VI International Meeting on Plant Breeding

“Understanding the plant-microbe interaction to innovative plant breeding”

PROCEEDINGS

GVENCK

October – 2022

THE INTERNATIONAL MEETING ON PLANT BREEDING

Understanding the intricate dynamics between plants and microbes stands as a cornerstone in pioneering innovative approaches to plant breeding. In a world grappling with uncertainties surrounding food security, leveraging plant-microbe interactions has emerged as a pivotal strategy in developing resilient, high-yielding cultivars. Scientists have ardently dedicated their efforts to crafting tools that transcend the challenges prevalent in agricultural landscapes.

In light of this pursuit, it is imperative to foster dialogues and discussions that elucidate these novel tools. Such exchanges are instrumental in cultivating a cohort of breeders adept at harnessing these innovations effectively, thereby ensuring their judicious application in both research and breeding practices.

The International Meeting on Plant Breeding, a component of the "Corteva Agriscience Plant Science Symposia Series," serves as a platform for these conversations. In its latest iteration, the focus shifted towards unraveling the significance of plant-microbe interactions in revolutionizing plant breeding methodologies. Recognizing the profound impact of integrated data analysis, the symposium aimed to underscore its pivotal role in propelling plant breeding programs forward.

Analyzing and monitoring data evolution across temporal scales becomes indispensable to accurately estimate parameters crucial for informed genetic selection. Therefore, the intent was to delve deeper into these discussions, fostering an environment conducive to the exchange, updates, and dissemination of knowledge, thereby amplifying the understanding and application of plant-microbe interactions in modern breeding paradigms.

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

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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 5th, 2022

08:00 - 08:30 AM → Jason Rauscher - Opening session (Corteva Agriscience)

08:30 - 09:30 AM → Marcio de Castro Silva Filho (ESALQ/Brazil)

09:30 - 09:45 AM → Research Presentation

09:45 - 10:45 AM → Juan E. Perez-Jaramillo (University of Antioquia, Medellín/Colombia)

10:45 - 11:00 AM → Break

11:00 - 11:15 AM → Research Presentation

11:15 - 12:15 AM → Marco Antônio Nogueira (EMBRAPA/Brazil)

12:15 - 14:00 PM → Lunch Break

14:00 - 15:00 PM → Cristiana Argueso (Colorado State University/USA)

15:00 - 15:15 PM → Research Presentation

15:15 - 16:15 PM → Matthew Hudson (University of Illinois campus, Urbana, IL)

16:15 - 16:40 PM → Break

16:40 - 17:40 PM → CORTEVA's representative

17:40 - 17:50 PM → "Roland Vencovsky" Award

17:50 - 18:00 PM → Closing remarks

October 6th, 2022

09:00 - 16:00 PM → MiniCourse - Dr. Juan E. Perez-Jaramillo (University of Antioquia, Medellín/Colombia)

October 7th, 2022

09:00 - 16:00 PM → MiniCourse -"Lights, camera, {pliman}! Analyzing plant images in R" - Tiago Olivoto (UFSC/Brazil).

SPEAKERS

Dr. Marcio de Castro Silva Filho

Marcio de Castro Silva Filho holds a degree in Agronomic Engineering from the Federal University of Lavras-UFLA (1984), a Master's in Genetics and Plant Breeding from UFLA (1989) and a PhD in Molecular Biology of Plants from the University of Louvain (1994), Belgium.

Full Professor at the Department of Genetics at Escola Superior de Agricultura "Luiz de Queiroz", University of São Paulo, Researcher and Pro-Rector of Graduate Studies at USP. Has experience in Genetics, with emphasis on Molecular Genetics of Plants, working mainly on the following topic: plant-insect-pathogen interaction.

Dra. Cristiana Argueso

Dra. Cristina has bachelor's degree and master's degree from Campinas State University and a Ph.D. from Cornell University. She currently serves as an assistant professor at Colorado State University, at the Department of Agricultural Biology.

She has already worked as a Research Associate in plant molecular biology at the University of North Carolina and was a Visiting Scientist in Plant Molecular Biology at the Max Planck Institute for Molecular Plant Physiology. The main focus of Argueso's lab is on the Plant hormone signaling pathways in response to pathogen infections and to plant-environment interactions.

Dr. Juan E. Perez Jaramillo

Juan E. Perez-Jaramillo holds a degree in Biology, from the University of Antioquia, and a Master's in Environmental Agrobiology, from the Public University of Navarre. Dr. Pereze-Jaramillo received his Ph.D. in Microbial-Plants Interactions from Leiden University, under the direction of the advisor Prof. Dr. J.M. Raaijmakers and co-advisor Dr. V.J. Carrión.

He has been developing studies about interactions between plants and microbial groups, aiming to understand how genes are involved in this process. In this field, he has participated in a study to investigate an actinobacterium from Cerrado soils and its aptitude to promote phosphorus solubilization in soybean plants. Dr. Perez-Jaramillo is now an Assistant Professor of Biology in the Institute of Biology at the University of Antioquia in Medellin, Colombia.

Dr. Marco Antônio Nogueira

Marco Antonio Nogueira, holds a degree in Agronomy from FCAV-UNESP (1994), a master's degree (1997) and a doctorate (2002) in Agronomy (Soils and Plant Nutrition) from ESALQ-USP, in a "sandwich" program at the University of Tübingen, Germany, and Visiting Scientist (Post-Doctoral) (2015/2016) at North Carolina State University.

He has been a Researcher A at Embrapa Soja since 2010, currently a member of the Internal Technical Committee and a member of the Management Committee of Embrapa's Biological Inputs Portfolio. Permanent professor and advisor at the Postgraduate Programs in Microbiology and Agronomy at the State University of Londrina. He has experience in Agronomy, with emphasis on Soil Microbiology and Biochemistry, working mainly on the following topics: soil quality bioindicators, biological nitrogen fixation, drought tolerance, and agronomic potential and environmental impact of urban and agro-industrial waste.

Dr. Tiago Olivoto

Son of family farmers, Agronomical Engeneer graduated from the UNOESC (2014), Master in Agronomy: Agriculture and Environment from the UFSM (2017) and Doctor in Agronomy with emphasis on Plant Breeding and Agricultural Experimentation by the UFSM (2020). He is currently Professor at the Department of Plant Science at the UFSC, working in Plant Breeding and Agricultural Experimentation.

He carries out activities related to the planning, conduction and evaluation of experiments with annual crops, with emphasis on the development and improvement of statistical-experimental methods for the evaluation of multi-environment assays in plant breeding. He has experience with the softwares: Gênes, GEA-R, R, SAS and SPSS. He has been developing packages for R metan software aimed at checking, manipulating, analyzing and presenting data from multi-environment assays and pliman , aimed at analyzing plant images.

Dr. Matthew Hudson

Dr. Hudson uses supercomputing and DNA sequencing to solve problems in plant, animal, and human genetics. His current research focuses on how crops are bred and on ways to treat and prevent plant, animal, and human diseases. He is particularly interested in the genetics of crop traits and the genetic and molecular interactions of soybeans with pathogens, pests, and other organisms, with a special interest in the interaction between soybean and its most economically important pest, the soybean cyst nematode.

SUMÁRIO

Classification of soybean populations for secondary macronutrient using machine learning and spectral data

Izabela Cristina de Oliveira[1], Dthenifer Cordeiro Santana[1]; Regimar Garcia dos Santos[1], João Lucas Gouveia de Oliveria[2], Paulo Eduardo Teodoro[2], Larissa Pereira Ribeiro Teodoro[2]

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Classifying soybean genotypes according to their nutritional characteristics can optimize time in soybean breeding programs. Using remote sensing technologies and Machine Learning (ML) techniques makes the genotype selection process even more efficient. Thus, the objective of this work was to classify soybean populations using information from secondary macronutrients, spectral data and ML techniques, seeking to find the best classification algorithm for these data and the best dataset for the algorithms. The experiment was carried out in the 2019/20 crop in the experimental area of the Federal University of Mato Grosso do Sul, municipality of Chapadão do Sul/MS. 103 F_2 soybean populations allocated in a randomized block design with two replications were evaluated. At 60 days after emergence, spectral images of the plant canopy were collected using a remotely piloted fixed-wing aircraft, Sensefly eBee RTK, with autonomous control of takeoff, flight plan and landing. The eBee was equipped with the Parrot Sequoia multispectral sensor. The spectral bands (SB) collected by the equipment were: red (660 nm), green (550 nm), NIR (735 nm) and Rededge (790 nm). The information acquired by the wavelengths made it possible to calculate the vegetation indices: NDVI, NDRE, GNDVI, SAVI, MSAVI, MCARI, EVI and SCCCI. To determine the levels of secondary macronutrients, the Bataglia methodology was adopted. The genotypes were divided into two groups using the k-means algorithm and expressed by a graph using principal components. For each nutrient, a boxplot of both clusters was generated, seeking to observe which set of genotypes obtained superiority in nutrient contents. Subsequently, the data were submitted to machine learning analyses. Spectral data were used as input variables for the models, and three different configurations were tested: using only spectral bands (SB), using only vegetation indices (IV) and using IVs+SBs. The performance of the models was evaluated according to the metrics of accuracy of percentage of correct classifications, F-score and Kappa coefficient. The performances of the models were submitted to an analysis of variance, evaluating the inputs, the ML models used and the interaction between them. If there was significance in boxplots were generated with the means according to the Scott-Knott test at a 5% significance level. In general, the Random Forest algorithm had the best performance for all accuracy metrics using the SB or IVs as input. Using the combination of SB+VIs the best algorithm was logistic regression.

Keywords: Calcium, Magnesium, Sulfur, Random Forest, Spectral Bands

Acknowledgements: CAPES.

Use of seed traits acquired by image analysis to select soybean genotypes resistant to the stink bug complex

Adriano Abreu Moreira[1]; Maiara de Oliveira[1]; Patricia Braga[1]; Ashley Noel Burricks[1]; Fernanda Smaniotto Campion[1]; Felipe Augusto Krause[1]; José Baldin Pinheiro[1]

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One of the major pest insects are stink bugs species that form the soybean's stink bug complex (STK). Resistance to STK is complex and of difficult selection, because it involves several traits and most of them are regulated by a high number of genes and are highly affected by the environment. The objective of this study was to assess the potential of seed traits to indirectly select soybean genotypes resistant to the stink bug complex. Twelve genotypes were selected from a RILs population as well as the parents, one susceptible and one resistant to STK, totaling fourteen genotypes. Four experiments were conducted in two growing conditions, one in which insect chemical control was carried out and the other where natural stink bug infestation was enabled. Ten traits were assessed and categorized in two groups, being the first group (FG) traits related to seed morphology and damaged area and the second group (SG) traits related to stink bug resistance. Morphology traits from FG were phenotyped trough image analysis performed by the Smart Grain® software, while the seed's percentage of damaged area (DSE) was assessed by treating seeds with the tetrazolium salt, acquiring images of 150 seeds per plot and then segmenting the images with the Field Image R package from the R software. The BLUPs were obtained for each trait to perform canonical correlation analysis (CCA) between FG and SG of traits with the metan package. CCA showed that only the first two pairs had a canonical correlation (*r*) significant by the Chi-square test ($p \leq 0.05$), thus intergroup associations can be established. The first canonical pair (CP) shows that DSE had the higher absolute canonical coefficient (CC) of 0.919 in the FG and tolerance index (TOL) had the CC (-1.074) in the SG. The canonical correlation between groups for this CP was 0.987 which shows a strong negative correlation between DSE and TOL. The second CP had a *r* of 0.974, with seed area (AS) having the CC (1.240) for the FG and in the SG hundred seed weight (MSC) had the CC (0.949). This is an indication of a positive correlation between AS and MSC, which is a trait related to compensation of stink bug damage. The third CP even though was not significant it presented a *r* of 0.821, being the main contributing traits DSE (1.279) and seed length to width ratio (LWR, CC = -2.131) for the FG, while weight of healthy seeds (PSD) and leaf retention (RF) had the CC (0.899; 0.866) in the SG. The canonical loadings for this CP suggest that the higher DSE and RF the lower PSD and LWR. Low LWR means a less round and more deformed seed which can be attributed to stink bug seed damage. Thus, DSE and AS are potential traits that could improve selection of resistant soybean genotypes. In addition, deeper studies considering LWR should be carried out because it shows a potential to select resistant genotypes and it is a trait of easy phenotyping, which favors selection in breeding programs with a high number of genotypes.

Keywords: High throughput phenotyping; Hemiptera: Pentatomidae; Plant breeding; *Glycine max*

Acknowledgements: I would like to thank the ESALQ's Genetics and Plant Breeding Graduate Program, the Genetics Department, the Diversity, Genetics and Plant Breeding Laboratory and CAPES for making this work possible.

Classification of soybean genotypes regarding physiological performance using spectral variables

Regimar Garcia dos Santos[1], Dthenifer Cordeiro Santana[1], Izabela Cristina de Oliveira[1], Larissa Pereira Ribeiro Teodoro[2], Paulo Eduardo Teodoro[2]

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The physiological characters of the soybean crop are correlated with its productivity, which has been proven through studies of genetic progress. The measurement of these characters requires complex equipment, specialized labor, in addition to being costly and time- consuming. Problems that can be solved using spectral bands and vegetation indices associated with remote sensing. The objective of this work was to identify the best machine learning technique for classifying F2 soybean population clusters based on their physiological characteristics using spectral bands and vegetation indices as input variables. The experiment was carried out in the 2019/2020 agricultural year, in the municipality of Chapadão do Sul, MS. Using a drone, the values of spectral bands (SB) and vegetation indices (IV) were collected from 194 soybean populations in F2. The physiological characteristics evaluated were: net photosynthesis (A), stomatal conductance (gs), internal concentration of CO2 (Ci), transpiration (E) and water use efficiency (USA). Using the k-means technique the samples were divided into two clusters, using Principal Components (PCA), the samples were partitioned into two groups based on their physiological behavior. SB+IV, SB only and IV only were evaluated as input variables. Using SB+IV, the technique with the highest classification capacity was the artificial neural networks (ANN) with 66.34% of correct classifications (CC), the J48 algorithm presented the best result using only SB (69.87% CC) and Logistic Regression (RL) obtained better response when using only IV's as input variable (68.95% CC). The results obtained demonstrate that the best way to make the classification is using only the SB as input variables in the J48 algorithm, reducing the time required and the chances of error during the step of calculating the vegetation indices.

Keywords: Machine Learning. Remote sensing. Physiology

Acknowledgements: CAPES.

DEVELOPMENT AND PERFORMANCE OF BIOFORTIFIED CHERRY-TOMATO HYBRIDS

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There is an increasing global demand for nutrient-enhanced food. Tomato (*Solanum lycopersicum* L.) is one of the species that can help meet these nutrient requirements due to the possibility of enriching fruits with compounds such as anthocyanins. Anthocyanins are the widest class of water-soluble pigments found in plants under numerous forms and are important for their anticarcinogenic, anti-inflammatory and potential to prevent metabolic diseases. The objective of this research was to estimate the combining abilities of purple cherry tomato inbred lines, developed at the Vegetables Breeding Laboratory (LMH) of Esalq/USP through a diallel arrangement, aiming to identify the best genotypes for new crosses, besides characterizing and identifying potentially outstanding hybrids suitable for releasing as new cultivars. For this purpose, seven purple cherry-tomato inbred lines were crossed to obtain 21 hybrids. Inbred lines and hybrids were grown in 5L pots in a greenhouse, and fruit yield per plant (PROD, kg.plant^{-1}), Number of fruits per plant (NFP, number.plant-1), average fruit mass (MMF, g.fruit-1), Fruit diameter (D, mm), Fruit length (C, mm), Shape Factor (FF, C/D) were evaluated in an experiment with three replicates and four plants per plot. Based on these data, a general characterization was performed and also the estimation of the general and specific combining abilities, significant differences among the genotypes studied regarding morpho-agronomic traits were found. Also, we performed a sensorial analysis based in a hedonic scale (1 - worse, 9 - best) for flavor, acidity, sweetness, appearance and texture. Hybrids H1-4, H1-6, H1-7, H2-6, H3-7 and H6-7 were the highest in PROD, probably because they were combinations between inbred lines with higher NFP and higher MMF, being these hybrids potentially candidates for new cultivars. All inbred lines presented significant GCA estimates for at least one of the variables studied in the diallelic analysis which is evidence that there are important additive effects that can be explored in new breeding programs using these inbred lines, especially L1 and L7, which have shown promise to increase both yield and average fruit mass, in the crosses they were involved. Finally, few combinations between inbred lines with significant SCA estimates according to each variable, being hybrids H1-4, H2-6 and H3-7 for PROD, hybrids H2-4 and H4-6 for MMF and hybrids H1-4, H5-7 and H2-6 for NFP. Through the selection index, hybrids H3-6 and H1-6 were classified as the best for the five sensorial traits.

Keywords: *Solanum lycopersicum* L.; anthocyanins; nutraceuticals; breeding.

DUAL-LAYER BIOLOGICAL NETWORK REVEALS TRANSCRIPTIONALLY MODULATED RGA GENES IN THE SMUT FUNGUS VS ENERGY-CANE BIOINTERACTION

Gustavo Schiavone Crestana[1]; Renato Gustavo Hoffmann Bombardelli[1]; Hugo Vianna Silva Rody[1]; José Antonio Bressiani[2]; Silvana Creste[3]; Claudia Barros Monteiro-Vitorello[1]

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Sugarcane (*Saccharum sp.*) presents great economic, environmental, and social importance worldwide. Traditionally used for sugar and ethanol production, this scenario has been changing with the development of novel genotypes, called energy-cane, as a source of fiber for renewable second-generation bioenergy. Although highly productive, such genotypes are susceptible to *Sporisorium scitamineum*, the causal agent of sugarcane smut disease, generating yield losses depending on the variety and environmental conditions. To investigate the differential behavior of plant defense mechanisms in contrasting energy-cane genotypes toward smut, we analyzed RNA-seq data of susceptible and resistant plants 48 hours after inoculation (hai). Using *Saccharum spontaneum* as a genomic reference, the transcriptomic analysis revealed a specific profile with 9,960 differentially expressed genes (DEGs) for the susceptible genotype and 2,220 DEGS for the resistant genotype. The RNA-seq data was integrated into a dual-layered biological network based on sugarcane-*Arabidopsis* orthology, containing metabolic (KEGG) and PPI (BioGrid) data. The largest connected component was composed of 8,548 nodes and 42,243 edges, and was used for the downstream analysis. Statistical inferences regarding centrality degree were used to cluster the nodes according to their connectivity. We also performed a Gene Set Enrichment Analysis (GSEA) after detecting sub-modules with the MCODE algorithm to determine gene set enrichment in the RNA-seq data. The GSEA analysis detected 40 MCODE sub-modules exhibiting enrichment within the susceptible and resistant plants. Interestingly, 6 sub-modules (42, 58, 83, 121, 318 and 333) harboring resistance gene analogs (RGAs) - related to plant defense against pathogens - were identified as positively enriched in the resistant plants. Additionally, those genes presented contrasting expression profiles of up- and down-regulated, respectively, within the comparison of resistant-susceptible plants. These results will be used as potential *input* for future functional studies and assist decision-making in sugarcane breeding programs. Furthermore, such approaches will enable the understanding of pivotal processes contributing to resistance/susceptibility in energy-cane, providing integrative knowledge toward a more sustainable agriculture.

Keywords: Biological network; Plant-microbe interaction; Sugarcane; Smut disease; Bioenergy

Acknowledgements: FAPESP, CNPq, Capes

Machine learning in the classification of soybean genotypes for primary macronutrient contents using UAV-multispectral sensor

Dthenifer Cordeiro Santana[1]; Regimar Garcia dos Santos[1], Izabela Cristina de Oliveira[1], Paulo Eduardo Teodoro[2], Larissa Pereira Ribeiro Teodoro[2]

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Using spectral data to quantify the content of nitrogen, phosphorus and potassium in soybean plants can help breeding programs to develop efficient genotypes in the use of fertilizers. And employing Machine Learning techniques to classify these genotypes according to nutritional content makes the analyzes performed in the breeding processes even faster and more accurate. Thus, the objective of the work was to find the best algorithm(s) and the best input input of the ML algorithms in the classification of soybean genotypes. A total of 103 F2 soybean populations were evaluated in a randomized block design with two replications. At 60 days after emergence (DAE) spectral images were collected with a remotely piloted aircraft (RPA) Sensefly eBee RTK fixed wing, with autonomous control of takeoff, flight plan and landing. The eBee was equipped with the Parrot Sequoia multispectral sensor. The reflectance values were obtained in the following spectral bands (SBs): red (660 nm), green (550 nm), NIR (735 nm) and Rededge (790 nm), which were used to calculate the vegetation indices (VIs). At the same time of flight, leaves were collected in each experimental unit to obtain the foliar contents of nitrogen, phosphorus and potassium. Data were subjected to a Pearson correlation analysis. Subsequently, principal components analysis was performed together with the k-means algorithm to define two groups: one whose genotypes have high foliar contents and the other whose genotypes have low foliar contents. Boxplots were constructed for each cluster according to the content of each nutrient within the groups formed, seeking to observe which set of genotypes obtained superiority in nutrient levels. Subsequently, the data were submitted to machine learning analyzes using the following algorithms: J48 decision tree, linear regression (LR), decision tree (DT), random forest (RF), artificial neural networks (ANN) and vector machine support (SVM). The clusters formed served as output variables for the classification models used. Spectral data were used as input variables for the models, and three different configurations were tested: using only SB, using only VIs and using SBs+VIs. The J48 and SVM algorithms presented the best performance in the classification of soybean genotypes. The best input configuration for the algorithms was using the spectral bands as input.

Keywords: Nitrogen, Phosphorus, Potassium, J48, Support Vector Machine, Spectral Bands

Acknowledgements: CAPES.

MULTI-TRAIT GENOME-WIDE ASSOCIATION STUDIES IDENTIFY LOCI RELATED WITH OIL PHENOTYPES IN ACROCOMIA ACULEATA

Evellyn Giselly de Oliveira Couto[1*]; Jonathan Morales-Marroquin[2]; Alessandro Alves Pereira[2]; Samuel B. Fernandes[3], Joaquim Adelino de Azevedo Filho[4], Carlos Augusto Colombo[4]; Maria Imaculada Zucchi[5].

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Facing the need of implement renewable energy sources to reduce environmental impacts, the macaúba oil palm (*Acrocomia aculeata* (Jacq.) Lodd. Mart) has stood out as a promising alternative for biofuels production, due to its high fruit production and sizable oil content in the mesocarp. Also, the processing of other parts of the fruit provide products to the cosmetics, food, and charcoal industry, along with discernable value in the commercial market. Despite the economic importance, macaúba is a non-domesticated neotropical palm, incipient in large-scale cultivation, besides genetic architecture studies in the species are scarce. Elucidating its genetic information can contribute to accelerate its domestication process. Furthermore, the quantification of simultaneous loci contributions for multiple traits, a phenomenon due pleiotropy or linkage genes, can be facilitated by using multivariate models in genome-wide association studies (GWAS). Therefore, we conducted *single-trait* and *multi-trait* GWAS models to identify SNP markers located in gene regions related to different phenotypic traits involved in fruit production and fruit pulp oil content. For this, 201 palms were randomly selected from a natural population; the fruits were collected within two years of production. Phenotypic measurements of 13 traits involved with fruit production, processing, and pulp oil content were obtained. Genomic libraries were prepared following the protocol of genotyping-by-sequencing using two restriction enzymes (ddGBS) for SNP markers detection. The SNP calling was performed using three different strategies since macaúba does not have a reference genome: using i) de novo sequencing, ii) the *Elaeis guineenses* Jacq. reference genome and ii) the macaúba transcriptome sequences. *Single-trait* and *multi-trait* GWAS models were fitted on the three genotypic datasets to detect candidate and/or pleiotropic genes involved with the traits. All phenotypic traits studied showed statistically significant differences and heritability values ranged from 63 to 95%. Traits that showed genotypic correlations above 0.8 were inserted into the *multi-trait* GWAS model. A total of 47 candidate genes in regions involved with different cellular pathways were detected in the *single-trait* GWAS, while the *multi-trait* GWAS detected 3 candidate genes that may be inserted in genes in pleiotropy or in linkage. Univariate and multivariate GWAS models can maximize the amount of information derived from the evaluation of multiple traits, once they allow the detection of pleiotropic or linked genes. The results achieved in this study revealed different gene regions associated with adaptive traits involved with fruit and oil production, allowing new genetic studies in macaúba for its domestication and pre-breeding.

Keywords: Neotropical oil palm, oil content, associative mapping, pleiotropic or linked genes.

Acknowledgment: We thanks FAPESP for the financial support in the development of this research and the IAC genetic resources group for the assistance in the phenotypic data obtention.

DESEMPENHO DE HÍBRIDOS DIALÉLICOS DE MILHO IRRIGADOS COM ÁGUA DE REUSO NO SEMIÁRIDO SERGIPANO

Henrique Rocha Azevedo Santos[1]; Jacilene Francisca Souza Santos [1]; Darliton Alex Silva Feitosa[1]; Jessica dos Santos Oliveira [1]; José Jairo Florentino Cordeiro Junior [1]; Gustavo Hugo Ferreira de Oliveira [1].
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A cultura do milho (*Zea Mays* L.) é uma das predominantes em todo o mundo, com destaque na região semiárida do estado de Sergipe, sendo importante para pequenos e grandes produtores. Em meio a limitação de recursos hídricos na região, faz-se necessário o desenvolvimento de genótipos tolerantes a águas especiais, ou de reuso. Objetiva-se avaliar o desenvolvimento de cruzamentos dialélicos de milho irrigados com água de reuso em condições de semiárido. Os genótipos foram cultivados em campo irrigado com água de reuso durante todo o ciclo da cultura, sendo um total de 29 genótipos, a parcela constitui-se de duas linhas de 4 metros, semeados com o espaçamento entre linhas de 0,7 m e entre plantas de 0,2 m. Posteriormente, foram realizadas avaliações de altura de planta, altura de espiga e produtividade de grãos por hectare. Por meio da análise de variância, observou-se a variabilidade existente entre os materiais para produtividade de grãos. Não foi observado variabilidade para altura de planta e altura de espiga. Os coeficientes de variação (CV) ficaram dentro da normalidade. Para produtividade de grãos os melhores genótipos foram os cruzamentos IAC AIRAN x KWS 9555, GNZ 19 x KWS 9822, GNZ 17 x KWS 9960, IAC AIRAN x KWS 9960 e a testemunha IAC 8053, sendo esses os que apresentam as melhores médias de produtividade de grãos, são elas 5632.130, 5328.810, 5303.270, 5284.110 e 5415.015 quilogramas por hectare, respectivamente. Tais dados nos fornecem as expectativas importantes do uso de água residuária em genótipos de milho, sendo uma alternativa de cultivo em região semiárida. Os genótipos selecionados podem ser incluídos em programas de melhoramento para síntese de populações adaptadas ao cultivo sob irrigação de água de reuso em condições semiáridas.

Palavras-chave: Genótipos, Produtividade de grãos; *Zea mays* L.
Agradecimento: Grupo de Estudo em Melhoramento Vegetal do Semiárido (GEMS), EMBRAPA Semiárido, Universidade Federal de Sergipe, FAPITEC-SE.

MAIZE YIELD POTENTIAL CAN BE DIFFERENTIATED BASED ON DIGITAL SIGNATURE IN JUVENILE STAGE

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The corn (*Zea mays* L.) field have been commonly monitored during its phenological development by technology focused on the phenotyping of high yield potential. In terms of plant breeding, the interest is to find the best way to predict, accurately and quickly, the grain yield of genotyping before maturity and select the best one, reducing human sources on the field work. The aim of this work was to determine the yield of corn still in juvenile stage through digital signature using vegetation indices. The experiment was carried out at embrapa's Experimental Farm, which is located in the municipality of Nossa Senhora da Glória - SE. A Randomized Block Design with Track Scheme was used. The plots were composed of two lines of eight meters each, with spacing of 0.20 m between plants. Four maize genotypes were evaluated in four replicates, distributed in three different spacings, which were 0.60: 0.70 and 0.80 m between lines. A total of seven flights were carried out on different dates, i.e.: 19; 26; 43; 57; 62; 69 and 75 days of flight after planting (DAP), using heights of 60 and 80 m. The harvested plots were adjusted to 13% to determine the grain yield. There was genotyping variability according to ANOVA. The productivity ranking was determined by the Tukey test. Thirty-seven vegetation indices were used. The heritability predicted by each index was determined to follow up with the selection of the best ones. Mixed models were performed to determine the temporal BLUP's (TBLUPS) of the indices. Temporal series was evaluated by TBLUPS vs DAP for the two flight heights, individually. It was verified that the Red (h^2= 64%) and TGI (h^2= 58%) indices for the altitude of 60 m presented the best results regarding the differentiation of materials in 43 DAP. The altitude of 80 m, presenting a very interesting results for the breeding program, with the BI; Blue, Green and TGI reaching the highest heritability values, presenting genotypic differences in 26 (h^2 52; 50; 60 and 62%, respectively) and 43 (h^2 73; 62; 73 and 70%, respectively) DAP. According to the genotypic differentiation found, it shows the possibility to obtain a genotypic digital signature, making it possible to make the choice of the best materials, before getting physiological maturity of the crop. The dates selected are related to the critical phenological period that concerns to the definition of productive potential. These results contribute significantly to the optimization of the resources invested during breeding process, because the use of high yield phenotyping in real-time can offer to the breeder the possibility of disposal of materials with undesirable or desirable characteristics, aiming to develop better varieties for the semi-arid region of Sergipe.

Keywords: Vegetation Indexes; Maize Breeding, Grain yield; UAV's; *Zea Mays L.*

Knowledge: Study Group on Plant Breeding in Semiarid (GEMS), EMBRAPA Semi-arid, Federal University of Sergipe, CNPQ.

OCCURRENCE OF ARBUSCULAR MYCORRHIZAL FUNGI SPORES ASSOCIATED WITH CASSAVA GENOTYPES WITH AND WITHOUT FOLIARY PSTHOGEN INOCULATION

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Cassava is an important crop as a food source, so it is essential that some factors that affect the development, productivity and health of plants, such as mycorrhizal dependence, should be studied. This work aimed to evaluate the sporulation of arbuscular mycorrhizal fungi in the absence and presence of inoculation of pathogens in cassava genotypes. The experiment was implemented at the Experimental Farm of the Faculty of Agricultural Sciences of the Federal University of Grande Dourados, in an enlarged block design, with six non-common treatments (BGM0682, BGM1659, BGM1698, BGM1726, BGM1733, BGM2011-34-41) and three controls. (Baianinha, IAC576, Kiriris). Experiments inoculated with anthracnose, bacteriosis, control 1 and control 2 were considered as blocks. Soil samples were collected in the 0-10 cm layer for spore extraction by the wet sieving method. The number of spores was performed using the Generalized Additive Model for Location, Scale and Shape with Type I Negative Binomial Family, followed by Tukey's test to compare the means of the genotypes. It was found that the genotypes and blocks analyzed exerted an influence on the amount of mycorrhizal spores, and the genotypes BGM 1698 and BGM 1659 exerted greater influence on the amount of spores of mycorrhizal fungi present in the soil.

Keywords: AMF spores; Symbiosis; Anthracnose; Bacteriosis; Manihot esculenta;

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Phenotypic alterations due to epigenetic changes in B73 maize (*Zea mays*) inbred line

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Maize is not only a worldwide cultivated crop of high economic relevance, but also a key model organism for genetic studies. The high diversity of the genome and the biogeographic localization of maize are two parameters that interact to produce a wide diversity of phenotypic and adaptative traits. The B73 maize inbred line, originated in a temperate climate from the Iowa state in the United States, was chosen to have its genome sequenced and used as reference in maize genetics studies. In Brazil, where the climate is tropical, the introduction and cultivation of B73 is recent, through a donation from Maize Genetics Cooperation Stock Center. The response to the environment and the maintenance of the genetic background, requires special attention when introducing B73 to the tropical region. Two cycles of self-pollination were carried out during the summer of 2018-2019 and 2021-2022, since the original seeds have arrived in Brazil. In this work, it was made the first seed comparison for morphological parameters, including color intensity by image analysis using the ImageJ software, collecting the following information: area, average gray value, perimeter, Feret diameter, integrated density, and shape descriptors, between the original sample with the S1 and S2 progenies of B73 cultivated in the tropical environment. Additionally, the seed weight was measured. It was observed differences for all the parameters analyzed. The color intensity increases from the original sample to the S2 generation. These results suggested that some descriptors may vary along with generations. These phenotypic variabilities across generations of the B73 adaptation to the tropical environment suggest an epigenetic accommodation with accumulation for some traits as seed color. The findings reinforce the importance of rigorous monitoring of introgressed genotypes in a new environment, especially for those used as references in genetic studies. Moreover, these results contribute to the understanding of the adaptation process to different environmental conditions of the maize spread around the world.

Keywords: maize; introgression; epigenetics; phenotype; tropicalization

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POTENTIAL BIOCONTROL AGENT (ISOLATE JAB01) AGAINST *Sclerotinia sclerotiorum*

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In Brazil, the fungus Sclerotinia sclerotiorum causes one of the most important diseases in soybean, with destructive potential due to its resistance structures that persist in the soil for years. Faced with the demand for sustainable control of white mold, the objective of this work was to evaluate the in vitro antagonist potential of the bacterial isolate JAB01. Double culture bioassays were carried out in PDA petri dishes, containing a disc of S. esclerotio mycelium held in the center, and bacterial plaque at one end to evaluate the production of diffusible substances. When the control treatment reached the edges of the petri dish, the diameter of the fungal colony was average in mm. For evaluation of sclerotia, the bacterial suspension was spread in PDA medium together with 2 and clerodia on the margins of the margins and after 7 days of evaluation of germination plates, it was germination plate. A plate was approved for the production of different organics in plate assays, where, isolated, they were identified superimposed on an alternative plate which was altered as they were altered with parafiled m and after the existence of volatile plates and subsequent to a volatile plate 3 days the mycelial growth of the fungus was evaluated. For all trials were control treatments. Scanning electron microscopy was performed to check for structural changes due to exposure to VOCs. Isolate JAB01 was sequenced using Novaseq6000 and Oxford Nanopore (MinION) technologies, Bowtie2, NanoFilt and Porechop were used for processing the reads. Genome assembly was performed with MaSuRCA and gene annotation with the Prokka tool. The identification of secondary metabolite gene clusters was performed with the antiSMASH v4.0 tool. The isolate was able to inhibit 67% of the mycelial growth of the fungus and 100% of the mycelogenic germination of sclerotia by the production of diffusible substances. As for the production of VOCs, it inhibited 78.71% of mycelial growth. The hyphae exposed to the VOCs of JAB01 showed the greatest number and size why the models were published to the control. In addition, eleven clusters were identified in the JAB01 genome responsible for the synthesis of secondary metabolites, including the antifungal compound Fengico, the siderogenics Petrogicin, Bacillibactin, Cerecidin and other unknowns encoding NRPS and RiPP without prior description. Therefore, JAB01 has the potential to inhibit the phytopathogen and its resistance structure, as well as other phytopathogens, and that is why we highlight its potential as a biocontrol agent.

Keywords: Antibiosis; Biological control; *In vitro* antagonism; White mold.

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