



IV Meeting Genetics and Plant Breeding of Rio de Janeiro

III INTERNATIONAL SYMPOSIUM ON GENETICS AND PLANT BREEDING

ABSTRACTS

November 05-07-2018

Convention Center Of Universidade Estadual
do Norte Fluminense Darcy Ribeiro-UENF

SCHEDULE



NOVEMBER 05, 2018

MORNING

- 8:00 - 9:00 am Registration
- 9:00 - 10:00 am Opening Session
- 10:00 - 10:30 am Coffee Break
- 10:30 - 11:30 am Lecture
"Soybean breeding in the genomic's era"
Speaker: PhD Steven J. Clough – USDA/University of Illinois

AFTERNOON

- 2:00 - 6:00 pm Mini Course
"Molecular tools to facilitate disease resistance breeding."
Speaker: PhD. Summaira Riaz - University of California - UC Davis



NOVEMBER 06, 2018

MORNING

- 8:00 - 12:00 pm Mini Course
"Molecular tools to facilitate disease resistance breeding."
Speaker: PhD. Summaira Riaz - University of California - UC Davis

AFTERNOON

- 14:00 - 15:00 pm Lecture
"Using genotypic selection strategies to accelerate the development of cassava varieties: the Embrapa's example"
Speaker: Dr. Eder Jorge de Oliveira - Embrapa Mandioca e Fruticultura
- 15:00 - 16:00 pm Lecture
"Cacao breeding in Brazil: Strategies and Achievements"
Speaker: Dr. Uilson Lopes - Comissão Executiva do Plano da Lavoura Cacaueira - CEPLAC

- 16:00 - 16:30 pm Coffee break
- 16:30 - 17:30 pm Lecture
"Twenty years of public Capsicum breeding for disease resistance at UENF"
Speaker: Dr. Rosana Rodrigues - Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF
- 17:30 - 18:30 pm Posters Presentation



NOVEMBER 07, 2018

MORNING

- 8:00 - 12:00 pm Mini Course
"Molecular tools to facilitate disease resistance breeding."
Speaker: PhD. Summaira Riaz - University of California - UC Davis

AFTERNOON

- 14:00 - 15 :00 pm Lecture
"Challenges for the management and control of plant viruses: understanding to combat"
Speaker: Dr. Marcelo Eiras - Instituto Biológico - SP
- 15:00 - 16:00 pm Lecture
"Grape breeding for disease resistance: above and below ground"
Speaker: PhD. Summaira Riaz - University of California - UC Davis
- 16:00 - 16:30 pm Coffee break
- 16:30 - 17:00 pm Lecture
"Rio Norte Sementes - Local seed company in association with UENF"
Speaker: Dr. Alexandre Pio Viana - Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF
- 17:00 - 17:30 pm Lecture
Functional Plant Breeding Journal – A new journal for breeders"
Speaker: Dr. Antônio Teixeira do Amaral Júnior - Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF
- 17:30 - 18:30 pm - Posters Presentation

Area: (Plant Breeding)

Genetic divergence of snap bean genotypes via multivariate analysis

Cruz, D.P.¹, Rocha, R.S.¹, Pereira, I.M.¹, Oliveira, T.R.A.¹, Sant'Anna, C.Q.S.S.¹, Chagas, J.T.B.¹, Gravina, L.M.¹, Gravina, G.A.¹, Jaeggi, M.E.P.C.¹, Entringer, G.C.¹, Santos, P.R.¹, Almeida, R.N.¹.

¹Agricultural Engineering Laboratory, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Snap bean is a very popular vegetable in Brazil and has shown promise in the Northwest region of Rio de Janeiro. However, one of the problems faced is the lack of specific cultivars for this region, therefore, breeding programs aimed at the highest yield of this species are necessary, to select and develop genotypes adapted to recommend to farmers. The objective of this work was to evaluate the genetic divergence in snap bean genotypes using multivariate analysis. The experiment was conducted at the Instituto Federal Fluminense-Campus Bom Jesus do Itabapoana-RJ. The experimental design was a randomized block with four replicates and 30 treatments. The plot was composed of 4 lines of 5m with spacing between lines of 1.0m and 0.5m between plants. Planting was done by sowing three seeds in each hole, ten days after planting, thinning was performed, leaving one plant per hole. Fifteen days after emergence the plants were tutored with bamboo and wire. The analyzes were performed based on the eight central plants of the row. Fertilizers followed the guidelines of soil analysis results. The cultural and phytosanitary treatments were done according to the recommended ones for the culture and the irrigation was done by sprinkling. The multivariate analysis was performed based on canonical variables for average number of snap per plant (ANSPP); average weight of snap per plant (AWSPP); average snap weight (ASW); number of seeds per snap (NSPS); length of snap (LS); snap width (SW); plant height (PH); total snap number (TSN); total snap weight (TSW); germination (GERM); flowering (FLOR); weight of one hundred seeds (WHS); snap productivity (SP); total number of seeds (TNS) and seed yield (SY). The first two canonical variables represented about 74.06% of the total variance. The dispersion plot allowed the formation of three genotypic groups based on the Mean Euclidean Distance, producing satisfactory interferences.

Key-words: genotypes, *Phaseolus vulgaris* L., canonical variables.

Support: CNPq, CAPES e FAPERJ



Plant Breeding

Quantification of the genetic order in passion fruit BC₂ genotypes

Vidal, R. F.¹, Viana, A. P.¹, Preisigke, S. da C.¹, Gonçalves Junior, D. H.¹, Santos, E. A.¹

¹ Plant Breeding Laboratory, Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The cultivation of passion fruit (*Passiflora edulis*) has been occupying a tropical fruit species being an agricultural alternative for small producers. The genus *Passiflora* is a large number of species being about 120 native of Brazil. Due to the great variability, the knowledge of genetic diversity between genotypes is important for the plant breeding, because there is a selection of superior genotypes in the segregating generations. The methods of diversity have been much more effective at improving average Euclidean distance. This method measures the dissimilarity between the genotypes by showing the genetic distance between them. In view of the exportation, the objective of this work is to estimate a genetic distance of 57 genotypes of full sibling families from passion fruit from the second generation of backcross (BC₂). The experiment was conducted in the experimental area of the Antonio Sarlo agricultural school, in the municipality of Campos dos Goytacazes-RJ. The characterization was performed based on eight characteristics being them of fruits of weight (mm), diameter (mm), shell thickness (g), pulp weight (g), seed number, seed size (mm) and total soluble solids content (Brix °). The data were submitted to grouping analysis by the UPGMA method, from the dissimulation matrix obtained by the Euclidean distance, with the aid of the Genes program. Genetic diversity was observed between the 57 genotypes which were grouped into 5 distinct groups being 3 groups with one genotype, group with 2 genotypes and the group with the other genotypes. Genetics 28 and 27, although familiar with BC₂, were in distinct groups. Group three consisted of two genotypes from different families. In the group with the highest number of genotypes is the recurrent parent (*Passiflora edulis*). This fact may be an indicator that the genotypes of BC have more and more genetically recurrent genitor. It is observed that there was genetic variability among and within the evaluated families, indicating, therefore, that it is possible to make selection within families.

Key-words: *Passiflora edulis*, dissimilarity, genome recovery

Support: UENF, FAPERJ, CAPES



Area: Plant Breeding

**Mature endosperm culture for the production of triploid plants of the hybrid (*Passiflora edulis*
x Passiflora setacea)**

Renan Carrari dos Santos¹, Rafael Walter¹, Otalício Damásio da Costa Júnior¹, Lidiane Miranda da Silva¹, Rodrigo Sobreira Alexandre³, Alexandre Pio Viana², Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia (LFIT) and ² Laboratório de Melhoramento Genético Vegetal (LMGV), Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamago, 2000. 28013-602, Campos dos Goytacazes, RJ, Brasil.

³ Departamento de Ciências Florestais e da Madeira (DCFM), Centro de Ciências Agrárias e Engenharias (CCAEE), Universidade Federal do Espírito Santo, UFES, Jerônimo Monteiro, ES, Brasil.

Endosperm culture is considered a direct method for the production of triploids. Triploid plants have larger organs, with greater capacity of biomass production and storage of photoassimilates. Triploid plants have great economic value and are also useful for the development of new cultivars. The objective of this work was to verify the effect of Thidiazuron (TDZ) on the endosperm culture of the *P. edulis* ‘UENF Rio Dourado’ x *P. setacea* hybrid for the production of triploid plants. In the laminar flow chamber the hybrid seeds without the integument were disinfested and later sectioned for the removal of the endosperm. Then, the endosperms were inoculated in culture medium containing the MS salts with 3% sucrose, 100 mg L⁻¹ myo-inositol and different concentrations of TDZ (0.00, 2.27, 4.54, 6.81 and 9.08 µmol L⁻¹). The experiment was conducted in a completely randomized design, with 5 replicates. Each replicate was composed of a Petri dish (90 x 15mm) with 10 explants. The Petri dishes were kept in a culture room with controlled temperature and luminosity. The evaluation was performed after 45 days. The callus percentage, callus diameter, callus texture, callus color and shoot formation were evaluated. There was callus formation in all treatments with TDZ. There was no difference in TDZ treatments for all variables, except for shoot formation. In TDZ treatments the diameter varied between 6.53 and 8.50 mm. The calluses from all treatments were compact. The calluses from all treatments with TDZ presented dark color, indicating a greater organogenic potential. The formation of new shoots was observed only in the treatment with 4.54 µmol L⁻¹ of TDZ. This is the first work describing the production of triploid plants from the endosperm culture in hybrids of *P. edulis* and *P. setacea*.

Key-words: polyploids, TDZ, passionfruit.

Support: UENF. This study was funded in part by the Coordination of Improvement of Higher Education Personnel - Brazil (CAPES) - Finance Code 001.



Area: Basic Genetics

Prospection of *Arabidopsis thaliana* natural accessions with high efficiency of association with *Gluconacetobacter diazotrophicus* Pal-5

Fabiano Silva Soares¹, Gonçalo Apolinário de Souza Filho¹

¹ Laboratory of Biotechnology, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Gluconacetobacter diazotrophicus is a plant growth-promoting bacterium potentially useful for agricultural production and for the phytoremediation of pollutants. Due to such high potential, it is important to understand the genetic and molecular bases involved in the interaction process with the plant, in order to potentiate the association. *Arabidopsis thaliana* is appropriate for this type of study because it is colonized by *G. diazotrophicus*, in addition to has a wide natural variation of ecotypes. We evaluated the growth promotion of a collection of 74 natural accessions of *A. thaliana* inoculated with *G. diazotrophicus* Pal-5. Seeds of *A. thaliana* natural accessions were surface-sterilized in 96% ethanol for 1 min and 2.5% NaCl for 10 min, washed six times with distilled water and then placed at 4 °C for 2 days to break dormancy. Seeds were planted into disposable cups (80 mL) containing a mixture of sterile vegetable soil and vermiculite (3:1, volume) and were placed in a growth room (23 °C, 12/12 h photoperiod, and relative humidity of 60%). *G. diazotrophicus* Pal-5 with DsRed Fluorescent Protein-labeled was grown on DYGs agar plates supplemented with kanamycin (50 µg/mL) and streptomycin (200 µg/mL) at 30 °C for 24 h. A single colony was transferred to liquid DYGs media and incubated at 30 °C, 250 rpm until it reaches the optical density (DO_{600nm}) 1.0. Twenty mL of *G. diazotrophicus* Pal-5 (10⁴ CFU/mL) in DYGs solution was inoculated to 10 days-old plants. The same amount of DYGs solution was used as control. There was one plant in each cup and six cups for each treatment. Plant leaf area was measured at 20 and 26 days after-inoculated. The fresh and dry weight of shoot and root parts was measured at 26 or 32 days after-inoculated. The *t*-test was conducted to compare the difference in plant growth promotion of the treatments and controls for each to *Arabidopsis* accessions. We observed that 53 natural accessions were responsive to the inoculation of the bacterium for at the very least one parameter evaluated. Among these, the accessions 0-A3 and 0-A7 showed repression of plant growth, while 0-C9, 1-E8 and 1-E10 showed promotion of plant growth compared to their respective non-inoculated controls. The results suggest that the plant response to *G. diazotrophicus* inoculation is genotype dependent. The crossbreeding between these contrasting genotypes and the progeny analysis from this crossing may reveal genes involved in the plant-bacteria interaction.

Key-words: Plant growth promoting bacteria, arabidopsis, leaf area.

Support: CAPES, CNPq, FAPERJ, FINEP and UENF.



Area: Plant Breeding

Title: Potential of resistance to *Bipolaris maydis* in popcorn hybrids originated from topcross crossing

Jhean Torres Leite¹, Divino Rosa dos Santos Junior¹, Rafael Nunes de Almeida¹, Valter Jario de Lima¹, Samuel Henrique Kamphorst¹, Talles Oliveira Santos¹, Rosimeire Barboza Bispo¹, Antônio Teixeira do Amaral Junior¹

¹Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Foliar diseases in the popcorn crop cause great investments in phytosanitary control, management techniques and adaptation of the growing season. This fact, obtaining genotypes resistant to the main diseases becomes a viable and sustainable alternative. Therefore, the aim of this study was to evaluate hybrids of popcorn from the topcross crossing, in terms of resistance to *B. maydis*. For this purpose, 15 inbred lines of the Active Germplasm Bank of UENF - L681, L683, L684, L685, L686, L688, L689, L690, L691, L692, L693, L694, L695, L696 and L204 were used in cross with the L270 tester. The experiment was conducted in a randomized complete block design with three replicates. The following characteristics were evaluated: spike weight (SW), in t/ha, and incidence of disease (ID), in percentage of injured leaf (Agrocères' scale). For data decomposition, a variance analysis was performed, with subsequent grouping of means by the Scott Knott test (5%). From the analysis of variance, it was possible to identify a significant difference between the treatments for the ID, showing presence of genetic variability among the evaluated hybrids. On the other hand, the SW characteristic did not present the same result, and it was not possible to identify more productive hybrids associated with this variable. The means test for the ID characteristic presented the formation of two groups, namely: L681xL270, L682xL270, L686xL270, L689xL270; and L692xL270, L691xL270, L696xL270, L694xL270, L204xL270, L693xL270, L695xL270, L688xL270, L684xL270, L683xL270, L685xL270, with higher and lower incidence respectively. The first group of hybrids presented ID ranging from 17.87 to 29.67%, while the second group ranged from 5.8 to 14.37%. The average estimate for SW among the evaluated hybrids ranged from 3.72 to 6.56 t/ha, but did not present a difference in the clustering test, forming only one group with the same denomination. However, the hybrids presented potential resistance to foliar diseases and, due to the importance of the study, it is necessary to assess the productivity and stability.

Key-words: Disease, helmintosporiosis, inbred line.

Support: This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brasil (CAPES) – Finance Code 001, and Faperj

Area: Plant Breeding

Silver nitrate in in vitro minimal growth of *Passiflora setacea* and *Passiflora edulis*

Roberta Aparecida de Sales¹, Rafael Walter¹, Naiara Lopes Brito¹, Renato Gobbi Vettorazzi¹, Clarissa Ribeiro Baptista, Renan Carrari dos Santos¹, Andressa Leal Generoso¹, Otalício Damásio da Costa Júnior¹, Lidiane Miranda da Silva¹, Vinicius de Freitas Manhães¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

In vitro minimal growth is a method of germplasm conservation for a short period of time. Frequent subcultures of the plant material are required in this technique. Since in vitro culture is effected inside closed flasks, the gas exchanges are hampered. Many gases like ethylene tend to accumulate inside the flasks. The addition of silver nitrate to the culture medium may inhibit the action of ethylene, retarding senescence and promoting in vitro conservation of *Passiflora*. Thus, the objective of this work was to verify the effect of silver nitrate (AgNO₃) on the in vitro minimal growth of *P. setacea* and *P. edulis*. Nodal segments of in vitro germinated seedlings were inoculated into flasks containing MSM medium containing 50% of the mineral salts, 3% of sucrose, 0,5 mg L⁻¹ of BA, 100 mg L⁻¹ of myo-inositol, pH adjusted to 5.7 before the addition of 7 g L⁻¹ of agar. The experiment was conducted in CRD in a 5x2 factorial scheme with five concentrations of AgNO₃ (0, 2, 4, 6 and 8 mg L⁻¹) added to the culture medium before autoclaving and two species (*P. setacea* and *P. edulis*), with five replicates. Each replicate was composed of a flask containing six explants. At the end of 68 days the survival, the plant height (PH), the shoot dry matter mass (SDMM) and chlorophyll *a* fluorescence (Fv/Fm) were evaluated. The survival was high in all treatments, except for the treatment without AgNO₃ for *P. edulis*. For PH and SDMM, for *P. edulis* it is observed that there were no differences between the treatments with AgNO₃. For *P. setacea*, the concentrations of 2 and 8 mg L⁻¹ of AgNO₃ promoted a lower PH and a lower SDMM. For *P. edulis* and *P. setacea*, Fv/Fm values demonstrate that the plants of all treatments were stressed due to in vitro culture, except for the treatment with 8 mg L⁻¹ of AgNO₃ for *P. edulis*. The ethylene must have been accumulated in all flasks, with 8 mg L⁻¹ of AgNO₃ for *P. edulis* being the most efficient concentration to inhibit the synthesis of ethylene. Under the conditions of this work, AgNO₃ can be used to inhibit the effects of ethylene on *P. edulis* and on *P. setacea*.

Key-words: Passionfruit, ethylene, germplasm conservation.

Support: This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001.



Area: Plant Breeding

Investigation of the genetic diversity of common bean (*Phaseolus vulgaris* L.) cultivars using molecular markers

Pablo Diego Silva Cabral¹, Gessica Ferreira da Costa¹, Leandro Pavani de Oliveira¹, Joao Hilario Neto¹, Jose Adalberto Gomes Alves¹

¹ Instituto Federal de Educação, Ciência e Tecnologia Goiano – IF Goiano, Rodovia Sul Goiana, Km 01, Zona Rural. 75901-970, Rio Verde, GO, Brasil.

The common bean (*Phaseolus vulgaris* L.) is a widespread crop in Brazil with dietary and economic importance, and it is cultivated primarily through family farming. Knowledge of genetic variability in landraces and improved bean cultivars is essential to explore the existing diversity, identify superior genotypes adapted to the climatic conditions of specific regions, and support genetic improvement strategies. Estimates of genetic diversity can be obtained using DNA molecular markers, and ISSR (inter simple sequence repeat) markers are widely used. The objective of this work was to evaluate the genetic diversity of 57 common bean genotypes, including accessions provided by the Brazilian Agricultural Research Corporation (EMBRAPA - Wheat), local genotypes of the Fortaleza community (Muqui-Espírito Santo) and commercial cultivars, using ISSR molecular markers. A total of 11 primers were used, generating 51 fragments, of which 39 were polymorphic (76.4%). The Polymorphic Information Content (PIC) ranged from 0.19 to 0.48, with a mean of 0.36. There was an unequal distribution between genetic distances, ranging from 0.00 to 1.0, and a mean of 0.44, evidencing wide genetic variability. The Pérola cultivar stood out as it showed the highest mean dissimilarity (0.76). The cluster analysis revealed the formation of eleven groups with a tendency to cluster genotypes by the region of origin and growth habit. There was a wide genetic diversity between the genotypes of the Fortaleza community and a narrower diversity for the EMBRAPA and commercial cultivars. ISSR markers have been shown to be efficient in quantifying the genetic diversity of genotypes, and the most divergent markers may be recommended for future conservation in germplasm banks.

Key-words: Bean plant; Molecular marker ISSR; Variability; Genetic breeding.

Support: FAPEG, CAPES and CNPq

Area: Plant Breeding

Agronomic performance of red and white rice cultivars in Rio de Janeiro State

Rafael Hydalgo Passeri Lima¹, Bruna Rafaela da Silva Menezes², Maurício Ballesteiro Pereira²,
Luiz Beja Moreira³

¹ Federal Rural University of Rio de Janeiro (UFRRJ) – Campos dos Goytacazes Campus, Rodovia do Açúcar, Km 5. 28022-560, Campos dos Goytacazes, RJ, Brazil.

² Department of Genetics, Institute of Biology and Health Sciences – UFRRJ, BR - 465, Km 7. 23.897-000, Seropédica, RJ, Brazil.

³ Department of Plant Science, Institute of Agronomy – UFRRJ, BR - 465, Km 7. 23.897-000, Seropédica, RJ, Brazil.

Red rice is a special type of rice with greater added value compared with white rice, which is due mainly to its functional properties such as high antioxidant content. However, red rice cultivars are usually less productive than white rice cultivars, and this is related to the fact that the latter have already undergone several breeding programs aimed at elevating traits associated with increased yield and better adaptability to different growing environments. The objective of this study was to evaluate agronomic traits of two red rice cultivars by comparing them with two white rice cultivars in three municipalities of Rio de Janeiro State. Eight traits were analyzed: panicles.m⁻², spikelets.panicle⁻¹, spikelet fertility, 100-grain weight, yield, stem length, panicle length, and plant height. The experiments were conducted in a rainfed system, with supplementary irrigation, under an organic production management. The trials were carried out in the 2016/2017 crop year, in three municipalities of Rio de Janeiro State, namely 1 - Campos dos Goytacazes; 2 - Seropédica; and 3 - Pinheiral. A randomized-block experimental design with four treatments and five replicates was adopted. Treatments were represented by the red rice cultivars ‘ENA AR-1601’ and ‘Vermelho Virgínia’ and the white rice cultivars ‘BRS Esmeralda’ and ‘IAC 201’. Data were collected from a usable area of 4 m² from each plot and subjected to individual analysis of variance for each location, and means were compared by Tukey’s test at the 5% probability level. After homogeneity of variances was detected, a combined analysis of data from the three locations was undertaken. No significant G×E interaction effect was observed for panicles.m² or yield. Cultivars ‘ENA AR-1601’ and ‘Vermelho Virgínia’ exhibited the highest means for those traits, showing higher values in Campos dos Goytacazes and Seropédica, but no statistical difference from cultivar ‘BRS Esmeralda’ in Pinheiral.

Key-words: yield, rainfed condition, *Oryza sativa*



Area: (Plant Breeding)

Phenotypic variability based on emergence variables among bean genotypes in the Northeast of Goiás

Alex Roniel Alves dos Santos¹, Raquel Gonçalves Silva¹, Daiza Dorn Sonda¹, Thauana Caroliny Souza Panasiuk¹, Jôsie Cloviane de O. Freitas¹, Fernando Higino de Lima e Silva², Eileen Azevedo Santos³

¹ Department of Plant Breeding, Universidade Estadual de Goiás – UEG, Av. Sra. de Santana, 598 - St. Santa Luzia, Posse - GO, 73900-000. ² Instituto Federal Goiano - Rodovia Sul Goiana, Km 01, Zona Rural - Rio Verde – Go. ³ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Beans are one of the most important constituents of the Brazilian diet for being an excellent protein source, carbohydrates and iron. There is great variability among cultivars and varieties of beans. The characterization of such variability may contribute to increase efficiency in conservation and the use of that germplasm for the breeding programs. For this, the use of high quality seeds is necessary for the success of the characterization. The aim of this work was evaluate the percentage emergence (EP) and emergence speed index (ESI) of 14 access of the genus *Phaseolus* and *Vigna*. The access were donated by small farmers from Goias northeast. The experiment was performed in styrofoam trays with 128 cells filled out with commercial substratum. For this, a total of 48 seedling was obtained for each cultivar and access. The evaluations for the analysis were carried out daily during a period of 19 days, counting the number of seedlings emerged. EP values above 80% were observed for genotypes evaluated. High phenotype variability was observed for the character ESI. The lowest ESI (3.5) was obtained for the cowpea. The highest ESI (7.9) was observed for the red bean. In conclusion the emergence percentage for all genotypes was high. For the ESI characteristic, there is variability, which is probably associated with the genetic divergence among the genotypes evaluated.

Key-words: *Phaseolus*, *Vigna*, germplasm characterization, emergence speed index, genetic resources.

Support: UEG

Area: Plant Breeding

Seed cryopreservation of *Cattleya tigrina*, a Brazilian orchid threatened with extinction

Renato Gobbi Vettorazzi¹, Virginia Silva Carvalho¹, Roberta Aparecida de Sales¹, Clarissa Ribeiro Baptista¹, Naiara Lopes Brito¹

¹Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The main limitation for cryopreservation of orchid seeds lies in the specific response of the different genotypes to cryopreservation protocols, making it difficult to generalize and develop a universal cryopreservation protocol. Therefore, the objective of this work was to verify the efficiency of the vitrification method in cryopreservation of *C. tigrina* seeds. The flower was pollinated and after five months the mature capsule was collected for use in the cryopreservation experiment. The seed viability test by the tetrazolium method was 47.4% and the water content before cryopreservation was 49.35%. Each treatment consisted of five replicates; each replicate consisted of a cryotube. The vitrification procedure consisted of the addition of 1 mL of osmoprotection solution in cryotubes containing 0.015 g of seeds for 30 minutes. Then the excess of this solution was removed and the seeds were subjected to dehydration by exposure to vitrificant solution (PVS2) for 30 minutes and 1 hour (0°C), before being immersed in liquid nitrogen (LN) for 1 hour. After immersion in LN, the cryotubes were rapidly heated to 40°C for 2 minutes. The PVS2 was removed and the seeds were immersed in wash solution for 15 minutes. It was also tested the viability of cryopreservation of the dry seeds without the use of the vitrifying solution. After cryopreservation, the seeds of all treatments were submitted to the tetrazolium viability test and to the *in vitro* germination test, in flasks containing B&G[®] semisolid culture medium suitable for orchids, incubated in a culture room under controlled conditions. At 90 days after cryopreservation, the protocorms presented similar morphology, with presence of rhizoids in the basal portion and formation of leaf primordia in the apical portion. For each treatment the viability test corresponded to the germination test, confirming the consistency of the tetrazolium method. The highest percentage of germination was observed in the treatment of direct germination (Control 1) (48.78%), followed by treatment of 1 hour in PVS2 without LN (Control 2) (23%) and 1 hour in PVS2 before immersion in LN (22.76%). Direct immersion of seeds in NL without PVS2 and immersion for 30 minutes in PVS2 before immersion in LN presented low percentage of germination (0.01 and 2.12%), not being effective for the conservation of this seeds. The high water content of the seeds and the effect of exposure time to PVS2 contributed to these results. The use of PVS2 for 1 hour reduced the free water content of the seeds, avoiding the formation of ice crystals when immersed in LN and consequently increased the germination rate. Therefore, the use of PVS2 for 1 hour before immersion in LN was fundamental to increase the germination rate of *C. tigrina* cryopreserved seeds, under the conditions described in this work.

Key-words: Orchidaceae, vitrification, germplasm conservation.

Support: FAPERJ



Area: (Basic Genetics)

Somatic Embryogenesis in *Passiflora edulis* Sims cv. “UENF Rio Dourado”

Kaliane Zaira Camacho Maximiano da Cruz^{1,2}, Nadia Botini^{1,2}, Ellen de Moura Vale^{1,2}, Claudete Santa-Catarina³, Vanildo Silveira^{1,2}

¹Biotechnology Laboratory, Center for Biosciences and Biotechnology (CBB), Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ²Unit of Integrative Biology, Genomic and Proteomics Sector – UENF, Campos dos Goytacazes, RJ, Brazil. ³Laboratory of Cell and Tissue Biology, Center of Biosciences and Biotechnology (CBB) – UENF, Campos dos Goytacazes, RJ, Brazil.

Somatic embryogenesis is an efficient development pathway for the *in vitro* regeneration of plants and with high potential of integration with breeding programs, when associated with cryopreservation and genetic engineering. The aim of this study was to carried out the induction and maturation phases of somatic embryogenesis in *Passiflora edulis* Sims, cv. "UENF Rio Dourado", and to perform a histomorphological analysis in embryogenic and non-embryogenic callus. Zygote embryos were used as explants for induction of callus in MS culture medium supplemented with auxin and cytokinin. Induced cultures were submitted to maturation in MS culture media supplemented with activated charcoal (AC) and polyethylene glycol (PEG). The percentage of induction of cultures was 100%, with 60% of embryogenic and 40% of non-embryogenic callus. The maturation treatment PEG 6% presented the highest embryogenic callus maturation rate with 14 cotyledonary embryos per Petri dishculture. The maturation treatment AC 1.5 g/L presented a mean of 7.1 cotyledonary embryos and the control treatments and the combination of PEG/CA did not allowed the formation of somatic embryos. Histomorphological analysis showed that the embryogenic callus was formed by small and isodiametric clumps of cells containing prominent nuclei and dense cytoplasm; these clumps were round structures bounded by a layer of organized cells. In contrast, non-embryogenic callus was friable or soft and translucent and comprised large, highly vacuolated, elongated cells. In conclusion, PEG was important for the maturation process of somatic embryos, being the first report of this maturation agent during somatic embryogenesis in *Passiflora* sp.

Key-words: Somatic Embryos, Polyethylene Glycol, *In vitro* Morphogenesis.

Support: CAPES, CNPq, UENF.

Area: (Applied Genomics)

Regulation of proteins during the somatic embryos development of *Carica papaya* L. ‘Golden’

Nadia Botini^{1,2}, Kaliane Zaira Camacho Maximiano da Cruz^{1,2}, Ellen de Moura Vale^{1,2}
Ricardo Souza Reis^{1,2}, Felipe Astolpho de Almeida^{1,2}, Claudete Santa-Catarina³, Vanildo Silveira^{1,2}.

¹Laboratory of Biotechnology, Center of Biosciences and Biotechnology (CBB), State University of North Fluminense Darcy Ribeiro (UENF), Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ²Unity of Integrative Biology, Genomic and Proteomics Sector, (UENF), Campos dos Goytacazes, RJ, Brazil, ³Laboratory of Cell and Tissue Biology, Center of Biosciences and Biotechnology (CBB) – (UENF), Campos dos Goytacazes, RJ, Brazil.

Carica papaya L. is an important tropical fruit tree of Brazil, since the country is the second largest worldwide producer of papaya. In this scene, somatic embryogenesis appears as an important biotechnological tool with potential for clonal propagation and regeneration of genetically modified plants. Despite the great advances in somatic embryogenesis protocols, the factors that regulate the somatic embryos morphogenetic evolution in *C. papaya* throughout the different developmental stages are still unclear. This work aimed to identify differentially regulated proteins at the different stages of somatic embryos during maturation of embryogenic cultures of *C. papaya*. Somatic embryos at globular, cordiform, torpedo and cotyledonary developmental stages were isolated and protein were extracted with urea/thiourea method. Samples desalted, trypsin digested, and analyzed in a nano LC-MS/MS mass spectrometer. Proteomics data were analyzed with Progenesis QI v.2.0 and the functional classification was performed using Bast2GO v4.1. Comparative proteomic analysis resulted in 495 identified proteins, with 48 differentially regulated. In the comparison between globular embryo and torpedo stages, 22 protein were upregulated and 24 downregulated. The comparison between torpedo and cordiform stages were observed 10 upregulated and 03 downregulated and in the comparison between the cordiform embryo and cotyledonary stages 2 upregulated and five downregulated. Differentially regulated proteins were classified into five classes according to the biological process, with the most representative were cellular processes, followed by metabolic processes, stimulus responses, and organization of cellular components or biogenesis. The differential regulation of these proteins in the different stages of development of the somatic embryos indicates that they can be candidates to act directly in the processes of the morphogenetic competence during the process of somatic embryogenesis.

Key-words: Morphogenesis, Somatic embryogenesis, Proteomics.

Support: CNPq, FAPERJ, CAPES.



Area: Plant Breeding

Genetic Diversity Among *Anacardium othonianum* Rizzini Mother Trees in the Goiás State

Fernando Hígino de Lima e Silva¹, Valéria Ferreira Oliveira¹, Fabiano Guimarães Silva¹, Paulo Sérgio Pereira¹, Mariana Buranelo Egea¹.

¹ Instituto Federal Goiano – IF Goiano, Rodovia Sul Goiana, Km 01, Zona Rural | Rio Verde – GO.

The caju-de-árvore-do-cerrado (*Anacardium othonianum* Rizzini) belongs to the family Anacardiaceae and is a plant with wide distribution in the Brazilian Cerrado, besides economical and social importance to the local population. Studies of the genetic and phenotypic variability of the native populations of this specie assists in strategies for conservation and breeding. The objective of this study was to quantify the genetic diversity by the physical, chemical and physicochemical traits of the *A. othonianum* Rizzini in thirty mother trees from a population of the northwestern goiano, municipality of Montes Claros de Goiás - Goiás. For this, the Euclidean Distance measurements were estimated and the cluster analysis obtained by the UPGMA method. A high variability was observed among the mother trees evaluated. Clustering by the hierarchical clustering method UPGMA formed four groups: group I, formed by one access; group II and group III, formed by tree access and group IV, formed for twenty-three access. The access 01 (group I) has more distinct genetic material and presented bigger dimensions of cashew apple. Peduncle mass, fruit width, SS/TA, a*, flavonoids concentration and pH were the main variables that contributed to the dendrogram groups formation. The cophenetic correlation coefficient for the hierarchical clustering method UPGMA was 0.82 ($p < 0.01$). There is genetic variability among the studied accesses, which makes it possible to indicate more promising accessions.

Key-words: cashew, native fruits, multivariate analysis, cluster

Support: FAPEG, CAPES and CNPq



Area: Plant Breeding

Use of SPAD - 520 in the evaluation of leaf chlorophyll content in popcorn inbred lines submitted to water stress

Rosimeire Barboza Bispo¹, Talles de Oliveira Santos¹, Valter Jáiro de Lima¹, Samuel Henrique Kamphorst¹, Divino Rosa dos Santos Júnior¹, Jhean Torres Leite¹, Fernando Rafael Alves Ferreira¹, Eliemar Campostrini¹, Antônio Teixeira do Amaral Júnior¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Popcorn, although widely appreciated in the country, requires a detailed physiological study, associated with water deficiency, that allows its efficient use in breeding programs. The studies of secondary traits shown good alternative to evaluate and characterize genotypes in different environments. The green index obtained by measurements of transmittance by the relative concentration of chlorophyll SPAD - 502 (*Soil Plant Analyser Development*), is a characteristic frequently monitored under several stresses to evaluate the *stay-green* effect in some cultures. The method is promising, inexpensive, easy to operate, non-destructive, allowing *in situ* assessments and providing results that allow its use as an evaluation criterion. The objective was to evaluate the relative concentration of chlorophyll by SPAD in popcorn inbred lines submitted to the water stress obtained from the Popcorn Germplasm Bank of the UENF. A total of 10 inbred lines (L61, L71, L65, L63, L75, L76, P6, P2, P7 and P3) were evaluated in a randomized complete block design with three replicates. The variable analyzed was the relative concentration of chlorophyll by SPAD obtained by reading three leaves at different plant heights: First leaf being the third below the tassel, Second (2nd) leaf below the insertion of the first ear and Third (3rd) leaf 3, two leaves below of the first ear. Data were submitted to analysis of variance and means were compared by the Scott Knott test at 5% probability. The results showed that there was a significant difference between the different leaves. In inbred lines L71, P2, P7 and P3, the mean for the SPAD of 3rd leaf differed from the means of First and 2nd leaves. In relation to the comparative analysis between the inbred lines, First leaf formed two groups with significant differences, being the first group composed of the L61, L71, L65 and L63; and the second groups contained the remaining others inbred lines. For 2nd leaf there were four groups, the first group being composed by the L61 and L63, the second group by the L71, L65 and L75, the third group by the P6, P2, P7 and P3 and the fourth group formed only by the L76 inbred line. For 3rd leaf, three groups were formed, the first group being composed of the L61 and L63, the second group formed by L71, L65, L75 and P6, and the third composed by the remaining inbred lines. According to the results obtained it is recommended for future studies with popcorn the realization of the evaluations in 2nd leaf and 3rd leaf, since these show difference in the relative concentration of chlorophyll by SPAD. Inbred lines L76, P2, P3, P6 and P7 showed the lowest means of SPAD when submitted to water stress in relation to the other strains.

Key-words: *Zea mays*, *stay-green*, green index.

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Area: Plant Breeding

Seed germination of segregating families from the passion fruit first backcrossing generation

Deurimar Herênio Gonçalves Júnior¹, Sandra da Costa Preisigke¹, Moisés Ambrósio¹, Ravena Ferreira Vidal¹, Eileen Azevedo Santos¹, Durval Félix da Silva Netto¹, Alexandre Pio Viana¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Passion fruit, *Passiflora edulis* Sims, is a fruit known for its characteristic natural flavor and medicinal purposes, is consumed mainly as juice. Brazil is the largest consumer and producer of the species. Seed dormancy is an important adaptive mechanism in many species and is generally lost during plant domestication because of selection that occurs through the collection and planting of seeds. The work aim was to evaluate the seeds germinative potential of full-siblings families from the recombination of RC₁ genotypes. It was compared the germinative potential of three families (F₁, F₂ and F₃) of full siblings from the recombination of the best genotypes for the characteristics resistant to the CABMV and productivity of the first backcrossing generation. To that end, 200 seeds from each crossing were sown in polystyrene trays and then placed in an automatic fog chamber for 5 weeks, each week the germination percentage of each family was evaluated. At the end of the fifth week, the germination percentage of family F_{FS2} was the highest, with 76%, followed by families F_{FS1} and F_{FS3} with 71% and 67%, respectively. The results also show that it is ideal to transplant the seedlings to larger containers in the fourth week after sowing, since there was a decrease in the germination of all families after this period. It's concluded that family F_{FS2} has the greatest germination potential among the three full-sib families evaluated for this characteristic.

Key-words: *Passiflora edulis*, seed dormancy, selection, CABMV.

Support: CNPq, CAPES, FAPERJ, UENF.



Area: (Plant Breeding)

Minimum number of assessment times to incidence of black-spot in leaves of papaya

Ramon de Moraes¹, Marcelo Vivas¹, José Tiago Barroso Chagas¹, Helenilson de Oliveira Francelino¹, Tiago Silva Jorge¹, Renato Santa Catarina, Adriana Azevedo Vimercati Pirovane

¹ Author affiliations (Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The number of measurements required for characteristics related to the genetic resistance of papaya becomes substantial in the condition that the evaluations require great personal effort, trained professionals and financial resources so that the obtained results are consistent. To increase the efficiency in the selection and recommendation of superior genotypes for the resistance to black-spot in papaya requires an adequate evaluation at field level. To evaluate the minimum number of measurements, this study used a randomized block design with six genotypes and four replicates. It was quantified in which leaves the first black spot symptoms emerged (FS), the incidence (%) of leaves with black spot symptoms (IBS), the severity of black spot on the fifth leaf (SBS5L) and on the leaf with axil attached at the first open flower (SBSFO). For the estimation of these parameters, disease intensity was quantified using four different methods: ANOVA, CPMCOV, CPMCOR, AEMCOR. We consider that between one evaluation and another in experiments that quantify diseases can be found a very high amplitude in the intensity, so, it should be prioritized then, by a characteristic that presents a smaller n and greater R², so that it is possible to obtain a characterization of the study material with a minimum reliability of the data, using the shortest possible time. In this work, we will consider a coefficient of determination equal to ninety percent. The characteristics IBS and SBSFO stood out for having a low number of measurements 5 and 3 measurements respectively, considering the principal correlation components method, thus qualifying these characteristics as excellent in the evaluation of attributes related to resistance to black-spot in papaya.

Key-words: *Asperisporium caricae*, genetic resistance, field control, *Carica papaya*,

Support: FAPERJ, UENF.



Area: (Applied Genomics)

Recurrent Genomic Selection in popcorn via different marker SNPs densities

Ismael Albino Schwantes¹, Janeo Eustáquio de Almeida Filho¹, Pedro Henrique de Araújo Diniz¹,
Antonio Teixeira do Amaral Junior¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Recurrent Selection (RS) increase the frequency of favorable alleles for economically important crop traits, which in the case of popcorn are the popping expansion and grain yield. However, it requires a lot of time, since each selection cycle demand three stages: progenies obtainment, evaluation and recombination of the superior families. With the use of the Recurrent Genomic Selection (SRG), the time required for each selection cycle can be shortened, as it enables the evaluation and recombination phases to be performed simultaneously, reducing the time needed to obtain each cycle for one harvest season. However, in the genomic selection dense panels of SNPs markers are used, which makes the cost of selection high. By this, the present study aim was to obtain selective accuracy using different SNPs markers densities. Grain yield (GY) and popping expansion (PE) were evaluated and field trials were carried out with 98 S₁ progenies, in two locations, under incomplete block design with three replications. The parents of these progenies were genotyped with a panel of 21.442 SNPs. Using Plink software, three filters were performed in the sequence: a) withdrawal of individuals with > 10% missing data; b) SNP discharge with > 5% missing data; and c) SNP discarding with Minor Allele Frequency-MAF <5%, resulting in 10,507 SNPs. From this point, several scenarios with reduction of the SNPs panel were tested. The Genomic best linear unbiased prediction (GBLUP) method was used to obtain the results. Results have demonstrated that the use of ~ 4,000 SNPs presented selective accuracy similar to the use of 10,507 SNPs. It is then concluded that considerable cost reduction can be achieved by using a reduced panel of SNPs.

Key-words: SNPs, GBlup, Popcorn

Support: Capes, Faperj

Area: Plant Breeding

Acibenzolar-s-methyl in the incidence and morphological characteristics of papaya genotypes inoculated with *Phytophthora palmivora*.

Tiago Silva Jorge¹, Silvaldo Felipe da Silveira¹, Marcelo Vivas², Luciana Aparecida Rodrigues³,
Laura Mathias Barroso¹, Josiane Leal Knupp¹

¹Department of Entomology and Plant Pathology, ²Department of Agricultural Engineering, ³Department of Soil Science, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The aim of this work was to demonstrate the effect of acibenzolar-s-methyl (ASM - a plant resistance chemical inducer) on the incidence of foot rot and on root characteristics of 14 papaya (*Carica papaya* L.) genotypes ('Tainung 01', Maradol, Golden, UC01, UC10, UC12, UC14, UC16, Sekati, JS -12, SS72-12, 36/7, 41/7 and 19), submitted or not to *Phytophthora palmivora* (*Pp*) zoospore suspension inoculation. The experiment was conducted in randomized blocks, arranged in 14x4 subdivided plots (ASM; without ASM and *Pp*; with *Pp*; and with *Pp*+ASM), with three replicates. The seedlings were growth in 1:1 (soil:sand) substrate in 290 cm³ tubes. The 20mg of the ASM per liter of water was sprayed until complete leaf coverage 3 d before pathogen inoculation and when the seedlings reached 60 days after planting. The pathogen was inoculated by adding 5mL of the 8x10⁴ sporangium's suspension per tube. In the inoculated plots, the incidence of dead seedlings was evaluated, and in the plots without *Pp* inoculation, the effect of ASM on root characteristics (length, surface area, volume) and plant height were evaluated. The data were analysed in the R statistic environmental and 5% of significance was found for major variables, including genotype x inducer interaction. The 'Tainung 01' was the only genotypes which increase its roots variable means, while for the others genotypes there was a decreasing in roots attributes in response to ASM sprays. However, considering the inoculated plots, there was no difference between the plots with or without ASM sprays. This is due probably to the high inoculum concentration used, culminating in the death of all the inoculated seedlings between seven to eleven days after inoculation. The 'Tainung01' hybrid presented the best root response to the ASM, being considered potential for further experiments involving resistance induction to papaya foot rot disease.

Key-words: Foot rot, *Carica papaya* L.

Support: Caliman Agrícola S/A, CAPES.



Area: (Plant Breeding)

Nodulation and productive potential of precocious black beans in the municipality of Macaé/RJ.

Larissa Jaina da Silva de Oliveira¹, Benedito Fernandes de Souza Filho², Silvino Amorim Neto², Paulo Ricardo dos Santos¹, Wanessa Francesconi Stida¹, Alexandre Gomes de Souza¹, Ana Kesia Faria Vidal¹, Maxwell Rodrigues Nascimento¹, Richardson Sales Rocha¹, Rafael Souza Freitas¹, Rogério Figueiredo Daher¹.

¹Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

²PESAGRO-RIO/CEPAAR/Estação experimental de Campos, Avenida Francisco Lamego, 134, Guarus-28080-000-Campos dos Goytacazes-RJ, Brasil.

Early black beans (*Phaseolus vulgaris* L.) are being cultivated practically all over Brazil. And to implement the productivity, there is the use of biological nitrogen fixation, in which the element present in atmosphere is converted in a way that is assimilable to the plants, since, the species has the capacity to associate symbiotically with several bacteria of the group of rhizobia. The present work aims to evaluate and select early black bean genotypes based on the level of nodulation and yield, in the municipality of Macaé / RJ in two environments in the year of cultivation 2016. Two trials of precocious black beans were conducted in different environments and evaluated 22 bean genotypes. The experimental design was in randomized blocks, with three replications. The plots were established by four lines with a length of 4.0 m each, the distance between lines was 0.5 m and the sowing consisted of 15 seeds per linear meter. The plot area was 4.0 m², taking into account only the two central lines less the 1.0 m border, since the total plot area was 8.0 m². The experiments of environments I and II were inoculated with rhizobia, with the participation of Embrapa Agrobiologia and Embrapa Solos. Regarding inoculation, grades 1 were given for weak nodulation, 2 for medium nodulation and 3 for good nodulation. The analysis of variance of the data revealed that in the I environment, the nodulation and yield variables obtained significant effects at 1% probability by the F test, whereas in the II environment, only nodulation presented significance (5% probability, by the test F). The coefficient of variation for the yield of precocious black beans is in accordance with those found in the literature, indicating good experimental accuracy. On the other hand, nodulation presented higher values, revealing low precision, regarding this variable. The average grain yield varied between the two cultivation environments, this variation may be related to the rhizobium inoculation, since the nodulations were weak, medium and good. Environment I obtained higher productivity compared to environment II. The inoculation in the environment I was good, whereas in the environment II it was weak.

Key-words: Biological nitrogen fixation, consumption, genotype.

Support: PESAGRO, EMBRAPA, UENF.



Area: Plant Breeding

***In vitro* culture of immature embryos of the passion fruit (*Passiflora edulis* Sims): A new tool for the passionfruit breeding programs**

Andressa Leal Generoso¹, Rafael Walter², Virginia Silva Carvalho², Sandra da Costa Preisigke¹, Alexandre Pio Viana¹

¹ Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ² Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Breeding programs of passion fruit have found difficulties in obtaining interspecific hybrids. One of the barriers is the abortion of the embryo. The rescue of immature embryos is a way to overcome this difficulty, however, in the literature there is no report of protocols for the culture of these embryos *in vitro* after the rescue. *In vitro* culture of immature embryos has not yet been reported in *Passiflora*. Thus, the objective of this work was to develop a protocol for the *in vitro* cultivation of immature zygotic passion fruit embryos. For each of the two stages of embryonic development: heterotrophic (globular and heart) and autotrophic (torpedo and cotyledonary), an independent experiment was set up. Each experiment was conducted in a 5x4 factorial design, in which five concentrations of sucrose (20, 40, 60, 80 and 100 gL⁻¹) were tested in combination with four concentrations of phytohormones gibberellic acid (GA3) and indole-3-acetic acid (IAA) (without phytohormone; 0.0571 μmol L⁻¹ of IAA + 0.0289 μmol L⁻¹ of GA3, 0.0571 μmol L⁻¹ of IAA, 0.0289 μmol L⁻¹ of GA3) with three replicates. Each replicate was composed of a Petri dish containing four embryos. Immature passionfruit fruits were collected 12 to 24 days after pollination (DAP) and disinfested in a laminar flow chamber. The embryos were excised under a microscope (Tecnival®) and inoculated into the culture media. Plates containing the embryos were kept in a growth room at 27±2 °C in the dark for 15 days and then transferred to light. After 37 days of germination, the seedlings were evaluated for the percentage of germination of normal seedlings, abnormal seedlings and non-germinated embryos. The seedlings were transferred to a new growth medium where they remained for 30 days and then the plants were acclimatized in the greenhouse. After 35 days, the plants were evaluated for survival, shoot length, leaf number, root volume, shoot, root and total dry matter mass. In the fruits with 20 to 24 DAP it was possible to detect all stages of development of immature zygotic passion fruit embryos. It is possible to rescue and cultivate *in vitro* heterotrophic and autotrophic immature zygotic embryos of passion fruit from germination to acclimatization. For the *in vitro* cultivation of heterotrophic immature zygotic passion fruit embryos, we indicated the use of 20 gL⁻¹ of sucrose combined with the phytohormones 0.0571 μmol L⁻¹ of IAA + 0.0289 μmol L⁻¹ of GA3 or only 0.0289 μmol L⁻¹ of GA3. For the *in vitro* cultivation of autotrophic immature zygotic passion fruit embryos, we indicated the use of 20 gL⁻¹ sucrose, without the addition of phytohormones. This is the first protocol developed for the *in vitro* cultivation of heterotrophic and autotrophic immature zygotic embryos of passion fruit.

Key-words: Sucrose, gibberellic acid, indole-3-acetic acid, zygotic embryos.

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Area: (Applied Genomics)

Molecular mechanisms involved in the interaction between plants and plant growth promoting bacteria *in vitro*

Tamires Cruz dos Santos¹, Fabiano Silva Soares¹, Mariana Ramos Leandro, Patricia Louzada Rangel Terra, Gonçalo Apolinário de Souza Filho¹

¹ Author affiliations (Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Plant growth promoting bacteria favor the development of plants through the production of phytohormones, biological nitrogen fixation, nutrient solubilization and biological control of phytopathogens. The mechanisms involved in promoting plant growth by endophytic bacteria are complex, and not all of them are yet elucidated, including molecular mechanisms activated during the association. The use of model plants such as *Arabidopsis thaliana* represents an important approach to elucidate such mechanisms, in a plant system of easy manipulation and widely studied. The objective of this work is to analyze the main pathways regulated in *Gluconacetobacter diazotrophicus* when co-cultivated with *Arabidopsis thaliana* plants. This way, we seek to identify bacterial mechanisms involved in this interaction. In this sense, *Arabidopsis thaliana* plants were grown for 10 days in MS medium and placed in contact with the bacterium for 24 hours. In order to characterize the molecular mechanisms activated in the bacterium, during the co-cultivation with plants, bacterial protein extracts were obtained and analyzed through large-scale proteomic analysis (mass spectrometry (LC-MS/MS)). When exposed in co-cultivation with *A. thaliana* plants, *G. diazotrophicus* presented an increase in its growth of 45.31% in relation to the culture isolated from the bacterium in MS medium. Co-cultivation between *G. diazotrophicus* and *A. thaliana* altered the pH of the medium. The proteomic analyzes allowed to identify 451 proteins, of which 51 were regulated in the presence of the plant, being 39 induced and 12 repressed. Some important routes were regulated, among which we can highlight: 5 proteins involved in the metabolism of carbon, 9 proteins involved with biosynthesis of secondary metabolites and 6 proteins involved with microbial metabolism in various environments. Of the proteins identified, 16 are described with "uncharacterized proteins", propitiating the future characterization of new proteins relevant to this microorganism. This work demonstrates the regulation of several bacterial molecular mechanisms during the initial phase of the interaction between *G. diazotrophicus* and *A. thaliana*.

Key-words: *Gluconacetobacter diazotrophicus*, *Arabidopsis thaliana*, Proteomics.

Support: FAPERJ, UENF, CAPES, CNPq



Area: Plant Breeding

Multivariate analysis for selection of bean lines inoculated with *Gluconacetobacter diazotrophicus* PAL5

Tâmara Rebecca Albuquerque de Oliveira¹, Geraldo do Amaral Gravina¹, Derivaldo Pureza da Cruz¹, Nathália Duarte da Silva¹, Camila Queiroz da Silva Sanfim de Sant'anna¹, Gustavo Hugo Ferreira de Oliveira², Milena Mangefeste Magalhães¹, Marília Amorim Berbert-Molina¹, José Tiago Barroso Chagas¹, Richardson Sales Rocha¹, Israel Martins Pereira¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

² Núcleo de graduação de agronomia, Universidade Federal de Sergipe – UFS, Rodovia Engenheiro Jorge Neto, km 3 – Silos . 49680-000, Nossa Senhora da Glória, SE, Brazil.

The need to increase bean pod yield requires larger fertilizer consumption. However fertilizer excessive use causes the deterioration of agricultural areas and increases crop conduction expenses. Thus plant growth-promoting bacteria appear as an alternative of agricultural sustainability. The aim of this report was to evaluate the performance of bean-pod strains under inoculation with *Gluconacetobacter diazotrophicus* PAL5. Between 2016 and 2017, six pod beans genotypes were evaluated in greenhouse. A completely randomized block design was used with four repetitions in a 6x2x2 factorial arrangement. The genotypes received the following treatments seeds inoculated and no inoculated with *Gluconacetobacter diazotrophicus* PAL5 and with and without NPK application. The phenotypic means of each genotype were used in the development of the biplots. Statistical analyses were performed in the R software, using the GGEbiplotGUI package for to generate the GT Biplot graph. The two first main components (FCs) represented 75.92% of the total variation in the biplot genotypes x characteristics (GT Biplot) analysis. The B2F1L7 treatment presented greater pod width and pod yield. The B2F1L2 treatment was highlighted for fostering longer pod lengths and B1F2L20 and B2F1L5 treatments were the most responsive to the 100 seed-weight variable. The B2F1L7, B1F1L3, B2F1L3, B1F1L7 and B2F1L4 treatments stood out for presenting above-average productivity, respectively. The UENF 7-6-1 strain, in the presence of *G. diazotrophicus* PAL5 (B2F1L7), was considered ideal, maintaining high productivity and phenotypic stability.

Key-words: *Phaseolus vulgaris* L.; Endophytic bacteria; GT biplot analysis.

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Area: (Plant Breeding, Basic Genetics or Applied Genomics)

Estimation of genetic parameters in bean genotypes

Richardson Sales Rocha¹, Derivaldo Pureza da Cruz¹, Tiago Barroso Chagas¹, Israel Martins Pereira¹, Mario Euclides Pechara da Costa Jaeger¹, Geraldo de Amaral Gravina¹, Tâmara Rebecca Albuquerque de Oliveira¹, Camila Queiroz da Silva Sanfim de Sant'Anna¹, Paulo Ricardo dos Santos¹, Lilia Marques Gravina¹

¹Agricultural Engineering Laboratory, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Bean-pod is a vegetable of national importance, especially in the Northwest Fluminense region. However, one of the main current challenges of breeding programs is the development of specific cultivars for this region that meet the demands of farmers. The objective of this work was to investigate ideal conditions for the selection of superior genotypes of bean-pods based on genetic parameters. The experimental design was a randomized block with four replicates and 30 treatments. The plot was composed of 4 lines of 5m with spacing between lines of 1.0m and 0.5m between parcels. Planting was done by sowing three seeds in each well, ten days after planting, thinning was performed, leaving one plant per hole. Fifteen days after emergence the plants were tutored with bamboo and wire. The analyzes were performed based on the eight central plants of the row. Fertilizers followed the guidelines of soil analysis results. The cultural and phytosanitary treatments were done according to the recommended ones for the culture and the irrigation was done by sprinkling. Statistical analysis was performed based on characteristics: mean number of pod per plant MNPP (un.); mean weight of pod per plant (g) MWPP; mean pod weight (g) MPW; number of seeds per pod (un.) NSP; length of pod (cm) LP; pod width (cm) PW; plant height (cm) PH; weight of one hundred seeds (g) WS100; total number of seeds (un.) TNS; grain yield GY (kg / ha). Statistical analyzes were performed using the GENES software. There was a significant effect in the treatments for all the characteristics, except for PH, the coefficients of experimental variation varied between 6, 13 and 26, 12. Heritability was considered moderate to high for most of the characteristics evaluated, which shows that there is enough genetic variability for the selection of high yield genotypes.

Key-words: heritability, *Phaseolus vulgaris* L., productivity.

Support: CNPq, CAPES e FAPERJ.

Area: Plant Breeding

Response of Snap Bean Lines to Charcoal Rot Disease

Geovana Cremonini Entringer¹, Pedro Henrique Dias dos Santos², Derivaldo Pureza da Cruz³, Gabriel Coda Vidal Seara⁴, Camila Queiroz da Silva Sanfim de Sant'Anna⁵, Geraldo de Amaral Gravina⁶

¹Engenheira Agrônoma. Doutora em Genética e Melhoramento de Plantas – UENF. ²Engenheiro Agrônomo. Doutor em Genética e Melhoramento de Plantas – UENF. ³Engenheiro Agrônomo. Mestre em Genética e Melhoramento de Plantas – UENF. ⁴Estudante de Agronomia – UENF. ⁵Bióloga. Mestre em Biociência e Biotecnologia – UENF. ⁶Engenheiro Agrônomo. Professor Associado da UENF.

Snap bean (*Phaseolus vulgaris* L.) is a vegetable of great acceptance and consumption all over Brazil, mostly in the southeast region, especially in Rio de Janeiro State. Yielded especially by small farmers, the crop is destined for the consumption of green pods. The average yield of snap bean in the southeast region of Brazil is approximately 37 mil t/year, and the state of Rio de Janeiro is responsible for 21% of this yield. Nevertheless, the marketing average of snap bean is about 600 t/year, when adding all resale units of the *Central de Abastecimento-CEASA* (Supply Central-CEASA) of the state. By this mathematics, the demand is higher than the supply, proving that the cultivation of snap bean is a profitable option for small producers of the north and northwest of Rio de Janeiro State. The purpose of this research was to survey *Macrophomina phaseolina* incidences on snap bean from the bank of snap bean germplasm at the *Universidade Estadual do Norte Fluminense Darcy Ribeiro*, so as to start a breeding program aiming at obtaining resistant cultivars. Twenty-nine accesses (F₁₀ lines) from the snap bean germplasm bank regarding the reaction to *Macrophomina phaseolina* were assessed. The evaluation was performed 20 days after inoculation, and the response of plants to infection was estimated by a graded scale from zero to five. Five promising accesses were chosen to be considered as genitors in the breeding program in view of resistance, which are related as follows: UENF 7-6-6, UENF 7-10-10, UENF 9-4-14, UENF 14-6-26, and UENF 14-22-102.

Keywords: Plant breeding, disease, yield

Support: UENF, FAPERJ

Area: Plant Breeding

Leaf spectrometry in identification of peppers resistant plants to *Xanthomonas euvesicatoria*

Rosimara Barboza Bispo, Gaspar Afonso da Graça, Maria do Socorro Bezerra Araújo, Cláudia Lougon Paiva de Almeida, Cláudia Pombo Sudré, Rosana Rodrigues

Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Campos dos Goytacazes, RJ.

Xanthomonas spp. causes bacterial spot, an important disease in sweet and chili peppers crops in many production areas in the world. To achieve better understand in this pathosystem new approaches, such as the use of leaf spectrometer in order to investigate physiological traits, have been used. Leaf spectrometer has the advantages to measure quickly and in non-destructive manner the area infected by bacteria. In this experiment, the objective was to correlate the leaf physiological traits with bacterial leaf spot resistance. The experiment was carried out in the greenhouse at UENF, Campos dos Goytacazes-RJ, Brazil. Experimental design consisted in completely randomized, with six treatments and five replications. We evaluated three genotypes of *Capsicum annum*, two resistant UENF 1381 and recombinant inbred line 317 in F₄ and one susceptible (ECW) to bacterial spot, inoculated and not inoculated with *X. euvesicatoria*. Physiological traits were measured during seven days after inoculation using a CI-710 Miniature Leaf Spectrometer. This device measures reflectance in the visible and infrared region (400-1000 nm). The traits used were: Normalized Difference Vegetation Index (NDVI); Greenness Index (G); Water Band Index (WBI); Carotenoid Reflectance Index (CRI), and Flavonol Reflectance Index (FRI). Data were analyzed by regression using GENES software. G, WBI and FRI traits were the ones that best differentiated the susceptible from the resistant genotype. There was significant decrease in the NDVI, G and CRI values in the susceptible genotype (ECW). These results are in agreement with the symptoms caused by the bacterial spot: yellowing leaves, defoliation in the plant and leaf dehydration. When comparing ECW and UENF 1381 genotypes in relation to FRI, on the last day of evaluations, we observed a lower index of flavonoids in the ECW susceptible genotype. These parameters contribute to the physiological understanding of plant-pathogen interaction and allow inferring about resistance.

Key-words: *Capsicum*, plant-pathogen interaction, breeding for disease resistance.

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Area: Plant Breeding

Potential of popcorn hybrids for the occurrence of ear rot

Rafael Nunes de Almeida¹, Marcelo Vivas¹, Divino Rosa dos Santos Junior¹, Julio Cesar Gradice Saluci¹, José Tiago Barroso Chagas¹, Mayara Casadini Carlos¹, Íris Petrolina Dutra¹, Antônio Teixeira do Amaral Júnior¹

¹ Agricultural Sciences and Technologies Center, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Among the diseases with the greatest potential for damage to the popcorn, the ear rot caused by the fungus of the genus *Fusarium spp.* It is one of the most relevant to the final quality of grains. The objective of this work was to assess the potential of popcorn hybrids for the incidence and severity of ear rot caused by *Fusarium spp.* The study was carried out at the Antônio Sarlo Agricultural College, Campos dos Goytacazes, RJ, Brazil. We obtained 28 test cross crosses between two test lines (P1 and L270) and 14 other lineages (female parents). Previous studies have pointed out that the line P1 is possibly susceptible to *Fusarium spp.*, whereas the line L270 is originated from the population 172 (which has resistance to *Fusarium spp.*). The hybrids were obtained during the 2017/2018 harvest. The competition test among the hybrids was implemented in the second harvest season of the year 2018. The experimental design was a randomized block, with three replicates, each experimental unit consisting in line of 25 plants. It was assessed the number of ears produced in the plot, the incidence and severity of pink rot in the ears. We used a diagrammatic scale already proposed in the literature and widely used in research for evaluation of corn ears. The plotted data in boxplot graphs were generated with the aid of the basic software package R. The ear production was smaller only for the hybrid L696xP1, not exceeding 20 ears. The incidence of the disease was high, both for the two lines and for the 28 hybrids generated. Hybrids L204xL270 and L681xL270 showed more elevated rates of disease incidence ranging from 75% to 100% of the infected ears. The L696xL270 hybrid showed a greater variation for the incidence rate of the disease, varying between 5% and 60%. For the hybrids from the crossing with the lineage P1, L688xP1 and L691xP1 presented variation between 35% and 60%, and 5% and 50% of incidence, respectively. The severity of the disease was high for the two test lines, with higher variation for the line P1. The hybrids L682xL270, L68xL270, L691xL270, L693xL270, L695xL270, and L696xL270 presented values for severity around 10% of the infected bean in the ears, with reduced variation. In addition, the hybrids L682xP1, L685xP1, L688xP1, L691xP1, and L695xP1 also presented variations around 10% for disease severity, also with reduced variation. It concluded that the L688xP1, L691xP1 and L696xL270 hybrids have greater potential for resistance to ear rot caused by *Fusarium spp.* Because they present a more reduced incidence and severity for the disease.

Key-words: *Zea mays*, *Fusarium verticillioides*, plant diseases, biotic stress.

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Area: Applied Genomics

Genomic identification, characterization and expression analysis of MBD gene family in soybean

Fernanda Coelho¹, Sara Sangi¹; Clícia Grativol²

¹Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ²Laboratory of Chemistry and Function of Proteins and Peptides, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

DNA methylation is an important epigenetic mark conserved in eukaryotes. Many studies have shown that DNA methylation plays central roles in genome organization, *imprinting*, transposon silencing and gene expression. In plants and animals, a set of proteins containing the methyl-CpG binding domain (MBD) are capable of recognizing and specifically binding to the methylated DNA. Epigenetic regulation in eukaryotic cells is performed by a complex set of connections and signaling between small RNA and chromatin remodeling. *Arabidopsis thaliana* genome contains 13 genes encoding possible MBD proteins. Considering that the role of MBD in soybean is still little explored, this study aims to identify and characterize MBD genes and proteins in soybean, as well as to evaluate the importance of these proteins in different tissues of the plant. Twenty-one proteins with a methyl-CpG binding domain (MBD) were identified in the soybean genome. Subsequent analyzes made possible to understand the frequency of each amino acid present in the MBD domain and its function in the methyl-CpG binding. To understand the evolutionary relationship between MBD proteins in soybean, we constructed a phylogenetic tree based on the amino acid alignments present in the MBD of the 21 proteins. The analyzes of soybean MBD protein alignment showed a small number of conserved and essential amino acids within the domain. We identified that the MBD9a and b proteins present several domains involved in gene regulation mediated by chromatin remodeling. These include PHD-finger domains (plant homeodomain) and a bromodomain, an acetyl-lysine binding domain found in chromatin-associated proteins and histone acetyltransferases involved in transcriptional activation. We also identified that MBD 8 and MBD 9, proteins involved in the control of flowering time in *Arabidopsis* ecotype C24 and MBD7, is required for active DNA demethylation. The expression profile of MBD genes in soybean seeds revealed that during the initial hours of germination a greater expression of MBD4b in comparison to other MBDs, possibly involved in the repair of DNA. The data obtained until now can help to clarify the role of MBDs in chromatin organization and regulation of transcription in soybean.

Key-words: DNA methylation, Epigenetic mark, Soybean

Support: FAPERJ and UENF



Area: Plant Breeding

Digital phenotyping for quantification of seed genetic diversity in *Passiflora* spp.

Renan Carrari dos Santos¹, Rafael Walter¹, Amanda Justino Acha¹, Henrique Duarte Vieira¹,
Rodrigo Sobreira Alexandre², Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia (LFIT), Universidade Estadual do Norte Fluminense Darcy Ribeiro, UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

² Departamento de Ciências Florestais e da Madeira (DCFM), Centro de Ciências Agrárias e Engenharia (CCAEE), Universidade Federal do Espírito Santo, UFES, Av. Gov. Lindenberg, 316, 29550-000, Jerônimo Monteiro, ES, Brazil.

The digital analysis of seeds images can be used to identify genotypes with characteristics of interest, using morphological data such as color, geometry, histograms and seed texture. The objective of the present study was to evaluate the efficiency of the digital analysis of seed images for the quantification of genetic diversity in *Passiflora* spp. The seeds of *P. edulis*, *P. setacea* and ten populations of *P. mucronata* were used for analyzes. Graundeye[®] mini equipment was used to capture the images and analyze the seeds. The equipment comprises a capture module and a software program for analysis. The capture module consists of an acrylic tray in which 50 seeds were placed for image capture by the high-resolution camera. The software generates graphs and spreadsheets from the captured information to facilitate interpretation of the seeds images. In this study, 334 seeds variables were obtained; 51 of these were related to color, 48 to geometry, 192 to histogram and 43 to texture. The genetic divergence of seeds characteristics was evaluated by Euclidean dissimilarity, UPGMA grouping and the relative contribution of the characters to divergence by the GENES program. Of the 334 evaluated variables, 88 were discarded because there was no variation. Thus, 36 color, 46 geometry, 133 histogram and 31 texture variables were analyzed. Analyzes were also performed with 10% of the variables that presented the highest relative contributions (Singh). With the dendrograms analysis, five groups were formed. The number of genotypes per group varied according to the analyzed variables (color, geometry, histogram and texture). *P. edulis* remained isolated for all groups of variables when evaluated separately and when evaluated together. The same is true for *P. setacea*, except for the color variables. In color variables *P. setacea* was grouped with five populations of *P. mucronata* (G1, G5, G7, G8 and G9). The only population of *P. mucronata* (G10) improved by EMBRAPA, remained isolated from other populations for all characteristics except for the texture of the seeds. Using only 10% of the variables together, we observed a small variation in the groups' formation. This fact makes evident that with only 25 variables (7 color, 6 geometry, 2 histogram and 10 texture) it is possible to explore the diversity of the *Passiflora* genotypes. These results stand out the great divergence in the seeds morphology of the studied populations. The use of the seed descriptors obtained through digital analysis using the Graundeye[®] System was efficient for the quantification of genetic divergence in *Passiflora* seeds.

Key-words: *P. mucronata*. *P. setacea*. *P. edulis*, Graundeye[®] System

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Area: Plant Breeding

Evaluation of genetic distance between Faba beans genotypes.

Chagas JTB¹, Rocha RS¹, Cruz DP¹, Moraes R¹, Oliveira TMA¹, Almeida RN¹, Santos PR¹,
Sant'Anna CQSS, Vivas M¹, Freitas Júnior SP²

¹ Agricultural Engineering Laboratory, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

²Federal University of Cariri – UFCA, Rua Ícaro de Sousa Moreira, s/n, Barro Branco - 63130-025, Crato – CE, Brazil

Faba beans are widely used in human food to provide energy and protein in Brazil, especially in the Northeast. Its production and consumption are restricted to specific regions of the Cerrado, Northeastern Brazil, plateaus, mountains, always associated with small crops and subsistence farming, so improvements in the conduct of cultivation are essential for producers' income and consequent maintenance man in the field. The objective of this study is to characterize morphological and agronomically twenty Faba bean accesses available in the germplasm bank of the Federal University of Cariri. The experiment was performed in randomized blocks with 6 plants per genotype. In order to estimate the genetic distance between the accessions, 07 quantitative characteristics (pod length, number of locules per pod, number of seeds per pod, pod width, seed length, seed width and weight of 100 seeds) and 04 tegument shape, background color, standard color and second standard color). Dissimilarity measures were estimated based on the Gower algorithm. The hierarchical groupings were performed by means of analyzes of the smallest distances and recalculated for new grouping by UPGMA (Unweighted Pair Group Method with Arithmetic Mean). The 20 genotypes were grouped into six groups where the first group had only the G25 genotype, the second group had similarity in the standard color between the G29, G09 and G53 genotypes, the third group had the G14 genotype, the fourth group had a similarity between the second The genotypes G51, G42, G55, G32, G41, G30, G16, G37, G40, the fifth group have similarity in the quantity of seeds between genotypes G17 and G56 and the sixth group has similarity in seed width genotypes G61 , G63, G69 and G73. The genetic divergence observed in the accesses that compose the germplasm bank is considerable in relation to the qualitative and quantitative characteristics, being the weight characteristics of 100 seeds and pod length that presented the greatest variation. The largest genetic distance for all of the evaluated morphological and agronomic characteristics found the lima bean G25 and G37 genotypes presenting distance (0:54).

Key-words: *Phaseolus lunatus*, Multivariate analysis, Genetic diversity

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Area: Plant Breeding

Benzyladenine and naphthaleneacetic acid in calogenesis of sunflower hypocotyls (*Helianthus annuus* L.)

Vinicius de Freitas Manhães¹, Rafael Walter¹, Renan Carrari dos Santos¹, Otacílio Damásio da Costa Júnior¹, Clarissa Ribeiro Baptista¹, Roberta Aparecida de Sales¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Lidiane Miranda da Silva, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Calogenesis for *in vitro* indirect organogenesis in sunflower is highly variable and depends on the genotype, the composition of the culture medium and the type of the explant. Thus, the objective of this work was to verify the formation of organogenesis potential callus in *Helianthus annuus* ‘Amarelo Alto’ hypocotyls at different concentrations of benzyladenine - BA and naphthaleneacetic acid - NAA. Seeds were disinfested and inoculated in MS medium with 30 g L⁻¹ of sucrose. The approximately 1 cm long hypocotyls were removed from 14-day-old *in vitro* germinated seedlings. The explants were inoculated into Petri dishes containing MS medium, White vitamins, 30 g L⁻¹ sucrose and 100 mg L⁻¹ myo-inositol. The experiment was conducted in a CRD, in a 3x5 factorial design with three concentrations of NAA (0, 2.68 and 5.37 µmol L⁻¹) and five concentrations of BA (0, 2.22, 4.44, 6.66 and 8.88 µmol L⁻¹) with 5 replicates. Each replicate was composed of a Petri dish with 5 explants. After 20 days in the culture room, the percentage of callus formation, callus diameter and callus color were evaluated. The data were analyzed using the Sisvar program. It is observed that, even in the absence of phytohormones, the hypocotyls of *H. annuus* formed callus. The overall mean of calogenesis was over 60%. The overall mean diameter of the callus was 14.16 mm. However, the color of the callus was different in the media with the presence of phytohormones, with yellowish and dark cream colors, whereas in the medium without phytohormones the calluses were translucent and white. The color indicates a greater organogenesis potential in callus cultivated in the medium with phytohormones, mainly BA. It is evident that the hypocotyl was efficient for the calogenesis *in vitro*. It is also evident that BA is necessary for the induction of callus with potential for organogenesis in sunflower.

Key-words: callus induction, phytohormone, organogenesis.

Support: This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001.



Area: Plant Breeding

Type of explant in *in vitro* calogenesis in two sunflower cultivars (*Helianthus annuus* L.)

Vinicius de Freitas Manhães¹, Rafael Walter¹, Clarissa Ribeiro Baptista¹, Renan Carrari dos Santos¹, Otalício Damásio da Costa Júnior¹, Roberta Aparecida de Sales¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Lidiane Miranda da Silva¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The calogenesis in sunflower, aiming at indirect organogenesis, is dependent on the genotype, the components of the culture medium and the type of explant. Thus, the objective of this work was to verify the effect of the genotype and different explants in the *in vitro* calogenesis of *Helianthus annuus*. The experiment was conducted in CRD in a 2x3 factorial scheme: two sunflower cultivars (Amarelo Alto and Anão) and three types of explants (cotyledons, hypocotyls and nodal segments), with five replicates. Each replicate was composed of a Petri dish with five explants. The explants were removed from 14-day-old *in vitro* germinated seedlings. The explants were inoculated in Petri dishes containing MS medium, White vitamins, 30 g L⁻¹ sucrose and 100 mg L⁻¹ myo-inositol, 26.64 µmol L⁻¹ BA and 5.37 µmol L⁻¹ NAA. After 20 days, the percentage of callus formation, callus diameter and callus color were evaluated. The data were analyzed using the Sisvar program. There were no differences related to the genotype. All explants formed callus (100%). There was influence of the explant type on the callus diameter. The cotyledons presented callus with larger diameter (18.54 mm), followed by the nodal segment (15.35 mm). Hypocotyl presented the callus with the smallest diameter (12.17 mm). For the callus color, it was observed that all the calluses had dark coloration, indicating organogenesis potential. Thus, all the explants proved to be responsible for the calogenesis of the two cultivars of *H. annuus* with potential use for indirect organogenesis.

Key-words: callus induction, phytohormone, organogenesis

Support: This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001.

Area: Plant Breeding

***In vitro* germination of grape seeds 'Niagara Rosada' (*Vitis labrusca* L.): culture medium and explant type**

Otalício Damásio da Costa Júnior¹, Rafael Walter¹, Renan Carrari dos Santos¹, Lidiane Miranda da Silva¹, Vinicius de Freitas Manhães¹, Joel Barbosa Cancio Pereira Soares¹, Clarissa Ribeiro Baptista¹, Roberta Aparecida de Sales¹, Daniel Pereira Miranda¹, Pedro Paulo Vieira Reis Júnior¹, Andressa Leal Generoso¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia (LFIT), Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Vine breeding programs target the selection of resistant and productive materials. Crosses are performed, the seedlings are assigned and the most promising genotypes are selected. Vine seeds have dormancy which can cause problems during germination. Thus, *in vitro* germination can overcome dormancy, ensuring success in seeds germination and in obtaining the plants from the most different crosses. Thus, this work aimed to test two different formulations of culture medium and three types of explants in the germination of 'Niagara Rosada' (*Vitis labrusca* L.) seeds. The experiment was conducted in CRD, in 3x2 factorial scheme (three explants and two culture medium), with four replicates. Each replicate consisted of five test tubes with one explant per tube. Two mechanical methods for breaking physical dormancy (seeds with cut in the micropyle and seeds with horizontal cut) were tested and intact seeds were used as controls. The culture mediums used were the complete MS medium and ½MS with half of the salts and the vitamins of White. Both mediums were supplemented with 30 g L⁻¹ sucrose and 2.5 g L⁻¹ activated charcoal. The explants were conditioned in a culture room with a temperature of 27±2°C and photoperiod of 16: 8 hours (light: dark) provided by daylight fluorescent lamps (OSRAM®). During the 35 days, the germination percentage, the germination speed index (GSI) and the accumulated germination rate were evaluated. At 35 days the number of leaves and the length of the seedlings were evaluated. Seedlings with developed root and shoot were considered germinated. The data were evaluated using the statistical program Sisvar 5.6. For the percentage of germination there was no influence of the culture medium. Seed cuttings were effective for breaking physical dormancy and increasing seed germination *in vitro* and the GSI. For the variables length of shoot and number of leaves, the ½MS was the most efficient medium. For the accumulated germination rate along the 35 days, it was observed that the horizontal cut in the seeds and the ½MS medium showed the best results, with 45% of germination. Thus, the horizontal cut in the seeds and the ½MS medium were the most efficient treatments for the *in vitro* germination of 'Niagara Rosada' seeds.

Key-words: vine, dormancy, MS medium.

Support: CNPq, UENF.



Area: Plant Breeding.

Use of minimum descriptors for S₁ families of *Psidium guajava*

Moisés Ambrósio¹, Alexandre Pio Viana², Sandra da Costa Presigke³, Flavia da Silva Alves¹, Natan Ramos Cavalcante¹, Rodrigo Moreira³, Géssica Xavier Torres¹, Deurimar Herênio Goncalves Junior¹.

¹²³Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Guava, *Psidium guajava* L., belongs to the family Myrtaceae, of the order Myrtales, in which it is composed of about 140 genera and 3,500 species of trees and shrubs, and 23 genera and 997 species were recorded. The work objective was to identify the descriptors with minimal efficiency for S₁ families of *Psidium guajava*. The families of this study were obtained through self-fertilization of guava tree breeding program superior genotypes (full siblings), from the Universidade Estadual do Norte Fluminense Darcy Ribeiro. The experiment was carried out at the Barra do Pomba Island Experimental Station, in Itaocara city, in Rio de Janeiro state Northwest Region. The experimental design was randomized blocks with 18 inbred families, three replicates and 10 plants per plot. A total of 61 guava genotypes (individual plants) were evaluated. Based on the distances generated matrices, the individuals were grouped by the UPGMA method (Unweighted, Pair Group Method with Arithmetic Mean) and the distance matrix with the 29 variables were compared to the distance matrices with less variables, using the packet Dendextend in program R. According to the dissimilarity generated matrix by the quantitative and qualitative variables, it was possible to establish the discrimination between the genotypes of the inbred families S₁ of *Psidium guajava*. Considering the results of the comparative analysis between the dendrogram containing all 29 descriptors with dendrogram with only leaf/stem or fruit descriptors, it is evident the need to use different descriptors in the genetic divergence characterization among the endogenous families S₁ of *Psidium guajava*. Thus, it isn't possible to indicate minimum descriptors for the culture.

Key-words: Diversity, Endogamy, Guava.

Support: UENF, FAPERJ and CAPES



Area: (Plant Breeding)

Genetic evaluation of polysora rust resistance in popcorn

Juliana Saltires Santos¹, Yure Pequeno Souza¹, Marcelo Vivas¹, Janeo Eustáquio de Almeida Filho¹, Gabrielle Sousa Mafra¹, Antônio Teixeira do Amaral Júnior¹

¹ Author affiliations (Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Genetic resistance to foliar diseases in popcorn allows higher yields at lower costs. In this way, the development of resistant genotypes becomes of great importance; but the realization of an efficient selection of parents and hybrids depends on the existence of genetic variability and the knowledge of the genetic control of the characteristics. Thus, the aim of this work was to estimate the genetic variance components of the combining ability, as well as reciprocal effect and to infer the genetic control of resistance polysora rust associated. 56 hybrid combinations were evaluated (and reciprocal F1`s), following the complete diallel design from eight genotypes (L88, L77, L76, L70, L55, L61, P8 and P1), in two harvest. A randomized block design with four replications was used. The severity evaluation was quantified by the percentage of leaf area with symptoms along the first leaf below the first ear with the aid of a diagrammatic scale. Five plants were evaluated in each plot and an average of three evaluations were performed, which were performed seven days after the female flowering. The variance components were estimated by REML using asreml pack and tests hypotheses about the genetic variance components were performed by the likelihood ratio test using Asreml Plus package. In the joint analysis of the genetic components of variance it was observed that independently of the harvest season, the non-additive genetic component presented greater importance for the polysora rust severity. No reciprocal effect was observed for the evaluated trait, revealing that there is no significant difference between the hybrids and their reciprocals. The component of variance of the interaction *RE* x harvest season for the characteristic polysora rust severity was significant at $P < 0.05$; however, these estimates were of low magnitude. The estimates of the components of variance of the interaction *CCG* x harvest season and *CCE* x harvest season presented significant differences ($p < 0.05$), indicating the existence of specific breeders and hybrids for each harvesting season. For this, it can be inferred that there is the possibility of obtaining new cultivars from crosses by more efficiently exploring the effect of allelic complementation and that environmental differences at harvesting season influence the selection of genitors and hybrids for resistance to polysora rust.

Key-words: Zea mays, genetic control, resistance diseases.

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Area: Plant Breeding

Phenotyping popcorn germplasm for drought tolerance based on tassel characteristics

Talles de Oliveira Santos¹, Rosimeire Barboza Bispo¹, Valter Jário de Lima¹, Jhean Torres Leite¹, Divino Rosa dos Santos Júnior¹, Samuel Henrique Kamphorst¹, Eliemar Campostrini², Antônio Teixeira do Amaral Júnior¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ² Department of Plant Physiology, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Water stress is one of the most common abiotic factors in tropical and subtropical regions. This condition limits the expansion of popcorn cultivation, a commodity much appreciated by Brazilian consumers. Add to this, the low availability of cultivars that have favorable agronomic characteristics and adapted to specific regions. Acting through plant breeding is the most viable alternative to obtain more tolerant/efficient genotypes under water stress conditions. The selection of germplasm for tolerance to water stress has been carried out in breeding programs based on tolerant plant indicator characteristics. Recent studies have shown a negative correlation between prolificity and number of branches and tassel size, pointing to selection of plants with shorter bends for gains in grain yield in environments with water stress. Based on this, the objective of this work was to evaluate the genetic divergence and the grouping of 15 open pollinated varieties of the Germoplasm Active Bank of the Universidade Estadual do Norte Fluminense based on three characteristics of the tassel: main stem length (MSL), number of branches (NB) and tassel length (TL). The experiment, with a randomized complete block design with three replications, was performed in a limiting water condition, imposed 15 days before anthesis until physiological maturity. The water potential of the soil was monitored with Decagon MPS-6 tensiometers to guarantee the condition of stress in the crop. Each experimental plot consisted of 23 plants in a row of 4.8 m with spacing of 0.20 m between plants and 0.80 m between rows. The measurements of MSL, NB and TL were sampled in five plants per plot. The data were submitted to analysis of variance and the means were compared by the Tukey test ($p < 0.05$). The genetic divergence between the accessions was determined based on the Gower distance and the grouping performed by the UPGMA method. By the means test, for the MSL characteristic, the accesses UNB2-C0 and UNB2-C8 presented the smallest measurements, 15 and 13.76 cm, respectively. For NB there was no significant difference between the accesses. For TL, the access CHZM 13134 was the one that presented smaller measure (8.06 cm). In the cluster analysis, where four groups were formed, the CHZM 13134 and UNB2-C0 accessions composed, on their own, one group each, being highly divergent from the others. Based on the characteristics evaluated in this study, these three accessions are indicated as being promising for future studies of selection of drought-tolerant genotypes, since the reduction of these measures points to productivity gains.

Key-words: Genetic resources, secondary traits, water stress.

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Area: Basic Genetics

Genomic and transcriptomic analysis, phylogenetic relationship and expression profile of defensins and LTPs in wild species and commercial cultivars of sugarcane

Leandro de Oliveira Silva¹, Jacymara Lopes Pereira¹, Lídia da Silva Pereira², Valdirene Moreira Gomes², Paulo Cavalcante Gomes Ferreira³, Clícia Grativol Gaspar de Matos¹

¹ Laboratory of Chemistry and Function of Proteins and Peptides, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ² Laboratory of Physiology and Biochemistry of Microorganisms, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ³ Laboratory of Molecular Biology of Plants, Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro – UFRJ, Cidade Universitária, 21044-020, Rio de Janeiro, RJ, Brazil.

Sugarcane is a major crop for sustainable energy production. *Saccharum* spp. is a hybrid resulting from the crossing of wild species *Saccharum officinarum*, called "noble cane", and *Saccharum spontaneum*. The hybridization aimed to combine the adaptability to adverse environments from *S. spontaneum* with increased ability to accumulate sucrose from *S. officinarum*. The high demands for sugarcane products requires the generation of hybrids resistant to diseases caused by fungi, virus and/or bacteria, whose main effect is the decrease of sugarcane. However, the molecular mechanism underlying the different defense capacities observed in hybrids and wild species has not yet been fully elucidated. The methodology involved computational analysis of genomic and transcriptomic sequences, expression profile using published RNA-sequencing libraries, construction of phylogenetic trees and prediction of tertiary structure of the identified proteins. Six defensins and nine LTP genes were identified in the sugarcane genome. Proteins predicted from the genes exhibited the typical conserved amino acid residues, and the phylogenetic trees suggest conservation between monocotyledonous and eudicotyledonous. The analysis of the promoter regions revealed characteristic transcription factors binding sites of AMPs. Expression analysis of these AMPs transcripts in RNA-seq libraries from sugarcane submitted to *Acidovorax avenae* infection showed increased expression of these two AMPs. In RNA-seq libraries from plants submitted to water deficit and inoculation with *Gluconacetobacter diazotrophicus*, defensins and LTPs seem to respond to water deficit, but not to beneficial bacteria. The three-dimensional modeling of defensins and LTPs showed a high structure conservation. The characterization of defensins and LTPs provided new elements for a better understanding the defense mechanisms of the different sugarcane hybrids.

Key-words: antimicrobial peptides, *Saccharum* spp., plant defense, bioinformatics

Support: CNPq, CAPES, FAPERJ



Area: Plant breeding

Selection and relative performance to the parents in a full-sib population of *Psidium guajava*

Carlos Misael Bezerra de Sousa¹, Alexandre Pio Viana¹, Rodrigo Moreira Ribeiro¹, Lucas Souza da Silva Leal¹, Flávia Alves da Silva¹, Durval da Silva Félix Netto¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Guava is a fruit appreciated worldwide, and Brazil is one of the main fruit producers in the world. However, one of the barriers to increase guava production is the low availability of cultivars. Therefore, the greatest challenge for breeders is the obtaining and availability of new cultivars. Therefore, the objective of this work was to estimate the components of genotypic variance, phenotypic variance, individual heritability, progeny selective accuracy, and the general population mean by REML / BLUP methodology for 11 full-sib families, aiming for greater genetic selection efficiency of promising individuals based on the most viable phenotypic characteristics of the guava breeding program. It was also decided to use the information from the parents of each of the 30 individuals to be selected within the families to verify if there was an improvement in the performance of the progenies in relation to their parents. The experiment was conducted in the UENF experimental area, Campos dos Goytacazes - north of the State of Rio de Janeiro, at Antônio Sarlo Agricultural College where 11 families of complete siblings were evaluated in a randomized complete block design with three replicates. The estimation of genetic parameters and the selection of the best genotypes based on the genetic value were performed by the statistical procedure REML / BLUP, using the Selegen-REML / BLUP software. The high estimates of heritability and selective genetic accuracy favored a high percentage of genetic gain for the fruit mass and pulp mass characteristics, mainly. When comparing the average of the 30 individuals selected with the general mean of the population, the best estimates of genetic gain were observed for pulp mass (27.45%) and fruit mass (26.58%). Other characteristics that presented mean predictions of positive gains were: mesocarp thickness (10.62%), fruit length (10.30%), TSS (6.62%) and fruit diameter (7.59%). Comparing the mean of the selected genotypes with the respective parents, these averages tended to be higher than their respective parents, except for individuals from family 3, who presented progenies with only equivalent values to the parents. This confirms that the strategy of selection through families of complete siblings, obtained from the crossing of individuals selected in previous generations, is efficient in generating breeding gains in the guava breeding program.

Key-words: *Psidium guajava* L., full-sib families, predicted genetic value.

Support: CAPES, CNPq, FAPERJ and UENF.



Area: Plant Breeding

Influence of gas exchange and sucrose on the *in vitro* germination and growth of sweet peppers (*Capsicum annuum*)

Rafael Walter¹, Daniel Pereira Miranda¹, Renan Carrari dos Santos¹, Otacílio Damásio da Costa Junior, Clarissa Ribeiro Baptista¹, Vinicius de Freitas Manhães¹, Roberta Aparecida de Sales¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Lidiane Miranda da Silva¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The accumulation of ethylene and the low gas exchanges cause various problems *in vitro* culture. The genus *Capsicum* has a high sensitivity to ethylene. Therefore, this work aimed to verify the effect of seal type and sucrose on the germination and *in vitro* growth of *C. annuum* var. *annuum*. Sweet pepper ‘Casca Dura Ikeda’ seeds were inoculated in ½MS culture medium in CRD, with 4 replicates consisting of a vial with 5 seeds each, in a 3x2 factorial scheme (three seal types and two concentrations of sucrose). The seal types were two layers of PVC plastic film, rigid polypropylene cover without or with two holes of 10 mm in diameter sealed with gas permeable membrane composed of two layers of tape microporous and a fluoroporo hydrophobic membrane polytetrafluoroethylene (PTFE). The sucrose concentrations were 0 and 20 g L⁻¹. The experiment was kept in cultivation room with temperature of 27 ± 2°C, photoperiod of 16/8 hours light / dark with a light intensity of 60 μmol m⁻² s⁻¹ provided by fluorescent daylight lamps OSRAM®. At the end of 45 days, germination, photosynthetic index (PI), green index (SPAD), chlorophyll *a* fluorescence (Fv/Fm), shoot length (SL), leaf area (LA), shoot mass (SM) and root volume (RV) were evaluated. The absence of sucrose promoted greater germination, 95%. However, for SPAD, SL, LA and SM the presence of sucrose in the culture medium resulted in higher values, promoted by the increase of carbon source to the culture medium. SL, LA and SM were also influenced by the sealing. For these three variables the use of the membrane promoted greater results. When we promoted greater gas exchanges the seedlings presented greater growth and accumulation of biomass. In relation to the photosynthetic apparatus (Fv/Fm), it was observed that the seedlings cultured with membrane were not under stress conditions. The opposite was observed with PVC film, indicating stress conditions due to the excessive sealing of the vials that diminished the gas exchanges. The PI is a more sensitive variable, because it accesses the photosystem II and I. For this variable there was interaction between the use of sucrose and the seal types. The lower PI (0.71) was observed in the seedlings cultured in bottles in the absence of sucrose and sealed with PVC film, while in all the other treatments the PI was above 2.2. It is evident that this combination is detrimental to the *in vitro* growth of *C. annuum*. The results of this study indicate that sucrose is not necessary for the *in vitro* germination of chili seeds. The membrane-sealed vials promote greater gas exchanges that are beneficial for the *in vitro* growth of sweet pepper.

Key-words: Seal type, sucrose-free medium.

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Area: Plant Breeding

Morphological markers for microspore stage selection for anthers culture in *Capsicum annum*

Joel Barbosa Cancio Pereira Soares¹, Rafael Walter¹, Pedro Paulo Vieira Reis Júnior¹, Renan Carrari dos Santos¹, Vinicius de Freitas Manhães¹, Otalício Damásio da Costa Júnior, Clarissa Ribeiro Baptista¹, Roberta Aparecida de Sales¹, Lidiane Miranda da Silva¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The *in vitro* anthers culture aims the production of haploid embryos from microspores. The stage of development of the microspore influences the androgenic response. The most responsive stages are uninucleate or binucleate. At these stages, the microspore still retains the sporophytic characteristics that allow its morphogenic reprogramming. Morphological markers can aid in the determination of these stages, helping to determine the correct anther collection moment. Thus, the objective of this work was to identify possible morphological markers relating the size of the floral bud with the stage of development of the microspore of different genotypes of ornamental peppers (*Capsicum annum* x *C. glabriusculum*). Flowers buds of the two parental (UENF 1750 and UENF 2030) and three hybrids were randomly collected and visually divided into three classes based on calyx and corolla size (petals smaller than sepals, petals and sepals of approximately the same size and petals larger than sepals). The diameter of the flower buds (BD), the diameter of the anther (AD), the length of the petals (PL), the length of the sepals (SL) and the length of the anthers (AL) were measured. The development stage of the microspore was determined for the anthers of each floral bud. The number of microspore mother cells (MC), the number of microspores in dyad (DY), the number of microspores in tetrad (TE), the number of uninucleate microspores (UN), and the number of pollen grains (PG) were determined. The data were subjected to analysis of variance ($P \leq 0.01$), and the means were separated by Tukey's test ($P \leq 0.05$). The broad sense heritability and the CVg/CVe relation were also determined by Software Genes. Significant differences were observed by F test for eight of the 10 traits related to flower bud morphology and microspore stage. Only the SL and TE did not show significant differences. With the exception of SL (64.97%), MC (69.81%), DY (3.81%) and TE (8.84%), the observed heritability values were greater than 80.00%, considered high. These values indicate that most of the total observed variability for these characters is due to genetic differences between them. The highest value for heritability was observed in a number of pollen grains (96.56%). The genetic and environmental variation coefficients ratio (CVg/CVe) was greater than 1.0 for five variables, SL, BD, AL, UNI and PG, indicating a favorable situation for selection. The flower buds with the same size of petals and sepals presented higher number of UNI. Thus, in order to obtain a greater number of uninucleate microspores, the anthers must be collected when the calyx and corolla are of the same size in *Capsicum annum*.

Key-words: Bud flower morphology, plant breeding, genotypes.

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Area: Plant Breeding

Luminous intensity and sucrose in the germination and in vitro growth of chili (*Capsicum annuum* var. *annuum*) with increased gas exchange

Rafael Walter¹, Daniel Pereira Miranda¹, Renan Carrari dos Santos¹, Otacílio Damásio da Costa Júnior, Clarissa Ribeiro Baptista¹, Vinicius de Freitas Manhães¹, Roberta Aparecida de Sales¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Lidiane Miranda da Silva¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

The luminous intensity and gases involved in photosynthesis and respiration directly interfere with the in vitro plant culture. Light is responsible for the processes of photosynthesis, photomorphogenesis and phototropism. Thus, the objective of this work was to verify the effect of light intensity and sucrose on the germination and on in vitro growth of *C. annuum* in flasks with ventilated membrane that allows greater gas exchange. Sweet pepper ‘Casca Dura Ikeda’ seeds were inoculated in ½MS culture medium in CRD, with 4 replicates consisting of a flask with 5 seeds each. In a 2x3 factorial scheme, two concentrations of sucrose (0 and 20 g L⁻¹) and three light intensities (60, 120 and 240 μmol m⁻² s⁻¹) provided by OSRAM® daylight fluorescent lamps were used. The vials were sealed with rigid polypropylene cap with two 10 mm diameter orifices sealed with gas permeable membrane, composed of two layers of tape microporous and a fluoroporo hydrophobic membrane polytetrafluoroethylene (PTFE). The experiment was kept in a culture room, with a temperature of 27 ± 2°C, photoperiod of 16/8 hours of light / dark. At the end of 30 days, germination, photosynthetic index (PI), green index (SPAD), chlorophyll *a* fluorescence (F_v/F_m), shoot length (SL), leaf area (LA), shoot mass (SM) and root volume (RV) were evaluated. The absence of sucrose promoted greater germination, 95%. The absence of sucrose promoted higher F_v/F_m and PI. In greater gas exchange, the increase of light intensity, in the absence of sucrose, induced the photoautotrophic growth of the plants. For the biometric variables SL, SM and RV the highest results were obtained in the medium supplemented with sucrose. The addition of the carbon source to the culture medium allowed a greater plant growth and higher SPAD. The luminous intensity influenced the SL. The plants at the lowest intensity (60 μmol m⁻² s⁻¹) reached a longer length. As the light intensity was low the plants growth in search of light, showing etiolation. The plants present greater values for SM and RV at higher light intensity. For LA there was interaction between the factors. The LA of the seedlings cultivated in the absence of sucrose and the lowest light intensity was 12.62 cm², while in the other treatments the leaf area was above 20 cm². Under the conditions of this experiment, in general, the increase of the light intensity in the presence of sucrose favored the growth of the pepper plants.

Key-words: Photoautotrophic growth, membrane-sealed vials, sucrose-free medium.

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Area: Plant Breeding

Incidence of *Bipolares maydis* in híbridos from topcrosses of popcorn

Divino Rosa dos Santos Junior¹, Jhean Torres Leite¹, Rafael Nunes de Almeida¹, Rosimeire Barbosa Bispo¹, Valter Jario Lima¹; Talles de Oliveira Santos¹; Kevelin Barbosa Xarvier¹; Marcelo Vivas¹, Fernando Rafael Alves Ferreira¹, Antônio Teixeira do Amaral Junior¹

¹ Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Fungi are the main pathogenic microorganisms in the popcorn crop, especially for foliar diseases. Among these, helminthosporiosis caused by *Bipolaris maydis*, that cause losses in the reduction of the photosynthetic area, early senescence and leaf necrosis, and a reduction of up to 40% in grain yield. Despite the availability of auxiliary methods of disease control, such as early planting, crop rotation and fungicide application, the most efficient control method is the use of resistant cultivars. In this context, the present work was outlined to evaluate the incidence of *B. maydis* in hybrids from top crosses. For the accomplishment, 15 lines of the popcorn bank of germoplasma of the UENF – L681, L682, L683, L684, L685, L686, L688, L689, L690, L691, L692, L693, L694, L695, L696 (originating from the population UENF14) e L204 (originating from the Hybrid IAC125) – in crosses with the L270 tester (inbredlines originating from the population PARA172, germplasm recognized as resistant to *Bipolaris maydis*). The experiment was conducted in a randomized complete block design with three replicates. The incidence was evaluated by means of the percentage of lesioned leaves, according to the scale of notes proposed by Agrocères. Data analysis was performed by means of a variance analysis and, later, the grouping of results by the Scott-Knott test at 5% level of significance. Based on the results of the analysis of variance, it was observed a significant increase in the disease in relation to the evaluation time in hybrids. From the grouping of means it was possible to verify the formation of two groups regarding the disease incidence character, in which the lowest rates were expressed by the following hybrids: L695XL270, L684XL270, L691XL270, L688XL270, L683XL270, L696XL270, L204XL270 and L685XL270 and the largest, by the following combinations: L682XL270, L692XL270, L689XL270, L681XL270, L693XL270, L686XL270 and L694XL270. However, hybrids showing the lowest averages for disease incidence exhibited potential for resistance to *B. maydis* and thus are potential genotypes to contribute to the reduction of damage in the photosynthetically active areas of the affected plants.

Key-words: Disease, resistance, genotypes.

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Area: (Plant Breeding)

Analysis of main components in fruit trees (*Psidium guajava*) to identify variables of greater importance.

Flavia Alves da Silva¹, Alexandre Pio Viana¹, Carlos Misael Bezerra de Sousa¹, Moisés Ambrósio¹, Sandra Costa Preisigke¹.

¹ Author affiliations (Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Principal component analysis (PCA) is very useful in plant genetic improvement, since it allows to simplify a data set, summarizing the information originally contained in a group of n variables in few components, which present the properties of retaining the maximum of the variance originally available in the population and the components are independent of one another. The objective of this work was to apply the PCA in a population of complete siblings of the guava breeding program in order to identify the most discrete variables. The variables evaluated were total yield per plant (YIELD), total fruit number (NTF), fruit mass (FM), fruit length (FL), fruit diameter (FD), mesocarp thickness (MT). The function `prcomp {stats}` was used and the function `ggbiplot {ggbiplot}` in software R. The variables that contributed most to identify the diversity among the individuals were NTF, FL and YIELD and the variables with higher weights in the last high vectors were MT and FD, respectively. To save time in the guava breeding program, it is possible to measure only the NTF, FL and YIELD variables without compromising the selection process, since these variables are capable of differing distinct groups within the population, allowing the discarding of the others.

Key-words: PCA, analysis multivariate, guava.

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Area: Plant Breeding

In vitro Germination Speed Index (GSI) of seeds with and without tegument and isolated embryos, from ten populations of *Passiflora mucronata*

Renan Carrari dos Santos¹, Rafael Walter¹, Lidiane Miranda da Silva¹, Otacílio Damásio da Costa Júnior¹, Vinicius de Freitas Manhães¹, Clarissa Ribeiro Baptista¹, Joel Barbosa Cancio Pereira Soares¹, Pedro Paulo Vieira Reis Júnior¹, Roberta Aparecida de Sales¹, Rodrigo Sobreira Alexandre², Henrique Duarte Vieira¹, Virginia Silva Carvalho¹

¹ Laboratório de Fitotecnia (LFIT), Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602 Campos dos Goytacazes, RJ, Brasil.

² Departamento de Ciências Florestais e da Madeira (DCFM), Centro de Ciências Agrárias e Engenharias (CCAEE), Universidade Federal do Espírito Santo, UFES, Jerônimo Monteiro, ES, Brasil.

Passiflora mucronata is a wild species with great potential for use in breeding programs. *Passiflora mucronata* can be used as a scion or in interspecific crosses with *P. edulis* because it has resistance to diseases that compromise passion fruit culture. Some selection programs explore this potential, evaluating the physiological quality of the seeds, seeking a homogeneous germination to obtain more uniform seedlings. Thus, the objective of this work was to evaluate the Germination Speed Index (GSI) of seeds with and without tegument and of embryos isolated, from ten populations of *P. mucronata*. The experiment was conducted in a CRD, in a 10x3 factorial scheme (ten populations and three types of explants: intact seeds, seed without integument and isolated embryos), with six replicates. Each replicate was composed of a flask with six explants. The explants were disinfested and inoculated in MSM medium with 30 g L⁻¹ of sucrose. The flasks were kept in a culture room with controlled light and temperature. Evaluation of seed germination was performed daily during 28 days, according to criteria established by RAS. The GSI formula was used to evaluate the germination speed. It was considered germinated the explant that emitted the primary root. All data were submitted to ANOVA and to the Tukey test ($P \leq 0.05$) using the Sisvar program. The explant type and the population influenced GSI of *P. mucronata* seeds. For the three explants used, intact seeds, seeds without integument and isolated embryo, the highest GSI were observed for the isolated embryo for all the ten populations. The intact seeds did not germinate. The smallest GSI were observed in the treatment with seeds without tegument, in which the GSI ranged from 2.14 to 4.93. The highest GSI were observed in the treatment with isolated embryo, in which the GSI ranged from 11.11 to 16.54. To obtain uniform seedlings and a high GSI we recommended the *in vitro* germination of isolated embryos of *P. mucronata*.

Key-words: Embryo culture, Restinga passion fruit.

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Area: Applied Genomics

Identification and characterization of antimicrobial proteins and peptides *Capsicum annuum* var. *annuum* and mechanism of action on the development of phytopathogenic microorganisms

Pereira L S¹, Walter R², Súdre C P³, Vieira F C¹, Rodrigues R³, Carvalho V S², Carvalho A O¹, Gomes V M¹

¹Laboratório de Fisiologia e Bioquímica de Microrganismo, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

²Laboratório de Fitotecnia, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

³Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Plants of the genus *Capsicum* are part of the Solanaceae family and represent a valuable genetic resource, since they have agronomic, pharmaceutical and industrial potential. In recent years proteins and antimicrobial peptides have been identified in plants of the genus *Capsicum* as a source of defense to phytopathogenic microorganisms. In this sense this work aims to identify and characterize antimicrobial proteins and peptides in plants of the genus *Capsicum* as potential antimicrobial molecules involved with plant defense. A study has been carried out on the action of the molecules identified on the growth of microorganisms of agronomic interest like the bacterium *Xanthomonas euvesicatoria*. Initially the seeds of *Capsicum annuum* L. (UENF accession 1381) were grown in a greenhouse and during the flowering period were self-fertilized, the seeds from the self-fertilization were cultivated for 15 days in Petri dishes containing half the concentration of the minerals of the MS medium, White's vitamin complex. The germinated seeds were transferred to glass flasks containing the same culture medium, where the plants were kept for 45 days. After this period the plants were inoculated with the bacterium *X. euvesicatoria* in two different concentrations 10^5 and 10^8 . The plants were grown for another 48 h and the samples (leaf and root) were collected in the periods of 12, 24 and 48 h and stored in liquid nitrogen for further extraction. It was performed a tricine gel electrophoresis in which the difference in the expression of protein bands at the different collection times was observed. The results of this work show that plants inoculated at 10^8 concentration showed a better pattern of protein expression after infection. An antibiogram with the *X. euvesicatoria* bacterium was carried out in which we observed that after 48h, the leaf extract was able to induce the formation of a growth inhibition halo of 0.47 mm in diameter from the extract of control plants (inoculated with water) and an inhibition halo of 1.92 mm in diameter from plant extract inoculated with the bacteria. With this study we hope to contribute to the identification and characterization of molecular candidates as sources of resistance to phytopathogenic microorganisms in plants of the genus *Capsicum*.

Key-words: Chili peppers, *Xanthomonas euvesicatoria* and Plant defense.

Support: UENF, CAPES, FAPERJ and CNPq.



Area: Plant Breeding

Common bean genotypes reaction to natural infection of powdery mildew in greenhouse

**Sabrina Cassaro¹, Elisangela Knoblauch Vieira de Andrade¹, Rosimara Barbosa Bispo¹,
Karina Kazue Nakamura Fukuji¹, Cláudia Lougon Paiva de Almeida¹, Rosana Rodrigues¹**

¹Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Powdery mildew is a disease caused by *Erysiphe polygoni* DC and has great importance in common bean. The disease occurs worldwide under moderate temperature (20 - 25° C) and low relative humidity, affecting the entire aerial part of the plant. It assumes economic importance when the infection occurs before flowering, causing a reduction in crop productivity. The objective of this work was to select resistant common bean genotypes, under natural pathogen infection. The experiment was conducted in a greenhouse at UENF, Campos dos Goytacazes-RJ, Brazil, from May to July of 2018. Eight genotypes of common bean, from the UENF's germplasm bank, were evaluated to powdery mildew reaction. The experimental design was completely randomized, with 10 replicates. Nine researchers, experienced and inexperienced in phytopathology, evaluated the severity of the disease for the analysis robustness, using rating scale varying from 1 (without symptoms) to 9 (100% of the leaf surface with symptoms and signs). A variance analysis and Tukey's test for mean comparison ($P < 0.01$) were performed using the Genes software. Of the nine evaluators, five formed three distinct groups among the genotypes, three formed four groups and one formed two groups. In general, 89% of the evaluators gave notes varying from 8.0 to 8.8 for genotype UENF 2250, classifying it as the most susceptible, because it contained leaves completely taken by the disease. Genotypes UENF 2252 and Bac-6 had leaves with none or at most three white-gray powdery masses, with notes between 1.0 and 2.4 (100% of the evaluators), being considered resistant to the pathogen and promising for use in resistance breeding programs. BAC-6 genotype is also moderately resistant to *Xanthomonas axonopodis* pv. *phaseoli*, and used as a resistance standard in several studies. Using rating scale was efficient to identify and select resistant common bean plants to powdery mildew with relative speed, easiness and precision.

Key-words: *Phaseolus vulgaris*, *Erysiphe polygoni*, breeding for diseases resistance.

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Area: Plant Breeding

Behavior of genotypic correlation in sour passion fruit population over four recurrent selection cycles

Natan Ramos Cavalcante¹, Alexandre Pio Viana², Moisés Ambrósio¹, Carlos Misael Bezerra de Sousa¹, Eileen Azevedo Santos³

^{1,2,3}Department of Plant Breeding, Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF, Av. Alberto Lamego, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

Obtaining gains from selection of superior genotypes requires knowledge of both the genetic variability available in breeding populations and of associations between traits for the development of genotypes with desirable agronomic features. The correlation between two traits may be of phenotypic, genotypic, or environmental nature, but only genotypic correlations — which involve an association of inheritable nature — are of greater interest in plant breeding. Moreover, numerous situations show that associations are transitory and their estimate may be changed according to the selection process to which breeding populations are subjected. Considering the above-described situation, the present study was developed to evaluate the associations between production and physicochemical-quality traits in population of passion fruit subjected to four cycles of recurrent intrapopulation selection. The following traits were analyzed: Number of fruits (NF); Production per plant (PROD); Fruit mass (FM); Fruit length (FL); Diameter of fruit (DF); Peel thickness (PT); Total soluble solids content (°Brix); and Percent pulp (PP). Was examined the correlation between qualitative and quantitative traits and how they correlate with the trait number of fruits (NF) throughout the first three cycles of recurrent selection and the current ongoing cycle (C4). This trait was chosen because it was evaluated in all cycles already performed and because it is strongly correlated with total fruit production per plant, precisely because higher-yielding plants with better nutritional quality are sought. In this regard, the correlation between NF and production was very strong in all cycles where total fruit production per plant was assessed (C2: 0.928; C3: 0.971; and C4: 0.951). Therefore, plants with elevated potential to produce a larger number of fruits are those presenting a larger production per area unit, which has been occurring throughout the cycles. The same is not true for fruit mass (FM), for which case heavier fruits were expected to mean a higher total production. On the contrary, negative values can be observed between NF and FM for all cycles, except C2, where the correlation was positive but very low (0.085), and considered null. The traits fruit length, fruit diameter, peel thickness, pulp percentage, and °Brix had a negative correlation with NF in most cycles; when the correlation was not negative, it was considered null or weak. This reinforces the need for acuity in the selection process, since these traits determine the final fruit quality, which should be a goal in a breeding program. However, these are negatively correlated with production and number of fruits, which are also highly desirable. In this way, breeding strategies should be adopted to overcome this obstacle in the breeding of passion fruit, wherein selection indices are an excellent alternative.

Key-words: *Passiflora edulis*, plant breeding, production.

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Area: Applied Genomics

Antimicrobial activity and mechanism of action of peptides from fruits of *Capsicum chinense* against phytopathogenic fungi

Layrana de Azevedo dos Santos¹, Gabriel Bonan Taveira¹, Lídia da Silva Pereira¹, Rodrigo da Silva Gebara¹, Rosana Rodrigues², Valdirene Moreira Gomes¹

¹ Laboratório de Fisiologia e Bioquímica de Microrganismos, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Av. Alberto Lamago, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil. ² Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Av. Alberto Lamago, 2000. 28013-602, Campos dos Goytacazes, RJ, Brazil.

A great concern with the overall food safety is related to significant production losses throughout the world crops caused by plant pathogens such as viruses, bacteria, fungi as well as other organisms. These losses represent more than 10% of the global food production yields. Due to the presence of an increasing number of pathogens resistant to several compounds, plant antimicrobial peptides (AMPs) have been attracting the attention of researchers in the attempt to develop new agents to control diseases and pests. In this way, different peptides with antimicrobial activity have been identified in different species of plants, including those of the genus *Capsicum*. Herein, we evaluate the antifungal activity and mechanism of action of peptides isolated from *Capsicum chinense* fruits against different fungi of agronomic interest. Initially, the proteins present in the pepper fruits were extracted in phosphate buffer pH 5.4 and precipitated with ammonium sulfate at 0-70% saturation. The extract obtained from the extraction was subjected to reverse phase chromatography using C18 column in HPLC system. The fractions obtained after chromatography (P1 - P10) were selected and submitted to antifungal assay against fungi *Colletotrichum gloeosporioides*, *Colletotrichum lindemuthianum*, *Fusarium oxysporum*, *Fusarium solani* and against the bacterium *Xanthomonas euvesicatoria*, in a concentration of 200 µg.mL⁻¹. From the fractions tested, the fraction denominated P5 presented high antimicrobial activity on species of genus *Fusarium*, and was selected and submitted to membrane permeability test and induction of reactive oxygen species (ROS). It was observed that when treated with P5 fraction, the *F. solani* fungus had its membrane permeabilized, besides presenting an increase of endogenous production of ROS. Later, the mechanism of action of these fractions and survey its combinatory effect with fluconazole against *Fusarium* species will be analyzed in order to find candidate for studies aimed improving ways of combating this fungi, and this strategy is even more interesting because it can minimize selection of resistant microorganisms.

Key-words: Genus *Capsicum*, Antimicrobial peptides, membrane permeabilization, reactive oxygen species

Support: UENF, CAPES, FAPERJ, CNPQ





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