TO DISEASES OF BLACK BEAN CULTIVARS GROWN UNDER RAINFED AND RESIDUAL SOIL MOISTURE CONDITIONS Ernesto López-Salinas, Oscar Hugo Tosquy-Valle, Bernardo Villar-Sánchez and Francisco Javier Ibarra-Pérez	247
GROWTH ANALYSIS OF EARLY GENOTYPES OF COMMON BEANS Adriano Stephan Nascente, Leonardo Cunha Melo and Paulo Holanda Rosa	249
PRODUCTIVITY, ADAPTABILITY AND STABILITY OF PRODUCTION OF SPECIAL GRAIN COMMON BEAN LINES IN DIFFERENT ENVIRONMENTS OF MINAS GERAIS, BRAZIL O.G. Brito, A.J. de Carvalho, J.E. de S. Carneiro, J.A.A. Moreira, M. Martins, L.C. Melo, L.C. Faria, H.S. Pereira, M.B. de Oliveira, J.C. Medeiros, T.L.P.O. Souza, P.S.C. Batista, M.L.Lacerda	251
RELEASE OF PINTO ‘RARÁMURI’ DRY BEAN FOR THE SEMIARID HIGHLANDS OF CENTRAL MEXICO Jorge A. Acosta-Gallegos, Yanet Jiménez Hernández, Victor Montero Tavera, Miguel Angel Martínez Gamiño, Mayra D. Herrera, José Luis Anaya López and James D. Kelly	253
SUBJECT MATTER INDEX - VOLUME 59	254
2016 MEMBERSHIP DIRECTORY	255
2015 FINANCIAL STATEMENT	269

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CONSERVATION AND CHARACTERIZATION OF NATIVE *PHASEOLUS VULGARIS* GERMPLASM FROM NORTHWESTERN ARGENTINA

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INTRODUCTION

The Active Germplasm Bank from Northwestern Argentina (BANOA), situated at the Salta Experimental Station of the National Agricultural Technology Institute (INTA-EEA-Salta), conserves an important common bean (*Phaseolus vulgaris* L.) collection of native wild populations and landraces. The BANOA bean collection, which was started in the 80s, consists of 700 accessions, including 400 landraces and 300 wild populations, collected in different regions of Northwestern Argentina. Germplasm collections must provide to breeders genetic variants, genes or genotypes, in order to respond to the challenges demanded by the new production systems. This requires the study and characterization of the preserved germplasm (Abadie and Berreta, 2001; Singh, 2001; De Ron et al, 2015). The aim of this work is to present the preliminary results of the evaluation of part of the BANOA bean collection based on morpho-agronomic characters, microsatellite markers and DNA sequences associated with domestication genes.

MATERIALS AND METHODS

A total of 128 wild populations from the BANOA bean collection were characterized based on 10 morpho-agronomic characters. Twenty pods and 30 seeds per population were measured and a principal components analysis (PCA) was performed. Also, six wild bean populations, selected based on their proximity to cultivated bean fields (< 1 km, > 2 km, and > 5 km), were analyzed with microsatellite markers. The DNA was extracted from seedlings of 10 individuals per population and amplified by PCR using four SSR markers. The amplified fragments were separated by 10% polyacrylamide gel electrophoresis. Allele frequencies for each marker were analyzed using the PowerMarker v3.25 program. On the other hand, two wild populations, two landraces and two commercial bean varieties were studied to analyze the partial sequences of the gene *PvTFL1y*. The amplified regions corresponded to exon I and part of exons II and III of the *PvTFL1y* gene. Sequences were analyzed with BioEdit and compared with the haplotypes described by Kwak et al. (2012).

RESULTS AND DISCUSSION

A Principal Component Analysis (PCA) was generated with 10 morpho-agronomic data: number of pods/plant (P/PL); 100 seeds weight (100 SW), days to 50% maturity (MAT), fruit length (FRL), fruit width (FRW), fruit thickness (FRT), number of grains/pod (GR/P), seed length (SL), seed width (SW) and seed thickness (ST). The first two components (PC1 and PC2) explained 61% of the total variability (figure 1). The variables that most contributed to the differentiation of the wild accessions were: seed length and width, and 100 seeds weight at PC1 and pods/plant, fruit length and grains/pod at PC2. Significant variability was observed for these morphological characters in the accessions analyzed. The spatial analysis performed based on the morphological data showed that the greatest diversity corresponds to accessions collected in

Rosario de Lerma and Chicoana departments in Salta province. The wild populations analyzed based on their proximity to domesticated beans showed differences in allele frequencies for some microsatellite markers. An average of 4.5 alleles per locus was observed over all the loci analyzed. Moreover, for some markers a correlation between the allele frequency and the proximity to crops was observed. After partial amplification of the *PvTFL1y* gene, sequences of approximately 1000 bp length were obtained. The landraces and wild populations analyzed corresponded to the A1 haplotype described previously by Kwak *et al.* (2012) for indeterminate phenotypes. Moreover, haplotypes were obtained for landraces and wild populations of *P. lunatus*, that were not previously described.

CONCLUSIONS

The morphological and molecular characterization confirmed the existence of a significant variability in the accessions conserved in the BANOA (De Ron *et al.*, 2004; Santalla *et al.*, 2005, Galván *et al.*, 2006) and a high degree of introgression in wild populations from domesticated germplasm. This alerts about the importance of conservation of the integer genetic variation of the wild populations in genebanks and also in their natural environments. On the other hand, the knowledge of the variability present in sequences associated with domestication genes it is useful to understand the origin and domestication of the common bean, especially considering the Andean domestication center, which still needs further studies. (Santalla *et al.*, 2004; Bittocci *et al.* 2013).

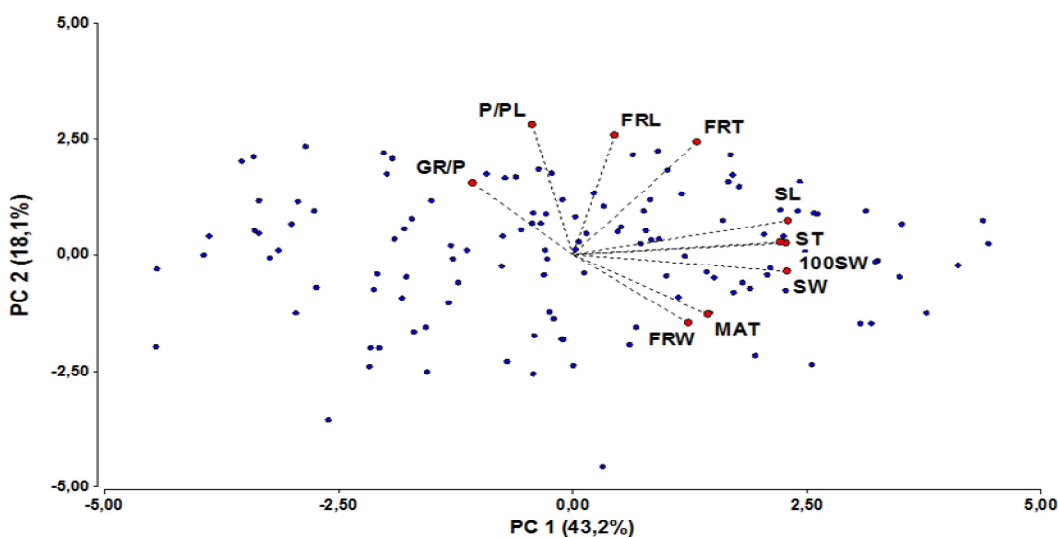


Fig.1. Principal Component Analysis plot using 10 morphological characters.

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