II International Meeting on Plant Breeding

Advances in Experimental Design and Statistical Analysis in Genetics and Plant Breeding

PROCEEDINGS

GVENCK

Genetics and Plant Breeding Group
“Prof. Roland Vencovsky”

October - 2018

THE INTERNATIONAL MEETING ON PLANT BREEDING

Due to the increasing global demand for food, fiber and fuel, different strategies must be taken by society for the development of the agricultural sector. Genetic improvement in plants can be considered one of the fundamental strategies in which geneticists and plant breeders are the protagonists of the development of more adapted and productive cultivars, assisting in the expansion of agriculture and the economy growth. This work demands a differential training of these professionals, requiring Masters and Doctorate degrees, as well as constant development of new technologies to be implemented in breeding programs.

The International Meeting on Plant Breeding is one of several events in the "Corteva Agriscience Plant Science Symposia" series. In this edition of the event, the topic addressed were the advances in experimental designs and statistical analysis applied to Genetics and Plant Breeding. The main purpose is that undergraduate, Masters and PhD students in Genetics and Plant Breeding, as well as professionals of companies or research institutions, improve their knowledge through discussions of relevant scientific topics.

The new techniques and methods discussed can be applied by students in their reseach and professionals from different areas can use them in research programs, helping to obtain new cultivars more productive, with tolerance or resistance to biotic and abiotic stresses and that meet the several objectives currently sought in cultivars development. This will enable gains to all those involved in the agricultural production system, increasing quality to consumers, profitability to farmers, abundance, and a more sustainable production.

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 events;
- Promotion of discussion on relevant topics in genetic and plant breeding;
- Technical visits to companies and public research institutions;
- Promote guidance of students through the "voice of the graduates", in which alumni with consolidated careers 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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PROGRAM

II INTERNATIONAL MEETING ON PLANT BREEDING

Advances in Experimental Design and Statistical Analysis in Genetics and Plant Breeding

October 3th (Wednesday)

07:00 – 08:00 – ***Material Delivery***

08:00 – 08:45 – Opening Session – Tabare Abadie - Corteva Agriscience - USA

08:45 – 09:45 – Lecture 1 - “Statistical Quantification of the Genomic Contribution towards Food and Energy-related Crop Traits”. Alexander Edward Lipka – University of Illinois – USA

09:45 – 10-15 – ***Coffee Break***

10:15 – 11:15 – Lecture 2 - “Genotyping and building linkage maps in complex autopolyploid species”. Antônio Augusto Franco Garcia – ESALQ/USP

11:15 – 12:00 – ***Poster Session 1***

12:00 – 14:00 – ***Break***

14:00 – 15:00 – Lecture 3 – “Artificial selection and the genetic architecture of economically important traits in Maize”. Natalia De Leon – University of Wisconsin - USA

15:00 – 16:00 – Lecture 4 – “Application of Secondary Traits from High-throughput Phenotyping for Yield Prediction”. Jesse Poland – Kansas State University – USA

16:00- 16:30 - ***Coffe Break***

16:30 – 17:30 – Lecture 5 – “Negative variance components for non-negative hierarchical data with correlation, over-, and/or underdispersion”. Clarice Garcia Borges Demetrio - ESALQ/USP

17:30 – 18:00 – ***Poster Session 2***

19:00 – ***Official Event Dinner***

October 4th (Thursday)

08:30 – 09:30 – Lecture 6 – “Genomics-Assisted Breeding for Autotetraploid Potato”. Jeffrey Endelman – University of Wisconsin - USA

09:30 – 10:00 – ***Coffee Break***

10:00 – 11:00 – Lecture 7 – “Genomic predictions for abiotic stress tolerance in maize and sorghum”. Maria Marta Pastina – Embrapa Maize and Sorghum - Brazil

11:00 – 11:15 – ***“Roland Vencovsky” Award***

11:15 – 11:30 – ***Closing Remarks***

SPEAKERS

Tabare Abadie

With 35 years of career in Plant Breeding, his areas of interest include Quantitative Genetics and Statistics as well as Technological Change in Large Organizations, Career Development, Education and Mentoring. Currently in Corteva Agriscience, Tabare leads the Research Effectiveness Team, responsible of building an educational and career development environment for research employees worldwide and to develop relations with Academia. Some of the programs under his supervision include the world wide Corteva Agriscience Plant Breeding Symposia, Fellowships and Internships. Before this assignment, he led a group responsible for the deployment of Molecular Breeding across species globally. Before coming to Iowa, Tabare was a Wheat and Barley Breeder at La Estanzuela (Uruguay) and a Full Professor in Plant Breeding at the Universidad de la Republica (Uruguay), and served as consultant for EMBRAPA CENARGEM (Brazil).

Alexander Lipka

Alexander Lipka received his Ph.D. in Statistics from Purdue University under the direction of co-advisors Prof. RW Doerge and Prof. George McCabe. Afterwards, he was a postdoctoral researcher under the supervision of Dr. Edward Buckler and Prof. Michael Gore. In this capacity, he conducted genome-wide association studies and genomic selection for a wide variety of crops and traits, most notably for vitamin levels in maize grain. He also co-developed the Genome Association and Prediction Integrated Tool (GAPIT) R package, which is currently widely used among the plant genetics research community. Dr. Lipka is now an Assistant Professor of Biometry in the Department of Crop Sciences at the University of Illinois in Urbana-Champaign.

Antonio Augusto Franco Garcia

A. Augusto F. Garcia has a PhD in Genetics and Plant Breeding (Luiz de Queiroz College of Agriculture - ESALQ, University of São Paulo - USP) and a postdoc in Statistical Genetics (Bioinformatics Research Center, North Carolina State University, USA). He is Associate Professor at Department of Genetics (ESALQ/USP), and leads a Statistical Genetics Laboratory with around 10 students (undergrads, MSC, PhDs and postdocs). He has been working on the development of statistical models to have a better understand of the genetic architecture of quantitative traits and to implement molecular breeding in several crops, including maize, sorghum and (specially) sugarcane. He participates of the National Institute of Science and Technology (INCT) of Bioethanol (FAPESP and CNPq). His research achievements include the development of a software (OneMap, and R package) that is used worldwide for building integrated genetic maps; several statistical methods for QTL mapping (including studies on heterosis and interaction G x E); and also methods for genotyping and mapping polyploids. He is editor of Theoretical and Applied Genetics.

Clarice G. B. Demétrio

Clarice G. B. Demétrio is a Professor in Experimental Statistics at “Luiz de Queiroz” College of Agriculture, University of São Paulo, Head of Exact Sciences Department. She has Degree in Agronomy, Master and PhD in Applied Statistics to Agriculture and Post-Doctoral at Mathematics Department, Imperial College of Science and Technology, London, England. She teaches for undergraduate and graduate courses and coordinates a research program dealing with Statistics in Agriculture. Clarice has published topics including generalized linear models and extensions and mixed models applied to Agriculture. She got the “Herman Callaert Leadership Award in Biostatistical Education”, Center for Statistics, Hasselt University, Diepenbeek, Belgium in May, 2006; the award “Best Contributed Paper from a Special Circumstance for the Americas”, during the IBC 2008, Dublin, Irlanda; the “Premio Anual del Proyecto Juárez Lincoln Marti” in 2009 and the “Rob Kempton Award for Outstanding Contribution to the Development of Biometry in the Developing World”, IBC 2010.

Jeffrey Endelman

Jeffrey Endelman is an Assistant Professor in the Department of Horticulture at the University of Wisconsin-Madison and a member of the graduate program in Plant Breeding and Plant Genetics. Endelman trained as a computational scientist (PhD Caltech) before discovering his passion for agriculture and retraining as a plant breeder at Washington State University (PhD) and Cornell (postdoc). Endelman leads the potato breeding program at UW-Madison, which releases new varieties for the chip, French fry, and fresh markets (potatobreeding.cals.wisc.edu). Current research interests include genomics-assisted breeding for autotetraploids, the development of inbred-hybrid breeding for potato, and the genetics of potato tuber appearance. Endelman teaches an undergraduate course on genetically modified crops and graduate courses on genetic mapping and polyploid genetics.

Jesse Poland

Jesse Poland is an Associate Professor at Kansas State University in the Department of Plant Pathology. He is appointed to the graduate faculty in Genetics, Plant Pathology and Agronomy where he serves as major professor and committee member for students in plant breeding and genetics. Dr. Poland is the Director of the Feed the Future Innovation Lab for Applied Wheat Genomics with focus on applying genomics tools to accelerate wheat breeding and develop climate resilient wheat varieties throughout the world. As Associate Director of the Wheat Genetics Resource Center, Dr. Poland leads research to characterize wild wheat germplasm and leveraging valuable genetic diversity for wheat improvement for increased resilience to biotic and abiotic stresses. The overall focus of the Poland Lab is on quantitative genetics, genomics and high-throughput phenotyping for use in breeding, diversity studies, and association genetics with the overall goal of understanding the wheat genome and increasing genetic gain in wheat breeding. In collaboration with public breeding programs, Dr. Poland is implementing the use of genomic selection methods to accelerate wheat breeding. In the area of germplasm development, Dr. Poland's group is focused on developing new breeding lines with resistance to the major pests of wheat including stem rust, stripe rust, leaf rust, Barley Yellow Dwarf virus and Hessian Fly while increasing the understanding of the genetic basis of these traits. To compliment advances in genomics, Dr. Poland's lab is actively developing and applying high-throughput phenotyping approaches for field-based evaluation of breeding lines with the primary focus being genetic characterization of heat and drought tolerance and development of improved germplasm. Dr. Poland currently supervises five graduate students as major professor and is mentor to nine post-doctoral scholars. He teaches graduate courses in plant genetics and serves as advisor for the plant breeding and genetic graduate student club.

Maria Marta Pastina

Maria Marta Pastina is a Statistical-Geneticist at Embrapa Maize and Sorghum in Brazil, and holds a bachelor degree in Agronomy (2004) and a PhD in Genetics and Plant Breeding (2010) from Luiz de Queiroz College of Agriculture, University of Sao Paulo, Brazil. She is currently working on quantitative genetics data analyses for maize and sorghum breeding.

Natalia De Leon

Natalia de Leon received her MS and PhD in Plant Breeding and Plant Genetics from the University of Wisconsin, Madison followed by a postdoctoral experience at Michigan State University. She then worked in the commercial sector for approximately two years before moving to the University of Wisconsin. She is currently a professor in the Department of Agronomy, Plant Breeding and Plant Genetics program at the University of Wisconsin, Madison. Her research program focuses on integrating different sources of information to accelerate translational research for enhanced crop productivity, specially focusing in maize.

SUMMARY

IMAGE ANALYSIS APPLIED IN COMMERCIAL CLASSIFICATION OF "NINJA" BROCCOLI

Ariadne Kaleda Marino[1]; Juliana Virginio da Silva[2]; Emmanuel Moreira Pereira[1]; Ben-Hur Mattiuz[1].
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Two types of broccoli can be found in the Brazilian market, the “ramoso” and the commonly known as "ninja". The “ramoso” type has smaller diameter stems and lateral branches and multiple harvests periods whereas the “ninja”presents single and terminal inflorescences of larger diameter and smaller flower buds. During the postharvest period, several changes may occur such as the loss of green color and the off flavors development. Color is a very important attribute for broccoli and the yellowing to which it is subjected is used to describe the adverse condition of the product quality resulting from the degradation of chlorophyll. Such process can be used as a tool to evaluate the quality and predict the shelf life of the product as well as its commercial class. The objective of this study was to evaluate the coloring of "ninja" broccoli through digital image analysis and to classify them commercially. The image of 28 broccoli were acquired in duplicate, 14 of which belonged to the "commercial" class and the rest to the "non-commercial" class, totaling 56 images. All of them were submitted to pre-processing in which the images were transformed into shades of gray and the backgrounds were excluded. The grayscale histogram of the images was individually plotted. Four images from each group were randomly separated for further validation. The average and the standard deviation were calculated and the final histogram of each group was generated at the end of the process. The final results show that the histograms of the "commercial" and "non-commercial" class, have well defined central points, although presenting an overlapping region. The validation showed an accuracy of approximately 90% of the classes. This pilot project showed the possibility to classify broccoli into two distinct groups (commercial or non-commercial) only by coloring analysis. Although further testing needs to be done to improve the technique, broccoli coloring analysis through imaging is a promising technique and an alternative to existing coloring techniques.

Keywords: *Brassica oleracea* L.; shelf life; image processing; color

ESTIMATING HERITABILITY OF SEED OIL CONTENT IN F5-DERIVED SOYBEAN RILs

Arthur Martins Almeida Bernardeli[1]; Maximiller Dal-Bianco Lamas Costa[1]; Rafael Delmond Bueno[1]; Luiz Cláudio Costa Silva[1]; Jéssica Nayara Basilio Silva[1]; Rafael Aguiar[1].

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Soybean [*Glycine max* (L.) Merr.] is one of the most important major crops worldwide, containing about 20% of oil in its seeds. Soybean germplasm collections have been reported to range from 8.1% to 27.9% for seed oil content (SOC). Then, improving soybean for high SOC may enhance its competitiveness in the market, especially due to its positive phenotypic and genetic correlation with grain yield. The estimates of genetic variance (σg2) and broad sense heritability (h2) for SOC trait is vital to know more specifically its genetic control and to infer about the genetic gain throughout the generations under selection. The objective of this research was to estimate h2 for SOC. Then, a single cross between two moderate SOC soybean accessions, PQMS80 and PQMS12, resulted in 269 F5-derived soybean RILs (recombinant inbred lines). They were submitted to field trials during summer 2017 in randomized complete blocks with two replications in two different locations (Capinópolis and Viçosa). Phenotyping consisted in measuring SOC in 20g of milled soybean seed sample performed by Antaris II FT-NIR. All the effects were considered random and the variance components were estimated by the expected mean squares in ANOVA. The h2 for each environment was the quotient between g2 and phenotypic variance. The results for h2 were 83.7928% and 80.6171% for Capinópolis and Viçosa, respectively. The trial carried out in Capinópolis provided higher magnitudes of genetic and phenotypic variances in comparison to Viçosa. However, the gap between these two estimates was shorter in the former environment, thus resulting in higher h2, despite the similar results for both locations. It is concluded that a considerable number of genes controls SOC, as shown in other related studies, but not as much genes such as those controlling yield. Despite the moderately high h2, it is complex to improve SOC, once improving oxidative stability in certain rates of fatty acids such as oleic, linoleic and linolenic must occur simultaneously.

Keywords: heritability; soybean; trial; variance

Acknowledgements: CNPq and FAPEMIG

CHECKING CONTINUOUS PATTERN OF SEED PROTEIN CONTENT IN F5-DERIVED SOYBEAN RILs

Arthur Martins Almeida Bernardeli[1]; Maximiller Dal-Bianco Lamas Costa[1]; Rafael Delmond Bueno[1]; Luiz Cláudio Costa Silva[1]; Jéssica Nayara Basilio Silva[1]; Rafael Aguiar[1].
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Soybean [*Glycine max* (L.) Merr.] is one of the most important crops worldwide, and protein accounts for about 40% of its total seed content. Improving soybean for high seed protein content (SPC) may enhance its competitiveness in human and livestock consumption. However, it is not easy to obtain high SPC soybean cultivars, once the inverse relationship between SPC and the major traits that are taken into consideration for selection. Investigating the pattern of the phenotypic data distribution leads the researcher to infer about the number of genes involved in its control, the environmental influence and the frequency of segregants to be selected. The objective of this research was to study SPC distribution by using a noramality test. To achieve it, a single cross between two high SPC soybean accessions, PQMS80 and PQMS12, resulted in 269 F5-derived soybean RILs (recombinant inbred lines). They were submitted to field trials during summer 2017 in randomized complete blocks with two replications in two different locations (Capinópolis and Viçosa). Phenotyping consisted in measuring SPC in 20g of milled soybean seed sample performed by Antaris II FT-NIR. Data was analyzed using ANOVA at a probability $p \leq 0.05$ level. Difference between means was compared using Fisher's Least Significant Difference (LSD) at a probability level ($p \leq 0.05$), and Lilliefors Test was used to investigate normality. A significant difference between the means was detected, and the genotypes differ from each other by a LSD of 7.220913 and 7.390623 for Capinopolis and Viçosa, respectively. The trials provided similar observed magnitudes for normality test, in which $D_{calc} = 0.492$ and 0.49 for Capinopolis and Viçosa, respectively. Then, both were non-significant under $p \leq 0.10$. Therefore, it is reasonable to study all the data through normal distribution, as a quantitative trait, and, due to the magnitude of LSD, breeders can exploit variability through selecting the top 4% transgressive genotypes that corresponds to the top SPC class.

Keywords: breeding; distribution; frequency; trial

Acknowledgements: CNPq and FAPEMIG

USE OF REML/BLUP FOR THE STUDY OF GENOTYPE X ENVIRONMENT INTERACTIONS IN PELE DE SAPO MELON HYBRIDS

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Melon plays an important role in the Northeast of Brazil, where it is responsible for more than 95% of the fruit production. The great majority of melon fruits produced is of the Yellow type. However, in recent years companies are trying to diversify the product, investing and cultivating other types of fruits. Among them is the melon of the Pele de Sapo type, which has been new branch of melon breeding programs for the deployment of novel cultivars. In order to launch new cultivars, genotypes must be tested in different years and environments. The present work had the objective to carry out the genotypic evaluation of twelve Pele de Sapo melon hybrids in the State of Rio Grande do Norte. Ten experimental hybrids and the two control hybrids, ‘Sancho' (Syngenta ®) and 'Grand Prix' (Sakata ®), were evaluated in assays conducted between September and November of 2016, in four municipalities of the Agropolo Mossoró-Assu: Mossoró (5º 11'S, 37º 21'W, altitude: 18 m), Baraúna (5º 05'S, 37º 38'W, altitude: 94 m), Assú (5º 34'S, 36º 54'W altitude: 27 m) and Ipanguassu (5th 05'S, 37 ° 38'W, altitude: 94 m). The experiments were conducted in a randomized complete block design with three replicates. We evaluated the total soluble solids content, using adigital refractometer. For the measurements, eight fruits per plot were sampled. Statistical analysis was performed according to the statistical model 54 of SELEGEN-REML/BLUP software. In the individual analyzes, genotypes differed between them in three (Mossoró, Assú and Ipanguassu) of the four assays, evidencing the genetic heterogeneity among the hybrids evaluated. As the assays were conducted in different municipalities, joint analysis was carried out to study the genotype x environment interactions. Genotypes were significantly different for soluble solids, confirming genetic heterogeneity among hybrids evaluated considering all four environments. Genotypes x environment interaction was significantly different, evidencing the differential behavior of the hybrids in the different municipalities. Regarding the soluble solids, all the hybrids presented values that meet the quality level for commercialization, soluble solids > 11%.

Keywords: *Cucumis melo*; soluble solids; selection

Acknowledgments: CAPES; UFERSA; UNESP

GENETIC PARAMETERS FOR THE SELECTION OF PELE DE SAPO MELON HYBRIDS

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In the melon-producing region of Agropolo Mossoró-Assú, it has been observed that the cultivation of Pele de Sapo melon is increasing every year and consequently companies are investing in the development of new cultivars. Thus, in the final stage of breeding programs, genotypes with the potential to become new cultivars should be evaluated. Therefore, experiments need to be conducted with special care in order to reduce experimental error. The objective of this work was to perform the genotypic evaluation of twelve Pele de Sapo melon hybrids in the State of Rio Grande do Norte. Ten experimental hybrids and two controls, 'Sancho' (Syngenta ®) and 'Grand Prix' (Sakata ®), were evaluated in trials conducted from September to November 2016 in four Agropolo Mossoró-Assu municipalities: Mossoró, Baraúna, Assú and Ipanguassu. The evaluated parameters were coefficient of variation (CV), average heritability and genetic accuracy. The experiments were conducted in a randomized complete block design with three replicates. The commercial productivity of the melon fruits and the total soluble solids content were evaluated. Statistical analysis was performed according to the statistical model 54 of SELEGEN-REML / BLUP software. The estimates of the CV for the two traits evaluated are within the range observed for the culture. The values verified for productivity can be classified as low for the assays in Mossoró and Assú (≤ 13.45) and average for the assays in Baraúna and Ipanguassu ($13.45 < CV \leq 45.79$). For soluble solids, the values were considered low in all assays, Mossoró, Baraunas and Ipanguassu (≤ 7.59), except for the Assú assays, considered as medium ($7.59 < CV \leq 14.90$). Estimates for average heritability showed differences between the two analyzed variables. The genetic accuracy for productivity was very high for the assays in Mossoró, Assú and Ipanguassu ($0.90 \leq Acg \leq 0.99$), and low in Baraúna ($0.10 \leq Acg \leq 0.40$). Concerning soluble solids, the results were very high in three trials Mossoró, Baraúna and Ipanguassu and high in Assú ($0.70 \leq Acg \leq 0.85$). Thus, considering the estimates of the genetic parameters, it can be stated that the assays were conducted with high precision, contributing to the safe selection of superior genotypes and reducing the experimental error.

Keywords: *Cucumis melo*; BLUP; productivity; soluble solids

Acknowledgments: CAPES; UFERSA; UNESP

SUPERVISED ARTIFICIAL NEURAL NETWORK APPLIED TO GUAVA CLASSIFICATION

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Brazil is one of the largest producers of citrus fruits and it stand out as producer of tropical fruits, such as guavas (*Psidium guajava* L.). After being harvested, guavas are sent to packing houses where they are classified and packaged. Traditionally, fruit selection is based on the human classification which evaluates and classifies the fruit according to predefined pattern established by São Paulo State Central Market (CEAGESP). The increase in the selectivity by the consumer market, combined with the fact that guava is highly perishable and sensitive to mechanical shocks, indicate the need for improvement in the classification process so that it is done faster, more accurately and with less handling. This study provides an evaluation of the use of the supervised artificial network MultiLayer Perceptron (MLP) as a tool to classify guavas *in silico* according to the quality parameters proposed by CEAGESP. In order to do this, 2600 random data were generated, divided into 26 classes according to the following characteristics: Sub-Group (Yellow, Greenish Yellow and Light Green), Class (5, 6, 7, 8, 9 and 10) and Category (Extra, Category I, Category II and Category III). All attributes were evaluated together in a single network, in order to try to classify the fruits at once. The MLP network was constructed containing 50 neurons in the intermediate layer, 26 neurons in the output layer, accuracy of 10^{-6} and learning rate of 0.01. The number of neurons in the output layer was determined by C-Class One method for encoding classes. The MLP network was trained in the ratio of 9:1, that is, 90% of the data was used in the training phase and 10% in the validation phase. At the end of the analysis, the MLP network was able to achieve an approximate 95% accuracy in the *in silico* guava classification and had an average time of 0.08s for a set of 100 guavas. The results indicate that the MLP network could be satisfactorily applied in packing houses to select guavas according to the criteria proposed by CEAGESP. Another important conclusion is that an automated process would reduce the excessive handling, therefore avoiding damage to the final product.

Keywords: multilayer perceptron; supervised classification; pattern recognition; post-harvest

PATTERN RECOGNITION OF MONOCOTYLEDONOUS VASCULAR BUNDLES WITH SECONDARY GROWTH

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Within the group of angiosperms, there are the monocotyledons that are characterized, among other factors, because they have diffuse and primary vascular bundles. However, there is a small set of monocotyledons that have atypical secondary growth. Among them, the species Dracaena marginata is characterized by presenting the primary and secondary vascular tissues of the amphivasal type. Histologic study using digital image analysis has helped characterize tissue and plant species. Aiming to characterize the primary and secondary amphivasal bundles of Dracaena marginata, 80 histological slides of these tissues were evaluated and, through algorithms implemented in Phyton, 33 attributes were determined according to classes of measures related to cell shape, density and structural regularity. These attributes were evaluated through Principal Component Analysis (PCA) and the weight of each measure was calculated. The attributes that had greater weight were selected and a new PCA was generated. The PCA with all attributes managed to reduce the sample space to 3 with a total variance of 77.7% of the original data. However, the graph resulting from the plot of the first main component with the second showed overlap between the primary and secondary xylem. This overlap is decreased when we consider the first and third components, but in this case, the other tissues were closer. The attributes with higher weights were: average cell area, entropy with sigma 30, radial density with radius 125 and lacunarity with radius 16. The PCA of these attributes was able to segregate all tissues with 84.1% of the total variation and without region of overlap. These results are in agreement with the particularities of each tissue in front of the cellular size, form of organization, disposition of the tissues and tissue growth. The evidences founds during this work are relevant because they indicate that, although the tissues analyzed are amphivasal, they have characteristics that segregate them both biologically and computationally. These results may help in the digital identification of these vascular tissues.

Key words: artificial vision; pattern recognition; plant histology; principal component analysis

STATISTICAL METHODS FOR THE STUDY OF ADAPTABILITY AND STABILITY IN SOYBEAN, NATURALLY INFECTED BY *Phakopsora pachyrhizi*

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The genetic breeding of soybean aims to obtain productive genotypes, so it is necessary that the genetic components, environment and the interaction between them be understood. The G x E interaction is the differential behavior of the genotypes against environmental. The objective was to study the G x E interaction and analyze the adaptability and stability of soybean genotypes under natural rust infection without fungicide. The experiment was conducted in the Genetic Breeding Program of the Federal University of Uberlândia. Fourteen soybean genotypes were evaluated, with 10 lines developed by the UFU Program (UFUS1117: 01, 02, 03, 05, 06, 07, 08, 09, 10 and 11) and 4 cultivars: UFUS 7415, UFUS Riqueza, TMG 801 and BRSGO 7560 in four seasons: 2013/14, 2014/15, 2015/16 and 2016/17, in a randomized complete block design. The G x E interaction was complex and the H^2 was 85.97% indicating superiority of genetic variation in relation to the environment. The average grain yield was 2284.13kg ha^{-1}. The genotypes UFUS 1117-01 and UFUS 7415 were identified by AMMI1, AMMI 2 and Centroid as being genotypes of high productive stability, however, by Centroid, UFUS 1117-01 it is specific for unfavorable environments while UFUS 7415 is wide adaptability. The UFUS 1117-07 showed wide adaptability by Centroid and high stability by AMMI1. The genotype UFUS 1117-09, UFUS 1117-06 and UFUS 1117-08 were identified as being adaptable to unfavorable environments, and UFUS 1117-10 and UFUS 1117-05 presented adaptability to favorable environmental by the Centroid method. It is concluded that the genotype UFUS1117-01 was identified by all methods as having high yield stability and may be indicated for crop regions with presence of Asian rust.

Keywords: *Glycine max*; G x E interaction; biometric analysis; cultivar recommendation

Acknowledgements: CNPQ, CAPES, FAPEMIG, soybean genetic breeding program - UFU and Federal University of Uberlândia

PHENOTYPICAL AND GENETIC CHARACTERIZATION OF ANGULAR LEAF SPOT RESISTANCE IN COMMON BEAN GENOTYPES

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Common bean (*Phaseolus vulgaris* L.) is one of the most cultivated legumes in the world, standing out as the main source of protein and calories for underdeveloped countries. Although the crop presents high productive potential, its average national productivity is still low and unstable due to the high number of diseases that affect the crop. Among the most important diseases, it highlights the angular leaf spot (ALS), caused by the fungus *Pseudocercospora griseola*, which presents wide genetic variability, providing constant breaks in the resistance of commercial cultivars. In recent studies, this disease showed a quantitative pattern of genetic resistance and therefore several QTLs are required to guarantee durable resistance. In order to obtain angular spot resistant cultivars, the choice of the parents to compose the crosses in a breeding program is of great importance. Therefore, the phenotypic and molecular characterization is essential, because it makes possible the selection of genotypes for crosses and the use of assisted selection as a tool for the breeder. In this work, a set of 81 accessions of the Germplasm (BAG) of the Agronomic Institute of Campinas were phenotyped for resistance to P. griseola and genotyped with microsatellite markers linked to the main QTLs of resistance to ALS. Allele frequencies, number of alleles per locus, expected heterozygosity (He) and observed heterozygosity (Ho) were calculated. An array of genetic dissimilarity was generated by by the modified Rogers distance, and hierarchical cluster analysis was performed using the UPGMA method. Polymorphism was detected in the 12 loci used with a mean number of 4 alleles per locus, the largest with 6 and the lowest with 2 alleles. Allele frequencies ranged from 0.01 to 0.91. The observed mean heterozygosity Ho (0.12) was lower than the expected heterozygosity He (0.54). Five groups were formed, revealing great genetic variability among the evaluated genotypes. Regarding the evaluation of severity to the angular spot, 19.7% of the accesses presented resistance to the disease, with emphasis on genotype AND 277 and IAC-Votuporanga, with a mean of 1.3 and 1.8, respectively. From a practical point of view, the molecular markers validated in this study demonstrated a great potential for use in the development of elite strains of common bean, since they are accessible to laboratories with different levels of infrastructure and highly efficient in the monitoring of genotypes bearing resistance loci to ALS.

Keyword: *P. griseola*; plant breeding; diversity genetic; molecular markers

GENETIC DIVERGENCE BETWEEN S_2 LINES OF MAIZE ESTIMATED BY AFLP AND CORRELATION WITH PERFORMANCE AGRONOMIC

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In the maize breeding programs the identification of parents with good combination capacity is a fundamental strategy for success in the development of high performance hybrids. Since the development of intermediate hybrids from partially interbreeding (S_2 or S_3) lines, can be an alternative to replace double or triple hybrids of lines with complete inbreeding, as it provides greater rapidity in obtaining, less variation and interaction in relation to the environment. AFLP markers are tools of molecular genetics, applied in diversity and genetic distance evaluations, identifying the variations of genotypes. The objective of this work was to compare the prediction of intermediate hybrids by means of molecular markers (AFLP) with the values obtained in the evaluation tests of the lines *per se* in the field. The evaluation test of LPE *per se* and of experimental hybrids between partially interbreeding (HELPE) lines was conducted in Londrina and Santa Tereza do Oeste, Paraná. The experimental design of randomized blocks with two replications per location was used, the plot was composed of a line of 5 meters in length and five plants per meter and two commercial single hybrids as controls (2B 810 from Dow AgroSciences and DKB 290 from Dekalb). The AFLP technique was efficient in identifying the higher genotypes through the correlation between the genetic distance and the variable grain yield (REND). It was observed that in relation to (REND), the controls (14.329 $kg.ha^{-1}$) were statistically similar ($p < 0.01$) when compared to the two most productive LPE hybrids (13.062 $kg.ha^{-1}$) with 91,2% of the average in relation to the controls. It is concluded that the lines 01 * 38/4 and 01 * 38/3 In addition to obtaining higher yields of grain (11.934 $kg.ha^{-1}$, 11.828 $kg.ha^{-1}$) were the highest genetic divergences, corroborating the data of hybrids 01 * 38/4 X02 * 33/1 (14.168 $kg.ha^{-1}$) and 01 * 38/3x02 * 1/1 (12.775 $kg.ha^{-1}$).

Keywords: genetic distance; *Zea mays*; partial lines

TRANSGENE ZYGOSITY AND PROTEIN EXPRESSION OF Cry1A.105 AND Cry2Ab2 IN ISOGENIC MAIZE HYBRIDS

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Commercial Bt maize hybrids in Brazil are obtained by crossing a transgenic inbred line with a conventional one, which results in Bt maize hybrids with their transgenic alleles in hemizygosis. The objective of this study was to determine whether Bt maize hybrids with transgenes in homozygosis express more Bt proteins than their hemizygous isogenic versions. We assessed five maize hybrids containing the transgenic event TC1507 x MON89034 x NK603. For each hybrid we obtained two isogenic versions: 1) with the transgenic event in homozygosis; and 2) with the transgenic event in hemizygosis. Homozygous hybrids were obtained by crossing two transgenic inbred lines, and its hemizygous isogenic versions were obtained by crossing the same parental inbred lines, but one of them as a non-transgenic line. During the V2 growth stage of the 10 maize hybrids, we pooled leaves of 13 plants from each hybrid in order to compose one biological replicate. Protein content was extracted from the leaves after pulverization by liquid nitrogen, buffer treatment (125 mM Tris pH 6.8; 20% glycerol; 1% SDS and 1% DTT) and precipitation in cold acetone for 16h. Trypsin was used for protein digestion (4h at 37ºC). Tryptic peptides were submitted to a mass spectrometry analysis (Q-EXACTIVE) to identify by spectral correlations the Bt proteins Cry1A.105 and Cry2Ab2 using SEQUEST-HT. Normalized spectral abundance factor was used to determine Bt proteins relative abundance between homozygous and hemizygous hybrids. Maize hybrids with the event TC1507 x MON89034 x NK603 in a homozygous state presented higher concentrations of Bt proteins Cry1A105 and Cry2Ab2, approximately twice the amount of Bt proteins in hemizygous hybrids. All five homozygous hybrids expressed more Cry1A.105 and Cry2Ab2 proteins than their isogenic hemizygous versions. The mean relative abundance of all hybrids for Cry1A.105 was approximately 8 times lower than for Cry2Ab2. In conclusion, as Brazil is facing a field-evolved resistance of *Spodoptera frugiperda* to Bt proteins, homozygosis of Bt events in maize hybrids could be deployed as a novel approach for insect resistance management. With its capacity to increase Bt protein expression, homozygosis of Bt events can play an important role in the high-dose strategy.

Keywords: *Zea mays*; Bt; transgene; concentration; hemizygous; homozygous

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IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF GENES FROM THE *AMMONIUM TRANSPORTER* SUBFAMILY 2 (*AMT2*) IN SUGARCANE (*Saccharum spp.*)

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It is crucial to clarify the mechanisms that affect the nitrogen use efficiency (NUE) in order to reduce the economic and environmental impact of the application of N fertilizers in agricultural systems. Therefore, this study aimed to conduct the molecular and functional characterization of members of the AMT2 subfamily from sugarcane by heterologous expression in mutants of *Saccharomyces cerevisiae* (strain 31019b) and *Arabidopsis thaliana* (*qko*), both defective in ammonium transport. Gene and regulatory region sequences of *ScAMT2;1* and *ScAMT3;3A* were identified in a bacterial artificial chromosome (BAC) library of sugarcane (cultivar 'R570'). The transcript levels analysis of *ScAMT2;1* and *ScAMT3;3A* in sugarcane showed a preferential expression in roots and mature leaves, respectively, and a distinct pattern between genes and organs depending on the ontogeny and the N status of the plant. The yeast complementation with AMT2 restored the mutant growth, with *ScAMT2;1* enabling higher ammonium absorption; however, the experiment did not indicate sensitivity to methylammonium (toxic ammonium analog). Arabidopsis wild type 'Col-0' transformed with the promoter region of *ScAMT2;1* or *ScAMT3;3A* directing the reporter genes *GUS* or *GFP*, demonstrated preferential expression in the endodermis/pericycle regions of roots and vascular region in shoots, being regulated by N availability and source. Arabidopsis *qko* overexpressing *ScAMT2;1*, *ScAMT3;3A* or transformed with *ScAMT2;1* driven by its endogenous promoter, grown *in vitro* with NH_4^+ as the sole source of N, significantly increased its biomass production compared to untransformed *qko*, especially for *ScAMT2;1*, indicating that these proteins are capable of transporting ammonium and complementing the mutant. When exposed to ^{15}N-labeled ammonium, plants overexpressing *ScAMT2;1* increased ammonium uptake by roots and nitrogen translocation to the shoots, possibly by xylem loading. The overexpression of *ScAMT3;3A* led to increased N remobilization from mature to young leaves and moderately increased root uptake under high NH_4^+. Our results characterize ScAMT2;1 and ScAMT3;3A from sugarcane as functional proteins, working with distinct properties and functions in ammonium transport according to the availability and source of N.

Keywords: *Saccharomyces cerevisiae; Arabidopsis thaliana;* nitrogen uptake; xylem loading; nitrogen translocation; nitrogen remobilization

GENETIC PROGRESS IN RECIPROCAL RECURRENT MAIZE SELECTION PROGRAM

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The objective of this work was to estimate the genetic progress with reciprocal recurrent selection in a maize crop from Universidade Federal de Lavras (UFLA), in Lavras, MG, Brazil, through the evaluation of top cross hybrids from progenies $S_{2:3}$ obtained from cycles 0, 3 and 6. We also aimed at obtaining estimates of the genetic components, verifying the maintenance of genetic variability during the cycles. A total of 1152 top cross hybrids were obtained from 192 progenies $S_{2:3}$ from the "A" and "B" populations, from cycles 0, 3 and 6 of the reciprocal recurrent selection (SRR) of the UFLA's maize breeding program. The experiment consisted of 1156 treatments, 192 top cross hybrids belonging to each of the six populations, and four controls, placed in a 34x34 square lattice, with two replicates, and two sites. Dehusked ear productivity was estimated by weighing total dehusked ears of each plot, obtaining total plot productivity in kilograms. With this data, the individual and joint analyzes were carried out through the mixed models approach. Initially, two models were compared, one considering homogeneity of variances for progenies within cycle and populations and the other considering heterogeneous variances by AIC and BIC criteria. For the two environments studied, the model considering heterogeneous variances was higher, obtaining lower values for the AIC and BIC selection criteria. Considering the model adjusted for heterogeneous variances, genetic components (genetic variance and heritability) were estimated for each population in each individual environment and for multiple environments. The genetic progress was estimated based on the average progenies productivity selected in each cycle. After six cycles of recurrent reciprocal selection, the genetic progress was 8%. The genetic variance values were stabilized, with a slightly increasing tendency, though, proving the existence of genetic variability in the populations, which suggests the possibility of success in future cycles selection. Although it was not the objective of the study, it was also noticed that there was an improvement of one population to the detriment of the other, but the populations showed satisfactory levels of variability, allowing the perennial process of reciprocal recurrent selection in the next years.

Keywords: Genetic Variance; Plant Breeding; Selection Gain; *Zea mays*

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MULTI-TRAIT STUDY FOR SOYBEAN RESISTANCE TO STINK BUG COMPLEX

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Breeding programs in recent years have combined many variables, mainly related to insect and disease resistance, in order to achieve genetic gain and superior progenies. However, it is necessary to identify the nature of cause and effects among the variables to evaluate the efficiency of different breeding strategies in obtaining high gains. Thus, the objective of the present study was to analyze the contributions of agronomic characters and resistance to stink bugs complex in relation to yield, through path analysis, besides constructing a selection index in a population of RILs with different degrees of resistance to stink bugs. The study was carried out with 260 lines being evaluated two crop seasons (2016/2017 and 2017/2018) in Piracicaba-SP, in alpha-lattice design with 3 replicates. The evaluated traits were: GW (grain weight), HSW (healthy seed weight), MPH (maturity plant height), TOL (Tolerance to stink bug complex, calculated by TOL=(GW-HSW)/GW), NDF (number of days to flowering), NDM (number of days to maturation), GFP (grain filling period) and WHS (weight of one hundred seeds). Principal component analyzes (PCA), correlations and unfolding on direct and indirect effects of the variables, and finally, a combination of variables for construction of the base index of Williams, were performed. The analyzes were carried in software R with "*Asreml"*, "*lavaan*" and "*semPlot"* packages, and the genetic effects were adjusted using an unstructured VARCOV matrix for the year effect, carried out through the mixed model approach with REML. Through the PCA analysis, it was possible to see that the characters HSW, GFP, NDF, and MPH have positive association with GW, and the variable TOL presents negative association with GW. After a first exploratory analysis, the correlations were made and it was identified that HSW had high positive correlation with GW (0.97) and TOL showed negative correlation with GW (-0.62). By unfolding the correlations, it was verified that HSW had multicollinearity with GW and, therefore, was excluded from the path analysis. However, the variables MPH and TOL showed a high relationship with GW, 0.45 and -0.34, respectively, in the path analysis. Hence, the variables GW, HSW, MPH, and TOL were combined to construct the index. It was verified that the index obtained high correlations with the characters GW, HSW, MPH and TOL, being 0.93, 0.97, 0.79 and -0.81. Thus, it can be stated that the proposed index using agronomic characteristics, resistance to stink bug complex and grain yield as main characters, can provide favorable gains in the selection of superior progenies.

Keywords: correlation; *Glycine max;* genetic gain; plant breeding

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GRAIN CHEMICAL QUALITY OF UPLAND RICE LINES

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Rice (Oryza sativa) is one of the most consumed grains on the world, being an excellent source of energy and is characterized as the main food for more than half of the world population. The majority of consumers prefer a uniform product with low content of broken and/or damaged grains with good cooking quality pan cooker, display dry and loose beans after cooking and remain soft even after cooling. The water absorption index is one of the parameters that determine the rice cooking quality. A good water absorption index during cooking is an important parameter for a variety, since the yield of cooked rice is directly proportional to that rate. Thus, the present work had as objective to measure the water absorption index of the line rice upland grains aiming to evaluate the chemical quality and to identify the superior lines. The experiments were conducted in two environments, Lambari and Lavras, in the 2016/2017 harvest. Thirty-six lines were used, including two checks (BRSMG Caravera and BRS Esmeralda), from the preliminary study of the upland rice genetic breeding program at the University of Lavras in partnership with Embrapa Rice and Beans and with Epamig. A randomized block design was used and individual and joint analyses of variance were performed. The experiment was carried out using 5 g of rice in 135 ml of distilled water, in each beaker, in a heating plate at 300 ° C. After 15 minutes of boiling, about 10 grains of rice were removed from each beaker and then placed on paper towel to dry for 5 minutes to remove water from the surface of the rice grains. After this time, the grains were weighed, thus determining the water absorption index, calculated by the volume of raw rice by the volume of cooked rice. The line CMG ERF 222-9 presented the highest water absorption index, 3.16 g, in a time of 25.82 minutes. While the line CMG ERF 85-12 presented the lowest water absorption index, 2.69 g, in a time of 23.82 minutes. Most of the lines presented a water absorption index between 2.85 and 2.93 g. However, there was no significant difference between the evaluated lines, but all of them obtained values within the desirable level, indicating that they fit the chemical quality desired by both the industry and the consumer.

Keywords: *Oryza sativa*; index; breeding; cooking

Acknowledgements: Cnpq; Capes; Fapemig

DESEMPENHO PRODUTIVO DE LINHAGENS DE MAMONA EM CONDIÇÕES DE SAFRA NO MUNICÍPIO DE BOTUCATU-SP

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A mamona (*Ricinus communis* L.) é uma matéria-prima versátil da qual originam-se produtos variados. Entretanto, seu potencial necessita ser explorado principalmente na região Sudeste, onde ainda há pouca expressividade. Assim, visando identificar linhagens de mamona mais produtivas e adaptadas à região, objetivou-se avaliar o desempenho produtivo na época de safra, no município de Botucatu - São Paulo. Para isso, foram utilizadas 20 linhagens S5 obtidas da População FCA Porte Baixo de Mamona, desenvolvidas pelo Programa de Melhoramento de Mamona do Departamento de Produção Vegetal, da Faculdade de Ciências Agronômicas FCA/UNESP, Botucatu o qual foi iniciado no ano de 1999, tendo como objetivo obter cultivares e híbridos para o Estado de São Paulo. O experimento foi desenvolvido nos anos de 2016 e 2017 na época de semeadura da safra, em delineamento experimental de blocos ao acaso com três repetições. A parcela experimental constitui-se por uma linha de 10 m de comprimento, com espaçamento entre linhas e entre plantas de 1,0 m. Após o completo desenvolvimento das plantas, foi realizado a observação de interesse agronômico da característica produtividade média dos grãos, sendo tomados dados da massa dos grãos dos frutos descascados por parcela de 10 m^2 e posteriormente realizada a estimativa em kg ha^{-1}. Os dados foram submetidos a teste de normalidade, e atendido o pressuposto, posteriormente a análise de variância. As médias foram comparadas pelo teste de Tukey a 5% de probabilidade, com uso do software Minitab® 18.1. O quadrado médio da análise de variância para linhagens, apresentou diferença significativa pelo teste F a 5% de probabilidade, indicando a existência de variabilidade genética entre as linhagens avaliadas. A média geral de produtividade de grãos foi de 1289,40 kg ha^{-1}, valor considerado baixo para a região, no entanto, todas as linhagens apresentaram valor superior a média nacional que é de 550 kg ha^{-1}. As linhagens 15 e 7 foram as mais produtivas com 1832,67 e 1795,33 kg ha^{-1}, respectivamente.

Keywords: *Ricinus communis* L.; Grãos; Potencial; Variabilidade

AVALIAÇÃO DE LINHAGENS DE MAMONA PARA PRODUÇÃO DE ÓLEO EM BARIRI-SP

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O interesse em estudos com novas fontes renováveis de energia tem sido despertado devido a crescente preocupação com o meio ambiente e em particular com as mudanças climáticas globais. A mamona (*Ricinus communis* L.), cuja a versatilidade permite a fabricação dos mais variados produtos similares ao petróleo, possui todos os requisitos base para ser utilizado como matéria-prima na produção de biodiesel, além disso, seu plantio pode ser uma alternativa para os sistemas de rotação de culturas que visem à sustentabilidade econômica e ambiental de biomas. Nesse contexto, objetivou-se com esse trabalho avaliar a produção de óleo entre linhagens de mamona, cultivadas no município de Bariri, São Paulo. Para isso, foram utilizadas 31 linhagens desenvolvidos pelo programa de melhoramento de mamona do Departamento de Produção Vegetal, da Faculdade de Ciências Agronômicas FCA/UNESP, Botucatu – SP, distribuídas em delineamento de blocos ao acaso, com quatro repetições. A semeadura foi realizada manualmente em Dezembro de 2016 (período da safra), utilizando-se três sementes por cova, e mantendo-se, após o desbaste, uma planta em cada cova. Cada parcela experimental foi constituída por uma linha de 2,5 m, com espaçamento de 1,0 m entrelinhas e 0,5 m entre plantas, totalizando 2,5 m^2 de parcela útil. A adubação e tratos culturais foram realizados de acordo com as indicações técnicas para o cultivo da mamona em São Paulo. Avaliou-se após o completo desenvolvimento da planta, o peso e o teor de óleo das sementes, calculando-se a porcentagem de óleo obtida por análise de amostra proveniente de lote homogeneizado, segundo metodologia soxhlet. Os resultados foram submetidos a análise de variância e as médias comparadas pelo teste Tukey a 5% de probabilidade, no software Minitab® 18.1. Houve diferença significativa ($p<0,05$) para ambas as variáveis analisadas. A linhagem 14 apresentou o melhor resultado em relação ao peso das sementes, com média equivalente a 668,47 g, entretanto diferiu estatisticamente apenas das linhagens 29, 15 e 6. Em relação ao teor de óleo, as linhagens 26, 30, 14, 27, 20, 7, 8 e 16 apresentaram melhores resultados, variando de 44,6 a 42,5%, entretanto, apenas a linhagem 28 diferiu destas, estatisticamente (29,07%). Tendo em vista que o teor de óleo de sementes de mamona varia entre 35 a 55%, as linhagens estudadas mostram-se promissoras para tal fim.

Keywords: *Ricinus communis* L.; Biocombustível; Mudanças climáticas

ENVIROTYPING FOR IDENTIFYING REGIONAL IMPACTS IN UPLAND RICE BREEDING STRATEGIES OVER THE LAST 30 YEARS IN BRAZIL

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Envirotyping is a novel terminology for a collective body of environmental-based breeding support systems. Crop physiologists have been used it to have a better knowledge of the environmental impacts within a target population of environments (TPE). It can be useful for providing new insights of crop adaptation and for restructuring breeder's selection strategies for specific conditions. This can be the case of the upland rice breeding program in Brazil, which occupies the largest worldwide rainfed growing-region and have faced a decreased of 70% in the cropped area in the last decade probably due to an increase in the drought risk. Considering that the magnitude of environmental impacts can provide useful information in designing new breeding strategies, we investigate here: (1) the shifts in drought-stress sensibility from traditional-type cultivars (from 1980s) to the modern-type cultivars (1990s and 2000s); (2) the breeding effectiveness to extend genetic gains observed at breeding's program nursery to the farm fields within the TPE. First, we used ORYZAv3 crop model to simulate 329472 near-iso environments based on two managements (rainfed water-limited and irrigated), 52 locations, 8 planting-dates, 4 soil types and 3 genotypes from the periods of 1980-1990, 1990-2000 and 2000s. Then, factorial-regression with environmental covariates were used to investigate regional patterns related to GxE interaction effects from 34 candidate cultivars between 2012-2014. For the modern-type cultivars, the selection differential (S, %) between commercial-checks and candidate cultivars were also evaluated for each trial. Results suggest that the long-term direct grain yield selection based on favorable environments at higher elevations (>700m a.s.l.) has led to a reduction of 12% (0.35% per year) in cultivars fitness for drought-prone conditions. Only 18% of Brazilian TPE represent environmental profiles similar to the breeding's nursery, where the maximum S% for grain yield was of 40%. However, the other 82% of the TPE is characterized by drought-prone environments with higher temperatures and lower elevations that limit crop adaptation. The maximum S% values under these conditions ranged from 0% to 10%, indicating the lower effectiveness in developing candidate cultivars. We recommend that the breeding program should be restructured to target specific drought-environments, and to priory efforts in lower elevations. It is possible that the use of envirotyping from the initial breeding stages can result in the optimization of selection practices for broadly adapted cultivars.

Keywords: crop model; genotype by environment interaction (GxE); ecophysiology; drought-stress

GENETIC DIVERSITY OF COTTON BASED IN INTRINSIC TRAITS OF FIBER

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Cotton (*Gossypium hirsutum*) is the main natural source of textile fiber, corresponding to 22.37 million tons of textile production worldwide. It is an important crop in the economy of countries as India, China, United States, Pakistan and Brazil. Brazil figures as the 5th largest producer, yielding 1.5 million tons of fiber. In the last decades, Brazilian cotton yield has increased due to the high level of technology applied in the field production, great climate conditions in the country and investments in crop breeding. The main goals of a cotton bedding program are to increase fiber yield, focusing in fiber content and quality, and to develop cultivars resistant to pests and diseases. Hybridzation is the main strategy employed to improve fiber quality, because it can recover favorable alleles and expand genetic diversity. In this context, studies aiming to understing the genetic diversity in germoplasm collections are essential for crop breeding, because they indicate potencial parents based on genetic variability. The goal of this study was to evaluate the genetic diversity of cotton genotypes using fiber intrinsic traits. In this study, we evaluated 20 genotypes from germoplasm collection owned by the Cotton Genetic Breeding Program (PROMALG) and two commercial cultivars (FiberMax 966 and DP 555), totalizing 22 cotton genotypes. The seven fiber intrinsic traits analyzed were: length, uniformity, strength, elongation, maturity index, short fiber index and micronaire index. Data were analyzed by using multivariate clustering methods and principal component analysis. In addition, we evaluated the genetic correlations between the different technological characteristics of the fiber. The analyses were performed with R Core Team software. The populations surveyed showed genetic variation for most of the characters under study. The fiber length consistency and strength were the traits with higher contribution to genetic diversity. The multivariate methods that we used showed similar results, in which genotype GABUFU14-09 stayed in a separate group. Furthermore, we found that most of the traits are correlated. In conclusion this study shows that some genotypes we evaluated here can be employed in breeding programs intended to increase variability. Additionally the intrinsic characteristics of fiber are an efficient tool in the study of cotton’s genetic diversity.

Keywords: *Gossypium hirsutum*, parental selection, fiber quality

ESTIMATING NATURAL CROSSING RATES IN *Capsicum chinense*

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Studies on the reproductive system of plants are important for the breeding of plants and conservation of genetic resources. Although Capsicum peppers are generally considered autogamous, they are capable of cross fertilization at varied rates, for the Capsicum chinense species it is observed an absence of information on the crossing rate. In this context, we aimed to estimate the natural crossing rate for C. chinense accessions using a set of morphological markers. Three divergent accessions (USP-CC15, USP-CC-28 and USP-CC35) from the ESALQ / USP Capsicum Germplasm Bank were selected based on morphological traits and flowering time. Each accession behaved both as donor and recipient of pollen, simultaneously. The experimental design consisted of three replicates of modules, which was composed of three plants, one of each genotype. These modules were placed in the field for the occurrence of pollination. Artificial hybridizations for all combinations between the parents were performed in order to verify the expression of the morphological markers in the progeny. Cross-fertilization between the parent plants resulted in morphologically distinct hybrids, easily identified in the field by observation. This methodology allowed to determine the direction of occurrence of the crossing and to compare the potential of each access as recipient and donor of pollen. The crossing rate was estimated by calculating the frequency of individuals different from the parent plant. A total of 732 individuals were evaluated, the average crossing rate was estimated at 13.06%, ranging from 0% to 40.59%. The highest mean self-fertilization rate was USP-CC28 (S = 98.39%), whose stigma was below the anther level. The USP-CC15 access had the highest crossing rate, mean of 30.38%, although as the male parent, it generated the lowest number of offspring. USP-CC35 showed an intermediate cross-breeding rate (7.19%) and was the genotype with the best pollinator capacity. On average 10.44% of the progeny from cross-fertilization of each genotype had USP-CC35 as the male parent. The results of this study indicate that the C. chinense species exhibited a mixed reproductive system that varied among the genotypes, and precautions are needed during breeding cycles and multiplication of germplasm.

Keywords: Capsicum peppers; mixed mating system; morphological markers; plant breeding

MOLECULAR AND PHENOTYPICAL EVALUATION OF BACKCROSSING POPULATION FOR ANTHRACNOSE RESISTANCE IN COMMON BEAN

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The use of resistant cultivars in common bean breeding programs stands out among the various strategies used to control diseases because of its inexpensiveness and efficiency. In this sense, anthracnose is an important disease that causes yield losses of up to 100% when infected seeds are sown in areas with high relative humidity and mild temperatures. The objective of this work was to perform phenotypic and molecular evaluation of a backcross population developed from the crossing of two elite cultivars of the carioca grain type, aiming to obtain new resistant and highly productive cultivars. The IAC-Formoso cultivar was the donor resistant parent and the BRS Pérola was the recurrent susceptible parent, with high yield. Two generations of backcrossing was performed followed by four generations of self-fertilization aiming the combination of the favorable alleles of both parents. Genotypes from the first backcross generation (F_1BC_1 FP population, IAC-Formoso x Pérola) were analyzed with 12 microsatellites and phenotypic evaluation was performed with the 65 anthracnose race in the F_4BC_2 progenies, in a randomized block design, with three replicates. The results of the phenotypic evaluation in the progenies were submitted to analysis of variance (ANOVA) and associated to the genotyping performed in previous progeny (F_1BC_1) with microsatellites previously associated to anthracnose resistance QTLs. By principal component analysis (PCA) of the genotypic data, the clustering showed that genotypes identified as 3, 5 and 8 had greater proximity to the recurrent susceptible parent Pérola. These genotypes were used as parents of the following progenies which were characterized as susceptible by phenotypic evaluations. On the opposite, a genotype identified as 17 in F_1BC_1 FP population showed greater proximity to the IAC-Formoso donor resistant parent. The progenies derived from that line were all resistant evidencing the efficiency of selection based on molecular marker analyses, even in early stages such as BC_1. Based on the phenotypic evaluation on F_4BC_2 FP progenies, 32% of the lines were considered highly resistant, 50% moderately resistant and 18% susceptible to anthracnose. The best resistant lines selected by phenotypic and molecular criteria are in a final cycle of evaluation of the agronomic and commercial traits of interest in order to measure the 'value of harvesting and use (VCU)' and to recommend a new great common bean cultivar to be released.

Keywords: anthracnose; microsatellites; plant breeding; carioca grain type.

Acknowledgments: FAPESP and CAPES.

LATE LEAF SPOT RESISTANCE AND AGRONOMIC CHARACTERS OF PEANUT LINES OBTAINED FROM A SYNTHETIC AMPHIDIPLOID

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The major Brazilian peanut (*Arachis hypogaea* L.) production is located in São Paulo State and foliar fungi diseases are the main issue in the crop management. It is known that many wild species of *Arachis* are resistant to leaf spots. This study aimed the comparison between F_5 lines obtained by hybridization of a synthetic amphidiploid and *Arachis hypogaea* cultivars regarding late leaf spot resistance (LLS).The progenies were evaluated for LLS resistance and for agronomic traits, using cv. IAC Caiapó as a control. The experiment was carried out in Pindorama, São Paulo State, Brazil, without chemical control of leaf diseases, in a randomized blocks design with three replications. The disease resistance was evaluated at 110 days after sowing, by assessing five random plants per plot. A diagrammatic scale was used with scores ranging from 1 to 9; 1 as absence of symptoms of LLS and 9 as high LLS infestation and defoliation. The agronomic traits evaluated were the yield and plant architecture. Though the best lines were not as resistant as the amphidiploid, but they had a better performance when compared to the cv. IAC Caiapó which is moderately resistant to late leaf spot. Agronomically, the lines are similar to the cv. IAC Caiapó based on architecture-associated traits but the yield of the lines were lower than the cv. IAC Caiapó.

Keywords: peanut breeding; wild species; disease resistance

Z INDEX IN THE SELECTION OF UPLAND RICE LINES

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Rice is the most important staple food for a large part of the world's human population, in order to meet world demand and the demands from the consumer market, a series of characteristics must be evaluated in a breeding program aiming at obtaining superior genotypes that combine important attributes for production and quality of the final product. The index selection theory is a good alternative for the breeder, since it allows combining multiple information contained in the experimental unit, so that the selection is based on a unique value involving all the others. The aim of the present study was to verify the efficiency of the sum of the standardized variables (Z index) in upland rice lines in order to identify genotypes that associate desirable characteristics for consumption. A total of 36 upland rice lines from the preliminary trial of upland rice breeding program of the Federal University of Lavras were evaluated. The experiments were conducted in Lavras-MG and in Lambari-MG, during the 2015/2016 agricultural year. The used design was the randomized complete block design with 3 replications and variance analyses were performed for all characters using Genes software system. In order to compose the index, the following characteristics were evaluated: grain yield, height, number of days for flowering, 1000-grain weight, income, yield, leaf blast incidence, and grain length/width ratio, 4 lines were selected using the selection index. The genetic gain was quantified for each trait and afterwards the sum of the gains was performed. There was a significant difference between the lines for all evaluated characters. It was observed positive gains for almost all traits, except for the yield character. The Z-index obtained a greater gain with the selection considering all the characteristics, the sum of the genetic gains of all the characteristics evaluated was 24.2% indicating that the Z index presented higher and balanced gains between the characters, being efficient for the selection of upland rice lines.

Keywords: *Oryza sativa*; Plant breeding; Multiple characters; Genetic gain

Acknowledgements: Capes, Cnpq, Fapemig

CLASSIC INDEX IN THE SELECTION OF UPLAND RICE LINES

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In breeding programs, it is common to measure several characters in order to practice the simultaneous selection for some of them. Rice breeding lines have a considerable amount of desirable characters, and the index selection theory is a good alternative for the breeder, since it allows combining multiple information contained in the experimental unit, so that the selection is based on a unique value involving all the others. The aim of the present study was to verify the efficiency of the Classic index of Smith and Hazel in upland rice lines in order to identify genotypes that associate desirable characteristics. The experiments were conducted in Lavras-MG and in Lambari-MG, during the 2015/2016 agricultural year. A total of 36 upland rice lines from the preliminary trial of upland rice breeding program of the Federal University of Lavras were evaluated. The used design was the randomized complete block design with 3 replications and variance analyses were performed for all characters using Genes software system. In order to compose the index, the following characteristics were evaluated: grain yield, height, number of days for flowering, 1000-grain weight, income, yield, leaf blast incidence, and grain length/width ratio, 4 lines were selected using the selection index. The genetic gain was quantified based on single and set of characters, there was a significant difference between the lines for all evaluated characters. The total gain obtained with the selection was 9.57%, but a higher gain was observed for the grain yield character, while the other characteristics presented lower results, indicating that the Classic index was not efficient in selecting superior rice lines for all desirable characters.

Keywords: *Oryza sativa*; Plant breeding; Multiple characters; Genetic gain

Acknowledgements: Capes, Cnpq, Fapemig

ESTIMATIVAS DE PARÂMETROS GENÉTICOS NO SEGUNDO CICLO DE SELEÇÃO DA POPULAÇÃO DE MILHO PC 0904

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Através do método de seleção recorrente, é possivel obter variedades de milho produtivas, com características agronômicas desejáveis tanto para serem utilizadas em cultivos, como também para extração de linhagens. A população de milho PC 0904, foi sintetizada no Programa de Melhoramento do IAPAR, a partir do intercruzamento de híbridos comerciais. Desta forma este trabalho teve como objetivo, estimar os parâmetros genéticos do segundo ciclo de seleção, das progênies de meio irmãos de milho, avaliando o potencial da população, e a eficiência do método utilizado para maior produção de grãos. O ensaio foi conduzido, nas estações experimentais do Instituto Agronômico do Paraná (IAPAR), de Londrina e Guarapuava, na safra 2015/2016, com duas repetições por local, avaliando 178 progênies, tendo para efeito de comparação três materiais: a variedade comercial IPR 164, desenvolvida pelo IAPAR; o material PC0904 resultante do ciclo I; e o híbrido simples P30F53 da empresa DuPont Pioneer. Sendo avaliado os caracteres de altura de planta e espiga (AP e AE), florescimento feminino (FF), prolificidade (PRO) e produção de grãos (REND), que para efeito da obtenção das estimativas de parâmetros genéticos, os quadrados médios de REND foram transformados para g/planta. A partir da análise conjunta, considerando o efeito aleatório, para o carater rendimento de grãos, para produtividade a média foi de 159,84 (g/plt). A estimativa de variância genética aditiva de 488,06 (g/plt), coeficiente de herdabilidade no sentido amplo de 51,15% e o ganho de seleção entre progênies foi de 7%, que equivale a 11,09 (g/plt). A partir das estimativas obtidas juntamente com os dados de produtividade, além dos caracteres agronômicos observados, pode se afirmar que a população de milho PC 0904, apresenta alto potencial tanto para continuidade do processo de seleção recorrente, para a obtenção de variedade comercial como também para a obtenção de linhagens e híbridos.

Keywords: *Zea mays* L.; Seleção Recorrente; Melhoramento de População; Produtividade

SELECTION OF LINEAGES, GENETIC PARAMETERS AND CORRELATIONS BETWEEN SOYBEAN CHARACTERS

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Soybean has great economic importance in the world accordingly, this legume has been exploited in breeding programs aiming to provide cultivars with extensive grain yield, tolerant to pests and diseases, and adapted to different soil and climatic conditions. Therefore, the objectives of this work were to evaluate genetic parameters and correlations between soybean traits to select lineages in order to increase yield and improve agronomic traits. Experiments were carried out on the *Capim Branco* farm, of the Federal University of Uberlândia, harvest 2016/2017. Fifteen morph-agronomic traits were assessed on twenty-two genotypes in a randomized complete block design with three replicates. Agronomic traits related to cycle, height, number of nodes and total pods have shown coefficients of genotypic determination higher than 70%. In addition, coefficients of variation of number of days to the flowering and number of days to maturity were equal to 3.79% and 4.87%, respectively, indicating high homogeneity of data and low random variation. Among evaluated traits, ten have presented the ratios between the coefficient of genetic variation (CVg) and coefficient of environmental variation (CVe) above one, demonstrating high success likelihood in the selection to these traits. Fifteen genotypes have presented grain yield above the national average of 2016/2017 harvest, which was 2882 kg h^{-1}. Significant phenotypic correlations between traits ranged from -0.49 to 0.89, however genotype correlation were higher than the phenotypic ones, indicating that genetic factors have contributed more than the environmental factors. Traits related to cycle, height and number of nodes in the main stem have presented measures of H^2 and CVg / CVe with extensive magnitudes, evidencing the possibility of selection lineages having superior traits in the Soybean Breeding Program of the Federal University of Uberlândia. In order to increasing grain yield, the traits Number of pods of three grains and Total number of pods were identified as appropriated to indirect selection based on the phenotypic and genotypic correlations. The 2IP14, B2P1, B2P28, B1P33 and 2AP11 lineages stand out as superior genotypes to direct selection.

Keywords: *Glycine max*; plant breeding; indirect selection; correlation;

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DIVERGÊNCIA GENÉTICA DO ALGODOEIRO ENTRE PROGRAMAS DE MELHORAMENTO DO BRASIL

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A cotonicultura brasileira se configura como um setor de alto nível tecnológico, havendo a demanda de investimento contínuo no desenvolvimento de novas cultivares, sendo que estes apresentam em geral, base genética estreita e há predominância de um pequeno número ocupando grandes áreas de cultivo. Logo, tem sido verificada a redução da variabilidade genética das cultivares, propiciando a ocorrência da vulnerabilidade genética e a redução da possibilidade de ganhos adicionais nas seleções em programas de melhoramento, em função do tamanho limitado do conjunto gênico. O objetivo do trabalho é detectar a diversidade genética de cultivares de algodoeiro dos programas de melhoramento do Brasil utilizando caracteres fenotípicos. O trabalho foi realizado em casa de vegetação, localizada no município de Uberlândia, Minas Gerais, Brasil, e conduzido em delineamento experimental de blocos completamente casualizados, com 18 genótipos e três repetições. Foram selecionados três cultivares de cinco programas de melhoramento de algodoeiro: BRS368, BRS372, BRS433, DPDeltaOpal, DP1228B2RF, DP1552B2RF, FM975WS, FM980GLT, FM982, IMA 2106GL, IMA5675 B2RF, IMA8405GLT, TMG45B2RF, TMG47B2RF e TMG82WS, pertencentes aos programas: Empresa Brasileira de Pesquisa Agropecuária, Monsanto, Bayer, Instituto Mineiro de Agropecuária e Tropical Melhoramento & Genética respectivamente, além de três genótipos provenientes do Programa de Melhoramento Genético de Algodoeiro da UFU: UFUJP-B, UFUJP-H e UFUJP-P. Foram realizadas avaliações de altura de plantas e diâmetro de caule quando as plantas estavam nos seguintes estágios fenológicos: V5, florescimento pleno e maturidade plena. Também foi determinado o peso médio de capulho e o rendimento de pluma. Realizou-se análise de variância, cálculo da distância de Mahalanobis, método hierárquico de ligação média entre grupos (UPGMA) e método de otimização de Tocher utilizando-se o programa GENES. No dendograma obtido pelo agrupamento UPGMA, a linha de corte foi realizada no ponto de alta mudança de nível (47% de dissimilaridade), separando os genótipos em 6 grupos, ao passo que, pelo método otimizado de Tocher, formaram-se 7 grupos. O maior grupo formado e mais diversificado apresenta cerca de 50% dos genótipos, com pelo menos um representante de cada programa de melhoramento, composto pelos genótipos DP1228, FM975, IMA8405, TMG45, IMA2106, BRS372, DP1552 e FM982 no método hierárquico, diferindo do método de otimização de Tocher, apenas na formação de um grupo a parte com os genótipos BRS372, DP1552 e FM982. Os genótipos IMA5675, UFUJPH, BRS368, FM980 e TMG47 formaram grupos isolados, sendo possível obter efeito heterótico e maior heterozigose em possíveis hibridações realizadas entre estes acessos. Os resultados indicam que apesar da detecção de divergência genética, há cultivares com similaridade entre todos os programas de melhoramento, e seu cruzamento deve ser evitado para manter a variabilidade genética e garantir ganhos de seleção.

Keywords: *Gossypium hirsutum;* vulnerabilidade genética; ganhos de seleção; rendimento de pluma.

DESCRITORES DA FASE VEGETATIVA EM SOJA PARA FINS DE DIFERENCIAÇÃO

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A soja é importante cultura da agricultura no mundo, movimenta grande parte do agronegócio brasileiro, sendo o Brasil o segundo maior produtor mundial, precedido pelo Estados Unidos. Na safra 2017/2018, a área cultivada foi de 35.022,8 mil hectares, de acordo com a Companhia Nacional de Abastecimento. O melhoramento genético foi responsável pela grande expansão da cultura, e com a promulgação da Lei nº 9456 de Proteção de Cultivares houve um grande estímulo às pesquisas públicas e privadas para o desenvolvimento de novas cultivares, mais produtivas e adaptadas as regiões brasileiras. Uma cultivar deve ser distinta, homogênea e estável para que se tenha sua proteção, sendo utilizado pelo Ministério da Agricultura Pecuária e Abastecimento (MAPA) descritores para diferenciação de cultivares, que são quaisquer características morfológica, fisiológica, bioquímica ou molecular. Atualmente existe apenas 37 descritores, sendo estes insuficientes para a distinção de cultivares de soja. Assim, objetivou-se neste trabalho, avaliar descritores da fase vegetativa de soja para fins de diferenciação das cultivares. O experimento foi realizado na safra 2016/2017, na estação experimental da Fazenda Capim Branco, pertencente à Universidade Federal de Uberlândia - UFU, no município de Uberlândia, Minas Gerais.Avaliaram-se 12 cultivares de soja (UFUS 6901, UFUS 7415, BRSMG 68, TMG 801, TMG 7062 IPRO, TMG 2158 IPRO, BRS 7270 IPRO, NA 5909 RR, NS 6909 RR, CD 2737 RR, P98Y30 RR e BMX Desafio RR). O delineamento experimental foi em blocos ao acaso, com três repetições. Cada unidade experimental foi constituída por quatro linhas, espaçadas entre si em 0,5 m. Foram amostradas 5 plantas aleatoriamente e avaliados, com auxílio de uma régua milimetrada, o comprimento de epicótilo (CE), largura da folha unifoliolada (LU) e comprimento do primeiro internódio (C1) em estádio V2. O coeficiente de variação de todas os caracteres oscilaram a 5,36% e 15,82% assemelhando às estimativas obtidos por outros autores. Os coeficientes de determinação genotípica (H^2) evidenciaram alta influência genética para todas os caracteres, com valores oscilando entre 83,80 a 91,78%. Para CE e C1 as cultivares foram separadas em 2 grupos e para LU em 5 grupos, pelo teste Scott Knott a 5% de significância. Conclui-se que comprimento do epicótilo, a largura da folha unifoliolada e comprimento do primeiro internódio são úteis para distinção de cultivares de soja.

Keywords: Cultivares; Descritores morfológicos; *Glycine max*; Melhoramento genético.

Acknowledgements: CNPq, FAPEMIG, CAPES.

INFERÊNCIAS NO NÚMERO DE CRUZAMENTOS POR PARENTAIS ENTRE DIALELO BALANCEADO E CIRCULANTE CONSIDERANDO COMPONENTES DE MÉDIA EM MILHO

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Na análise dialélica estuda-se o delineamento genético, provendo estimativas de parâmetros úteis na seleção de genitores, bem como o entendimento dos efeitos genéticos envolvidos na determinação dos caracteres quantitativos. O objetivo desse estudo foiavaliar a eficiência dos dialelos circulantes em relação aos dialelos balanceado sem recíprocos, quanto às estimativas da capacidade geral de combinação (CGC) e da capacidade específica de combinação (CEC). Os experimentos foram conduzidos em três ambientes distintos no Estado do Paraná, Brasil. O delineamento experimental utilizado foi em blocos ao acaso com três repetições por local. Foi realizado o cruzamento dialélico balanceado entre 12 populações parentais de milho e estimada a CGC e CEC para os modelos balanceados e circulantes em diversos tamanhos de cruzamentos por parental (s=3, 5, 7 e 9). A magnitude da herdabilidade e a presença da interação G×A influenciam diretamente no número mínimo de cruzamentos por parental, no modelo dialélico circulante em milho. Neste modelo, tanto a presença quanto ausência dos parentais avaliados, em relação à variável florescimento feminino (FF), foi constatada alta correlações com as estimativas de CGC obtidas no dialelo balanceado. Já nas estimativas de CEC para FF, verificou-se um aumento substancial nas correlações com o modelo balanceado, quando se utilizou s próximo da metade do número de parentais. Para produtividade de grãos, (REND) em relação à CGC, as correlações tenderam a se estabilizar acima de 0,70 a partir de s=7, ou seja, mais da metade do número de cruzamentos por parental no modelo balanceado. A CEC para REND, considerando s=3 com avaliação de parentais, permitiram obter estimativas de correlação em dialelos circulantes superior em todos os ambientes, quando comparado com os resultados sem parentais.

Keywords: *Zea mays* L.; Capacidade Geral de Combinação; Capacidade Específica de Combinação; interação GxA.

FIFTY YEARS OF COMMON BEANS BREEDING PROGRAM FROM FEDERAL UNIVERSITY OF LAVRAS

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Common beans crop in Brazil has undergone great changes in the last fifty years. In the past it was cultivated only by family farmers, but today it also raise the interest of rural entrepreneurs. The success of the crop in these two production systems depends on the obtaining of new cultivars, which is done exclusively by breeding programs of public institutions. One of these programs is from Federal University of Lavras (UFLA), which is completing half a century. The aim of this study was to make a critical analysis of the UFLA common beans breeding program and to estimate its genetic progress (GP) for grain yield. For this, a survey was made on the history of the program. To obtain GP, we used data from the elite lines experiments conducted in Lavras, MG, from 1994 to 2017. In these experiments the lines are evaluated for two years, being totally replaced after that period. The cultivars Carioca, Carioca-MG and Ouro Negro were used as controls. A combined variance analysis was performed, that is, the correction of the lines averages by the common controls. Afterwards, the linear regression coefficient (b) was estimated using the number of biennials as independent variable and the adjusted means of the five best lines in each biennium as dependent variable. The estimate of GP was obtained by the estimator: $GP = (b / L1 x100)$, where $\overline{L}1$ corresponds to the estimate of the average performance of the five best lines in the first biennium of evaluation. The program objectives are to develop new cultivars, obtain information that can help the work of breeders and train students in genetics and plant breeding. In this context, success has been achieved. Despite the limitations from a program of a public institution, it was possible to register twelve cultivars. In addition, the basic studies performed contributed substantially to autogamous plant breeding, not only of common beans but also of other crops. A total of 119 dissertations, 43 thesis and 401 articles were produced with the crop, with data from 120 harvests carried out so far. In the period considered 275 lines were evaluated, in an average of 27.5 lines per biennium. The estimated GP was 0.35% per year. Considering that in the selection the emphasis is also in obtaining plants with good architecture and grains of better quality, this progress can be considered expressive.

Keywords: *Phaseolus vulgaris*; elite lines; genetic progress.

Acknowledgment: CNPq, Capes, Fapemig

SELEÇÃO DE GENITORES E POPULAÇÕES SEGREGANTES DE FEIJÃO COM RESISTÊNCIA A MURCHA DE FUSÁRIO

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A cultura do feijoeiro (*Phaseolus vulgaris*) pode apresentar perdas na produtividade de grãos na presença de doenças. Entre aquelas que a acometem, está a murcha de fusário, provocada por Fusarium oxysporum f. sp. phaseoli (Fop). Por isso, neste sentido foi empregado dialelo parcial para avaliar a capacidade combinatória de linhagens de feijão tipo carioca para a obtenção de genitores e linhagens com resistência ao Fop. Foram realizados cruzamentos entre seis genitores que apresentam algum nível de resistência (BRS Ametista (A), BRS Notável (B), CNFC 15086 (C), BRSMG Uai (D), BRS FC402 (E) e CNFC 15082 (F)) e sete genitores suscetíveis (BRS Sublime (G), CNFC 10762 (H), CNFC 15475 (I), BRS Cometa (J), BRS Estilo (K), CNFC 15097 (L), BRSMG Madrepérola (M)). As populações segregantes foram avaliadas em três anos (2015, 2016 e 2017), nas gerações F2, F3 e F4, respectivamente, em área infestada naturalmente, em Santo Antônio de Goiás – GO, na época do inverno. Também foram utilizadas três testemunhas e os ensaios foram conduzidos em delineamento experimental de blocos completos ao acaso, com quatro repetições e parcelas de três linhas de três metros. Para avaliar a severidade da doença utilizou-se uma escala de notas variando de 1 (resistente, sem sintomas) a 9 (plantas mortas). Foram realizadas análises de variância, teste de médias de Scott-Knott, análises dialélicas e também foram estimadas as capacidades combinatórias dos genitores e populações. Considerando a análise conjunta, houve diferença significativa na reação à murcha de fusário das populações e nas capacidades gerais de combinação dos genitores. A testemunha B (3,2a) apresentou maior resistência e K (6,1d) e J (8,2e) foram muito suscetíveis. Entre os genitores do grupo 1, C e E apresentaram estimativas de gi que indicam que as populações formadas por eles são mais promissoras e que, consequentemente, esses são os melhores genitores para esse caráter. Mesmo no grupo 2, houve variação nas estimativas de gi e as linhagens I e L se destacaram, contribuindo para a geração de populações mais resistentes. Considerando as médias das populações e as estimativas de gi dos genitores, as populações que se destacaram foram E x L (3,3a), F x I (3,4a), C x I (3,5a), B x I (3,7a), E x I (3,7a), C x L (3,8a), E x J (3,8a) e A x L (3,9a). Estas populações são as mais promissoras para a obtenção de linhagens de feijão com bom nível de resistência à murcha de fusário.

Keywords: *Fusarium oxysporum*; capacidade combinatória; dialelo; *Phaseolus vulgaris*

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