VII International Meeting on Plant Breeding

"Plant breeding for the ESG world: preparing for climate changes, food security, sustainability and quality"

PROCEEDINGS

GVENCK

Genetics and Plant Breeding Group
"Prof. Roland Vencovsky"

October – 2023

THE INTERNATIONAL MEETING ON PLANT BREEDING

Plant breeding is one of the fundamental strategies for the development of more adapted and productive cultivars, particularly in a world surrounded by uncertainty on food security. Given this scenario, scientists have been putting great efforts into the development of tools that could help to overcome challenges faced every day in the field. Therefore, we feel that discussions around these new tools are important to build next-generation breeders who will make them useful and effective, ensuring its correct application within research and breeding.

The International Meeting on Plant Breeding is one of several events that compose the "Corteva Agriscience Plant Science Symposia Series”. In the seventh edition, the main topic we intended to address was how to integrate the ESG (Environmental, Social, Governance) approach with plant breeding, highlighting the challenge of achieving high productivity with environmental and social security. The negative social and environmental impacts of severe climate change are becoming increasingly evident, and what are we doing to mitigate them? This is a discussion that involves experts from all fields. Therefore, in this year's edition, we promote insights into how social and corporate environmental governance have enabled new levels of social and environmental responsibility to be achieved, in the academic sphere and in private companies, with a focus on plant breeding

GVENCK

The Genetics and Plant Breeding Group “Prof. Roland Vencovsky” (GVENCK) is composed by graduate and undergraduate students in Genetics and Plant Breeding at “Luiz de Queiroz” College of Agriculture (ESALQ/USP), under coordination of Professor Dr. José Baldin Pinheiro. Our mission is to integrate academics, professors and professionals with the goal of improving the training of future breeders and geneticists.

The main activities of the group are:

- Organization of scientific and training events;
- Promotion of discussion on relevant topics in genetic and plant breeding;
- Technical visits to companies and public research institutions;
- Promote the guidance of young talents under training from the “alumni voice”, in which the alumni with consolidated careers will share professional experiences;
- Promote moments and opportunities for interaction between students, professors and researchers outside the university;
- Establishment of partnerships with companies and public institutions.

ORGANIZATION

Coordination

José Baldin Pinheiro

Leonardo Martins Brandão

Givanildo Rodrigues da Silva

Secretary

Marcela Martinez

Treasury

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ACKNOWLEDGEMENTS

The organizing committee is thankful for all the support provided by Corteva Agriscience, ESALQ (“Luiz de Queiroz” College of Agriculture), Department of Genetics, The graduate program in Genetics and Plant Breeding.

PROGRAM

October 4th, 2023

8:00 – 18:00 → MiniCourse 1 – Juliana Erika de Carvalho Teixeira Yassitepe & Sophia Gerasimova – “Construção de vetores e transformação genética de milho”
8:00 – 18:00 → MiniCourse 2 – Filipe Matias & Rafael Tassinari – “Enviromics and phenomics applied on Plant Breeding”

October 5th, 2023

7:30 - 8:00 → Accreditation
8:00 - 8:30 → Jason Rauscher - Opening session (Corteva Agriscience)
8:30 -9:30 → 1st Lecture – Saulo Chiega (Grupo SG) - “Soluções em Sustentabilidade Corporativa”
9:30 - 10:15 → Coffee-Break + Posters
10:15 - 10:30 → Abstract presentation – Alessandra Koltun - “Metabolomics enlighten mechanisms for higher drought tolerance in barley overexpressing uncoupling protein 1”
10:30 - 11:30→ 2nd Lecture - Juliana Erika de Carvalho Teixeira Yassitepe (EMBRAPA Agricultura Digital) – “Developing new biotech varieties for an environmentally changing world”
11:30 - 12:30 → 3rd Lecture - Sophia Gerasimova (GCCRC) - “Genome editing for trait improvement in crops”
12:30 - 14:00 → Lunch Break
14:00 - 15:00 → 4th Lecture – Elisa Salas (CIP) – “The biofortified, heat and drought tolerance potatoes – one successful case in Latin-American”
15:00 - 15:45 → Coffee-Break + Posters
15:45 - 16:00 → Abstract presentation - Juliana A. V. Nonato – “Phenotypic evaluation of transgenic and gene editing maize lines for a new maize receptor-like kinase likely involved in drought stress”
16:00 - 17:00 → 5th Lecture - Rafael Tassinari (UFG) – "Enviromics as a Tool for Participatory Breeding"

October 6th, 2023

8:00 - 8:30 → Accreditation
8:30 - 9:30 → 6th Lecture - Mateus Sanquetta (ECO$_2$ Consulting) - “The future of plant breeding: next-generation breeding strategies for climate-ready cultures”
9:30 - 10:15 → Coffee-Break + Posters
10:15 - 10:30 → Abstract presentation - Gustavo C. Jacobassi – “Near infrared spectroscopy for predicting sucrose content in sugarcane breeding trials”
10:30 - 11:30 → 7th Lecture - Filipe Matias (Syngenta) – “Career and social media: building experiences in plant breeding and marketing yourself”
12:30 - 14:00 → Lunch Break
14:00 - 15:00 → 8th Lecture - Julien Linares (Corteva Agriscience) – “The opportunities and challenges of modelling novel introduced genetic variation in breeding populations”
15:00 - 15:45 → Coffee-Break + Posters
16:00 - 17:00 → “Vencovsky Awards”

SPEAKERS

ELISA SALAS MURRUGARRA - Elisa is an agronomist graduated from the Universidad Nacional Agrária La Molina (Lima – Peru) and obtained her master's degree in Plant Breeding at the same university in 2002. Currently, Elisa is an Associate Researcher in Genetics, Genomics and Crop Improvement (DCE-GGCI) at the International Potato Center (CIP), in Lima (Peru), where she joined 19 years ago and since 2016, she is president of the Association Latin American Potato Association (ALAP). She has a solid experience of 21 years in potato genetic improvement, being responsible for the crossing, evaluation, selection of families and advanced clones of two important populations: The Biofortified (Iron and Zinc) population and the Low Tropics Virus Resistance (LTVR) population with heat and drought tolerance.

FILIPE INÁCIO MATIAS - Filipe has a degree in Agronomy from the Federal University of Uberlândia (UFU, Uberlândia/MG), a Master's degree in Agronomy from the Universidade Estadual Paulista Júlio de Mesquita Filho (UNESP, Jaboticabal/SP), a PhD in Genetics and Plant Breeding from the University of São Paulo (ESALQ/USP, Piracicaba/SP) and did post-doctoral programmes at the University of Wisconsin (Madison/WI). He held the position of Research Scientist at North Dakota State University (Fargo/ND) and is currently Lead in Applied Phenomics at Syngenta Seeds LATAM. Throughout his career, Filipe has developed scientific experiments in partnership with Embrapa Gado de Corte (Campo Grande/MS, Brazil), focused on the genetic improvement of tropical forage crops. His experience covers various crops, such as maize, potatoes, wheat and tropical forage plants. His interests include areas such as communication, quantitative genetics, genomic selection, GWAS, phenomics, high-yield phenotyping, image analysis and R programming.

JULIANA E. DE C. T. YASSITEPE - Juliana is an Agronomist graduated from the Federal University of Lavras (2002), Master and Doctor in Genetics and Plant Breeding from the same University (2005) and from the Escola Superior de Agricultura de Luiz de Queiroz (ESALQ/USP) (2009), respectively, and carried out his post-doctorate at the University of Delaware, in the United States between 2011 and 2013. Juliana worked as Researcher in Genomics and Forestry Biotechnology at Votorantim Celulose e Papel, also at Fibria Celulose. She is currently a researcher at Embrapa Digital Agriculture and leads the Plant Genetics team at the Center for Research in Genomics Applied to Climate Change (GCCRC), which was established by Embrapa, the State University of Campinas (Unicamp) and the State Research Support Foundation. of São Paulo (Fapesp).

JULIEN LINARES - Julien earned his BS in Animal Science from the University of California, Davis, MS in Plant Breeding from Iowa State University before starting his PhD in Horticulture and Agronomy at UC Davis where he worked to understand how transgenes interact with native germplasm and design novel testing methodologies. Julien currently leads the global deployment of precision phenotyping traits for the Seed Product Development team at Corteva Agriscience bringing validated technology in data science, imaging and robotics to breeders and data collection teams worldwide. Julien has been with Corteva since 2010 and has held many roles. In 2011, Julien took a position within the maize stress product development team to develop new drought tolerant corn hybrids successfully aiding launch of the Aquamax brand while concurrently working with the agronomic transgenic traits team to identify transgenes that provide higher yields. In 2023, Julien was recognized as an associate laureate within Corteva for his work in developing technologies and processes that have the potential to deliver significant impact.

MATEUS NIROH INOUE SANQUETTA - Mateus is a Forestry Engineer who graduated from the Federal University of Paraná. He is studying for a master's degree in Forestry Engineering at the Federal University of Paraná and in Forestry and Natural Resources at the Warnell School of Forestry and Natural Resources - University of Georgia. He is a specialist in forest biometrics, remote sensing, carbon, ESG, sustainability and climate change. He is the author of more than 100 publications and has taken part in conferences in different countries. He is Managing Editor of Urban Forestry Urban Greening magazine. He was a project manager at reNature Investments (Holland) and a specialist consultant at Casa da Floresta. Mateus is Founder and Technical Director of eco$_2$ Consulting, a company founded in 2021 that works in ESG, Decarbonization, Projects and Strategies for the Carbon Market. Co-founder and Operations Director of SEYVA, a forestry business consultancy focusing on Performance Management of forestry operations, forestry planning, market intelligence, valuation and forensics.

RAFAEL TASSINARI RESENDE – Dr. Rafael is a Forestry Engineer graduated from the Federal University of Viçosa (UFV) (2012), Master in Genetics and Plant Breeding from the Escola Superior de Agricultura Luiz de Queiroz (ESALQ/USP) (2014), PhD in Genetics and Plant Breeding (2017) from UFV, as well as in Forest Science at the same university (2019). Currently, he is a major professor at the Federal University of Goiás (UFG), working in Breeding, Statistics and Biometry and advisor in the graduate programs in Genetics and Plant Breeding (PPGGMP) at UFG and Forestry Sciences (PPG-CFL) at the University of Brasilia (UnB). In addition, he is also a researcher at the scientific startup TheCROP. He has specialization in areas such as Biometrics, Quantitative Genetics, Biotechnology (Genomics), Geographic Information Systems (GIS), with application in studies of Enviromics and Computational Process Optimization.

SAULO PADOIN CHIELLE - Saulo has a degree in Environmental Engineering from the Lutheran University of Brazil. He also has an MBA in Business Management from the Getúlio Vargas Foundation and a Master's degree in Environmental Impact Assessment from the La Salle University Centre. He is currently CEO of Grupo SG - Sustentabilidade e Gestão (SGBIO/SGTECH/SG Comunicação). He also was a researcher at IEITEC - Instituto Empresarial de Incubação e Inovação Tecnológica (Canoas/RS), where he contributed to the field of technological innovation. As an environmental advisor and consultant, he has guided corporations in their quest for eco-efficiency and socio-environmental responsibility. He has taught postgraduate courses in business management, the environment and corporate sustainability. His expertise extends to the areas of Innovation and Entrepreneurship, Negotiation, Business Management, Environmental Management and Corporate Sustainability. He is also an experienced speaker and offers courses and training in areas such as sustainability (socio-environmental responsibility and eco-efficiency), business management and personal and professional development.

SOPHIA GERASIMOVA – Dra. Sophia is a biologist graduated from Novosibirsk State University (NSU) and a geneticist from the Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences. Furthermore, Sophia was a doctoral student at the Gregor Mendel Institute, in Austria and also carried out her post-doctorate at the Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences. At this same institute, Sophia works as a Senior Researcher and head of the Agricultural Biotechnology Group, in addition, she is an assistant professor at Novosibirsk State University (NSU). Sophia currently conducts research at the Genomics for Climate Change Research Center (GCCRC), working with the development of genome editing test systems based on the transient expression of genetic constructs in protoplasts and embryonic cells. Her main research focus is plant biotechnology and genome editing.

SUMMARY

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METABOLOMICS ENLIGHTEN MECHANISMS FOR HIGHER DROUGHT TOLERANCE IN BARLEY OVEREXPRESSING UNCOUPLING PROTEIN 1

Alessandra Koltun[1]; Juliana Yassitepe [1,2]; Vinicius Almeida[1]; Zoe Wilson[3]; Pedro Barreto[1*]; and Paulo Arruda[1**]

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Drought significantly stresses agricultural systems and ongoing global climate changes are expected to worsen water scarcity-related risks, requiring innovative solutions such as crop engineering. Barley (*Hordeum vulgare* L.), a vital cereal crop and research model, was chosen to investigate Arabidopsis UNCOUPLING PROTEIN 1 (AtUCP1), a mitochondrial inner membrane protein known for enhancing stress response and plant performance. This study aimed to assess whether UCP1 overexpression improves barley drought tolerance while identifying the metabolite production triggered by this protein. Three events were selected based on their high mRNA expression levels and AtUCP1 protein accumulation for further phenotyping under drought conditions. Physiological parameters were estimated at five stages: well-watered, severe drought stress, and 2 h, 6 h, and 10 h after rehydration. Plants overexpressing AtUCP1 displayed robust drought tolerance, with minimal stress symptoms enduring for up to 12 days without irrigation. In contrast, wild-type (WT) plants suffered severe drought stress, taking 10 hours to fully recover after rehydration. Moreover, AtUCP1-overexpressing plants demonstrated significantly higher photosynthetic activity under well-watered conditions, during severe drought, and after 6 h rehydration. Notably, the AtUCP1ox L2 event exhibited nearly double the photosynthetic efficiency of WT plants in all tested conditions. Metabolic profiling of barley leaf samples, particularly the L2 event, revealed a significant induction of drought stress-associated metabolites. The saccharopine pathway, known for its response to various abiotic stresses, showed substantial upregulation in AtUCP1ox plants during severe drought stress and early recovery phases. Finally, a metabolic shift from lysine to α-aminoadipate was observed, with reduced lysine levels in AtUCP1ox events, leading to the accumulation of saccharopine, pipecolate, and α-aminoadipate. These findings highlight metabolic changes associated with enhanced drought tolerance in AtUCP1-overexpressing barley.

Keywords: mitochondrial protein; abiotic stresses; functional genomics; saccharopine pathway.

NEAR INFRARED SPECTROSCOPY FOR PREDICTING SUCROSE CONTENT IN SUGARCANE BREEDING TRIALS

Gustavo Candido Jacobassi[1]; Thiago Willian Almeida Balsalobre[1]; Nathan Euclair Pinto[1]; Roberto Giacomini Chapola[1]; Hermann Paulo Hoffmann[1]; Monalisa Sampaio Carneiro[1*]

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Sugarcane is an important crop due to its use for sugar production and as a renewable source of energy like biofuel and biomass electricity. Genetic breeding aims, among other traits, to increase the sucrose content in sugarcane. Routinely, the sucrose content estimates were performed in the intermediate and advanced stages of breeding through a laborious methodology that grinds the cane stalks. The combination of near-infrared spectroscopy (NIR) and machine learning allows us to obtain calibration curves for predicting phenotypic data. The MicroNIR OnSite-W can capture NIR spectra from stalks directly in the field without destroying the biological material. Thus, this study aimed to construct a calibration curve for predicting the sucrose content of the juice (POL%J) using MicroNIR. The NIR data were collected from 50 genotypes of the Brazilian Panel of Sugarcane Genotypes (BPSG) and from genotypes of breeding trials from the Sugarcane Genetic Breeding Program of the UFSCar, between 2020 and 2023. As a reference method, conventional laboratory analysis were conducted from the POL%J values. UNSCRAMBLER (CAMO Technologies) and SPECTRAL SOFT (Spectral Solutions) software were used for data analysis. Different chemometric preprocessing was tested and standard normal variate (SNV) plus the first Savitzky-Golay derivative with 5-point window was selected. The outliers were excluded by applying the Mahalanobis distance with a 90% confidence interval. The calibration curve was constructed using a partial least squares (PLS) regression model. To ensure a good prediction, the data set was randomly divided into a calibration set (70% of the samples) and a cross-validation set (30% of the samples). In this study, we obtained 2,461 data points and 72,2% are on the calibration curve. The root mean square error of calibration (RMSEC) and the root mean square error of validation (RMSEV) were 0,93 and 0,95, respectively. The coefficients of determination to calibration (R^2C) and cross-validation (R^2V) were 0,92 and 0,91, respectively. These results showed that the calibration curve for POL%J has a high correlation with the reference values and suggest that the prediction error from external validation may be acceptable. The near-infrared spectroscopy can be used in the initial stages of sugarcane breeding programs to assist in the early selection of genotypes with high sucrose content.

Keywords: *Saccharum* spp.; phenotypic data; sugar; MicroNIR; machine learning.

PHENOTYPIC EVALUATION OF TRANSGENIC AND GENE EDITING MAIZE LINES FOR A NEW MAIZE RECEPTOR-LIKE KINASE LIKELY INVOLVED IN DROUGHT STRESS

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The increase in global temperature is causing climate change observed in various regions of the world. In the face of this scenario, urgent efforts are needed to develop drought-tolerant cultivars. Genetic transformation and gene editing are biotechnological approaches that can be used to explore plant tolerance to abiotic stress. The gene ZmDRIK1, for example, is a pseudo-kinase similar to a receptor-regulated by biotic and abiotic stresses, including drought. Under biotic and abiotic stress, ZmDRIK1 is negatively regulated to release the expression of these stress-responsive genes. Despite this role, pseudo-kinases are understudied in plants. In order to understand the function of ZmDRIK1 in maize, we examined the phenotypic response of maize events that harbor modifications on the DRIK gene. A drought response experiment was performed using overexpression (drik1-OV1, drik1-OV2, and drik1-OV3) and loss-of-function (drik-KO1, drik-KO2, and drik-KO3) maize events. The experiment was conducted in a greenhouse facility of the Genomics for Climate Change Research Center (GCCRC-UNICAMP 2016/23218-0), equipped with internet access temperature- and LED light-controlled environments for photosynthesis enhancement. Plant phenotyping was performed by evaluating parameters such as photosynthesis, stomatal conductance, recovery from water stress, and water use response. On average, edited and transgenic events restored phenotype and growth similar to wild plants. However, under normal irrigation conditions, the edited DRIK event with a 214 bp deletion (drik-KO2) exhibited more wilting under water stress, indicating a decrease in turgor pressure compared to controls. No significant differences were observed for transgenic, knockout, and control plants regarding photosynthetic efficiency, stomatal conductance, total plant biomass, and plant height. Collectively, the phenotypic results of plants subjected to water stress suggest the existence of possible compensatory stress response pathways of DRIK1 in maize. The function of this pseudo-kinase requires further investigation in plants, including experiments on specific tissues and developmental stages.

Keywords: Drought tolerance; transgenic maize; genome editing; *Zea mays*

IMPACT OF LYSINE CATABOLISM IN STRESS RESPONSE REGULATION

Ana Lúcia Mendes Pinheiro[1]*; Viviane C. H. da Silva[1]; Alessandra Koltun[1]; Maísa S. Pinto[1]; Maria Helena F. Bruno[1]; Priscila Z. Ramos[1]; Juliana Yassitepe[1]; Paulo Arruda[1]

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Lysine catabolism is involved in the stress response of plants, animals, and microorganisms. The saccharopine pathway (SacPath) is a conserved lysine catabolism pathway in eukaryotes and prokaryotes, known for contributing to stress responses mainly due to osmolyte production and aldehydes detoxification. Pipecolate and proline are produced after LKR/SDH activity and can help alleviate the cellular impact of osmotic, salt, and drought stress. In addition, AASADH properties of converting not only AASA, but a wide range of aldehydes as substrates is interesting for helping the cell to detoxicate aldehydes toxic levels as the enzyme converts it to non-toxic carboxylates. In prokaryotes, the conversion of lysine to AASA can be performed without the intermediate production of saccharopine, catalyzed by lysine dehydrogenase (LYSDH). In the seawater model bacteria, *Silicibacter pomeroyi*, LYSDH, and SacPath enzymes are both present. Still, LYSDH is 100-fold more expressed than LKR and SDH enzymes in high salted conditions when supplemented by lysine. In the thermophile bacteria *Geobacillus stearothermophillus*, only the LYSDH pathway is present. Another lysine catabolic route in plants, N-hydroxy-pipecolic acid (NHP) pathway, also produces pipecolate and is associated with a biotic stress response. As LYSDH pathway is preferentially expressed in stressful conditions in extremophile bacteria, we are investigating the impacts and contributions of LYSDH in plant stress tolerance by overexpressing LYSDH genes in maize and characterizing LYSDH and SDH enzymes heterologous produced in *E. coli* for their kinetic properties, thermostability, optimal pH and substrate utilization. The selected genes were successfully cloned into pTf101.1 and C729p7o2x35s-Act (DNA Cloning Service) plasmids for overexpression in maize, using traditional cloning with restriction enzymes. The constructs were confirmed by sanger sequencing. For maize transformation, ears were harvested 12 to 15 days after pollination, transformed with *Agrobacterium tumefasciens* containing plasmid of interest, and regenerated using tissue culture. For all constructs, 33 experiments were performed, using 14.903 embryos and obtaining 67 positive events. Transgenic plants overexpressing LYSDHs will be phenotyped for drought stress and biotrophic infection responses. LYSDH and SDH selected enzymes were also successfully produced after heterologous cloning and expression in *E. coli* using ligase-independent cloning protocol into pNIC28-Bsa4 vector. With this work, we expect to contribute to the understanding of lysine catabolism, looking to develop crops resilient to the challenges imposed by climate changes.

Key words: lysine catabolism; maize; drought stress; biotic stress

IDENTIFYING POTENTIAL MAIZE GENOTYPES PRIOR TO PHYSIOLOGICAL MATURITY THROUGH IMAGE-BASED ANALYSIS

Barbara N. Santos[1*]; Kelvin P. F. Ferreira[1]; Mario S. R. Barreto[1]; Jacilene F. S. Santos[2]; José J. F. C. Junior[1] e Gustavo H. F. de Oliveira[1]

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High-Throughput Phenotyping (HTP) has revolutionized maize (*Zea mays* L.) genotype selection in breeding programs, enhancing speed and precision. The integration of drones has further streamlined this process, although it is essential to customize HTP protocols for specific programs and regions. This study aimed to develop, implement, and validate an image acquisition protocol for early maize genotype identification in a semi-arid region. To this end, we conducted experiments over two cropping seasons. In the 2021 protocol establishment experiment, we assessed grain yield for four maize genotypes at three row spacings (0.60, 0.70, and 0.80 m) using a randomized complete block design (RCBD) with four replications. Experimental units consisted of two 8-meter rows in strips. We conducted seven drone flights at 60 and 80 meters altitude on various dates (26, 43, 57, 62, 69, 75, and 107 days after planting - DAP). In the 2022 validation trial, we evaluated grain yield for 50 maize genotypes using an RCBD with two replications. Plots included two 5-meter rows, and drone flights were performed at 40, 60, and 80 meters altitude on days 27 and 46 DAP. From captured RGB images, we extracted 29 vegetation indices, from which we selected the most appropriate based on repeatability analyses. Results indicated that flights at 80 meters altitude yielded the best vegetation index performance. However, the choice of vegetation index varied between the establishment and validation experiments, with TGI being selected in the latter case. Temporal Blups allowed us to distinguish differences between genotypes as early as 27 DAP, enabling early selection. Therefore, we infer that the strategy of flying at 80 meters altitude is the most suitable for image acquisition and early maize genotype selection. Although a precise flight date was not determined, it is evident that distinguishing and identifying promising genotypes before the physiological maturity stage is feasible, resulting in significant optimization of time and resources invested in the maize cultivar selection process.

Keywords: *Zea mays* L.; Plant Breeding; Blups; VANTs.

Acknowledgements: Universidade Federal de Sergipe, ao Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), ao Grupo de Estudos em Melhoramento Vegetal do Semiárido (GEMS) e a EMBRAPA Semiárido.

FACTOR ANALYSIS AS A TOOL IN THE SELECTION OF PARENTS IN COMMON BEAN

Domingos Jeque[1*], Julio Augusto de Castro Miguel Miguel[2], João Vitor Carvalho Cardoso[3], Rafaela Pereira Carvalho[4] , Danilo Gomes[5], Vinicius Quintão Carneiro[6]

Escola Superior de Agricultura "Luiz de Queiroz" da Universidade de São Paulo (ESALQ/USP)[1], Universidade Federal de Lavras (UFLA)[2], Universidade Federal de Lavras (UFLA)[3] , Universidade Federal de Lavras (UFLA)[4] , Universidade Federal de Lavras (UFLA)[5], Universidade Federal de Lavras (UFLA)[6].

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Common bean (*Phaseolus vulgaris*) is one of the most vital legumes cultivated globally, playing an essential role in global food security. The success of autogamous plant breeding programs critically depends on selecting the right parents. In this context, various methods described in the literature are based on information about parents and their offspring's behavior. This study aimed to select common bean parents of the red commercial type using factor analysis. Specifically, we sought to identify promising parents for crossbreeding and future Value for Cultivation and Use (VCU) trials. We evaluated 48 red bean lines from UFV and CIAT origins in experiments conducted during the 2020 and 2021 rainy seasons and the 2022 dry season at the Center for Scientific and Technological Development of the Federal University of Lavras, Lavras, MG. The experimental design used in all experiments consisted of randomized blocks with three replicates. The evaluated characteristics included grain yield ($kg.ha^{-1}$), grain appearance, and plant architecture. Individual and joint variance analyses were conducted for all assessed traits, along with the Scott-Knott mean grouping test and factor analysis. The results revealed significant effects of lineages and interactions between lineages and cultivation environments. Simultaneous selection based on grain appearance and plant architecture was carried out through factor analysis, where the first and second factors (Plant architecture and grain appearance) explained 53.04% and 28.23% of the variation, respectively. Together, these two factors explained 81.27% of the total variation. Some lineages, such as BRSMG-Marte, UFV-5, CIAT-2, and CIAT-5, stood out as promising for both characteristics. Others, like BRSMG Ouro Vermelho and VR-25, proved suitable for specific traits, such as grain appearance. Additionally, lineages CIAT-11, CIAT-21, CIAT-22, PAUD, CIAT-7, CIAT-3, UFV-8, UFV-15, and UFV-12 excelled in plant architecture. These results indicate that factor analysis is a valuable methodology that can be employed in parent selection, whether for specific or multiple traits. The identified promising lineages have the potential to enhance the efficiency of genetic breeding programs by providing high-quality genetic material for grain appearance, plant architecture, and both traits.

Keywords: *Phaseolus vulgaris*, red bean, factor analysis, plant breeding.

Acknowledgements: CAPES, CNPQ e FAPEMIG.

MIXED VARIETY SOYBEAN PRODUCTION: EVALUATION OF YIELD POTENTIAL

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The production of soybeans (*Glycine max*) plays a crucial role in global agriculture due to its economic and food importance. However, the growing demand for soy-derived products and the environmental challenges associated with soybean production have led to the search for innovative strategies to optimize production and increase productivity. In this context, the usage of mixtures of seeds from different cultivars can be considered a promising alternative. The main objective of this study was to investigate the feasibility of soybean production through the sowing of mixtures of commercial cultivars in different proportions. To achieve this, field evaluations and digital phenotyping were conducted over 15 treatments of 6 cultivars and 9 mixtures of different proportions in a randomized design. Standard field procedures for fertilization and pest control were adopted through the season. The field evaluations were carried out through the collection of grain yield data. The digital phenotyping was performed using an unmanned aerial vehicle equipped with a RGB camera to evaluate NGRDI and canopy coverage, aiming to understand the uniformity of development and maturity of the mixtures. In the first season, the average yields of cultivars and mixtures were 4360 kg ha^{-1} and 4086 kg ha^{-1} respectively, while in the second season they were 4490 kg ha^{-1} and 4492 kg ha^{-1}. The results showed that the mixture of cultivars provide stable yield, with the harvested yield being only 1,39% lower than the expected yield (based on the weighted average of the mixture components) in the first season and 0,07% higher in the second season. The average canopy coverage of the individual cultivars was 81,67%, while the average of the mixtures was 86,58%, meaning there's no impact on crop development based on this variable. NGRDI results were -0,15 with a coefficient of variation of 16,87% for individual cultivars while -0,14 and 18,70% for mixtures, showing no difference in the uniformity of maturity process. In conclusion, the use of mixtures of soybean cultivars in different proportions can be a promising alternative to optimize production and increase food production security.

Keywords: soybean production; cultivar mixtures; digital phenotyping; canopy coverage; NGRDI.

DERIVATION OF ENVIROMICS MULTIMARKERS FOR UPLAND RICE AND THE IMPORTANCE OF THEIR COVARIABLES.

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Rice (*Oryza sativa* L.) is one of the staple foods in the Brazilian diet, and therefore, its cultivation and productive independence are strategically essential for ensuring the population's food security. Within rice farming, selecting the appropriate genotype for planting is the factor that most strongly impacts the outcome of the endeavor. In order to support this decision-making process, *enviromics* has been applied with the objective of selecting genotypes with higher productive potential for specific areas of interest. The aim of this study was to generate and analyze the contribution of enviromic markers to the total upland rice production data in Brazilian territory. The experimental data were provided by Embrapa Rice and Beans and involved the evaluation of 2,119 rice genotypes in 187 municipalities or localities across the country, spanning the period from 1982 to 2018. For the generation of enviromic markers, data from the SoilGrids, WorldClim, and NASA POWER platforms were used, resulting in a total of 393 environmental covariates collected. The generation of enviromic markers was performed using the Monte Carlo method, with 10,000 iterations and always considering the presence of the 187 municipalities where the Embrapa experiments were conducted. The Random Forest package and the IncMSE method were used to evaluate the importance of each covariate for the model applied throughout the Brazilian territory. The top-ranked covariates were the coefficient of variation for seasonal precipitation, the percentage of coarse fragments in the 30-60 cm soil layer, and the density of organic carbon in the 5-15 cm layer. Together, these covariates were the most important in the environmental index in 98.81% of cases, with the precipitation-related covariate considered the most important for the environment in 84.35% of cases. Although *enviromics* does not aim to explain the effect of environmental covariates on the study object, it is interesting to observe the clear relationship between precipitation rates and their variables related to crop productivity. Additionally, the percentage of coarse fragments can reduce soil drainage capacity and create a compacted layer that hinders root growth and penetration. Organic carbon density, on the other hand, plays an important role in providing water and other nutrients to the plant and contributes to the maintenance of microbial activity. Given the vast size of the Brazilian territory and the intricate demands for constructing an *envirome*, it is crucial to prioritize obtaining the highest quantity and diversity of environmental data for a more comprehensive characterization of the environment. We observed the presence of covariates from all three repositories analyzed in the covariate importance ranking, emphasizing the ongoing need to maintain a robust and up-to-date database for environmental variables.

Keywords: Remote sensing; precision breeding; geoinformatics; rice cultivation.

Acknowledgements: We thank CAPES and FAPEG for the project funding.

USE OF ALTRUISTIC VECTOR WITH MORPHOGENIC GENES TO INCREASE TRANSFORMATION EFFICIENCY IN B104 MAIZE LINES

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The transcription factors Baby Boom (Bbm) and Wuschel2 (Wus2) are morphogenic genes (MR) that respectively promote cell proliferation during embryogenesis and maintain stem cells in the shoot meristem. MR has increased transformation efficiency in previously difficult-to- transform plant species in recent years. In the first studies, *Bbm* and *Wus2* were included in the same plasmid as the gene of interest (GOI) and were frequently integrated into the genome, generating undesirable phenotypes. A new transformation approach, called "altruistic transformation", uses co-infection with two Agrobacterium strains. One strain delivers a T-DNA conferring morphogenic gene expression, while the other delivers a gene of interest (GOI). Using the altruistic approach for maize transformation with morphogenic genes and GOI, this work aims to enhance the efficiency of the B104 maize line. We tested the ratio of 9:1 (Agrobacterium-GOI to Agrobacterium-MR genes) against 1:1. Few events had abnormal phenotypes with the 9:1 ratio and the number of positive events was higher with the 9:1 ratio (66 vs 40) for the altruistic transformation, which contains the MR *Bbm* and *Wus*. Half of the embryos were transformed in our transformation experiments with only one Agrobacterium strain containing the T-DNA harboring the GOI. The other half was transformed with two Agrobacterium strains, one containing a T-DNA binary plasmid with GOI and the other containing a T-DNA binary plasmid with MR (1:1 ratio). We also tested two ratios of Agrobacterium with GOI to Agrobacterium with MR 1:1 and 9:1. The maize transformation protocol used was based on Aesaert et al. (2022). We tested the effectiveness of a new approach that includes MR genes compared to our previous protocol without them. The test used a 1:1 ratio of Agrobacterium-GOI to Agrobacterium-MR genes and the vector pLAPAU14. The results indicated that the altruist protocol outperformed our routine protocol. We obtained 53 positive plants utilizing MRs and eight without MRs. However, some abnormal events were still observed. We then tested the ratio 9:1 (Agrobacterium-GOI to Agrobacterium-MR genes) with 1:1, and only very few events had abnormal phenotypes using 9:1 ratio. In addition, the number of positive events was superior using 9:1 ratio, 66 versus 40. On average, the transformation efficiency was 0.5% for the experiments without MR and 3.3% with MR. When we tested the two MR ratios, we observed, on average, 1.29% for 1:1 and 2.2% for 9:1. Maize transformation efficiency was increased by MR, with a 9:1 ratio outperforming 1:1 in both transformation efficiency and absence of abnormal plants.

Keywords: altruistic vector; maize; morphogenic genes; transformation.

WHEAT CULTIVAR EVALUATION IN THE SOUTH OF MINAS GERAIS

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Brazil is expected to produce approximately 10.8 million tons of wheat in the 2022/23 agricultural year, with the largest producers being the states of Paraná and Rio Grande do Sul. However, other states are promising for wheat cultivation, such as Minas Gerais. However, the increase in this production is directly linked to the improvement of wheat cultivars adapted to growing conditions, which contributes to meeting the country's need for this cereal. Therefore, the aim of this study was to evaluate the agronomic performance of wheat cultivars in VCU trials in the south of Minas Gerais. Two experiments were conducted under dryland conditions in two locations, one in Itutinga (IT) and another in São Gonçalo do Sapucaí (SG). A total of 27 cultivars from different breeding programs were evaluated in experiments laid out in a randomized complete block design with four replications and five 5.0 m long rows. The following traits were evaluated: hectolitre weight (HW, kg/hL), thousand-seed weight (TSW, g) and grain yield corrected to 13% moisture (GY, kg/ha). Data were analyzed in the R environment using mixed model approach with interblock recovery information and the Scott-Knott test to cluster the phenotypic adjusted means. GGE biplot analysis was performed to assess the adaptability and stability of the cultivars. Based on the experimental coefficient of variation (CVe), there was middle and high experimental precision for HW (CVe=14.6 % IT and 7.2 % SG) and follow the selective accuracy (SA) there was high precision for TSW (SA= 0.86 IT and 0.98 SG; CVe=8.6 % IT and 3.0 % SG) and low for GY (SA= 0.19 IT and 0.57 SG; CVe=27.0 % IT and 23.4 % SG). There were significant differences between locations for TSW and GY, and among cultivars for TSW, allowing them to be grouped into five groups by the Scott-Knott test. There was no significant effect for the interaction between cultivars and locations. The wheat line with the highest TSW was UB 1813604 (50.9 g) and the one with the lowest TSW was TBIO Sintonia (34.2 g). According to GGE biplot analysis, TBIO Duque and ORS Feroz performed better than the others and cultivars with the best stabilities were IPF 89223 and PF 190015. It is concluded that it was possible to identify potential wheat cultivars based on phenotypic performance and stability for cultivation in the South of Minas Gerais.

Keywords: Adaptability; stability; yield; wheat breeding.

Acknowledgements: The authors would like to thank CAPES, CNPq, Embrapa and FAPEMIG for their financial support and EPAMIG for its technical support.

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