



IV ISGPB

IV INTERNATIONAL SYMPOSIUM ON GENETICS
AND PLANT BREEDING

HOW HAS PLANT BREEDING CONTRIBUTED TO
FOOD SECURITY?



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do Norte Fluminense Darcy Ribeiro (UENF)

Anais do IV Simpósio Internacional de Genética e Melhoramento de Plantas

Realização



Suporte



**Anais do IV International Symposium on
Genetics and Plant Breeding**

Editores

Catiane dos Santos Braga
Cleudiane Lopes Leite
Roberta Aparecida de Sales
Adriana Azevedo Vimercati Pirovani
Rosimara Barboza Bispo
Talles de Oliveira Santos
Rafaela Pereira Duarte
Larissa Maximiano Resende
Rosimeire Barboza Bispo
Divino Rosa Santos Junior
Jhean Torres Leite
Ramon de Moraes
Rosieli Barboza Bispo
Danielle Lâmega

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Larissa Maximiano Resende

Doutoranda em Genética e Melhoramento de Plantas

Catiane dos Santos Braga

Doutoranda em Genética e Melhoramento de Plantas

Colaboradores

Adriana Azevedo Vimercati Pirovani

Doutora em Genética e Melhoramento de Plantas

Roberta Aparecida de Sales

Doutoranda em Genética e Melhoramento de Plantas

Ramon de Moraes

Doutor em Genética e Melhoramento de Plantas

Rosieli Barboza Bispo

Doutoranda em Genética e Melhoramento de Plantas

Danielle Lâmega

Mestranda em Genética e Melhoramento de Plantas

Docentes do Programa de Genética e Melhoramento de Plantas – UENF

Alexandre Pio Viana – D. Sc.
Melhoramento de Fruteiras. pirapora@uenf.br

Antônio Teixeira do Amaral Júnior – D. Sc.
Melhoramento Vegetal. amaraljr@uenf.br

Clícia Grativol Gaspar – D.Sc.
Química Biológica. cgrativol@uenf.br

Geraldo de Amaral Gravina – D. Sc.
Produção Vegetal / Fitotecnia. gravina@uenf.br

Gonçalo Apolinário de Souza Filho – D. Sc.
Biologia Molecular. goncalos@uenf.br

Helaine Christine Cancela Ramos – D.Sc.
Melhoramento Vegetal e Marcadores de DNA. helainecr@uenf.br

Marcelo Vivas – D.Sc.
Melhoramento Vegetal / Estatística. mrclvivas@hotmail.com

Messias Gonzaga Pereira – Ph. D.
Melhoramento Vegetal. messias@uenf.br

Rogério Figueiredo Daher – D.Sc.
Produção Vegetal / Melhoramento de Forrageiras e Estatística.
rogdaher@uenf.br

Rosana Rodrigues – D. Sc.
Melhoramento Visando Resistência à Doenças e Recursos Genéticos
Vegetais. rosana@uenf.br

Silvaldo Felipe da Silveira – D. Sc.
Fitopatologia. silvaldo@uenf.br

Telma Nair Santana Pereira – Ph. D.
Citogenética Vegetal e Recursos Genéticos Vegetais. telmasp@uenf.br

Vanildo Silveira – D.Sc.
Biotecnologia/Proteomica Comparada e Morfogênese in vitro.
vanildo@uenf.br

Valdirene Moreira Gomes – D.Sc.
Biotecnologia / Proteômica associada à Resistência a Doenças.
valmg@uenf.br

Virginia Silva Carvalho – D. Sc.
Cultura de Tecidos. virginia@uenf.br

Leonardo Siqueira Glória – D.Sc.
Genética e Melhoramento. leonardogloria@uenf.br

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PREFÁCIO

Simpósios são importantes eventos científicos para transmissão de conhecimento, aproximação de participantes, sejam eles estudantes ou profissionais, impactando a interação com pesquisadores de renome nacional e internacional, além de movimentar a economia regional, e ser uma oportunidade para as empresas apresentarem suas demandas por produtos e serviços.

Nesse sentido, o Grupo de Estudos “Ganho Genético”, vinculado ao Programa de Pós-Graduação em Genética e Melhoramento de Plantas da Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, com o objetivo de alavancar as inovações do agronegócio e movimentar a economia da região Norte Fluminense promove o “IV Simpósio Internacional de Genética e Melhoramento de Plantas” o tema “Como o melhoramento de plantas tem contribuído para a segurança alimentar?”.

Este evento é uma oportunidade para profissionais, especialistas e estudantes discutirem como o melhoramento de plantas tem contribuído para a segurança alimentar mundial e para mitigar os efeitos nocivos das mudanças climáticas, assim como atender as demandas dos agricultores e consumidores. O evento busca discutir como as novas tecnologias do melhoramento de plantas, aliadas aos recursos genéticos vegetais, podem contribuir para a busca de características-alvo, face a necessidade do desenvolvimento agrícola sustentável.

A segurança alimentar é um importante tema para a movimentação da economia regional. As discussões sobre essa temática enriquecem o debate acadêmico-inovador, gerando ideias alvissareiras para o desenvolvimento de agronegócio economicamente viável e ambientalmente sustentável, gerando benefícios desde a produção de insumos, transporte e beneficiamento de produtos até a comercialização.

PROGRAMAÇÃO

May 24		
Time	Activity	Speaker
14:00	Institutional video	-
14:10	Opening session	UENF Dean (Raul Ernesto Lopez Palácio) Coordinator of the Graduate Program in Genetics And Plant Breeding (Alexandre Pio Viana) Head of the Genetic Breeding Laboratory (Antônio Teixeira do Amaral Júnior) Coordinator of the Ganho Genético (Jhean Torres Leite)
14:30	Plant Sciences Symposia Series (PSSS)	Jason Rauscher - Corteva
14:40	Immersion in germplasm: Genetics resources as the basis for food security	Moderator: Prof. Dra. Telma Nair Santana Pereira - UENF
14:45	From conservation to the use of plant genetic resources	Flávia França Teixeira - EMBRAPA
15:15	Global foundation institute	Neil Hausmann from - Bill and Melinda Gates Foundation
15:45	Coffee Break	Institutional video
16:10	PSSS - Career skills	Ex-Ganho Genético (Renato Santa Catarina) - UENF
16:20	Accelerating Breeding Results with Precision Phenotyping	Nathan D. Coles (Corteva Agriscience)
16:50	Round table	Speakers of the day
17:20	Closing of the first day	Moderator: Prof. Dra. Telma Nair Pereira Santana - UENF
May 25		
Time	Activity	Speaker
14:00	Innovations in plant breeding to contributed to food security	Moderator: Prof. Dr. Messias Gonzaga Pereira - UENF
14:05	Abiotic stresses: Molecular breeding showing results for the	Cláudia Teixeira Guimarães

	medium and low investment sectors	
14:35	PSSS - Career skills	Ex- NuGEM (Cátia Meneguzzi - Corteva Agriscience)
14:45	Stresses abióticos (Associações simbióticas e estresse nutricional)	Fátima Bosetti (Corteva Agriscience)
15:15	Best works (Presented with a video)	3 best works (Genetic Resources, Plant Breeding, Genomics) 10 minutes each
15:35	Coffee Break	Institutional video
16:05	New tools to mitigate the effects of biotic stresses and increase yield	Marlonni Maurastoni Araujo - North Carolina University
16:35	The global search for drought stress tolerance in Phaseolus beans	Dr. Paul Gepts - University of California, Davis
17:05	Round table	Speakers of the day
17:30	Closing of the second day	Moderator: Prof. Dr. Messias Gonzaga Pereira - UENF/membro do ganho

May 26

Time	Activity	Speaker
14:00	Predictions to the global feed: breeding strategies against hunger	Moderator: Alexandre Pio Viana- UENF
14:05	Technologies enabling plant breeding for sustainable agriculture	Mai Komatsu (Corteva Agriscience)
14:35	Crop Improvement for circular bioeconomy systems	Charlie Messina - University of Florida
15:05	PSSS - Career skills	Intergen Speaker - Melina Prado (GVENCK) - ESALQ
15:35	Coffee Break	Laboratories video and GG video
16:05	Roots of the Second Green Revolution	Jonathan Lynch - Penn State University,
16:35	Enviromics: a tool to optimize breeding trials and develop more resilient	Roberto Fritsche-Neto - (IRRI), Philippines.

	genotypes for the climate change effects	
17:00	Round table	Mai Komatsu - Corteva
17:30	Closing event	Ganho Genético Team



RESUMOS

**A qualidade e conteúdo dos resumos publicados são de inteira responsabilidade de seus autores.*

Area of concentration: Plant Breeding

**CORRELATION AND PATH ANALYSIS OF TRAITS CONTRIBUTING TO
FRUIT YIELD IN GRAPES ‘BRS TAINÁ’ GRAFTED ONTO DIFFERENT
ROOTSTOCKS**

OLIVEIRA; Carlos Roberto Silva de¹, SILVA; Francismary Barros¹, FELINTO FILHO; Ezildo Francisco¹, MENDONÇA JÚNIOR; Antônio Francisco de², PONTES; Glácia Maria de Alencar³, LEÃO; Patrícia Coelho de Souza⁴

¹UFRPE - Universidade Federal Rural de Pernambuco - Bolsista CAPES/Facepe, carlos.robertooliveira@ufrpe.br, francismarybarrosdasilva@gmail.com, ezildoff@gmail.com

²UFRPE - Universidade Federal Rural de Pernambuco - antonio.mendoncajunior@ufrpe.br

³UNIVASF- Universidade Federal do Vale do São Francisco - gciaalencar@gmail.com

⁴Embrapa Semiárido, patricia.leao@embrapa.br

Grapes are the third most exported fresh fruit in Brazil, the semi-arid region of São Francisco Valley is recognized for its table grapes production. Qualitative and quantitative traits in grapes can be affected by using different rootstocks due to the scion/rootstock interaction, associated with the edaphic and climatic conditions. Through correlation and path analysis is possible to identify which traits make a large contribution to yield. Therefore, the objective was to study the association of ‘BRS Tainá’ fruit yield cultivated onto different rootstocks with 11 morpho-agronomic traits, during the first production cycle. The experiment was carried out under field conditions, from July to December 2021, in Petrolina, PE, Brazil. The scions were trained in a horizontal trellis system, 3.5 x 2.5 m spacing, with localized drip irrigation. The experimental design was in randomized blocks with eight treatments (rootstocks) and four replications. The rootstocks were Ramsey, Teleki 5C, 101-14 MgT, IAC 313, IAC 572, IAC 766, Paulsen 1103, e SO4. Phenotypic correlation and path analysis were estimated to the following variables: pruning weight; stem diameter; number of canes; bud fertility index; number of bunches; weight, length, and width of the bunch; weight, length, and diameter of the berry; and yield. Significant effects of the rootstock were observed for the variables bud fertility index, number of bunches, and berry diameter. Estimates of significant phenotypic correlations ranged from -0.51 (stem diameter and bud fertility index) to 0.84 (berry length and diameter). The path analysis showed that a large part of the variation in estimated mean yield (0.59) was explained by the effect of morpho-agronomic traits evaluated. Therefore, other traits need to be evaluated for increasing the coefficient of determination. The direct effect of berry diameter on yield in the path analysis was significant (0.80) deserving special attention from the breeder during rootstock selection.

KEYWORDS: Table grapes; Phenotyping correlation; Tropical viticulture.



Area of concentration: Plant Breeding

MACHINE LEARNING FOR CLASSIFICATION OF SOYBEAN POPULATIONS FOR INDUSTRIAL CHARACTERISTICS BASED ON SPECTRAL VARIABLES

SANTANA; Dthenifer Cordeiro¹, OLIVEIRA; Izabela Cristina¹, SANTOS, Regimar Garcia¹; SILVA; Celí Santana¹, TEODORO; Larissa Pereira Ribeiro², TEODORO; Paulo Eduardo²

¹UNESP – Department of Agronomy, State University of São Paulo (UNESP), Ilha Solteira 15385-000, Brazil, dthenifer.santana@unesp.br; izabela.oliveira@unesp.br; regimar.garcia@unesp.br; celi.santana@unesp.br

²UFMS – Department of Agronomy, Federal University of Mato Grosso do Sul, Rodovia MS 306, km. 305, Caixa Postal 112, 79560000 – Chapadão do Sul, MS, Brazil. eduteodoro@hotmail.com; larissa_ribeiro@ufms.br

Soybean genotypes have distinct characteristics of industrial variables, especially with regard to oil and protein. Quantifying these values using high-precision phenotyping technologies combined with data processing through machine learning algorithms makes it easier, faster and more accurate to obtain this information. In the literature, there is little information on intrinsic factors to grains such as oil, protein, fibers, ash, etc., especially with regard to data from high-precision phenotyping and using computational intelligence algorithms. Thus, the objective of this work was to find a machine learning algorithm and inputs with the best performance for soybean classification according to industrial data intrinsic to the grains. Soybean farming was implemented in the 2019/20 crop in the municipality of Chapadão do Sul - MS, Brazil, in the experimental area of the Federal University of Mato Grosso do Sul. The experiment was implemented in the field in randomized blocks with two replications, 194 F₂ populations of soybean were evaluated. Spectral data were obtained from the crop using Red, green, near-infrared and infrared wavelengths and the vegetation indices NDVI, NDRE, GNDVI, SAVI, MSAVI, MCARI, EVI and SCCCI were calculated. Industrial characteristics of the grain were also evaluated: protein, oil, ash and fiber. First, the data were submitted to a correlation analysis expressed by a correlation network. Subsequently, a cluster analysis forming clusters by the Kmeans method was performed and two groups were formed and expressed by the principal component analysis (PCA). With the genotypes separated into groups, the data were submitted to machine learning analyses, that were: Artificial Neural Networks, J48 Decision Trees, Logistic Regression, REPTree, Random Forest, Random Tree and Support Vector Machine. The machine learning algorithms that had the best performances were artificial neural networks and Decision Tree. As for the tested inputs, the best results were obtained with spectral bands.

KEYWORDS: Remote sensing; High precision phenotyping; Vegetation indices.



Area of concentration: Plant Breeding

GENETIC POTENTIAL OF INTERVARIETAL HYBRIDS BETWEEN LOCAL VARIETIES OF SWEET CORN TO SHORTEN THE CYCLE

SOUZA; Rosenilda de¹, OGLIARI; Juliana Bernardi², ULIANA; Cassiane³, WENDLING; Tamires Schapuis⁴, REICHERT JÚNIOR; Francisco Wilson⁵

¹Universidade Estadual do Norte Fluminense Darcy Ribeiro – Pós Doc 10-Faperj, rosenilda@pq.uenf.br

²Universidade Federal de Santa Catarina – Docente, jbogliar@gmail.com

³Universidade Federal da Fronteira Sul – Bolsista, cassianeuliana1@gmail.com

⁴Universidade Federal da Fronteira Sul – Bolsista, tami.schapuis@hotmail.com

⁵Universidade Federal de Santa Catarina – chicowrj@gmail.com

Obtaining early sweet corn genotypes is one of the demands of genetic breeding, considering that this type of corn is marketed as fresh corn, which occurs around 21 days after female anthesis, between R3 and R4 stages. Local varieties tend to have a longer cycle as a result of farmer management. Therefore, the objective of the present work was to evaluate the genetic potential of the combination of six local maize varieties, carrying the *su1su1* genotype, aiming at shortening the vegetative cycle. The intervarietal hybrids were evaluated using the full diallel method (Griffing method II), containing 15 F₁'s hybrids and six parents. The genotypes were evaluated in two environments, in a complete randomized block design with three replications. The results of the diallel, individual and joint analyses, and the magnitude of the mean squares associated with the general and specific combining ability, denote the existence of variability for cycle shortening, with superiority of the quadratic component \hat{G}_i , associated with additive gene effects. Such verification is common in diallel in which the parents did not undergo previous selection for the character being studied, as is the case of local varieties. Genotypes 741B, 2276A and 319A showed negative estimates for the effects of the general combining ability (\hat{g}_i), favorable to selection to reduce the number of days from emergence to tasseling, with values of -1.69, -1.67 and -0.22 days, respectively. The best combinations, with negative specific combining ability (\hat{s}_{ij}) estimates, were 2029A x 319A (-2.62), 2255A x 741B (-1.97), and 2255A x 319A (-1.95). The sweet corn varieties *sugary1*, conserved *in situ* – *on farm* in the extreme west region of Santa Catarina, have the combining potential to shorten the cycle, with favorable results for genetic breeding aimed at the conservation and use of this local germplasm.

KEYWORDS: *Zea mays* L.; *sugary1*; Full diallel.

Area of concentration: Plant Breeding

**GENOTYPE X ENVIRONMENT INTERACTION FOR ADVANCED TABLE
GRAPE PROGENIES IN SÃO FRANCISCO VALLEY**

PONTES; Glácia Maria de Alencar¹, ISHIKAWA; Francine Hiromi¹, OLIVEIRA; Carlos Roberto Silva de², SILVA; Francismary Barros², FELINTO FILHO; Ezildo Francisco², LEÃO; Patrícia Coelho de Souza³

¹UNIVASF - Universidade Federal do Vale do São Francisco - gciaalencar@gmail.com, francine.hiromi@univasf.edu.br

²UFRPE - Universidade Federal Rural de Pernambuco - Bolsista CAPES/Facepe, carlos.robertooliveira@ufrpe.br, francismarybarrosdasilva@gmail.com, ezildoff@gmail.com

³Embrapa Semiárido, patricia.leao@embrapa.br

Plant breeding has been a strong ally in increasing the productivity and quality of table grapes. This study aimed to evaluate the agronomic performance of table grape progenies in different locations in the Submédio São Francisco Valley. The experiments were carried out under field conditions between March and October 2021, on vines in the first production cycle, grafted onto rootstock 'SO4'. Five progenies (45, 54, 64, 80 and 81) were evaluated in seven commercial areas in the Vale do Submédio São Francisco. The scions were trained in horizontal trellis system, 3.0 x 2.0 m spacing, with drip irrigation. The experimental design was in strips, with five replications (plants). The variables evaluated were: production (PR), in kg.plant⁻¹; bunch mass (MC), in g; number of bunches per plant (NC); length (CC) and width (LC) of bunches, in cm; berry mass (MB), in g; berry length (CB) and diameter (DB), in mm; soluble solids (SS); total acidity (AT) and ratio (SS/AT). There was a significant interaction between genotypes and environments for all variables evaluated. Location three provided the best performance of variables related to production, except NC, as location four had the highest average (74.56). For the chemical variables SS and AT, the means of the progenies showed the highest values (22.0 and 0.52) at site two, but the SS/AT ratio was higher at sites five and three (55.36 and 48.21). About all environments, progeny 80 was superior for MC, LC, MB, CB and DB, however the highest PR was obtained by progeny 45 with 19.3 kg.plant⁻¹. Progeny 81 had the highest values for SS (24.56) and ratio (60.11), while progeny 80 was the most acidic (0.63). Based on the results, location three was the one that provided the best agronomic performance, and progeny 45 being the most productive in all locations.

KEYWORDS: Genotype-by-environment interaction; Table grapes; Tropical viticulture.



Area of concentration: Plant Breeding

TIME TO INOCULATION OF OVULES FOR THE *IN VITRO* GRAPEVINE EMBRYO RESCUE

CUNHA; Marcos Andrei Custodio da¹, AMORIM; Marilúcia Ribeiro², MELO; Nataniel Franklin de³, LEÃO; Patrícia Coelho de Souza³

¹UNIVASF - Universidade Federal do Vale do São Francisco - Bolsista CAPES, andreymarcos347@gmail.com

²UPE – Universidade de Pernambuco - Estagiária, mariluciar261@gmail.com

³Embrapa Semiárido, nataniel.melo@embrapa.br, patricia.leao@embrapa.br

The Vale do Submédio São Francisco accounts for about 99% of total Brazilian grape exports, reaching volumes of 49.3 thousand tons in 2020. The objective of this study was to evaluate time to inoculation of grape ovules to increase the efficiency of the method of vine embryo rescue. The crosses were carried out using as parents 'BRS Isis' ♀ x 'CNPUV 24' ♂, grown in the Experimental Field of Bebedouro, Embrapa Semiárido - Petrolina, PE. The treatments were represented by three different time to inoculation of ovules (T1: six weeks after pollination; T2: seven weeks after pollination and T3: eight weeks after pollination). A completely randomized design with five replications was used, with 20 berries as the experimental unit. The quantified variables were: number of inoculated ovules, number of rescued embryos, number of germinated embryos and germination percentage. The effect of the time to collect the bunches and inoculation of ovules was significant, with T3 increasing the number of inoculated ovules (30.2) and rescued embryos (15.2). Inoculation of grape ovules six weeks after pollination (T1) is not recommended, as it presented the lowest values for number of inoculated ovules and rescued embryos, consequently, no germination was obtained on this treatment. The variables number of germinated embryos and germination percentage did not differ statistically between treatments T2 and T3. The germination percentage in T2 was 50%, while in T3 it was 65%. It is recommended the inoculation of ovules eight weeks after pollination since it increases the efficiency of the embryo rescue technique in the seedless table grape breeding.

KEYWORDS: *Vitis* sp.; Tissue culture; Table grape breeding.

Area of concentration: Plant Breeding

**PATH ANALYSIS FOR THE ORNAMENTAL COMPONENTS OF PEPPER
(*Capsicum annuum*) VIA MIXED MODEL METHODS**

GOMES; Fátima de Souza¹, DA SILVA; Luiza Thaiany², DE PAULA; Allyson Gabriel Santos³, SILVA; Taylor Johnny Patricio⁴, CUSTÓDIO, Gabriela Cristina Alves⁵, PIMENTA; Samy⁶

¹UNIMONTES - Universidade Estadual de Montes Claros - Bolsista CAPES, fatimaagro27@gmail.com

²UNIMONTES-Universidade Estadual de Montes Claros-Bolsista CNPq, luizathaianydasilva1@gmail.com

³UNIMONTES-Universidade Estadual de Montes Claros - Bolsista CNPq, allyson.agro.eng@gmail.com

⁴UNIMONTES-Universidade Estadual de Montes Claros-Bolsista BIC/UNI, contatotaylorasilva@gmail.com

⁵UNIMONTES-Universidade Estadual de Montes Claros -Bolsista CAPES, gabrielac.agro@gmail.com

⁶UNIMONTES - Universidade Estadual de Montes Claros, samy.pimenta@unimontes.br

Path analysis becomes more effective when based on predicted genotypic values ($u+a$) than when applied on phenotypic values, resulting in more accurate inferences, increasing efficiency in indirect selection in the plant breeding program. The objective was to evaluate, through path analysis, based on ($u+a$) via REML/BLUP methodology direct and indirect effects of the ornamental components, the basic variable being the average fruit mass (MMF) and the explanatory variables: flowering cycle (CF), maturation cycle (CM), average fruit length (CMF) and average fruit diameter (DMF). The experiments were carried out in the experimental area of UNIMONTES, Campus Janaúba-MG. The contrasting accessions UNI 01 and UNI 05 were used as parents and the F_1 generations and subsequent F_2 population were obtained. Thirty potential genotypes (lower CF) were selected in F_2 to compose the $F_{2.3}$ generation, generating 30 families with eight individuals, totaling 240 plants/individuals advanced by the Genealogical Method (Pedigree). The genotypic values of the families were predicted by the BLUP procedure, using the computer program Selegen – REML/BLUP. For the trail analysis, the statistical software R Development Core Team® version 4.1.3 was used, under weak multicollinearity for the analyzed data. The decomposition of the ($u+a$) through the trail analysis showed that the trail coefficient does not satisfactorily explain the variations in MMF, as indicated by its determination value ($R^2 = 0.55$) and the high residual effect (0.74). The direct and indirect effects of CF, CM, CMF and DMF on MMF were positive and negative. The direct effects were superior to the indirect ones on MMF when analyzing the ornamental component CMF. In general, none of the components considered obtained a direct relationship greater than 80%, which would be ideal for a direct selection on MMF. The CMF presented the highest estimate of direct effect on MMF (0.38) among the other components.

KEYWORDS: BLUP; Genealogical Method; $F_{2.3}$ Population.



Area of concentration: Plant Breeding

VINE ROOT STOCKS TOLERANT TO WATER DEFICIT: INFLUENCE ON PHOTOSYNTHESIS AND STOMATIC CONDUCTANCE

SILVA; Alessandro Gomes da¹, ARAÚJO; Rafaella Rodrigues², CHAVES; Agnaldo Rodrigues de Melo³, LEÃO; Patrícia Coelho de Souza³

¹UFRPE - Universidade Federal Rural de Pernambuco - Bolsista CAPES/CNPq, alegomes1996@gmail.com

²UNIVASF- Universidade Federal do Vale do São Francisco - Bolsista CNPQ, rafaellarodrigues333@hotmail.com

³Embrapa Semiárido, agnaldo.chaves@embrapa.com, patricia.leao@embrapa.br

The vine is one of the most economically important fruit trees in the world. The development of canopy and rootstock cultivars more adapted and tolerant to biotic and abiotic stresses it is one of the main objectives of the genetic improvement of the vine. This study aimed to characterize the photosynthesis and stomatic conductance of vine rootstocks in water deficit conditions. The experiment was carried out during 128 days between August and December 2021 at the Experimental Field of Bebedouro, Petrolina, PE. Plant vases containing 25 liters of soil from a cultivated area with vine and corrected for fertility were used, with irrigation located by drip. The treatments consisted of seven rootstocks: 101-14 MGT, IAC 313, IAC 572, IAC 766, Paulsen 1103, Ramsey e SO4. Each rootstock was submitted to three irrigation depths as a function of the reference evapotranspiration (20, 50 and 80% of ETo), with daily laminas calculated based on climatic information from the Automatic Meteorological Station. The experimental design was randomized blocks with four replications, in subdivided plots, with the main plot being the irrigation depth and the subplot, the rootstocks. The variables evaluated were: photosynthesis (A) and stomatic conductance (gs), using IRGA with readings every 15 days. There were significant differences between the rootstocks, especially 'Ramsey', '101-14 MGT' and 'Paulsen1103', in all irrigation depths and dates evaluated. 'Paulsen 1103' rootstock presented the highest values of photosynthesis and stomatic conductance under water stress conditions, demonstrating greater tolerance to water deficit. Complementary studies associating other variables and long-term in field are important for validation of rootstocks tolerance to water stress.

KEYWORDS: Physiology; Viticulture; Water stress.



Area of concentration: Plant Breeding

AGRONOMIC PERFORMANCE OF EXPERIMENTAL PURPLE-FLESHED SWEET POTATO GENOTYPES IN A COMMERCIAL CROP IN OESTE PAULISTA

MELO; Elisa Patrícia Ramos¹, LEAL; João Lucas Pires¹, OLIVEIRA; Guilherme José Almeida¹, TOROCO; Bruno da Rocha¹, GUERREIRO; João Carlos Tadeu¹, ZEIST; André Ricardo²

¹UNOESTE – Universidade do Oeste Paulista, lisaramosmelo@hotmail.com, bolsista CNPQ, joaolucasliresleal@gmail.com, guilhermejaost@hotmail.com, bolsista FAPESP, bruno-toroco@hotmail.com, joao.carlos.guerreiro@hotmail.com

²UFSC- Universidade Federal de Santa Catarina, andre.zeist@ufsc.br

The sweet potato crop has great economic and social importance in Brazil is widespread in almost all regions. The state of São Paulo is the second largest producer of sweet potatoes being the Oeste Paulista the main producing region of this tuberous root. Despite the considerable importance of culture in the region, the predominant genotypes are obsolete, of low productivity and do not meet the demands of the consumer market. Therefore, the objective was to select experimental genotypes of purple-fleshed sweet potato in terms of agronomic characteristics, thus aiming, obtain plants that meet the needs of producers in the West Paulista region. The experiments were carried out in Álvares Machado-SP in commercial farming of a partner producer of the Center for Studies in Olericulture and Fruit Growing of Oeste Paulista, Universidade do Oeste Paulista – Unoeste, Campus II. Installation took place in the month 10/2021 (spring-summer cycle) and the harvest with 140 days. A block experimental design with randomized treatments was adopted. Evaluating the experimental genotypes UZBD-U2-12, UZBD-K-25, UZBD-U2-10, UZBD-F-21, UZBD-U1-15, UZBD-K-78, UZBD-U1-29, UZBD-F-06 and as a witness to the commercial cultivar SCS370 Luiza. The characters evaluated were: total tuberous root production (TTRP), in t ha⁻¹, production of commercial tuberous roots (PCTR), in t ha⁻¹ and average mass of commercial roots (AMCR), in t ha⁻¹. It was found that the UZBD-U1-12 genotype presented superior results compared to the others in relation to the TTRP and PCTR, for AMCR was no statistical difference between the genotypes. It is concluded that the UZBD-U1-12 genotype achieved better results under the cultivation conditions of the Oeste Paulista region, and may be indicated to continue the sweet potato breeding program.

KEYWORDS: *Ipomoea batatas*; Superior genotypes; Genetical enhancement.

Area of concentration: Plant Breeding

**GENETIC VARIABILITY IN F₂ POPULATION OF CHILI PEPPERS WITH
ORNAMENTAL INTEREST**

SILVA; Taylor Johnny Patricio¹, GOMES; Fátima de Souza², DE PAULA; Allyson Gabriel Santos³, DA SILVA; Luiza Thaiany⁴, CORDEIRO; Rodolfo Andrade⁵, PIMENTA; Samy⁶

¹UNIMONTES – Universidade Estadual de Montes Claros – contatotaylorsilva@gmail.com

²UNIMONTES – Universidade Estadual de Montes Claros – fatimaagro27@gmail.com

³UNIMONTES – Universidade Estadual de Montes Claros – allyson.agro.eng@gmail.com

⁴UNIMONTES – Universidade Estadual de Montes Claros – luizathaianydasilva1@gmail.com

⁵UNIMONTES – Universidade Estadual de Montes Claros – rodolfo.cordeiro.mg@gmail.com

⁶UNIMONTES – Universidade Estadual de Montes Claros - samy.pimenta@unimontes.br

Chili peppers of the genus *Capsicum annuum* belong to the Solanaceae family and can be used for various purposes, such as ornamental plants. The use of morphological descriptors allows the identification of genetic variability in chili pepper progenies that can be selected for ornamental purposes. The objective was to identify the level of genetic variability existing within the segregating population of chili pepper, *C. annuum*, with ornamental interest. The experiment was conducted in a greenhouse in the Experimental Area of the State University of Montes Claros (Unimontes), Janaúba-MG Campus, Brazil. The F₂ population was obtained from two contrasting parents Uni 01 and Uni 07 in relation to traits of ornamental value. From the total number of plants, 333 genotypes were randomly considered for qualitative evaluation of corolla color (CC), anther color (CA), fruit length (CF), fruit diameter (DF) and fruit color at maturity (CFM), both considering five replications per genotype. For the CF and DF variables, measured quantitatively, the frequency distribution of continuous variables was used to obtain the values related to the proposed classes for each descriptor, based on the form of the Brazilian National Service for the Protection of Cultivars (SNPC). Descriptive statistics of the Mode type were used for the final classification of the genotypes. For the analyses, the statistical software GENES was used. The results of each descriptor were interpreted by percentage. For the CC descriptor, 99% of the flowers are white and only 1% of the flowers are white with violet margins. A phenotypic variation was also observed for CA, with 89% of the genotypes being pale blue and 11% violet. The CF descriptor ranged from 3% very short, 32% short, 38% medium, 25% long and 2% very long. The fruit diameter showed 2% of the genotypes very small, 9% small, 74% medium and 15% large. Variability was also observed in the CFM, in which it diverged in 5% orange and 95% red. There is genetic variability that can be explored for the characteristics considered in this study, thus enabling the selection of genotypes with ornamental potential in this population.

KEYWORDS: *Capsicum annuum*; Breeding of ornamental plants; Morphological descriptors.



Area of concentration: Plant Breeding

EXPERIMENTAL STRAWBERRY HYBRIDS TARGETING PLANTS ADAPTED TO BRAZILIAN GROWING CONDITIONS

OLIVEIRA; Guilherme José Almeida¹, TOROCO; Bruno da Rocha¹, GUERREIRO; João Carlos Tadeu¹, MELO; Elisa Patrícia Ramos de¹, PIERI; Julia Roberta Sanches de¹, ZEIST; André Ricardo²

¹Unoeste - Universidade do Oeste Paulista, guilhermejaost@hotmail.com; bruno-toroco@hotmail.com, joao.carlos.guerreiro@hotmail.com, lisaramosmelo@hotmail.com

²UFSC – Universidade Federal de Santa Catarina, andre.zeist@ufsc.br

The strawberry is of great relevance to the national market, as it is a fruit with a characteristic appearance and flavor, it is highly appreciated and demanded by the population. However, it is a culture that needs high investments, making its production more expensive. One of the main costs is the importation of seedlings and the use of cultivars poorly adapted to our soil and climate conditions. Thus, the objective was to select experimental strawberry hybrids adapted for cultivation in tropical climates based on production characteristics. The experiments were carried out at the Universidade do Oeste Paulista, Campus II in the years 2020/21. An enlarged block experimental design was adopted, using the interleaved checks 'Albion', 'San Andreas' and 'Pra Estiva'. Experimental 205 hybrids obtained from intraspecific crosses were evaluated, 116 belonging to the UZAP population (cross 'Albion' × 'Pra Estiva') and 89 UZSP (cross 'San Andreas' × 'Pra Estiva'). For harvesting the fruits, those that completed the maturation stage were collected, considering commercial fruits those with a mass greater than 10 g and without defects. The fruits were evaluated for the parameters total number of fruits (NTF, plant⁻¹), number of commercial fruits (NFC, plant⁻¹), total fruit mass (MTF, g plant⁻¹), commercial fruit mass (MFC, g plant⁻¹). The analysis of variance was performed to obtain the genotypic, phenotypic and residual correlation, variance and covariance matrices. Of the 205 experimental strawberry genotypes, a total of 8, 16, 4 and 5 were superior to commercial controls for the parameters NTF, NFC, MTF and MFC, respectively. However, only the genotypes UZAP-68, UZAP-26, UZAP-45, UZAP-38, UZAP-41, UZAP-12, UZAP-24, UZAP-73 were superior to commercial controls for all parameters explored. Therefore, to continue the breeding program, 21 experimental hybrids were selected in terms of yield characteristics.

KEYWORDS: *Fragaria x ananassa* Duch; Strawberry production; Superior genotypes.

Area of concentration: Plant Breeding

**SELECTION OF EXPERIMENTAL STRAWBERRY HYBRIDS BY
PARAMETRIC RANK SUM INDEX**

TOROCO; Bruno Da Rocha¹, OLIVEIRA; Guilherme José Almeida¹, PIERI; Júlia Roberta Sanches de¹, GUERREIRO; João Carlos Tadeu¹, MELO; Elisa Patrícia Ramos de¹, ZEIST; André Ricardo²

¹UNOESTE - Universidade do Oeste Paulista - Bolsista FAPESP, bruno-taroco@hotmail.com; guilhermejaost@hotmail.com; joao.carlos.guerreiro@hotmail.com; lisaramosmelo@hotmail.com

²UFSC - Universidade Federal de Santa Catarina – Docente do departamento de fitotecnia, andre.zeist@ufsc.br

Brazil depends almost entirely on imported commercial strawberry cultivars, which leads to higher costs for producers and less adaptation of the genotypes. To reverse this scenario, it is necessary to focus more on improving the strawberry plant in Brazil, which requires the payment of royalties. Therefore, the evaluation and selection of hybrids adapted to tropical climate conditions is of great importance. The objective of this work was to select experimental day-neutral strawberry hybrids, using a selection index. A total of 205 experimental hybrids obtained from intraspecific crosses were evaluated, 116 belonging to the UZAP population (cross 'Albion' × 'Pra Estiva') and 89 UZSP (cross 'San Andreas' × 'Pra Estiva') comparing them with three cultivars commercial 'Albion', 'San Andreas' and 'Pra Estiva'. The design was adopted in enlarged experimental blocks, using the interleaved controls 'Albion', 'San Andreas' and 'Pra Estiva'. Selection index was estimated for total number of fruits (NTF, plant⁻¹), number of commercial fruits (NFC, plant⁻¹), total fruit mass (MTF, g plant⁻¹), commercial fruit mass (MFC, g plant⁻¹), average weight of commercial fruits (MMFC, g fruit⁻¹), color and brightness. The harvest of the fruits was carried out when in the stage of maturation and with weight above 10g, in addition to the absence of defects in them. High heritability was obtained ($\geq 97.2\%$), selection gains of 40.4, 44.79, 64.91, 72.64, 18.96, 14.36 and 16.01% were observed for the parameters NTF, NFC, MTF, MFC, MMFC, Color and Brightness. The selected genotypes had means of 62.35, 49.38, 669.89, 585.82, 12.25, 2.17 and 5.65. The experimental genotypes UZAP-50, UZAP-62, UZAP-69, UZAP-45, UZAP-24, UZSP-35, UZSP-06, UZSP-17, UZAP-68, UZAP-94, UZAP-73, UZSP-48, UZAP-26, UZAP-38, UZSP-31, UZSP-47, UZAP-41, UZAP-116, UZSP-64, UZAP-12 and UZAP-19 were indicated by the rank sum selection index. The respective experimental strawberry genotypes are promising for breeding programs aimed at the development of superior cultivars.

KEYWORDS: *Fragaria* x *Ananassa* Duch; Superior genotypes; Genetic improvement.

Area of concentration: Plant Breeding

**PHENOTYPING ANTHRACNOSE RESISTANT INTEGRATING SEVERITY
VARIABLES AND LEAF REFLECTANCE INDICES**

BISPO; Rosimara Barboza¹, ARAUJO; Maria do Socorro Bezerra², SUDRÉ; Cláudia Pombo¹, RODRIGUES; Rosana¹

¹UENF- Universidade Estadual do Norte Fluminense Darcy Ribeiro, rosimara.barboza@gmail.com

¹UENF- Universidade Estadual do Norte Fluminense Darcy Ribeiro, cpombo@uenf.br

¹UENF- Universidade Estadual do Norte Fluminense Darcy Ribeiro, rosana@uenf.br

²UNEMAT- Universidade do Estado do Mato Grosso, mariasbserrita@gmail.com

Developing anthracnose resistant cultivars of sweet and chili peppers has been a challenge for plant breeders. This work aimed to evaluate recombined lines of *Capsicum annuum* for anthracnose resistance integrating ten resistant variables and investigating the viability of indirect selection by canonical correlations. Twenty-five F_{5,6} families, and two inbred lines, UENF 1381 (resistant) and UENF 2285 (susceptible), were evaluated. The treatments were arranged in a randomized block design, with three replications and five plants per plot. Based on the severity, the area under the disease progress curve (AUDPC), incubation period (IP) and latency period (LP) of immature and ripe fruits were estimated. The leaf reflectance indices evaluated were NDVI (Normalized Difference Vegetation Index), NPCI (Normalized Pigmented Chlorophyll Index), CTR2 (Carter Indexes), TCARI (Transformed Carter Index), ARI2 (Anthocyanin Reflectance Index) and RENDVI (Red-edge Normalized Difference Vegetation Index). The correlation coefficients (r) for the first and second canonical pairs were 0.81 and 0.67, respectively, indicating that traits related to resistance are associated with variables related to reflectance indices. In the first canonical pair, LP of immature fruits and IP of mature fruits were associated with the variables NDVI, CTR2 and RENDVI. The LP relationships of immature fruits occurred in the same direction (negative), as the LP of mature fruits were related in the opposite direction (positive). In the second canonical pair, the LP of immature fruits was positively associated and in the same direction with CTR2 and RENDVI, while the LP of mature fruits was related in the opposite direction. Leaf reflectance indices, NDVI, CTR2 and RENDVI can be used in the selection of anthracnose resistant genotypes, becoming an indirect selection option for genetic gains in *Capsicum*, in addition to being a non-destructive and faster method.

KEYWORDS: *Colletotrichum scovillei*; Disease resistance; Plant Disease Phenotyping.



Area of concentration: Plant Breeding

RECURRENT SELECTION IN *Passiflora*: DOES IT ALLOW EFFECTIVE GAINS FOR CABMV RESISTANCE?

MENDES; Débora Souza¹, LIMA; Joameson Antunes¹, RODRIGUES; Cleidiane Alves², CAVALCANTE; Natan Ramos¹, SANTOS; Eileen Azevedo³, VIANA; Alexandre Pio¹

¹UENF- Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsistas FAPERJ/CAPES/CNPq, deborasouzamendes@yahoo.com.br, joameson.lima@unemat.br, natancavalcante2@hotmail.com, pirapora@uenf.br

²UFV- Universidade Federal de Viçosa - Bolsista CAPES, cleidiane10rodrigues@gmail.com

³UNEMAT- Universidade do Estado de Mato Grosso- Bolsista CAPES, eileen.azevedo@unemat.br

Nowadays the passion fruit woodiness disease is the most harmful viral disease to the passion fruit (*Passiflora edulis* Sims) cultivation and, in Brazil, is caused by the pathogenic agent cowpea aphid-borne mosaic virus (CABMV). The objective of this study was to implement recurrent selection, aiming the development of passion fruit cultivars resistant to CABMV and high agronomic performance. The experiment was carried out in the municipality of Campos dos Goytacazes, Rio de Janeiro - Brazil, in a randomized block design consisting of 90 full-sibs families, with three replications and three plants per plot. Symptom evaluations were performed fortnightly, over a period of 15 months, using a rating scale, for young leaves and for the total plant area. The area under the mean disease progress curve (AUDPC) was estimated and the total production per plant (PROD) was evaluated. The analysis of estimation of variance components and prediction of genetic gains were performed using the REML/BLUP procedure (*restricted maximum likelihood/best linear unbiased prediction*). According to phylogenetic analysis, the presence of CABMV was confirmed in the experimental area, being responsible for infecting passion fruit plants. At the end of the evaluations, all the plants showed symptoms of the disease, with different levels of severity. For families RS32 and RS33, the largest number of individuals selected for PROD was obtained. AUDPC values ranged from 468.75 to 1717.50 for individuals 438 and 604, respectively. In the selection for AUDPC, families RS91 and RS84 were highlighted with the highest number of resistant individuals selected. Recurrent selection applied to full-sibs families is efficient to obtaining high genetic gains for AUDPC and PROD, allows the selection of promising genotypes that can be used as parents to obtain progenies, to compose the next cycle of recurrent selection.

KEYWORDS: REML/BLUP; Passion fruit; Passion fruit woodiness disease.



Area of concentration: Plant Breeding

EFFECT OF SEED PRIMING ON RADICLE PROTUSION OF SOYBEAN SEEDS UNDER ABIOTIC STRESSES

ARAÚJO, Paula Machado de¹; GRATIVOL, Clícia²

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista Doutorado UENF, araujo.bio.md@pq.uenf.br

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro, cgrativol@uenf.br

Seed germination is characterized by the protrusion of the embryonic axis through the seed coat. The germination process can be influenced by environmental factors, such as temperature, water availability, and soil salinity. In recent years, the seed priming method has been an efficient strategy to enhance emergence and grain yield, in addition to increasing tolerance to abiotic stresses. In this work, we aimed to evaluate the effect of seed priming on the germination of soybean (*Glycine max*) seeds under saline and osmotic stress, considering the cultivars BR-16 (drought-sensitive) and Embrapa 48 (drought-resistant). Disinfested seeds were treated with NaCl and mannitol at concentrations of 0 (control), 100, 200, and 300 mM, and germinated at 28 °C. For priming, we treated the seeds with a 30% polyethylene glycol (PEG) 8000 solution for 6 hours at 28°C. Then, the seeds were dried at 32 °C for 48 hours and germinated, following the same germination procedure for the treatments with NaCl and mannitol. After 72 hours of imbibition, the radicles were manually sectioned to weigh the fresh mass and measure the area using the ImageJ program. To compare the values of fresh mass and radicle area in the different treatments, the Tukey test was performed, with a significance level of 95%, in the GraphPad Prism program (version 7.0). The cultivar BR-16 primed seeds showed higher germination rate, fresh mass, and radicle area in both saline and osmotic stresses than non-primed seeds. Primed seeds of cultivar Embrapa 48 showed a higher germination rate at 300 mM NaCl concentration, higher fresh mass, and radicle area under both stresses. This work helps to elucidate the impacts of abiotic stresses during soybean germination and shows how the use of priming before germination could enhance radicle emergence under drought and saline stress conditions, mainly in the drought-sensitive cultivar.

KEYWORDS: Drought; Salinity; Germination.



Area of concentration: Plant Breeding

**INFLUENCE OF ROOTSTOCKS ON VIGOR AND BUD FERTILITY OF AN
ADVANCED TABLE GRAPE PROGENIES IN SÃO FRANCISCO VALLEY**

SILVA; Francismary Barros¹, OLIVEIRA; Carlos Roberto Silva de¹, FELINTO FILHO; Ezildo Francisco¹, PONTES; Glácia Maria de Alencar², LEÃO; Patrícia Coelho de Souza³

¹UFRPE - Universidade Federal Rural de Pernambuco - Bolsista CAPES/Facepe, carlos.robertooliveira@ufrpe.br, francismarybarrosdasilva@gmail.com, ezildoff@gmail.com

²UNIVASF- Universidade Federal do Vale do São Francisco - gcialencar@gmail.com

³Embrapa Semiárido, patricia.leao@embrapa.br

The development of seedless grape cultivars with high natural bud fertility adapted to the semi-arid tropical climate of Brazil is the goal of national and international grapevine breeding programs. Then, the objective of this research was to evaluate the vegetative vigor and the fertility index of buds of 'Progeny 53', an advanced progeny of Embrapa's genetic breeding program, which is in the final validation step on different rootstocks in the São Francisco Valley. The experiment was carried on during two production cycles (July/2021 and January/2022). The scions were trained in a horizontal trellis system, with spacing 3.5 m x 2.5 m and drip irrigation. The treatments were represented by eight rootstocks: 101-14 Mgt, IAC 313, IAC 572, IAC 766, Paulsen 1103, Ramsey, SO4 e Teleki 5C. The experimental design was in randomized blocks, in split plots in time, with four replications. The variables evaluated were: fresh mass (FM) of branches eliminated after pruning in kg plant⁻¹, stem diameter (SD) in mm, number of lateral branches after pruning (NB), and bud fertility index (FI). The data obtained were submitted to analysis of variance. In all variables, treatments showed independent behavior between rootstocks and production cycles. The effect for cycles was significant for the variables FM, SD and FI, being the second cycle superior. The fertility index (FI) presented an average value of 0.75 bunches bud⁻¹, which represents a satisfactory bud fertility. There was no influence of rootstock on FM, NB and FI of vines 'Progeny 53' in the second production cycle. Ramsey rootstock increased the stem diameter of the vines compared to the 'IAC 572', however the other rootstocks did not show significant differences.

KEYWORDS: Table grape; Grape breeding; Tropical viticulture.



Area of concentration: Plant Breeding

EUCALYPTUS GENOTYPE SELECTION FROM IMAGE ANALYSIS USING "DEEP LEARNING" ARTIFICIAL NEURAL NETWORKS

NASCIMENTO; Elis do¹, SILVA; Silas Eduardo da², POSTINGUEL; Rafael Barros³,
BARRETTO, Vitor Corrêa de Matos⁴, TOMAZ; Rafael Simões⁵

¹UNESP-São Paulo State University - Bolsista PIBIC-CNPQ, elis.nascimento@unesp.br

²UNESP-São Paulo State University - Bolsista PIBIC-CNPQ, silas.eduardo-silva@unesp.br

³UNESP-São Paulo State University - rafael.postinguel@unesp.br

⁴UNESP-São Paulo State University - vitor.barretto@unesp.br

⁵UNESP-São Paulo State University - rafael.tomaz@unesp.br

Eucalyptus spp. is native to Australia, belongs to the family Myrtaceae, and has more than 700 catalogued species. These species have such diverse physical and chemical properties that make the eucalyptus have several uses. The genetic improvement of the specie has shown to be of great importance, considering the demands of producers and pulp, coal and furniture industries. In this work we aim to develop an artificial neural network to act in the selection process of larger and more vigorous eucalyptus seedlings in nursery production. The genotypes can then be photographed sequentially; the images interpreted by the network; and selected. For this purpose, 127 *Eucalyptus grandis* seedlings sown in tubes with Carolina Soil compost were considered. At 50 days after sowing, the plants were photographed: 1 top viewpoint photo and 3 lateral viewpoint photos, rotating the plant 120° degrees. Plant height was also measured. The attributes of the images were obtained by means of the "OpenImageR" package of the R software. Through the "H2O" package, it was possible to model ANNs capable of identifying patterns and selecting plants. It was considered 75% of the data for ANN training and 25% for testing. An architecture with an input layer with 20 attributes of the images; two intermediate layers with 20 neurons each; and an output layer with the binary result for plant selection was evaluated in 50 repetitions. ANNs with satisfactory results were obtained for seedling selection based on the images. The average correlation coefficient of the plants selected only based on height and based on image analysis was 94.7958%. Such result is quite satisfactory and encouraging, since it allows the automation of the plant selection process by means of intelligent machines.

KEYWORDS: Eucalipto; Artificial Intelligence; Pattern recognition.



Area of concentration: Plant Breeding

**WORKING IN THE DEVELOPMENT OF A SUSTAINABLE AGRICULTURE:
WHAT ARE THE GENETIC EFFECTS INVOLVED IN THE NITROGEN USE
EFFICIENCY IN POPCORN?**

SANTOS; Talles de Oliveira¹, BISPO; Rosimeire Barboza¹, SIMÃO; Bruna Rohem¹, LIMA, Valter Jário de¹, AMARAL JUNIOR, Antônio Teixeira do¹

¹Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) - tallesdeoliveira@live.com, rosimeirebarboza1@hotmail.com, rohembruna@gmail.com, valter_jario@hotmail.com, amaraljr@uenf.com

Nitrogen (N) is essential for sustaining life on Earth and plays an essential role in plant growth. However, the excessive use of nitrogen fertilizers causes not only economic but also ecological damage. In the context of the environmental damage caused by agriculture, global maize improvement programs aim to develop varieties that use nitrogen efficiently to reduce the consumption of nitrogen fertilizer in the soil. To obtain relevant information for popcorn improvement, this work was considered useful, aiming to investigate the genetic mode of action of nitrogen use efficiency (NUE) of popcorn under contrasting conditions of N availability. To this end, four contrasting NUE lines and their 12 hybrids, including reciprocal hybrids derived from a complete diallel, were grown in a greenhouse. The experiment was conducted in randomized complete blocks, with three replicates under high (100% – 224 mg L⁻¹) and low (10% – 22.4 mg L⁻¹) N conditions, defined by the Hoagland solution, modified for the nitrate source. In V6, plants were harvested and dried to obtain dry matter values and N content determination by the Kjeldahl method. The analysis of variance and Diallel proposed by Griffing were performed. Significance ($p < 0.01$) was found for the interaction between the estimates of the effects of general (GCA) and specific (SCA) combining ability and reciprocal effect (REC) in the two conditions of N to NUE. At high and low N, the magnitudes of the quadratic components associated with GCA and SCA showed greater significance of the nonadditive effects. Based on the above, it is concluded that the selection of hybrids with high allelic complementation is the best way to achieve more promising yields under normal and limited conditions of nitrogen in the soil, contributing to agricultural sustainability and the registration of better varieties for the national agribusiness.

KEYWORDS: Abiotic Stress; Nutritional Stress; Diallel Analysis; *Zea mays everta*.



Area of concentration: Plant Breeding

**THE DISCRIMINATION OF SUPERIOR INBRED LINES AND HYBRIDS OF
POPCORN FOR NITROGEN USE EFFICIENCY WITH AIM TO DEVELOP A
SUSTAINABLE AGRICULTURE**

FULY, Lara Moreira Catarino¹; SANTOS; Talles de Oliveira¹, BISPO; Rosimeire Barboza¹, SIMÃO; Bruna Rohem¹, LIMA, Valter Jário de¹, AMARAL JUNIOR, Antônio Teixeira do¹

¹ Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) – fulylara@gmail.com, tallesdeoliveira@live.com, rosimeirebarboza1@hotmail.com, rohembruna@gmail.com, valter_jario@hotmail.com, amaraljr@uenf.com

In global agriculture, nitrogen (N) is essential for increasing the productivity of crops of commercial interest. However, the increasing use of nitrogen fertilizers not only has serious environmental impacts, but also increases the production costs of important crops such as popcorn. Given the need to develop a sustainable agricultural model, increasing nitrogen use efficiency (NUE) through plant breeding programs is the most viable strategy from an economic and sustainability perspective. To obtain relevant information for the improvement of popcorn from UENF, this work was developed with the objective of evaluating the responses of popcorn genotypes under contrasting conditions of N availability for NUE, efficiency in absorption (NUpE) and transport (NUtE) of N. For this purpose, four contrasting lines for NUE (P2 and P7: efficient; L75 and L80: inefficient) and their 12 hybrids – derived from a cross in a complete diallel scheme – were grown in a greenhouse. The experiment was conducted in a randomized complete blocks scheme, with three replicates under high (100% – 224 mg L⁻¹) and low (10% – 22.4 mg L⁻¹) N conditions. In V6, plants were harvested, and dried to obtain dry matter values and determination of N content by the Kjeldahl method. Analyzes of variance and Tukey tests were performed. For NUE, NUpE, and NUtE, at high N content, lines P7 and L75 and P2 and L75 stood out, respectively. At low N, P7 stood out for NUE and NUtE, while P2 stood out for NUpE. Among the hybrid combinations, P2×L75 stood out for NUE, while P7×L75 and P2×L75 stood out for NUpE and NUtE, respectively. In this sense, P2×L75 combination is an alternative to increase productivity without expensive nitrogen fertilization when nitrogen content is limited.

KEYWORDS: Abiotic Stress; Nitrogen Acquisition; Diallel Analysis; *Zea mays everta*.



Area of concentration: Plant Breeding

YIELD PERFORMANCE OF *Coffea arabica* CLONES

ORNELAS; Daniela Oliveira¹, CARVALHO; Carlos Henrique Siqueira de², HOTZ; Aline Lenzi³, BARTELEGA; Lucas³, MATIELLO; José Braz³, ALMEIDA, Saulo Roque de³

¹ Embrapa Café – Researcher/ CNPq DTI-B, dani.ornelas@hotmail.com

² Researcher Embrapa Café/Fundação Procafé, carlos.carvalho@embrapa.br

³ Researchers Fundação Procafé

The development of sexually propagated varieties of *Coffea arabica* takes about 25 years of work to launch a new commercial variety. The use of selected clones, however, can reduce this process, allowing the exploitation of heterosis in hybrids and the commercial use of segregating plants with resistance to diseases, pests, and good cup quality. The objective of this research was to evaluate the yield performance of clones selected for resistance to coffee leaf rust (*Hemileia vastatrix*) and leaf miner (*Leucoptera coffeella*), in the coffee breeding program of Fundação Procafé, in partnership with Embrapa Café. The experiment was carried out from 2015 to 2021 with six harvests, in a randomized block design, with four replications and six plants per plot, in Varginha, MG, Brazil. The following genotypes were evaluated: clones CL3, CL13/16, CL10/18, and CL6/32 (resistant to leaf miner and to rust), clones 3-27(379), and CL3-27(1087) (with resistance to coffee leaf rust) and the commercial varieties Catuaí Amarelo IAC 62, Acauã Novo and Arara. Data analysis was performed using the R Software. The productivity of the CL13/16, CL10/18, and CL6/32 clones was higher than that of the commercial varieties, indicating that they are good candidates to compose a clonal variety.

KEYWORDS: Coffee leaf miner; Coffee leaf rust; Clonal propagation.



Area of concentration: Plant Breeding

WATER STRESS IN GERMINATION STAGE OF POPCORN GENOTYPES: GENETIC EFFECTS

FIGUEIREDO; Jardel da Silva¹, CARVALHO; Carolina Macedo¹, SILVA; José Gabriel de Souza¹, SILVA; Samuel Pereira da¹, LEITE; Jhean Torres¹, KAMPHORST; Samuel Henrique¹

¹UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – RJ, jardel.figueiredo7@gmail.com; carolinamacedocarvalho@gmail.com; jgabrielshs@gmail.com; samuelvip26@gmail.com; torresjhean@gmail.com; samuelkampho@hotmail.com

Water unavailability is an important theme to be discussed in plant breeding, as it's the most frequent event in the crops. Its occurrence affects directly the agriculture productivity. The goal of this work was, under two contrasting water conditions, to estimate the combining ability of 45 popcorn diallel hybrids in the seedling germination stage. The water conditions (WC) applied were 25% (WS) and 70% (WW) of the water retention capability of germination paper. The traits evaluated were germination velocity index (GVI), seventh-day germination (GER), shoot length (SL), shoot dry weight (SDW), root length (RL), root dry weight (RDW), root-shoot ratio (RSR), maximum number of roots (MNR), network area (NA), specific root length (SRL), network length (NL), network volume (NV). The results showed that comparison between WSs had the tendency of decreasing germination traits (GVI and GER), shoot traits (SL and SDW), RL, RDW, MNR, NA, NL, NV; and increasing SRL and RSR. The traits that had differences for ECA were GVI, in WS, RDW, NA, SRL, NL, NV, in WW, and GER and RDW for both WC. For GCA, the differences occurred for GVI in WS; GER, SDW, MNR, and RL in WW; and for RDW, RSR, NA, SRL, NL, and NV in both WC. The success of plant breeding programs in drought tolerance in germination and seedling stages can be achieved through the use of hybrids, due to non-additive genetic effects (ϕ_s) are responsible for available control traits in the seedling stage.

KEYWORDS: Non-additive genetic effects; Hybrids; Combining ability.



Area of concentration: Plant Breeding

GENETIC SELECTION OF EUCALYPTUS HYBRID PROGENY TEST IN THE NORTH OF MINAS GERAIS

BARBOSA; Talles Aquino Guedes¹, PEREIRA; Rodrigo Araújo de Assis², SANTOS; Glêison Augusto dos³, GARUZZO; Marlon dos Santos Pereira Birindiba⁴

¹UFV - Universidade Federal de Viçosa - Bolsista Embrapii, talles.barbosa@ufv.br

²UFV - Universidade Federal de Viçosa - Bolsista Embrapii, rodrigo.a.pereira@ufv.br

³UFV - Universidade Federal de Viçosa - Departamento de Engenharia Florestal, gleison@ufv.br

⁴UFV - Universidade Federal de Viçosa - Bolsista FAPEMIG, marlon.garuzzo@ufv.br

The Eucalyptus has approximately 700 botanically recognized species and can thrive in hostile environments, since there is a high diversity of characteristics and adaptive strategies in species and provenances. Considering the aspects, the present study aimed to select potential drought tolerant Eucalyptus hybrids for the IMAvol ($m^3/ha/year$) character in a progeny test in the municipality of Buritizeiro, Minas Gerais, Brazil. A randomized block design was used, with 220 distinct clones, 20 repetitions, one tree per plot and spacing of 9 m^2 . The trees were evaluated for diameter at breast height (DBH, cm) and height (m) at 1.5 years. After analyzing the traits using the Selegen REML/BLUP Software, the genetic parameters were estimated and the ranking of potential progenitors by their genetic values (u+a) and potential clones using the genotypic value (u+g) were obtained. The result showed for the trait IMAvol, individual heritability (h^2a) equal to 0.32. The estimate of h^2a is classified as moderate when it ranges from 0.15 to 0.50. The predicted values for the genetic gains (u+a) of the trait IMAvol in the selection of potential progenitors, vary from 65.78% to 76.20% for the ten potential progenitors. The gain of the best progenitor, belonging to family 25, presents an additive value considered to have a high capacity to transmit its genetic merit to the descendants, being important for recombination programs. In the selection of clones, the gains related to the genotypic value (u+g) of individuals show values for the ten potential clones from 74.01% to 88.23%. These individuals can be recommended for vegetative propagation, especially the first classified, belonging to family 25. Therefore, the estimated genetic parameters show sufficient genetic variability for the selection of materials, and the selection of potential progenitors and clones shows individuals with high genetic and genotypic value for the IMAvol character.

KEYWORDS: Forest Breeding; Potential Clones and Progenitors; Drought Tolerance.

Area of concentration: Plant Breeding

**EVALUATION OF SUGARCANE CLONES IN THE SOIL AND CLIMATE
CONDITIONS OF LINHARES-ES**

CARVALHO; Carolina Macedo¹, BITENCOURT; Celso², PORTO; José Marcos Terra²,
FERNANDES, Tamys Luiz ², CARNEIRO FILHO, Josil de Barros ², PEREIRA, Willian²

¹ UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – Graduanda em Agronomia, estagiária da UFRRJ - CCG carolinamacedocarvalho@gmail.com

² UFRRJ – Universidade Federal Rural do Rio de Janeiro Campus Campos dos Goytacazes – Pesquisador do PMGCA, celso.bitencourt@terra.com.br, josemarcosporto@yahoo.com.br, tamyslf@ufrj.br, melhoramento_clm@yahoo.com.br e willianpereira@ufrj.br

The Sugarcane Genetic Improvement Programs (PMGCA)/RIDESA are pillars of the Brazilian sugar-energy sector. They contribute with productive and healthy cultivars, suitable for mechanized harvesting and adaptable to the diversity of environments. The PMGCA-UFRRJ develops research in regions of high climate and soil restriction, covering the states of RJ, ES, BA (south region) and MG (northeast region). This research had studied sugarcane clones in an advanced stage of experimental evaluation (EF), aiming at the selection of genotypes adapted to regional edaphoclimatic conditions, superior to commercial standard cultivars. The experiment was installed in June-2018, in at the company Linhares Agroindustrial S.A. (LASA), in Linhares-ES. A total of 33 genotypes, 29 clones and 4 controls were evaluated. The experimental plots consisted of three lines of six meters spaced at 1.5m. The experimental design used was in randomized blocks with 3 replications. The harvest and final evaluation took place 17 months after planting for the characteristics: stalk yield (TSH), total recoverable sugar (TRS) and sugar yield per hectare (SYH). Means were compared by cluster using the Scott-Knott test at 95% confidence. The genotypes with the highest yield of stalks were clones RB068027, RB068528 and RB048517, with averages of 186,2, 191,4 and 212,6 t ha⁻¹, respectively. These clones, in the same order, also stood out for TAH, with averages of 23,6, 25,6 and 25,6 t ha⁻¹. The average productivity of these three clones were 44 and 46% above the cultivars RB867515 and RB966928, currently the most planted in Brazil. In addition, another 11 genotypes presented similar results to the commercial ones for TCH and 10, for TAH. The clones RB068027, RB068528 and RB048517 are promising, therefore, it is recommended to continue the studies, aiming at in-depth knowledge about TCH, ATR and TAH for future commercial releases and the continuous contribution to the Brazilian sugar-energy sector.

KEYWORDS: Productivity; *Saccharum officinarum*; Genetical enhancement

Area of concentration: Plant Breeding

LEAF VENATION RATE IN *Coffea canephora* L. TO SELECT DROUGHT-TOLERANT CLONES

SILVA; Gabriel Permanhane da¹, ROBERTO; Carlos Eduardo de Oliveira², RAMALHETE; Gabriel Pereira³, SOBREIRA; Franciele Barros de Souza⁴, SILVA; Josimar Aleixo da⁵, SOARES; Taís Cristina Bastos⁶

¹UFES - Universidade Federal do Espírito Santo - Bolsista CAPES, permanhaneg@gmail.com

²UFES - Universidade Federal do Espírito Santo - Bolsista CAPES, duh_kadu@hotmail.com

³UFES - Universidade Federal do Espírito Santo, gabrielramalhete@gmail.com

⁴UFES - Universidade Federal do Espírito Santo, francielesouza@gmail.com

⁵INCAPER - Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural, josimaraleixo_@hotmail.com

⁶UFES - Universidade Federal do Espírito Santo, tcbsoares@gmail.com

Droughts and rising global temperatures encourage the search for adapted genotypes of *Coffea canephora*. Since leaf hydraulics is directly related to the plants' "water-use efficiency" (WUE), we aimed to quantify the venation rate (VR) in Conilon genotypes, which diverge for drought tolerance. Under factorial scheme (2 (irrigation) x 6 (genotype)), with four replications of one plant, ten-month plants were grown in pots and subjected to progressive limitation (DEF treatment) in irrigation, every 15 days, until reaching 30% of the Control treatment's water status. Six genotypes were used - parentals 120T (tolerant) and 109S (susceptible), 2 pre-selected progenies from the 120x109 population (4S and 3T) and 2 pre-selected from the 109x120 population (44S and 6T). Two leaf fragments (2cm) from each plant, fixed and stained, were used. Slides were mounted and photographed under optical microscope (5X). Images were analyzed in ImageProPlus, and VR was quantified in mm/mm². Results were submitted to ANOVA and Scott-Knott ($P < 0.05$). Under Control, the highest VR means were observed in the tolerant 120T (41.86 mm/mm²) and 3T (39.14 mm/mm²) clones, and the lowest in the susceptible 44S (18.34 mm/mm²). Despite this, there was no significant difference between the 6 clones (p-value: 0.650). Under DEF, 3T showed the highest mean (54 mm/mm²), differing from the other 5 clones. However, it did not differ from Control, suggesting a constant VR in both conditions. All other 5 genotypes showed significantly higher means (p-value: 0.047) under DEF than Control. Nevertheless, this difference was greater in susceptible clones. As hypothesized, leaves developed under water stress presented higher VR, which may promote vascular redundancy, mitigating cavitation. However, in this study, tolerant genotypes tended to show, in addition to responsiveness to water stress, high VR also under normal conditions. VR seems to be useful in directing the choice of *C. canephora* drought-tolerant materials.

KEYWORDS: Conilon coffee; Leaf hydraulics; Water-stress.



Area of concentration: Plant Breeding

**RELATIONSHIP AMONG RESISTANCE TO LEAF BLIGHTS AND
AGRONOMIC TRAITS IN POPCORN INBRED LINES**

SOUZA; Ana Lucia Rangel de¹, GOMES; Lavínia Santana Ladeira², ANDRADE JÚNIOR; Marcelo Serafim de³, COSTA; Juliana Santa Barbara⁴, GONÇALVES; Gabriel Moreno Bernardo⁵, VIVAS; Marcelo⁶

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC UENF Nota 10, rangelana.agro@gmail.com

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista PIBIC UENF Nota 10, laviniasladeiragomes@gmail.com

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC CNPq, marcelojunior.A@hotmail.com

⁴UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC CNPq, jusbcosta@gmail.com

⁵UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PDR10 FAPERJ, gabriel.goncalves@pq.uenf.br

⁶UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor UENF, vivas@uenf.br

Although the popcorn culture has gained great expression in the Brazilian market in recent years, there are still serious limitations in some aspects, such as obtaining genotypes that are productive and resistant to productivity-limiting diseases such as helminthosporiose. In this context, the present study aimed to understand the relationship between helminthosporiose and the variables of greater economic value through Principal Component Analysis (PCA). The experiment was carried out in Campos dos Goytacazes - RJ, where 35 inbred lines of popcorn were evaluated. The experiment was performed as a randomized complete block design with 3 replications. The plants were sown in single rows of 3 m, 90 cm apart and 20 cm between plants. For the evaluation of severity, 5 plants were chosen from each plot, evaluated three times in an interval of 10 days, with the aid of diagrammatic scales. The variables evaluated were Grain Yield (GY), Popping Expansion (PE), resistance to *Bipolaris maydis* (BM) and resistance to *Exserohilum turcicum* (ET). The graph generated by PCA Biplot explained 68% of the data variations, with the variable GY being negatively correlated with the variable BM. The PE and ET variables showed a positive correlation. From the analyzes it was possible to verify that the L69 and L292 lines are associated with high GY and the lines L217 and L594 associated with higher values of PE. As the variables GY and BM are negatively correlated, lines L69 and L292 has higher GY and resistance to BM.

KEYWORDS: Maize; Helminthosporiose; Cluster analysis.



Area of concentration: Plant Breeding

USE OF HIGH-THROUGHPUT PHENOTYPING IN EUCALYPTUS PLANTATIONS PRODUCED IN CONVENTIONAL AND BGC TUBES

MINGORANCI; Vitória Costa¹, RIBEIRO, Arthur Lopes ¹, FABRINO; Franco Monici¹, LIMA; Ronaldo Cintra¹, BARETTO; Vitor Côrrea de Mattos¹, TOMAZ; Rafael Simões¹

¹São Paulo State of University (Unesp), Dracena, vitoria.c.mingoranci@unesp.br, arthur.l.ribeiro@unesp.br, franco.fabrino@unesp.br, ronaldo.c.lima@unesp.br, vitor.barretto@unesp.br, rafael.tomaz@unesp.br

Sustainable thinking becomes a challenge when it comes to the production of forest seedlings with quality and homogeneity, since the use of containers from non-renewable sources is still frequently applied. Thus, the use of technologies that measure such parameters, such as the analysis of aerial images, is necessary, showing results with greater accuracy. This work aimed to perform, through the use of high throughput phenotyping, a comparative analysis of eucalyptus plants produced in conventional system and BGC tubes. For this purpose, an experiment was considered in a randomized block design, unbalanced, considering a total of 85 seedlings with 190 days of age, installed in 2x2 m spacing. At 120 days after transplanting, plant height, and stem diameter at breast height were evaluated. Additionally, Phantom 4 V2 drone flights were performed every 30 days after transplanting. Aiming at high-throughput phenotyping, orthomosaics were constructed using OpenDrone Map software, analyzed using the FIELDImageR package of R software. The different types of tubes did not prove to be influential in the development of the seedlings, since the degradation of the BGC did not hinder the development of the plant. No differences were detected by means of the Tukey test. Similarly, the analysis of the VARI index of individual plants showed no significant difference between the development of plants with and without BGC. We thus evaluate that the BGC tube is a possible substitute for the conventional tube, in the challenge of production and development of forest species. Furthermore, it increases the use of containers that meet the need for the principles of sustainability, associated with technologies such as image analysis, in breeding.

KEYWORDS: Technology; Sustainability; Forest species.



Area of concentration: Plant Breeding

GENOTYPE SELECTION OF BIXA ORELLANA FROM IMAGE ANALYSIS USING ARTIFICIAL NEURAL NETWORK

SILVA; Silas Eduardo da¹, NASCIMENTO; Elis Maria do², POSTINGUEL; Rafael Barros³,
BARRETTO; Vitor Corrêa de Mattos⁴, TOMAZ; Rafael Simões⁵

¹UNESP-São Paulo State University - Bolsista PIBIC-CNPQ, silas.eduardo-silva@unesp.br

²UNESP-São Paulo State University - Bolsista PIBIC-CNPQ, elis.nascimento@unesp.br

³UNESP-São Paulo State University - rafael.postinguel@unesp.br

⁴UNESP-São Paulo State University - vitor.barretto@unesp.br

⁵UNESP-São Paulo State University - rafael.tomaz@unesp.br

Urucum was originated from Tropical America and is a plant belonging to the Bixaceae Family with the botanical name *Bixa orellana* L. Its economic importance is due to the content of bixin, a dye substance present in its seeds. The genetic improvement of the species has shown to be of great importance, considering the demands of producers and the food and pharmaceutical industries. In this work we aim to develop an artificial neural network (ANN) to act in the selection process of urucum genotypes, larger and more vigorous in nursery production, which demands manpower and time. The urucum seedlings can then be photographed sequentially; the images interpreted by the ANN; and selected by it. For this purpose, 137 urucum seedlings were considered, sown in tubes with Carolina Soil compost. At 50 days after sowing, the plants were photographed: 1 top viewpoint photo and 3 lateral viewpoint photos, rotating the plant 120° degrees. Plant height was also measured. The attributes of the images were obtained by means of R software packages "FIELDImageR" and "OpenImageR". By means of ANN algorithms it was possible to model networks capable of identifying patterns and selecting plants. An architecture with an input layer with 20 attributes of the images, two intermediate layers with 20 neurons each, and one output layer with the binary result for plant selection was evaluated. Fifty repetitions were evaluated. ANNs with satisfactory results were obtained for seedling selection based on the images. The average correlation coefficient of the plants selected only based on height and based on image analysis was 83.30%. This result is quite satisfactory and encouraging, since it allows the automation of the plant selection process by means of intelligent machines.

KEYWORDS: Urucum; Artificial Intelligence; Pattern recognition.



Area of concentration: Plant Breeding

TILLERING AND SUGAR ACCUMULATION OF SUGARCANE GENOTYPES IN THE FINAL STAGE OF SELECTION

BARCELOS; Letícia Fernandes Tavares¹ BITTENCOURT; Celso², PORTO; José Marcos Terra², FERNANDES; Tamys Luiz², CARNEIRO FILHO; Josil de Barros², PEREIRA; Willian⁶

¹UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – Graduanda em Agronomia, estagiária da UFRRJ - CCG, leticiaftbarcelos@gmail.br

²UFRRJ – Universidade Federal Rural do Rio de Janeiro, Campus Campos dos Goytacazes – Pesquisador do PMGCA, celso.bitencourt@terra.com.br, josemrcosporto@yahoo.com.br, tamvslf@ufrj.br, melhoramento.clm@yahoo.com.br e willianpereira@ufrj.br

The genetic improvement of sugarcane is based on the development of more productive cultivars, more resistant to pests and diseases, better adapted to mechanized harvesting and tolerant to water stress. In this focus, the Sugarcane Genetic Improvement Program (PMGCA) of UFRRJ operates in RJ, ES, south of BA and northeast of MG, regions with water deficit in most of the sugarcane development. The objective of this work was to evaluate 21 genetic materials, 19 clones and two controls, in the final stage of experimentation (Fe) in the cultivation of plant cane in a place with limited water and soil with low fertility. The experiment was installed in March 2018, at Linhares Agroindustrial S.A. (LASA), a region with a hot humid tropical climate and periods of drought. The experimental plots consisted of three lines of six meters, with 1.5 m between the lines. The experimental design was in randomized blocks with three replications. The harvest was carried out at 14 months, and the following variables were evaluated: tillering, average stalk weight and technological quality, represented by the total recoverable sugar (TRS). The clones showed significant differences in the parameters evaluated, however, three clones (RB128522, RB108556 and RB108519) were superior to the others in all parameters. These three clones were similar to the control RB925345, and superior (37%) to the control RB867515 in relation to the number of stems. Tillering and average weight per stalk demonstrate better clone development and are important components of productivity. In addition, they presented higher TRS, which is essential for the economic return of the producer and better processing in the industry. From these results and their relationship with other parameters, these clones demonstrate a potential for multiplication and later release as commercial cultivars.

KEYWORDS: Breeding; Experimentation; Clones.

Area of concentration: Plant Breeding

**GENETIC DIVERSITY OF SOYBEAN GENOTYPES BASED ON
AGRONOMIC CHARACTERS**

OLIVEIRA; Lawrência Maria Conceição de Oliveira¹, SILVA; Leonardo Corrêa da²

¹UFV - Universidade Federal de Viçosa - Bolsista Iniciação Científica IFTO - *Campus* Araguatins 2020-2021, law.maria16@gmail.com

²IFTO – Instituto Federal do Tocantins – *Campus* Araguatins - Professor, leocalvino@yahoo.com.br

Genetic diversity helps in the selection of divergent and complementary parents. The objective of this work was to evaluate the genetic diversity among 24 soybean lines in the extreme north of Tocantins through agronomic characters, in the 2020/2021 harvest. The experiment was conducted at the Institute Federal of Tocantins - *Campus* Araguatins. A randomized block design with three replications was used. Each plot consisted of 2 lines of 4 meters in length, spaced at 0.50 meters. Were evaluated the number of days to flowering (NDF), number of days to harvest (NDH), plant height (PH), stem diameter (SD), number of pods per plant (NPP), number of seeds per pod (NSP), plant tipping (PT) and hundred grain mass (HGM). The generalized Mahalanobis distance was used as a dissimilarity measure and, after, the clustering by the Tocher method. The relative importance of characters was determined by Singh method. All analyzes were performed using the Genes program. The largest and smallest distances obtained were between lineages L4 and L25 (219.34) and L14 and L15 (2.83), respectively. The formation of seven distinct groups was obtained. Groups I and II grouped most of the lineages, followed by groups III, IV and V, with two representatives in each, while groups VI and VII grouped one lineage each. The order of contribution of the characters to the divergence between the lineages was PH (53.01%), HGM (17.13%), SD (8.90%), NDF (7.27%), NDH (6.15 %), NSP (3.97%), NPP (3.97%) and PT (0.85%). Thus, in order to obtain superior genotypes that present high values for the components of productivity and height suitable for mechanical harvesting, lineages L5, L7, L8 and L12, belonging to group II, may be crossed with lineages L10 or L24 (group III), L21 (group VI) or L25 (group VII).

KEYWORDS: Clusting; Genetic dissimilarity; *Glycine max* L.



Area of concentration: Plant Breeding

PERFORMANCE OF POPCORN GENOTYPES UNDER LIMITING CONDITIONS OF PHOSPHORUS

SIMÃO; Bruna Rohem¹, BISPO; Rosimeire Barboza¹, SANTOS; Talles de Oliveira¹, FULY; Lara Moreira Catarino¹, LIMA; Valter Jário de¹, KAMPHORST, Samuel Henrique¹, AMARAL JÚNIOR; Antônio Teixeira do¹

¹ UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – RJ, rohembruna@gmail.com; rosimeirebarboza1@hotmail.com; tallesdeoliveira@live.com; larafuly@hotmail.com; valter_jario@hotmail.com; samuelkampho@hotmail.com; amaraljr@uenf.br

The expansion of agriculture combined with the need for sustainable cultivation is one of the biggest challenges for the scientific community that works on the generation of new cultivars adapted to abiotic stress conditions. Among the stresses, the low availability of phosphorus (P) has great importance, because its natural source is finite, and its deficiency is a limiting factor for the growth and development of crops. In this context, the objective of the work was to evaluate the responses of P use efficiency (PUE), uptake (PU_pE), and utilization (pUtE) of P in popcorn genotypes under contrasting conditions of P supply. To this end, four lines of popcorn (P2, P7, L75, and L80) and their respective F₁s hybrids including the reciprocals were grown under conditions of low (P-) and high (P+) P availability in complete blocks with three repetitions in a greenhouse. At the V6 stage, the plants were harvested and oven-dried for dry matter measurement and determination of P content. In P- the P7 strain stood out for PUE, PU_pE, and PUtE, L80 stood out for PUE and PUtE and L75 and P2 stood out only for PUtE and PU_pE respectively. In P+, strain L75 stood out for PUE and PUtE while L80 stood out only for PU_pE. Of the hybrid combinations in P-, P7×L80 stood out for PUE and PUtE, while L75×L80, P2×P7, and P7×P2 stood out for PU_pE. In P+, for PUE and PUtE the L75×L80 and L75×P2 hybrids stood out while the L80×L75, L80×P7, and P7×L80 hybrids stood out for PU_pE. In this aspect, the combination P7×L80 showed promise in P-limiting conditions, being an alternative for biomass increase and consequently productivity in popcorn, demanding a smaller amount of phosphate fertilization.

KEYWORDS: *Zea mays* L. var everta; Abiotic stresses; Nutritional Stress.

Area of concentration: Plant Breeding

IS THERE HETEROSIS FOR PHOSPHORUS USE EFFICIENCY AND GROWTH OF POPCORN UNDER LIMITING CONDITIONS OF THIS NUTRIENT?

BISPO; Rosimeire Barboza¹, SANTOS; Talles de Oliveira¹, SIMÃO; Bruna Rohem¹, FULY; Lara Moreira Catarino¹, LIMA; Valter Jário de¹, KAMPHORST, Samuel Henrique¹, AMARAL JÚNIOR; Antônio Teixeira do¹

¹ UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – RJ, rosimeirebarboza1@hotmail.com; tallesdeoliveira@live.com; rohembruna@gmail.com; larafuly@hotmail.com; valter_jario@hotmail.com; samuelkampho@hotmail.com; amaraljr@uenf.br

Phosphorus (P) is a fundamental nutrient for plants and one of the most used in agriculture worldwide. Its depletion is an imminent concern because it is a non-renewable natural resource. A strategy to mitigate the problems related to P is the development of crops that efficiently acquire and use it. However, for popcorn, these studies are still scarce. In this aspect, under conditions of high (P+) and low (P-) P availability, the objective was to evaluate differences in P use efficiency and growth of popcorn plants, as well as to estimate relative heterosis (RH) values. To this end, four inbred lines (L) and their respective F₁s hybrids (H) were used, including reciprocals, which were cultivated until the V6 stage for evaluation of the characteristics of plant height (PH), leaf length (LL), and width (LW), and stem diameter (SD). After harvest, leaf (LDM), stem (SDM), and root (RDM) dry matter and analyses to determine P use efficiency (PUE), P uptake efficiency (PUpE), and P utilization efficiency (PUtE) were performed. Given the comparison between the P condition, LDM, and SDM, although they maintained a similar pattern of average reduction between L and H, the values were higher for H, with RDM having a higher reduction. PUE and PUpE had higher values in P- conditions, while PUtE had higher values in P+ for both L and H. In P- condition, RH was positive only for PH (82.2%), LW (59.2%) and SDM (0.3%) and in P+ condition, negative only for PUtE (-1.4%), LL (-15.7%) and LDM (-0.3%). In general, for all traits simultaneously, negative RH values, in P- condition, evidenced higher sensitivity of H in relation to their genitors. It is necessary to expand the variables studied to allow conclusions, however, apparently, additive action is perceived in the control of these traits.

KEYWORDS: *Zea mays* L. var everta; Hybrids; Abiotic Stresses; Nutritional Stress.



Area of concentration: Plant Breeding

PRODUCTIVITY OF SUGARCANE GENOTYPES UNDER LOW FERTILITY AND WATER DEFICIT CONDITIONS

COSTA; Aline da Silva¹, MENDES; Monara Abreu², CARNEIRO FILHO, Josil de Barros³, BITENCOURT; Celso⁴, PORTO; José Marcos Terra⁵ PEREIRA; Willian⁶

¹UFRRJ - Universidade Federal Rural do Rio de Janeiro – Agrônoma Residente, ascbispo@gmail.com

²UFRRJ - Universidade Federal Rural do Rio de Janeiro – Bolsista FAPUR, monaraabreu01@gmail.com

³UFRRJ - Universidade Federal Rural do Rio de Janeiro – Agrônomo, melhoramento_clm@yahoo.com.br

⁴UFRRJ - Universidade Federal Rural do Rio de Janeiro -Agrônomo, celso.bitencourt@terra.com.br

⁵UFRRJ - Universidade Federal Rural do Rio de Janeiro – Tec. Agrícola, josemarcosporto@yahoo.com.br

⁶UFRRJ - Universidade Federal Rural do Rio de Janeiro - Agrônomo, willianpereira@ufrj.br

Brazil is the world's biggest producer of sugarcane. In the 2020/21 harvest, 654.5 million tons were produced. The development of highly productive sugarcane cultivars, adapted to dry environments, with low fertility and high added value, has been one of the bases for the expansion of sugarcane in several regions of the country. Therefore, breeding programs must develop cultivars that best adapt to such conditions, since these factors influence the productivity of this crop. Thus, the aim of this work was to evaluate the productivity of different sugarcane varieties under water deficit and low fertility conditions, in the first cut. The experiment was developed in the experimental area at Linhares Agroindustrial (Lasa, Linhares-ES). The experimental design used was in randomized blocks, with three replications. To compose the treatments, 33 cultivars were evaluated. Each plot was formed by three grooves with six meters and 1.5 m of spacing. The conventional planting system was chosen, using billets with three buds. Harvest and final evaluation took place 17 months after planting. The average was compared by cluster using the Scott-Knott test at 95% confidence. The varieties that stood out, differing statistically from the others and with the highest yields were the RB128534, RB108017, RB108519, RB068030, RB108544, RB128536 e RB128515, reaching 170,2; 160,7; 145,4; 145,2; 138,8; 135,5 e 133,9 t ha⁻¹, respectively. Based on the results, it is concluded that the clones under study are promising and should continue the subsequent phases of selection with a view to future commercial release.

KEYWORDS: RB128534; TCH; Breeding.



Area of concentration: Plant Breeding

SOURCES OF RESISTANCE TO *XANTHOMONAS EUVISICATORIA* IN ORNAMENTAL GENOTYPES OF *Capsicum* spp.

SILVA; Ronei Costa¹, DE ASSIS ALVES, Thayllon¹, BENTO, Cíntia dos Santos², Machado M. J³, ROSA, D. F. M³

¹UFES - Universidade Federal do Espírito Santo – Mestrando, roneicostasilva@hotmail.com

¹UFES - Universidade Federal do Espírito Santo – Mestre, thayllonalves@gmail.com

²UFES - Universidade Federal do Espírito Santo – Professora, cintia_bento@yahoo.com.br

³UFES - Universidade Federal do Espírito Santo – Graduando, matheus.machado-@hotmail.com

³UFES - Universidade Federal do Espírito Santo – Bacharel, danifrosa2009@hotmail.com

Xanthomonas euvesicatoria is among the bacteria that cause the most losses in peppers of the genus *Capsicum* in Brazil. The experiment was carried out in a greenhouse at the Federal University of Espírito Santo, Campus of Alegre. For resistance to bacterial spot, 41 accessions of *Capsicum* spp. from the germplasm bank of the Federal University of Espírito Santo, Campus of Alegre, the cultivar Ikeda (negative control) and the genotype UENF 1381 (positive control), thus, 43 genotypes. The experimental design used was completely randomized with eight replications, totaling 344 plants. For the inoculation of the genotypes, the isolate ENA 4135 of *Xanthomonas euvesicatoria* was used. Two concentrations were used, one for the hypersensitivity reaction at a concentration of 1.0×10^8 CFU/mL and another for the quantitative reaction at a concentration of 1.0×10^5 CFU/mL. Syringes and hypodermic needles were used to inoculate the bacteria (Riva-Souza et al., 2007; Pimenta et al., 2016). In the evaluation of the hypersensitivity response, presence or absence of necrosis was observed in the inoculated leaves. For the quantitative assessment, the grade scale was used. The scores assigned to the symptoms ranged from 1 to 5, being directly related to the level of development of the disease. In the Scott-Knott test at 5% significance, the hits that were statistically equal to the control mean were: 8, 9, 28, 30, 40, 49, 51, 66, 70, 74, 87, 60 and 91. The genotypes that showed resistance when compared to the control were 2, 3, 5, 25, 48, 56, 59, 62, 66, 68, 76, 80, 81, 82, 85 and 89. incubation period, the greater the severity of the epidemic in the culture. Nine genotypes were identified that stood out for not showing symptoms, these were: 5, 48, 62, 68, 76, 80, 81, 82 and 89.

KEYWORDS: Pepper; Bacterial spot; Disease resistance.



Area of concentration: Plant Breeding

SELECTION OF POPCORN INBRED LINES RESISTANT TO *Exserohilum turcicum*

GOMES; Lavínia Santana Ladeira¹, JUNIOR; Marcelo Serafim de Andrade², VALADARES; Fernanda Vargas³, PEREIRA; Luana Coimbra⁴, SALUCI; Júlio Cesar⁵, VIVAS; Marcelo⁶

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista FAPERJ, laviniasladeiragomes@gmail.com

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC CNPq, marcelojunior.A@hotmail.com

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista Doutorado CAPES, fernanda_valladares@hotmail.com

⁴UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC UENF Nota 10, coimbraluana10@gmail.com

⁵UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista Doutorado CNPq, juliosaluci@gmail.com

⁶UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Professor, vivas@uenf.br

Among the grains produced in Brazilian agribusiness, corn is in second place in the cultivation scale. According to the National Supply Company, there was a production of approximately 115 thousand tons in the 21/22 crop year. Popcorn, treated as a special type of corn, has gained more and more space in this market, given the increase in consumption and the differentiated selling price. Popcorn consumption can bring benefits, as it has vitamins and antioxidant compounds, for example. The occurrence of diseases that affect popcorn plantations makes it necessary to implement studies aimed at selecting more resistant genotypes. Within this context, the disease known as northern corn leaf blight (NCLB) is relevant, caused by the fungus *Exserohilum turcicum*. Currently, this disease is considered one of the main foliar diseases of corn, as it can compromise up to 90% of production. Thus, the use of resistant cultivars becomes more economical and effective to minimize the overall impact. The aim of this study was to evaluate the level of resistance of 37 popcorn inbred lines to NCLB. For this, the inbred lines were evaluated in a field experiment, in the municipality of Campos dos Goytacazes-RJ, in RBD with three replications, in the 2019/2020 off-season. The lines were evaluated using a diagrammatic scale, in three moments, and an average was estimated. Although the coefficient of variation (CV) was high (84%), the analysis of variance indicated a significant difference between treatments ($p=0.05$). Of the 37 genotypes, 33 showed low severity, while the genotypes L268, L328, L270 and L626 were considered susceptible.

KEYWORDS: Northern corn leaf blight; Plant disease.



Area of concentration: Plant Breeding

**CONTRIBUTION OF PLANT BREEDING TO MAIZE PRODUCTION IN
EAST AFRICA FOR 30 YEARS: WHAT IS THE MAIN EXPLANATION?**

PEDRO; César^{1,2}, MAÇOLA; Maria Angélica¹, CARVALHO; Eduarda Mendes¹, CHARIMBA; Alcides Mário^{1,2}, SAMPO; Mercês da Graça Calisto¹, SOUZA; João Cândido¹

¹UFLA - Universidade Federal de Lavras - Bolsista CAPES, Programa de Melhoramento de Milho, cpedroscentia@gmail.com, maria_marcola@hotmail.com, eduarda.carvalho@estudante.ufla.br, charimbalcides@gmail.com, merces.sampo@estudante.ufla.br, cansouza@ufla.br

²Instituto de Investigação Agrária de Moçambique, Centro Zonal Nordeste, Posto Agrônômico de Nampula

The East Africa (EA) population reached 469 million in 2022, it could reach 851 million in 2050 and the demand for food is expected to grow in the coming years. Maize is an important staple food of EA, where they face challenges such as food insecurity, low production and environmental degradation. Maize production can be increased by expanding the harvested area, managing the crop and increasing the yield of the cultivars, although the last two are not separated, yield is essential to achieve food security in a socially and environmentally sustainable way, which is possible by plant breeding, which has grown all over the world. However, in EA, changes in maize production are not easily perceived, due to several socioeconomic and environmental factors. The objective was to study the maize production, yield and growth of the harvested area, in the last 30 (1991 to 2020) years in EA and to discover the main variables that explain the increase in production. Secondary data were obtained from FAO and a linear regression analysis was performed considering the dependent (production, area and yield) and independent (year) variables, later as independent (production and area) and dependent (production) variables. In addition, the exponential model was used to estimate the growth rate considering 1991 as year zero. Production (857415 tons: 4.22%), yield (27.351 kg/ha: 1.76%) and harvested area (317253 ha: 2.46%) grow every year. Production grows by 24996 tons (0.12%)/kg of yield and 2.515 tons (0.0000001%)/hectare of maize. However, yield and area explain 85% and 86%, respectively, for the total variation in production. Measuring the contribution of maize breeding to EA is essential to determine its effectiveness and establish a baseline for research interventions.

KEYWORDS: *Zea mays*; yield of cultivars; Harvested area; Growth.



Area of concentration: Plant Breeding

SELECTION OF POPCORN INBRED LINES FOR RESISTANCE TO DISEASES AND AGRONOMIC TRAITS

GONÇALVES; Gabriel Moreno Bernardo¹, COSTA; Juliana Santa Barbara², SOUZA; Ana Lucia Rangel de³, GOMES; Lavinia Santana Ladeira⁴, VASCONCELOS; Luana Cruz⁵, VIVAS; Marcelo⁶

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista PRD10-FAPERJ, gabriel.goncalves@pq.uenf.br;

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista PIBIC-CNPq, juliana.sbc1@hotmail.com;

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC NOTA 10, rangelana.agro@gmail.com;

⁴UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista FAPERJ IC, laviniasladeiragomes@gmail.com;

⁵UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista Doutorado CAPES, luanavasconcelos16@hotmail.com;

⁶UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor UENF, vivas@uenf.br

The UENF Popcorn Breeding Program is one of the most promising popcorn improvement programs in Brazil, with several cultivars registered in recent years. The registered cultivars seek, in addition to agronomic potential, a superior ability to overcome biotic and abiotic stresses. To classify the set of lines from the UENF seed bank seed with the best agronomic performance and resistance to leaf blight caused by *Bipolaris maydis* (BM) and *Exserohilum turcicum* (ET), they were evaluated in the field in two crops seasons in Campos dos Goytacazes-RJ. In total, 190 lines were evaluated in two experiments in randomized complete blocks design with three replications. The elite lines were selected using the Mulamba and Mock selection index. The variables considered were: popping expansion (PE); grain yield (GY), BM and ET severity. PE ranged from 3.33 ml.g⁻¹ (min) to 41.7 ml.g⁻¹ (max); GY ranged from 4.94 kg.ha⁻¹ to 3965.2 kg.ha⁻¹; BM ranged from 0% to 42.5%; and ET ranged from 0% to 79.94%. The heritability of PE and GY was ~0.65, of BM of 0.8 and ET of 0.02. With that, the selection of the 60 superior lines brought gains of 1.37 ml.g⁻¹ in the average of PE, 204 kg.ha⁻¹ in GY and reduction of 2% in the severity of BM, without significant alterations in ET. The results for CE, RG and BM are a good indication of potential for selection, and the existence of interaction between the two growing seasons should not be considered a problem at this stage of the breeding program, which also aims to obtain hybrids from these lines, which should show greater vigor and, possibly, greater stability.

KEYWORDS: Selection index; Northern corn leaf blight; Southern corn leaf blight.



Area of concentration: Plant Breeding

QUALITY OF TUBEROUS ROOTS OF ORANGE-FLESHED SWEETPOTATO EXPERIMENTAL GENOTYPES IN THE WEST SÃO PAULO

GUERREIRO; João Carlos Tadeu¹, SILVA; Edgard Henrique Costa¹, LEAL; João Lucas Pires¹,
CORREIA; Wellington Giovani¹, MELO; Elisa Patrícia Ramos de¹, ZEIST; André Ricardo²

¹UNOESTE – Universidade do Oeste Paulista, joao.carlos.guerreiro@hotmail.com, edgard@unoeste.br,
joaolucaspiresleal@gmail.com, wellingtoncorreia777@gmail.com, lisaramosmelo@hotmail.com

²UFSC – Universidade Federal De Santa Catarina, andre.zeist@ufsc.br

West São Paulo is the largest national sweetpotato production site. Part of the production is exported to several countries, mostly European and South American, which are demanding in the quality of tuberous roots. There is a high demand for orange-fleshed sweetpotato for export, mainly due to the significant concentration of beta-carotene in this vegetable, as this compound is a precursor of vitamin A, which is important for the prevention of human diseases, especially in children and pregnant women. The genotypes cultivated in West São Paulo are obsolete and have a low-quality standard of tuberous roots. There is demand for the development of new genotypes to meet export standards. Thus, the objective of this work was to evaluate the quality of orange-fleshed sweetpotato tuberous roots. The experiment was carried out in a randomized block design, with four replications, in the municipality of Alvares Machado-SP. Five experimental genotypes developed by Universidade do Oeste Paulista (Unoeste) were evaluated (UZBD F-09, UZBD F-34, UZBD U2-05, UZBD U2-19 and UZBD C-14) plus 'Beauregard' as a commercial control. The root quality was assessed by the flesh color (FC) using a grade scale and skin thickness (ST). Aiming at higher pulp yield, thinner skin is sought. The UZBD U2-05 genotype presented ST of 0.1750 mm, being superior to the other genotypes and to the control 'Beauregard' that presented ST of 0.2000 mm. As for FC parameter, the genotype with the best performance was UZBD F-09 (intense orange), compared to the control cultivar (intermediate orange). The experimental genotypes UZBD U2-05 and UZBD F-09 showed better tuberous root quality.

KEYWORDS: *Ipomoea batatas* L. Lam.; Beta-carotene; Exportation.



Area of concentration: Plant Breeding

ANALYSIS OF GENETIC GAINS IN PROGENY TEST OF EUCALYPTUS HYBRIDS

FREITAS; Ricarla de Cássia Batalha de¹, SILVA; Leonardo de Souza², SANTOS; Glêison Augusto dos³, GARUZZO; Marlon dos Santos Pereira Birindiba⁴

¹UFV - Universidade Federal de Viçosa - Bolsista Embrapii, ricarla.batalha@ufv.br

²UFV - Universidade Federal de Viçosa - Bolsista Embrapii, leonardo.silva22@ufv.br

³UFV - Universidade Federal de Viçosa - Departamento de Engenharia Florestal, gleison@ufv.br

⁴UFV - Universidade Federal de Viçosa - Bolsista FAPEMIG, marlon.garuzzo@ufv.br

The genetic breeding is one of the factors responsible for the increase in average productivity and reduction in the turnover of Eucalyptus plantations. In addition, it's one of the reasons why Brazil is a world reference in planted forest of this genus. The present study aimed to estimate genetic parameters and select potential progenitors and superior clones for the silvicultural trait DBH (Diameter at Breast Height). The Eucalyptus were evaluated for DBH (Diameter at Breast Height) at 1.5 years in a progeny test in the municipality of Ibiai, Minas Gerais, Brazil. The experiment consisted of 220 families developed at the Research Nursery of the Forest Engineering Department of the Universidade Federal de Viçosa - UFV. The planting was done in a randomized block design, one plant per plot and spacing of 9 m². The traits were analyzed via Selegen REML/BLUP Software. After analysis, the genetic parameters were estimated and the ranking of potential progenitors by their genetic values (u+a) and potential clones using the genotypic value (u+g) were obtained. The parameter estimates for the trait DBH was individual heritability (h²a) equal to 0.33. The predicted values for genetic gains (u+a) of the trait DBH in the selection of potential progenitors revealed estimates from 24% to 28% for the ten potential progenitors. In the selection of clones, the gains related to the genotypic value (u+g) of individuals for the trait DBH shows values for the ten potential clones from 26% to 32%. The genetic parameter indicates success in testing progenies and favorable conditions for breeding programs. In addition, the breeding population showed gain in the silvicultural trait DBH, favoring the availability of superior genetic material for silviculture.

KEYWORDS: Forest Breeding; Genetic Selection; Drought Tolerance.

Area of concentration: Plant Breeding

**COMBINING ABILITY IN POPCORN FOR SOUTHERN CORN LEAF
BLIGHT RESISTANCE**

JUNIOR; Marcelo Serafim de Andrade¹, SALUCI; Júlio Cesar ², PEREIRA; Luana Coimbra³,
SOUZA; Ana Lucia Rangel de⁴, VALADARES; Fernanda Vargas⁵, VIVAS; Marcelo⁶

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Bolsista PIBIC CNPQ, marcelojunior.A@hotmail.com

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Bolsista Doutorado CNPQ, juliosaluci@gmail.com

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Bolsista PIBIC UENF Nota 10, coimbraluana10@gmail.com

⁴UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Bolsista PIBIC UENF Nota 10, rangelana.agro@gmail.com

⁵UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Bolsista Doutorado CAPES, fernanda_valladares@hotmail.com

⁶UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro- Professor, vivas@uenf.com

Popcorn is a food appreciated in many countries around the world, including Brazil. However, crop yield may be reduced due to the occurrence of leaf diseases such as southern corn leaf blight (SCLB), which can be controlled with the use of resistant genotypes. The objective of this work was to evaluate the combining ability between popcorn lines previously selected for resistance to SCLB. Diallel crosses were performed between 4 inbred lines of popcorn, obtaining 6 hybrids. These were evaluated in a greenhouse in randomized blocks with 5 replications and inoculated by the fungus *Bipolaris maydis* causing SCLB. The plants were grown in pot filled with 5L of substrate, at 30 days after sowed the plants were sprayed with a suspension of 1×10^4 conídios.mL⁻¹. 20 days after inoculation, severity was evaluated in the fifth expanded leaf of each plant. The data were submitted to variance analysis and diallelic analysis only of F₁s by Griffing method. There was a significant effect on the general combining ability (GCA) and specific (SCA), however the GCA values were higher. The GCA effects on parents indicated the L443 lineage with the lowest values, followed by the L322 line, which is of interest in the analysis of disease data. As for SCA, the hybrids L443 x L292 and L322 x L594 presented the lowest values. Among the lines evaluated, L443 presented the best potential to reduce the severity of SCLB. Due to the results, it is possible to conclude that the L443 strain can be used as a genitor to obtain resistant hybrids.

KEYWORDS: *Zea mays*; *Bipolaris maydis*; Helminthosporiosis.



Area of concentration: Plant Breeding

**EVALUATION OF CULMS AND SUGAR OF SUGARCANE CLONES IN THE
T3 PHASE IN LINHARES-ES**

SANTOS; Jane Ribeiro dos¹, CARNEIRO FILHO; Josil de Barros², BITENCOURT; Celso³, PORTO; José Marcos Terra⁴, PEREIRA; Willian⁵

¹UFRRJ-Universidade Federal Rural do Rio de Janeiro – Agrônoma Residente, janerribs@gmail.com

²UFRRJ-Universidade Federal Rural do Rio de Janeiro – Agrônomo, melhoramento_clm@yahoo.com.br

³UFRRJ-Universidade Federal Rural do Rio de Janeiro – Agrônomo, celso.bitencourt@terra.com.br

⁴UFRRJ- Universidade Federal Rural do Rio de Janeiro - Técnico Agrícola, josemarcosporto@yahoo.com.br

⁵UFRRJ – Universidade Federal Rural do Rio de Janeiro – Agrônomo, willianpereira@ufrj.br

Sugarcane, a perennial grass belonging to the genus *Saccharum*, is used in Brazil not only for the production of sugar and ethanol, but also for the internal generation of electricity, corresponding to about 19.1% of the national energy matrix. The present work aims to evaluate the productivity and technological quality of the field of 27 sugarcane clones, in the third stage of sugar selection (T3), looking for development factors such as: higher productivity, tolerance to water stress and resistance to diseases and pests. The experiment was carried out in the agricultural area of Destilaria Lasa, in Linhares, Espírito Santo. The experimental design used was in randomized blocks, with 27 treatments (24 clones and 3 controls) and 3 replications. The experimental unit consisted of 3 furrows, 6 m long, 1.5 m apart. The analysed variables STH, STR and SYH, were submitted to analysis of variance using the F test at the 95% confidence level. When the F test showed significance in ANOVA, the Scott-Knott test was applied at 95% confidence to compare the means of the quantitative variables. Through the analysis, it was possible to identify that the clones – RB108519, RB108544 and RB108556 – showed good yields, in addition to having similar productivity to standard sugar stalks, such as RB867515, the most planted variety in Brazil and RB92579, the most cultivated in the region northeast. However, more research is needed to confirm the potential of the clones studied. Considering that Brazil is the world's largest producer of sugarcane, it is extremely important that similar research continues to be carried out so that there are more and more quality clones with greater productivity in the country.

KEYWORDS: Productivity; Selection; ANOVA.



Area of concentration: Plant Breeding

PHENOTYPIC VARIABILITY IN POPULATION OF INDOGAMIC FAMILIES S₁ OF ELEPHANT GRASS FOR BIOENERGY PURPOSES

LEITE; Cleudiane Lopes¹, SANTANA; Josefa Grasiela Silva¹, AMBRÓSIO; Moisés¹, DAHER; Rogério Figueiredo¹

¹UENF- Universidade Estadual do Norte Fluminense Darcy Ribeiro, cleudiane.lobes25@gmail.com, grasi_agronomia@hotmail.com, ambrosio_20007@hotmail.com, rogdaher@uenf.br

Elephant grass (*Pennisetum purpureum* Schum.) is a grass with high productive potential and has been investigated as a renewable energy source for its biomass. A strategy not yet explored in the improvement of elephant grass is the production of hybrids from inbred lines. In this study, 195 genotypes comprising 11 inbred S₁ families from the elephant grass breeding program were evaluated to distinguish phenotypic variability from qualitative characters. Seeds of the S₁ generation obtained by self-pollination of elephant grass accessions from the UENF BAG were sown in trays and transplanted to the field at 45 days after seedling emergence. The experiment located at the Experimental Station of the State Center for Research in Agroenergy and Waste Utilization (CEPAAR) in Pesagro-Rio, Campos dos Goytacazes, the design was in randomized blocks with three replications, with an experimental plot consisting of a single plant, with spacing 1.5 m between plants and 1 m between rows. The thirteen qualitative descriptors used were growth habit (HC), plant height (AP), basilar tillering intensity (IP), internode color (CI), sheath color (CB), sheath hairiness (PB), shape ligule (FL), ligule pubescence (PL), leaf blade position (PLF), leaf blade color (CLF), midrib width (LNC), midrib color (CNC), hair on the leaf adaxial surface (PFA). Data were submitted to multiple correspondence analysis (MCA) to verify dissimilarities between genotypes and between descriptor categories. The most divergent genotypes belong to the F01, F02, F05, F07, F08, F09 and F11 families and the variables that present the greatest contributions to this result were CB, AP, HC, and IP. These preliminary results of dissimilarity of inbred families will be used together with quantitative trait evaluations to identify superior genotypes with desirable traits of interest.

KEYWORDS: Renewable energy; Dry mass; Multivariate analysis.

Area of concentration: Plant Breeding

SELECTION OF POPCORN INBRED LINES RESISTANT TO *Bipolaris Maydis*

COSTA; Juliana Santa Barbara¹, PEREIRA; Luana Coimbra², GOMES; Lavinia Santana Ladeira³, JUNIOR; Marcelo Serafim de Andrade⁴, GONÇALVES; Gabriel Moreno Bernardo⁵, VIVAS; Marcelo⁶

¹UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PIBIC CNPq, costa.julianasb@gmail.com

²UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista PIBIC UENF Nota 10, coimbraluana10@gmail.com

³UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista IC FAPERJ, laviniasladeiragomes@gmail.com

⁴UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – Bolsista PIBIC CNPq, marcelojunior.A@hotmail.com

⁵UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista PDR10 FAPERJ, Gabriel.goncalves@pq.uenf.br

⁶UENF – Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor UENF, vivas@uenf.br

Obtaining genetically resistant genotypes to southern corn leaf blight (*Bipolaris maydis*) is a strategy to mitigate the damage caused by this pathogen. Thus, the objective of this study was to identify genotypes tolerant to *B. maydis* according to their degree of severity. A total of 35 popcorn lines were evaluated in an experiment conducted in Campos dos Goytacazes - RJ. A randomized block design with three replications was used, totaling 105 plots. Each experimental unit consisted of single rows 3 meters long, 0.9 m apart rows and 0.20 m between plants, resulting in a density of 55,000 plants per hectare. The severity of *B. maydis* was measured using a diagrammatic scale, 3 times after flowering. Each evaluation consisted of analyzing the leaf attached to the first ear in 5 plants per plot. From the analysis of variance, a mean comparison test was performed, calculating the least significant difference (LSD) by the T test. As a result, the lines L353, L628, L394, L292 and L441 had lower rates of susceptibility to the pathogen. On the other hand, the genotypes with the highest severity were L654, L74, L209, L52 and L202. Among the lines that showed high susceptibility to *B. maydis*, L654 stood out as a highly susceptible material, being considered an interesting material for studies of genetic inheritance or other research related to the fungus. Resistant lines, on the other hand, should compose the group of promising genotypes for combination in crossing schemes or obtaining a synthetic population.

KEYWORDS: Southern corn leaf blight; *Zea mays* L.; Plant disease.



Area of concentration: Plant Breeding

WHAT IS THE IDEAL TIME OF IMMERSION IN SULFURIC ACID TO BREAK DORMANCY OF SWEET POTATO SEEDS?

CORREIA; Wellington Giovani¹, CARBONERA; Maiara Zenni², SILVA JUNIO; André Dutra³, OLIVEIRA; Guilherme José Almeida¹, TOROCO; Bruno da Rocha¹, ZESIT; André Ricardo²

¹Unoeste – Universidade do Oeste Paulista, welligtoncorreia777@gmail.com, guilhermejaost@hotmail.com, bruno-toroco@outlook.com

²UFSC – Universidade Federal de Santa Catarina, andre.zeist@bol.com, maiaraufsc@hotmail.com

³UFV – Universidade Federal de Viçosa, andrejunior018@gmail.com

In sweet potato breeding, it is necessary to carry out crosses between parents that will generate seeds that will originate the new plants. However, these seeds have a hard and thick tegument that prevents germination. Thus, to that can occur the germination it is essential the rupture of this physical impediments. The main technique employed is chemistry, with the use of sulfuric acid. However, there are few studies that determine the appropriate time for these seeds to remain immersed, ensuring a high percentage of germination and seedling vigor. Thus, the objective was to identify the effects of immersion times of seeds in sulfuric acid on germination and initial growth of sweet potato seedlings. Sweet potato seeds were obtained from July to September 2021 in polocrosse blocks in Presidente Prudente-SP, in the experimental area of CEOFOP. The seeds were immersed in sulfuric acid (H₂SO₄) 98% for time intervals, where 0 was the control followed by periods of 20, 40, 60, 80 min. The study was carried out in a completely randomized design with ten replications and each replication consisted of 25 seeds. The percentage of germination, germination speed index (GSI), dry mass of whole seedlings and length of the largest root and shoot were evaluated. The germination percentage and GSI improved as the immersion time increased, reaching the maximum point at 53.30 min, in which the maximum estimated values were 90.19% and 26.54, respectively. For the parameters dry mass, length of the largest root and length of the shoot, an increase was observed up to the limit of 55.00, 37.63 and 44.44 min of immersion, respectively. Thus, the immersion time of 53 min is the most suitable for breaking dormancy.

KEYWORDS: *Ipomoea batatas* Lam; Breeding; Chemical scarification; Seed germination.



Area of concentration: Plant Breeding

MYCELIAL GROWTH OF *Exserohilum turcicum* IN DIFFERENT CULTURE MEDIA

PEREIRA; Luana Coimbra¹, SOUZA; Ana Lúcia Rangel¹, COSTA; Juliana Santa Barbara², VASCONCELOS; Cruz Luana³, GONÇALVES; Gabriel Moreno Bernardo⁴, VIVAS; Marcelo⁵

¹UENF - Universidade Estadual do Norte Fluminense - Bolsista IC UENF-Nota 10 coimbraluana10@gmail.com; rangelana.agro@gmail.com;

²UENF - Universidade Estadual do Norte Fluminense – Bolsista PIBIC-CNPq, juliana.sbc1@hotmail.com;

³UENF - Universidade Estadual do Norte Fluminense – Bolsista Doutorado CAPES, luanavasconcelos16@hotmail.com

⁴UENF - Universidade Estadual do Norte Fluminense – Bolsista PRD10-FAPERJ, gabriel.agrobio@gmail.com

⁵UENF - Universidade Estadual do Norte Fluminense – Professor UENF, mrclvivas@hotmail.com

Helminthosporiosis is one of the main plant diseases that affect corn and is caused by the fungus *Exserohilum turcicum*. Genetic improvement is the most efficient way to avoid the disease and that is why studies of the fungus are essential. However, the inoculation of this fungus in the selection of superior genotypes is always a challenge due to the low efficiency of the inoculum. Thus, the objective of this study was to select the best culture media that provide better sporulation of *E. turcicum*. The experiment performed evaluating five culture media that provided the best mycelial growth. The experiment was carried out in a randomized complete block design with ten replication. The media used were PDA (potato, dextrose, agar), V8 (vegetable juice), LCHA (lactose, casein, agar), AV (oat, agar) and CF (corn flour, peptone, dextrose, agar). In each culture media a small chunk of ~6mm from the colonies of the fungus was transferred. The plates were incubated in BOD at a temperature of 25 °C ± 2 °C and a photoperiod of 12h. Mycelial growth was evaluated daily by measuring the colony diameter (cm) in two opposite directions, with the aid of a ruler. All cultural media differed statistically from each other, according to the ANOVA. The media that allowed the best mycelial growth was CF (6.17 cm), followed by BDA (5.75 cm), V8 (5.56 cm), LCHA (5.49 cm) and AV (5.06 cm). From the results obtained, it can be said that the corn flour media was the best for mycelial growth in the experimental conditions, but BDA is a media most used in routine preparations and its use should not be discarded, since it was the second best growing medium.

KEYWORDS: Popcorn; Northern leaf blight; Maize.



Area of concentration: Plant Breeding

PRODUCTIVITY AND TECHNOLOGICAL QUALITY OF SUGARCANE CLONES IN LINHARES-ES

FERNANDES; Letícia Spolador¹, BITENCOURT; Celso², PORTO; José Marcos Terra²,
FERNANDES, Tamys Luiz ², CARNEIRO FILHO, Josil de Barros ², PEREIRA, Willian²

¹UFRRJ - Universidade Federal Rural do Rio de Janeiro – Residente em Agronomia,
leticiasf.rural@gmail.com

²UFRRJ – Universidade Federal Rural do Rio de Janeiro Campus Campos dos Goytacazes – Pesquisador
do PMGCA, celso.bitencourt@terra.com.br, josemarcosporto@yahoo.com.br, tamyslf@ufrj.br,
melhoramento_clm@yahoo.com.br e willianpereira@ufrj.br

Sugarcane culture is present in a diversified way in the economy of several capixaba municipalities. The production of sugarcane for juice and cachaça, for animal feed and for the production of sugar and ethanol are inserted in a context of technological innovation, especially in genetic improvement, in which new cultivars make more efficient use of natural resources. The present work was developed with the objective of evaluating potential clones of the Sugarcane Genetic Improvement Program (PMGCA -UFRRJ), in the experimental phase (FE) of second ratoon, regarding agricultural productivity and technological quality. The variables analyzed were ATR (total reduced sugar), ARC (reducing sugar in the stem), TAH (ton of sugar per hectare), TCH (ton of sugar per hectare) and fiber. The PMGCA-UFRRJ develops research in the northern region of Espírito Santo, which presents productive environments with water restriction, low soil fertility and hot humid tropical climate. The experiment was installed in June 2017, in a commercial area of the company Linhares Agroindustrial S.A. (LASA), in Linhares - ES. The second ratoon harvest occurred in October 2020, 13 months after the previous harvest. The experimental design was randomized block design with three repetitions. Ten genetic materials were used - two witnesses and eight potential clones. Each plot was composed of 3 rows of 6 meters, spaced at 1.5 meters. The results obtained were submitted to analysis of variance (ANOVA) and the Scott-Knott grouping of means test at 95% confidence level. There were significant differences among ARC, ATR and TAH treatments, with three superior genotypes standing out. RB 128515, RB 128536, RB 108519 presented, respectively, average values of ATR 126.18, 134.52 and 136.61, and TAH values 9.84, 11.77 and 12.18. The results help in the understanding of the genetic potential of the genotypes, contributing to future releases of sugarcane cultivars.

KEYWORDS: Technological innovation; *Saccharum officinarum*; Genetical enhancement.



Area of concentration: Genomic Analysis

PLASTID MARKERS AS A TOOL FOR CHARACTERIZATION OF PECAN CULTIVARS: A NOVEL SET OF MICROSATELLITES TOWARD SPECIES BREEDING

OLIVEIRA; Joana Nascimento Mercedes de¹, NAGEL; Jordana Caroline², POLETTO; Tales³, GUTERRES; Suelen Martinez⁴, BEISE; Dalvan Carlos⁵, STEFENON; Valdir Marcos⁶

¹Universidade Federal de Santa Catarina – Mestranda PPGRGV, Bolsista CNPq, ojoana140@gmail.com

²Universidade Regional Integrada do Alto Uruguai e das Missões, jordananagel@san.uri.br

³Universidade Federal de Santa Maria, talespoletto@gmail.com

⁴Universidade Federal de Santa Catarina - Doutoranda PPGRGV, Bolsista CAPES, suelenguterres1996@gmail.com

⁵Universidade Federal de Santa Catarina - Doutorando PPGRGV, Bolsista CAPES, dalvanbio@gmail.com

⁶Universidade Federal de Santa Catarina - Bolsista de produtividade CNPq, valdir.stefenon@ufsc.br

Pecan is an important perennial species introduced in southern Brazil more than 80 years ago with cultivars originating from the USA. The expansion of planted areas in Brazil is limited due to the poor performance of some cultivars in regions climatically different from the original distribution area of the species. The development of cultivars adapted to the Brazilian edaphoclimatic conditions is, therefore, needed. As the correct identification of registered cultivars is essential for the development of pecan breeding programs, this study aimed at using a novel set of plastid microsatellite markers for identifying possible misassignments in Pecan cultivars from southern Brazilian orchards. Twenty-four plants of eight commercial cultivars and three plants from open-pollinated origin were genotyped using ten plastid microsatellite markers. These markers were developed from the plastid genome of the pecan cultivar Imperial. The genetic relationship between plants was evaluated using Principal Component Analysis (PCA) and UPGMA clustering. The plastid markers, which have a maternal inheritance in pecan, clearly represented the parental relationship among cultivars Shawnee, Jackson, Success, and Barton. The low genetic differentiation between cultivars Shawnee and Jackson reflected the close relationship of half-sibs since both have cultivar Schley as the maternal parent. The samples of cultivar Barton formed a single clade in the UPGMA cluster analysis. On the other hand, there was no consistent grouping of plants identified as Imperial, Melhorada, Mahan, Jackson, Shawnee, Success, as well as those from open-pollinated origin. Thus, samples named Barton have the same genetic patterns, while some samples named Imperial, Melhorada, Mahan, Jackson, Shawnee, and Success are probably misassigned. The plastid microsatellite markers used in this study are relevant tools for advancing breeding programs of pecan, through the selection of genotypes, characterization of genetic diversity, and identification of genitors.

KEYWORDS: *Carya illinoensis*; Molecular markers; Marker-assisted selection.



Area of concentration: Genomic Analysis

THE COMPLETE CHLOROPLAST GENOME SEQUENCE OF *Euterpe Precatoria*

SCHARDONG; Iago Beffart¹; LOPES, Ricardo², COELHO; Alexandre Siqueira Guedes³

¹UFG - Universidade Federal de Goiás – Mestrando PPGGMP, iago.biotec@gmail.com

²Embrapa Amazônia Ocidental, ricardo.lopes@embrapa.br

³UFG - Universidade Federal de Goiás – Professor Associado, alexandre_coelho@ufg.br

Açaí palm (*Euterpe precatoria*) is an Amazonian tree species and is widely used for food and crafting purposes. Given its economic relevance, there is a wide interest in its conservation and breeding. Despite this interest, little is known about the genomics of *E. precatoria*. In this work we publish the complete chloroplast genome sequence of the species. Chloroplast genomes are known for having a conserved structure and are useful to explore evolutionary questions and to provide markers that unveil the genetic diversity within and between species. Our objective was to assemble and characterize *E. precatoria*'s plastid genome and to perform a comparative analysis to other species within the *Arecaceae* family. Using Illumina reads, the assembly was obtained using the Fast-Plast pipeline. Gene content, as well as tRNA and rRNA sequences were annotated using the GeSeq web interface. Microsatellite loci were identified using MISA. The comparative analysis of the chloroplast genomes of different species of *Euterpe* was carried out using mVISTA. The phylogenomic relationship between the plastid genome of *E. precatoria* and those of other 13 species within *Arecaceae* was also estimated. The final assembly size was 159,282 bp and presented the expected quadripartite structure. A total of 113 genes were annotated, of which 95 were single-copy and 18 were duplicated in the inverted regions. A total of 276 microsatellite loci were identified, the majority of which composed of mononucleotide motifs. The mVISTA analysis confirmed that a major part of plastid genomes is composed of very conserved sequences, especially in gene-coding regions. The phylogenomic tree revealed a closer proximity between *E. precatoria* and *E. oleracea*. Complementing its conserved organization, cpDNA of *E. precatoria* presents the same gene content as of other *Euterpe* species. Our results contribute to open the way for future evolutionary and comparative analysis within *Arecaceae*.

KEYWORDS: Açaí; cpDNA; Genome assembly.



Area of concentration: Genomic Analysis

IDENTIFICATION OF NEW AND CANONIC microRNAs IN THE SUGARCANE (*Saccharum spontaneum*) GENOME

CARDOZO, Luciele de Léo¹, ARAÚJO, Paula Machado de²; GRATIVOL, Clícia³

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista CNPQ IC, cardozoluciele@gmail.com

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista Doutorado UENF, araujo.bio.md@pq.uenf.br

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro, cgrativol@uenf.br

Sugarcane belongs to the monocot group of plants and is the major source for producing sugar and ethanol. Brazil is the largest producer of sugarcane and the largest exporter of sugar. Recently, three reference genomes were published for sugarcane, which highlighted its genomic complexity. MicroRNAs (miRNAs) are non-coding RNAs capable of regulating gene expression post-transcriptionally and act in several biological processes in plants. Most of the work on the characterization of miRNAs in sugarcane has used transcriptomic sequences or genomes of phylogenetically related species. The identification of miRNAs in the sugarcane genome may contribute to the discovery of species-specific miRNAs. In this study, we aimed to identify known and new miRNAs in sugarcane (*Saccharum spontaneum*) and their potential miRNA-encoded peptides (miPEPs) using bioinformatics tools. Initially, 52 small RNAs sequencing libraries were obtained, and the reads were filtered for size and quality. The filtered libraries were submitted to the miRCat2 program to identify known and new miRNAs. The obtained miRNAs were aligned against the mature miRNAs in the miRBase database using the BLASTN algorithm, and 472 canonical miRNAs and 1,419 potential new miRNAs were identified. Two putative miPEPs from miR408 were identified on chromosomes Chr3A and Chr3C. First, the genomic sequences in which the miR408 precursor is located on chromosomes Chr3A and Chr3C were obtained using the Bedtools program by adding 500 base pairs before the precursor. Such regions were subjected to a search for Transcription Start Sites (TSS). Next, ORF prediction was performed using the ORFfinder tool, and only ORFs starting after the TSS regions were considered. The translated ORFs resulted in two identical putative miPEPs of 55 amino acids. The results obtained in this research may increase the number of miRNAs identified in sugarcane and contribute to the understanding of how miRNAs regulate different biological processes in this species.

KEYWORDS: Bioinformatics analysis; Small RNA-seq; miPEPs.

Area of concentration: Genomic Analysis

**N-USE EFFICIENCY TRAITS IN MAIZE GENOTYPE RESPONSIVE TO
Herbaspirillum seropedicae INOCULATION REVEALED BY
TRANSCRIPTOMIC AND PROTEOMIC APPROACHES**

IRINEU; Luiz Eduardo Souza da Silva¹, SOARES; Cleiton de Paula², ALMEIDA; Felipe Astolpho de³, SILVEIRA; Vanildo⁴, OLIVARES; Fabio Lopes⁵

¹UENF - Universidade Estadual do Norte Fluminense - Doutorando LBCT, luizeduardobio@outlook.com

²IFRR - Instituto Federal de Roraima - Campus Novo Paraíso - Professor, cleiton.soares@ifrr.edu.br

³USP - Universidade de São Paulo – Pós-Doutorando IC, flp_astolpho@hotmail.com

⁴UENF - Universidade Estadual do Norte Fluminense - Professor LBT, vanildo@uenf.br

⁵UENF - Universidade Estadual do Norte Fluminense - Professor LBCT, fabioliv@uenf.br

Microbial technologies are essential to achieve food security in a future sustainable way. *Herbaspirillum seropedicae* is a diazotrophic bacterium used in bioinoculants for maize and sugarcane. Inoculation efficiency, growth and productivity may be related to the plant's ability to absorb the nutrients provided by the soil and microbial activities. This work aims to decipher the mechanism responsible for the N-uptake and assimilation of maize genotype responsive to *H. seropedicae* using omics. For this, seeds (Dekalb 7815) were disinfected and germinated on Germitec paper for 72 hours in a growth chamber. Seedlings were transplanted into 2L pots with 2mM CaCl₂ solution and separated into control and inoculated, which received 20mL of inoculum containing 2x10⁷ cells/mL⁻¹ of *H. seropedicae* strain HRC54, remaining for five days in a growth chamber. For Transcriptomic and proteomics, roots were separated into triplicates and macerated in liquid nitrogen. RNA was extracted, and sequencing libraries were prepared and sequenced on the Illumina platform. The transcripts obtained were analyzed by bioinformatics. Proteins were extracted, subjected to mass spectrometry (ESI-MS/MS), and mass spectra were analyzed using PLGS and ISOquant software. To correlate omics results with N-accumulation, chlorophyll content was measured by SPAD, and the expression of the gene chlorophyll a-b binding protein 1 (CAB-1) in the leaves was analyzed by RTq-PCR. Transcripts of Nitrate Transport 2, High-Affinity Nitrate Transporter and Protein NRT1 were down-regulated, and the Nitrate Transport 1 and another Protein NRT1 were up-regulated. On the other hand, transcripts of Nitrate Reductase and glutamate synthase were up-regulated. Proteins of N-metabolism, Nitrate Reductase, Glutamine Synthetase and Glutamate Dehydrogenase were all up-accumulated. In addition, the chlorophyll index was higher, and the gene CAB-1 was 4.36 fold-changed, more expressed in inoculated plants. These results evoke the importance of N-use efficiency traits to increase the responsiveness to microbial inoculants from a plant breeding perspective.

KEYWORDS: Bioinoculants; Nitrogen; Plant Breeding.



Area of concentration: Genomic Analysis

MACHINE LEARNING AS A DIGITAL TOOL FOR GENOMIC ANALYSIS

COSTA; Weverton Gomes da¹, CELERI, Maurício de Oliveira², BARBOSA, Ivan de Paiva³, BORÉM, Aluizio³, NASCIMENTO, Moyses², CRUZ, Cosme Damião¹

¹Federal University of Viçosa, Department of General Biology, Bioinformatics laboratory, wevertonufv@gmail.com, cdcruz@ufv.br.

²Federal University of Viçosa, Statistics Department, Computational Intelligence Laboratory and Statistical Learning – LICAE, mauricio.celeri@ufv.br, moysesnascim@ufv.br.

³Federal University of Viçosa, Department of Agronomy, ivanbarbosa.agro@gmail.com, borem@ufv.br

Machine learning is one of the most used digital tools today. Several studies have already demonstrated the high potential of this tool in genomic analysis. In this sense, this study aimed to evaluate and compare the predictive performance of various machine learning methods within G-BLUP through GWS. F2 population formed by 1000 individuals was simulated and genotyped with 4010 SNP markers. Twelve traits were simulated from a model considering epistatic effect, with QTL numbers ranging from eight to 480 and heritability of 0.5 or 0.8. Machine learning methods used were: multilayer perceptron (MLP), radial basis function (RBF), decision trees (DT), bagging (BA), random forest (RF), boosting (BO) and multivariate adaptive regression splines (MARS) considering additive and non-additive model. The results obtained were able to demonstrate the strong effect of heritability and the increase in the number of QTL on the values of R^2 and RMSE. The MARS methods presented higher R^2 values for traits with 8 QTLs, for both heritability scenarios. When increasing the number of QTLs (40 or more) it was observed that the RBF presented the highest R^2 values, followed by G-BLUP, RF, BA, and BO, and always above the general average for the traits with 50% heritability. For traits with 240 and 480 QTLs, the non-additive MARS methods presented high R^2 values, considering the standard error only smaller than the G-BLUP. The methods MLP and RBF, similarly to G-BLUP, showed substantial improvement the higher the QTLs. The BO method demonstrated greater sensitivity to heritability and showed the best results when the scenarios were of greater heritability and 40 or more QTLs. Machine learning methods are powerful tools for predicting genetics values with epistatic gene control in traits with different degrees of heritability and different numbers of control genes and should be carefully considered in genomic selection analyses.

KEYWORDS: MARS; Predictive and selective accuracy; Quantitative trait loci.



Area of concentration: Genomic Analysis

CALLOSE BIOSYNTHESIS AND DEPOSITION IN THE SOYBEAN EMBRYONIC AXIS DURING GERMINATION UNDER ABIOTIC STRESSES

OLIMPIO; Geovanna Vitória¹, SANGI; Sara², GRATIVOL; Clícia³

¹UENF - State University of the North Fluminense Darcy Ribeiro, Bolsista IC - CNPQ, geovannavop@gmail.com

²UENF - State University of the North Fluminense Darcy Ribeiro, Bolsista doutoranda - CAPES sarasangi@pq.uenf.br

³UENF - State University of the North Fluminense Darcy Ribeiro, - cgrativol@uenf.br

Environmental stresses directly affect plant development and, consequently, crop production. In response to stress, callose synthase (GSL) can be induced as a plant defense mechanism. The GSL family is related to the formation of protective barriers in the cell wall, but in soybean the genes that synthesize this polymer have not yet been characterized. Thus, this work aimed to identify the genes involved in callose biosynthesis in the soybean genome and to analyze callose deposition in embryonic axes during germination under abiotic stresses. To identify the GSLs, the soybean (*Glycine max*) genome database available in Phytozome v12 using the hidden Markov model (HMM) and their phylogenetic relationship was analyzed by the MEGA X program. Twenty-three GSL genes were identified and formed four clusters in the soybean genome. To investigate gene expression changes, we used embryonic axis RNA-seq libraries at 0, 3, 6, 12 and 24 HAI (hours after imbibition) available on the Soybean Expression Atlas platform. The data show that some GSLs are required throughout the embryonic axis germination process. In particular, the *GmGSL10* gene that remained highly expressed throughout germination. We quantified relative callose fluorescence at 6, 12, 18 and 24 HAI under heat stress (40°C), water stress and fluorescence microscopy to analyze the 3 and 24 HAI untreated spots. Comparatively, the 24HAI time point had a higher callose deposit compared to 6 HAI, and this difference is certified with extreme points microscopy. All treatments under stress had high callose deposition when compared to untreated throughout germination. Our results reveal that the stress response by callose deposition is a potential component of resistance. Callose, which can eventually influence the development of a future healthy seedling under environmental stresses can form the reinforcement that the cell wall needs during the germination stages.

KEYWORDS: GSL; Sprouting; Environmental stresses.



Area of concentration: Genomic Analysis

IDENTIFICATION AND CHARACTERIZATION OF NEW ANTIMICROBIAL PEPTIDES IN FRUITS OF THE *Capsicum* WITH INHIBITORY ACTIVITY AGAINST *Colletotrichum scovillei*

RESENDE, Larissa Maximiano¹; OLIVEIRA, Arielle Pinheiro Bessiatti Fava²; SOUSA, Lorrán Yves Machado de²; CARVALHO, Mariana Agueiras²; MELLO, Érica de Oliveira³; CARVALHO, André de Oliveira³; RODRIGUES, Rosana⁴; GOMES, Valdirene Moreira⁵

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Estudante doutorado, larissa.resende@live.com

²UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Estudante mestrado

³UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor Associado LFBM

⁴UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor Associado LMGV

⁵UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro – Professor Titular LFBM

The crop peppers presents great challenges due to diseases caused by fungi such as Anthracnose (*Colletotrichum* spp). The proteomic investigation of defense components can help to understand the mechanisms of plant resistance to pathogens and help to mitigate the impact of these diseases. Antimicrobial Peptides (AMPs) are low molecular weight proteins that have a broad spectrum of inhibitory activity against microorganisms. The objective of this work is to identify and characterize AMPs in the genus *Capsicum* and to evaluate the growth inhibition (IC) potential of the fungus *Colletotrichum scovillei*. The AMPs were extracted from the pericarp of *Capsicum chinense* peppers accession UENF 1751. The extract was submitted to the steps of ion exchange chromatography, molecular exclusion, and reversed phase in HPLC system for protein purification and mass spectrometry for characterization by AMP families according to similarity. A PIN II protease inhibitor was identified and named CcF4-Pin II, and at 50 µg.mL it was able to inhibit by 30% the enzymatic activity on the Bapna substrate. We evaluated the IC potential of the fungus *C. scovillei* with 2000 cells/well and found that CcF4-PinII at 200 µg.mL inhibits 31% of growth. Another fraction that has not yet been characterized, called F1, showed a strong IC of the same fungus. With only 25 µg.mL the percentage of CI was 44%. From now on, we will characterize and investigate the mechanism of action that this fraction causes in the inhibition of fungal growth through microscopic analyzes with fluorescent probes. With the results obtained, we hope to describe new antimicrobial peptides from *Capsicum*. And contribute to the studies of proteins with biotechnological potential to mitigate diseases caused by microorganisms as a tool to improve the management of pepper culture.

KEYWORDS: AMPs; Inhibition of fungal growth; Pepper.



Area of concentration: Plant Genetic Resources

IN VITRO GERMINATION AS A STRATEGY FOR CONSERVATION OF NATIVE GENETIC RESOURCES WITH ECONOMIC VALUE

GUTERRES; Suelen Martinez¹, GIRARDELLO; Gabriel Menegusso², BEISE; Dalvan Carlos³, OLIVEIRA; Joana Nascimento Merces de⁴, STEFENON; Valdir Marcos⁵; PESCADOR; Rosete⁶

¹Universidade Federal de Santa Catarina–Doutoranda PPGRGV suelenguterres1996@gmail.com

²Universidade Federal de Santa Catarina -bolsista PIBIC/CNPqgiraa33@hotmail.com

³Universidade Federal de Santa Catarina - Doutorando PPGRGV, Bolsista CAPES dalvanbio@gmail.com

⁴Universidade Federal de Santa Catarina - Mestranda PPGRGV, Bolsista CAPES ojoana140@gmail.com

⁵Universidade Federal de Santa Catarina - Bolsista de produtividade CNPq valdir.stefenon@ufsc.br

⁶ Universidade Federal de Santa Catarina - Bolsista de produtividade CNPq rosete.pescador@ufsc.br

The exuberance of shapes and colors, and their low maintenance demand and easy adaptation, make bromeliads popular among landscapers who recognize their potential economic value as an ornamental species. *Vriesea reitzii* Leme e Costa is an epiphytic bromeliad endemic to the Atlantic Forest, with great ornamental potential. The micropropagation of wild or ornamental bromeliads and the establishment of *in vitro* multiplication protocols allow the production of seedlings on a large scale for commercialization. Light is a very important factor in the development of plants as they are a source of energy in photosynthesis and have a photomorphogenic effect. This work aimed at investigating the influence of different light spectra on the germination of *Vriesea reitzii* seeds. *Vriesea reitzii* seeds were disinfected and germinated in an MS culture medium in the absence of PGRs, under different light spectra: fluorescent lamps and white, red, blue/red, or blue LED lamps. Seedlings germinated in the fluorescent light spectrum showed superior results in the variables number of germinated seedlings, several leaves, seedling height, root size, dry mass, and fresh mass. Regarding the pigment contents, the highest amount of chlorophyll *a* was observed in the germinated seedlings in the fluorescent light spectrum. The highest chlorophyll *b* and total chlorophyll levels were observed in seedlings germinated in the blue and white light spectra. The highest levels of carotenoids were observed in seedlings submitted to the blue light spectrum. In summary, we conclude that all treatments had similar germination rates, while the fluorescent spectrum was highlighted in the seedlings size variable when compared to other treatments. The total chlorophyll and carotenoids contents revealed high rates along with the light spectrum blue.

KEYWORDS: Micropropagation; Pigment content; LED lights.



Area of concentration: Plant Genetic Resources

PHENOLOGY OF PUMPKIN ACCESSIONS IN ALTA FLORESTA-MT, BRAZIL

BRAGA; Catiane dos Santos¹, LOPES; Danielle Vieira Rodrigues², SOUZA; Sérgio Alessandro Machado³

¹UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro - Bolsista CAPES, catianedsbraga@gmail.com

²UNEMAT - Universidade do Estado de Mato Grosso, danielierodriguesbio@hotmail.com

³UNEMAT - Universidade do Estado de Mato Grosso, sergiobioufpel@yahoo.com.br

Phenology analyzes morphological changes that are related to the culture cycle and is essential for plant breeding. To characterize the phenology of *Cucurbita moschata* Duchesne collected in Southern Amazon, eleven pumpkin accessions (UNEMAT 015, 016, 017, 018, 019, 020, 021, 022, 023, 024, and 025) were described using the following scale of scores: (0) floral bud emergence, (1) floral bud development, (2) floral bud developed, (3) floral bud one day before anthesis, (4) anthesis (5) initial fruit development, (6) final fruit development, and (7) mature fruit. The experiment was installed in field conditions in randomized block design, with four replications at the State University of Mato Grosso in Alta Floresta-MT. During the growing of the crop, temperatures ranged from 30 °C to 32 °C, while the total precipitation ranged from 203 mm to 321 mm. The accessions developed floral buds and flourished from November 2018 to February 2019. In March 2019, they reached the maturity of their fruits. Pumpkins are allogamous with monoecious flowers, consequently, the phenology is described for male and female flowers. The phenology for male flowers ranges from the appearance of the floral bud to anthesis. UNEMAT 017, 019, and 023 were the first accessions to achieve the complete male flowers phenology with an average of 23 days. UNEMAT 016 was the latest to complete the phenological stages (30 days). The female phenology ranges from the emergence of the floral bud to the total ripening of the fruit. UNEMAT 024 achieved in 57 days the phenological stages and was characterized as the earliest. The longest cycle, with an average of 93 days, was UNEMAT 018. All accessions reached the phenological cycle complete. The results will help to guide small farmers in the planning of their plantations, in addition to guiding new studies in the plant breeding field.

KEYWORDS: *Cucurbita moschata*; Phenology; Genetic Resources.



Area of concentration: Plant Genetic Resources

HAPLOID INDUCTION AND OBTAINING DOUBLE-HAPLOID IN SUPERSWEET CORN

LUCENA; Vitor Joaquim de¹, OLIVEIRA; Juliana Moraes Machado de², HODA; Otavio Gabriel Lalau³, FERREIRA; Josue Maldonado⁴, FREGONEZI; Bruno Figueiró⁵

¹UEL – Universidade Estadual de Londrina – Bolsista FAUEL, vitor.joaquim.lucena@uel.br

²UEL – Universidade Estadual de Londrina – Bolsista FAUEL, juliana.machado51@uel.br

³UEL – Universidade Estadual de Londrina – Bolsista FAUEL, otavio.gabriel@uel.br

⁴UEL – Universidade Estadual de Londrina – Bolsista CAPES, fregonezi.bruno@uel.br

⁵UEL – Universidade Estadual de Londrina – Departamento de Biologia Geral, josuemf@uel.br

Double-haploid synthesis has been widely used to speed up the process of inbred line production, in common corn. However, there are few reports of the use of the technology in supersweet corn. The objective of this work was the production of double-haploid lines and determine the induction rate of PI4003 inducer in crosses with different supersweet corn genotypes. Six genotypes of supersweet corn were pollinated by the inducer population PI4003 at an isolated area. The seeds obtained were classified as, diploid seeds with purple endosperm and embryo, putative haploid seeds with purple endosperm and non-purple embryo, and seeds without marking and with non-purple endosperm and embryo. In a greenhouse, the putative haploid seeds were sown in trays of 64 cells, containing turfa Sphagnum. At the V2-V3 stage, a roguing was performed on the most vigorous plants, leaving only haploid plants. The chromosomal doubling was realized by the injection of 100 µL/seedling solution of colchicine (0.125%) and DMSO (0.5%), 3 -5 mm above de shoot apical meristem. An average germination of 85.7% was obtained. The induction rates ranged from 2.3% and 38.7%, SD3005 population was the best number. Although, inside of putative haploids, truly haploid plants ranged from 3.4% and 36.7%, showing high false positive rates. An overall mean of chromosomal duplication success of 15.3% was obtained, generating fertile plants that produced double-haploid lines of supersweet corn.

KEYWORDS: *Zea mays var. saccharata*; Chromosomal doubling; Inbred lines.

