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ABSTRACTS

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NDSU NORTH DAKOTA STATE UNIVERSITY

ÁREA: CITOGENÉTICA

CHROMOSOME NUMBER CHARACTERIZATION OF *Catasetum ornithoides* SPECIES

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The genus Catasetum LC Richard ex Kunth currently has 168 recognized species, and Brazil is the main area of its occurrence, with about 100 species listed. The aim of this work was to determine the chromosome number of Catasetum ornithoides, contributing to the understanding of the group taxonomy, their evolutionary relationships and chromosome number variation of the genre. It was used root meristems collected from in vivo C. ornithoides orchids. The roots were subjected to the cell blocking process with a Trifluralin® solution at concentration of 3 µM for 18-24 hours at 4ºC and then washed in distilled water with three consecutive changes at intervals of 15 minutes. After washing with distilled water, the material was fixed in a methanol: acetic acid (PA) solution in a ratio of 3:1, wherein the meristems were transferred to Eppendorf tubes of 1.5 mL. It was added in the tubes 200 µL of Pectinase SIGMAR at 34°C for 2h. In the enzymatic maceration procedure, the meristems were removed from the fixative solution and washed 3 times with 15 minute intervals in distilled water. The slides preparation was performed by dissociating the root meristem and subsequently air drying in rapid movements, and placed on a heater plate at 50°C for 5 minutes. The slides were stained in a Giemsa 5% solution for 3 minutes at a temperature of 23°C, washed twice in distilled water and dried again on a heater plate. The slides were photographed, and it was identified 20 cells in prometaphases, using a 100X lens from a photomic binocular microscope (Leica ICC 50) coupled to a computer with the software LAZ EZ V1. 7.0. It was analyzed the C. ornithoides cells in metaphase stage, which presented chromosome number of $2n=42$. Despite the existence of cytogenetic studies of the Orchidaceae family, the basic number of chromosomes is still unclear, hampering studies of karyotype evolution regarding the estimation of ploidy level, mainly from the genus Catasetum. Thus the determination of the number of chromosomes of C. ornithoides has great importance, since there are no records in the literature on cytogenetics of this species that give further information that may assist the taxonomy, breeding programs and evolutionary aspects. It is likely that in the polyploidy event complex involved in the diversification of various species, structural chromosomal changes can occur and be maintained through vegetative reproduction. Such studies can provide important information about the affinities of a species with others, assisting in understanding genetic variations involved in the group evolution. Therefore, the chromosome number can provide important information about the affinities of a species with others, and together with other cytological features, assist the understanding of genetic variation. Once the chromosomes constitute the genetic material itself, any changes in them are always significant.

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UNREDUCED GAMETES (2N) IN PAPAYA GENOTYPES TREATED WITH COLCHICINE

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The polyploidy is an important tool in the evolution, adaptation, and plant breeding because it produces new genes combinations increasing the plant variability. In nature, most polyploidy has arisen by sexual polyploidization or by unreduced gametes (2n gametes). The 2n gametes can be cytologically detected by the presence of the triad and dyad in the late telophase II. This study aimed to estimate the frequency of unreduced gametes (2n gametes) in plants JS12 and SS72 / 12 treated with colchicine (JS12: F1P10- F1P12 and SS72/12: F7P13 and F7P01). JS12 and SS72/12 were also included as control. Flower buds were collected in fixative solution (ethanol and acetic acid - 3: 1) and kept at 4°C until the slide preparation. The slide preparation was performed following the routine used in the laboratory. The observations were made under an optical microscope Olympus BX60. A total of 500 post-meiotic products (monads, dyads, triads and tetrads) were counted. The frequency of 2n gametes was estimated as follows: frequency 2n gametes = (1M + 2D + Tr) / (2D + 1M + 3TR + 4T), where M is the number of monads, D number of dyads, Tr number of triads and T number of tetrads. The numerator (1M + 2D + Tr) represents the total number of 2n gametes observed. The denominator (1M + 2D + 3TR + 4T) represents the total number of gametes. The JS12 and SS72/12 lines and the genotype F7P13, treated with colchicine, had a low frequency of 2n gametes (0.56%, 3% and 2%, respectively) and high percentage of viable pollen grains (89.8%, 97.5%, and 94.30%, respectively). Genotypes treated with colchicine, F1P10, F1P12 from JS12, had high frequency of 2n gametes 18.8% and 34.9%, and low pollen grain viability, 13.7% and 1.87%, respectively; these two genotypes are autotetraployd according to the number of chromosomes (2n=36 chromosomes). The genotype F7P01 from SS72 / 12, the frequency of 2n gametes was 8.39% and the pollen grain viability, was 6.87%. Genotypes from JS12 treated with colchicine had monads frequency ranging from 0% to 25.3%. Based on the data, it can be concluded that the frequency of 2n gametes is higher in genotypes JS12 treated with colchicine than in SS72/12 treated genotypes. The frequency of 2n gametes is related to the low pollen grain viability due to unbalanced gamete, which reduces its viability.

NUMBER OF OVULES PER OVARY IN THREE GENOTYPES OF PAPAYA (*Carica papaya* L.)

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Seed production is directly related to the number of viable ovules since abnormal or aborted ovules do not produce seeds. Thus, the objective of this study was to estimate the total number of ovules and the percentage of normal and abnormal ovules in hermaphrodite and female plants collected on the JS12, SS72/12 and the hybrid UENF/Caliman-01. Five buds/variety/sex at anthesis were collected in 70% ethanol. In the laboratory, ovules were removed from the ovarian cavity and it was counted the viable and non viable ovules under a microscope stereoscope. Ovules were considered abnormal when they had a reduction in size compared to other normal ovules. The means were compared by Student's t-test for independent samples, considering results statistically significant for values of $p \leq 0.05$. The rates of normal ovules were transformed using arc-sen $\sqrt{x(\%)}$. Statistical analyzes were carried out by Infostat v2010 software. The mean number of total ovules/ovary observed in female flowers was 811, 883 and 999 for JS12, SS72/12 and UENF/Caliman-01, respectively. For hermaphrodite flowers, the ovule mean was 655 for JS12, 848 in SS72/12 and 884 in the hybrid. The t test showed significant differences for number of total ovules/ovary from female and hermaphrodite flowers in all genotypes, as well as for viable ovules. Moreover, the number of viable ovules among genotypes was significantly in JS12 and SS72/12 for female and hermaphrodite flowers. There were not observed diferences betweem JS12 and UENF/Caliman-01 for the number of normal ovules in hermaphrodite flowers. In relation to the total number of ovules per ovary it was not observed difference between JS12 and SS72/12 for female flowers and for hermaphrodite flowers in SS72/12 and the hybrid. The line SS72/12 had the highest percentage of viable ovule (97% in hermaphrodite flowers and 96% in female flowers), while the line JS12 showed the lowest percentage (67% in hermaphrodite flowers and 88% in female flowers). It was observed that the average of ovules is statistically higher in female flowers for all genotypes studied and the UENF/Caliman-01 had the highest number of ovule, in female and hermaphrodite flowers, as well as the highest percentage of viable ovules.

CHARACTERIZATION OF MITOTIC CHROMOSOMES OF *SOLANUM LYCOPERSICUM* L. VAR. ROQUESSO

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The tomato (*Solanum lycopersicum* L.) stands out as one of the most produced crops in the world. In the Brazilian market, there are several tomato cultivars from different groups such as Santa Cruz, Italiano, Caqui, Cereja and Penca. Furthermore, there are regional varieties within Group Santa Cruz such as Roquesso produced in Espírito Santo, which presents greater adaptability to environmental differences and tolerance to diseases such as rot of final blossom. The introduction of tomato hybrids, Roquesso lost niche market and was restricted to a few organic farmers. However, these characteristics may be useful in plant breeding programs. Thus, it is necessary to know the range of the genetic aspects. Therefore, the present study aimed to obtain metaphase chromosomes to set the karyogram. We used root meristems from seeds germinated in Petri dishes for cytogenetic analysis. After germination, roots with 1.0 cm of length were submitted to the blocking process using aminoprofos-methyl (APM) and Oryzalin. During the blocking process, concentrations of 3 µM and 4 µM were used for different exposure times (14 h, 15 h, 16 h, 18 h, 19 h, 20 h and 22 h), at approximately 4°C. Then, roots were fixed in methanol: acetic acid [3: 1]. After 24 hours, roots were undergone to the process of enzymatic maceration in a water bath at 34°C using distilled water and Pectinase [1:10] and [1:12] at different times (1 h 30 min, 1 h 40 min, 2 h 2 h 30 min to 2 h 35 min). Slides were prepared according to the technique of dissociation of root meristem, air-dried on hot plate at 50°C and stained with 5% Giemsa solution. The methodology used in pre-treatment, enzymatic maceration and mitotic block resulted in metaphase chromosomes suitable for characterization of morphology. The best results were obtained using the concentration of Antitubulínico APM at 3 µM for a period of 18 h, soaking 2h and 30min. Regarding to the antitubulínico Oryzalin, the best results were obtained at a concentration of 4 µM for a period of 19 h, soaking 2 h and 35 min. The diploid number of the analyzed accession was characterized as 2n = 24 chromosomes, two metacentric (3:06) and the other sub metacentric. Chromosome 1 had a secondary constriction in the short arm. The mean length of chromosomes ranged from 1.80 (12) to 3.26 µm. The material enabled the assembly of karyogram and provided information about the organization of the chromosomes of the variety, which can be used by tomato breeding programs.

TOXICITY OF THE DIFENOCONAZOL IN *Lactuca sativa*

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Agrotoxics are largely used on agriculture, but they are toxic to living beings and contaminate the environment. In order to elucidate the damage caused by these compounds, some analyzes are used, such as macroscopic (germination and radicular growth) and microscopic analyzes (mitotic index, chromosome and nuclear aberrations) which are carried out in plant models. The objective of this work was to evaluate the toxic potential of difenoconazol, a fungicide, by macro and microscopic analyzes in *Lactuca sativa*. The experiment was carried out on a completely randomized design with five concentrations of the active principle, with five replicates. Thirty seeds of *Latuca sativa* were germinated in Petri dishes with 15mL of solution and the negative and positive controls, respectively water and triflurarin. The dishes were covered with aluminum foil to avoid the light influence and stored in BOD at 24°C. During the period of 48h of exposition, germination was monitored at an interval of 8 hours. After this period, radicular growth and IVG were measured. In order to perform the microscopic analysis, two slides were prepared per dish, totalizing 10 slides per treatment with approximately 1,000 cells each, totalizing 10,000 cells per treatment. The microscopic analysis was performed in order to count the chromosome aberrations and aneuploidies (mitotic index, chromosome and nuclear alterations). Difenoconazol promoted macro and microscopic alterations on *Lactuca sativa* treated roots, depending on the used concentration. This active principle was phytotoxic because it promoted a delay on germination and on radicular growth in the most part of concentrations when compared to the negative control. On the microscopic analysis, a decrease at mitotic index occurred and an increase at chromosome and nuclear alterations occurred regarding to the negative control on the higher concentrations. Thus, difenoconazol presented a cytotoxic effect for roots. This principle presents mixed action because it caused aneugenic and clastogenic effect, which were frequent on lost, sticky and bridge chromosomes when compared to the controls. It is concluded that difenoconazol presented toxic effect to roots treated by the most concentrations evaluated.

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MEIOTIC BEHAVIOR OF ARAÇAS (*P. guineense*).

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Psidium spp. belongs to Myrtaceae family and is mainly represented by guava (*P. guajava*) and araçá *(P. cattleyanum* and *P. guineense*). Guava is susceptible to the nematode *Meloidogyne enterolobii* and araçá are considered to be the source of genes for nematode resistance. Guava is diploid (2n=2x=16 chromosomes) and araçá presents cytotypes with different ploidy levels ranging from tetraploid to octaploid. The objective of this research was to analyze the meiotic behavior of *P. guineense*. In order to do that, flower buds at different developmental stages were collected and fixed in Carnoy 3: 1 (ethanol: acetic acid) for meiotic analysis and flower buds were collected at anthesis and immersed in alcohol 70% for pollen viability. Slides were prepared by squashing anthers into drops of acetic carmine 1%. The meiotic index and pollen viability were estimated. In order to estimate the meiotic index, the anthers were macerated with drops of acetic carmine 1%. The meiotic index was estimated by the ratio of the total normal tetrads by total post-meiotic products. Normal tetrad was considered the one with four nuclei with the same size; any deviation was considered abnormal (monads dyad, triad, and polyads). Pollen viability was estimated by using Alexander's triple stain. Five slides were prepared and 100 pollen grains viable and non-viable were counted, counting a total of 500 grains. Empty pollen grains and pollen grains with contracted protoplasm were considered unviable. All slides were observed by optical microscope (Olympus BX60). The meiosis was normal, about 82.7 % of cells presented normal nuclear division and 17.3% showed abnormalities as laggard chromosome and chromosome bridges; these abnormalities can produce unbalanced or aneuploid gametes. The meiotic index was 59.4%, a low value that suggest that the species has unstable meiosis. There was a high frequency of triads, probably due to the meiotic abnormalities, resulting from mechanisms FDR and SDR. These mechanisms might produce unreduced gametes type (2n). The pollen viability was 47%, considered low, and the most of unviable pollen grains presented contracted protoplast. It was also observed many pollen grains with irregular shapes and sizes. About 20.6% of pollen grains presented four germinative pores instead of two, the usual number of most plant species.

ÁREA: MARCADORES MOLECULARES

PRODUCTION OF INTRAVARIETAL HYBRIDS OF COCONUT: MORPHOLOGICAL AND MOLECULAR GENOTYPING

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The fidelity of coconut crosses is highly important. However, 100% of the legitimacy of hybrids cannot be obtained, considering that the pollination is not totally controlled. Although, mechanisms of controlling pollination are adopted, genetically impure seeds are obtained because of contaminant factors. The color of each coconut plant has great importance for the identification of cultivars as well as for the identification of legitimate hybrids during germination, acting as a morphological marker and accelerating the selection of standardized plants. But the morphological marker is not always viable, depending on the cross. Thus, this study aimed to identify SSR markers that allow the recognizing of pure intravarietal hybrids for experimental and commercial purposes. Therefore, leaf samples of 13 dwarf coconut populations were collected, wherein each population was represented by 20 genotypes. From the collected samples, the DNA extraction was done using the DNeasy Plant Mini Kit (QIAGEN) and, in addition, each one of the 13 populations formed a Bulk, composed of the set of leaf samples of the genotypes used for representing each population. After that, amplification reactions were performed using the 13 bulks representing each population and applying 57 pairs of microsatellites pre-selected from specific literature, besides unprecedented primers. The PCR reactions were executed using a volume of 20 µl, according to Baudouin (2009) and, the PCR products were underwent to the capillary electrophoresis system under fluorescence. Finally, the resulting data of electrophoresis were tabulated and underwent to analyses in the softwares GenAlEx and Mega 5.0. For the crosses between Green Dwarf x Red Dwarf and their reciprocals, the identification through morphological marker is effective. For the crosses Green Dwarf x Yellow Dwarf and Red Dwarf x Yellow Dwarf, the morphological marker is only effective when the Yellow Dwarf is used as female genitor. From the results of this study, it was possible to elect 10 primer pairs with potential for identifying Green Dwarf x Yellow Dwarf hybrids and 12 primer pairs with potential for identifying Red Dwarf x Yellow Dwarf hybrids. Thus, it is possible to identify pure seeds of intravarietal hybrids (Green Dwarf x Yellow Dwarf and Red Dwarf x Yellow Dwarf) in a precise and safe way, because for those crosses the methodology of identification based on the color of the seedling is not an alternative 100% viable. The molecular genotyping is the only viable alternative, specifically, regarding to the cross between Green Dwarf and Yellow Dwarf, when the green dwarf is used as female genitor.

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SSR PRIMERS SELECTION FOR STUDY OF GENETIC STRUCTURE OF INBREED FAMILIES OF GUAVA

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Molecular markers have been used as tools in different stages of breeding from the characterization of germplasm to the final stages of marker assist selection (MAS). Additionally, this technology may significantly contribute to the basic knowledge of the culture, character study and to estimate the proportion of homozygous loci. Among the available molecular markers, microsatellites (SSR) are still the most used class of markers for several of purposes. The highly mutable nature of microsatellites makes them potentially powerful markers to distinguish DNA polymorphism between closely related genotypes. In guava, dozens of microsatellites have been identified and characterized, and the genomic location of many of these was determined by genetic mapping. The objective of this work was to investigate the potential of microsatellite markers to detect polymorphism in three inbreed families of guava to provide subsidies for the improvement program developed in UENF. Thus, DNA was extracted from 10 plants of each family originated from a generation of selfing in bulk using the CTAB method. In total, 16 microsatellite primers originally described for *Psidium guajava* were tested. The amplified fragments were separated by capillary electrophoresis to visualize the results. Within the 16 analyzed primers, one primer has not worked, 10 were considered monomorphic and five polymorphic alleles were considered varying by more than five base pairs. The markers were efficient in detecting differences between the families evaluated and will be used in later works for molecular characterization, especially regarding to the structure of genetic variability and quantification of the level of inbreeding in genetic materials, contributing to the structuring of the breeding program.

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RECOVERY OF RECURRENT GENOME PASSION FRUIT BY OF DNA MARKERS

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The transfer of resistance genes from wild species for commercial passion fruit has been done through interspecific hybridization followed a program of backcrossing. To save time and increase the response speed of programs, breeders resort to auxiliary tools such as molecular markers. The microsatellite markers allow monitoring the trait in transfer and to identify individuals with a higher proportion of the recurrent parent genome. In this work, we aimed to verify the recovery of recurrent genome passion fruit in the first backcross population segregating (RC_1) using microsatellite markers. The DNA of each genetic material (1 genotype *P. edulis*, 1 *P. setacea*, 1 F_1 hybrid and 187 plants RC_1) was extracted using the CTAB method, and 6 microsatellite primers were used. Based on genetic distances, it was found the formation of three groups: Group I formed by RC_1 and *P. setacea* individual, group 2 comprising four individuals RC_1 and group III formed by the F_1 hybrid, *P. edulis* and 182 RC_1 plants. The highest genetic similarity was obtained between genotype 1 generation RC_1 and the recurrent parent *P. edulis*, while the lowest similarity was obtained between *P. edulis* and *P. setacea* species, highlighting the large genetic distance of these commercial and wild varieties, respectively. The average percentage of recovery of recurrent genome in segregating population was 76%. Genotype 6 with 90% of the recurrent parent alleles can be used as parent for establishment the RC_2 population, since this individual had no symptoms of infection CABMV.

Financial support: CNPq, FAPERJ, UENF

MICROSATELLITE SCREENING IN PARENTS AND HYBRIDS OF *Passiflora* TO SUBSIDIZE THE CONSTRUCTION OF GENETIC MAPS

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The diseases are the main factors that limit the expansion of the cultivated area of passion fruit in Brazil. Among them, passion fruit woodiness disease (PWD) induced *Cowpea aphid-borne mosaic virus* (CABMV) is considered the most economically important. There is no reports of passion fruit cultivars resistant CABMV. Thus, the interspecific cross has important implications in the Passiflora breeding program, particularly in order to introgress genes of resistance from one species to another which is susceptible. Molecular markers have been used as a tool in different stages of breeding from the characterization of germplasm to the final stages of marker assistant selection (MAS). The aim of this work was to establish SSR markers for use in genetic mapping studies aimed to identify loci that control resistance to CABMV. DNA was extracted from leaves of the parent *P. edulis*, *P. setacea* and an interspecific hybrid by using the CTAB method. 129 SSR primers developed for *Passiflora edulis* and *P. setacea* were tested. The amplified fragments were separated by capillary electrophoresis for visualization of the results. The optimal annealing temperature for each primer ranged 56-65°C. 25 of the 129 primers were tested considered polymorphic alleles varying by more than five base pairs. The SSR markers were efficient in discriminating genotypes and may be used in genetic mapping and selection of resistant genotypes to CABMV.

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HETEROLOGOUS AMPLIFICATION OF MICROSATELLITE MARKERS IN *VOCHYSIA BIFALCATA* WARM.

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Vochysia bifalcata Warm. has economic and environmental importance. Its environmental importance is due to its use for recovering degraded areas. Reforestation programs require information about the influence of devastation to genetic variability of the species. DNA Molecular markers are useful tools to get this information, in particular the microsatellites or SSR. The use of SSR technique is generally high-cost, which prevents the use of this method for several species. However, the evolutionary proximity among certain species allows that *primers* developed for a related species can be used successfully to other species. The objective of this study was to evaluate the transferability of microsatellite markers originally developed for *Qualea grandiflora* Mart. in *V. bifalcata* to Vochysia bifalcata Warm. In order to test the transferability of such primers, eight SSRs markers developed for *Q. grandiflora* were tested with DNA samples of *V. bifalcata*. Therefore, leaf samples of five individuals of *V. bifalcata* were collected in a population in Parque Nacional do Caparaó-ES. The samples were stored in silica gel and used for DNA extraction by CTAB method. PCRs were performed with 15 µL per sample under the following conditions: 1.5 mM MgCl2, 20mM50mM of TrisKCl pH 8.4, 0, 2 mm of each nucleotide (dNTP), 0.8 µm *primer*, 1 unit of Taq polymerase and 20 ng of genomic DNA. Amplifications were performed in thermal cycler (Applied Biosystems Veriti model), under the following conditions: 1 minutes 94° C, followed by 35 cycles with three steps: a) 1 minute at 94° C, b) temperature shit specifies for each initiator and c) 1 minute at 72° C, with a final step of 10 minute 72 c. Amplified fragments were separated by electrophoresis on polyacrylamide gel 10in 1 x TBE buffer, to 100 Volts for five hours. The gels were stained in solution of ethidium bromide and photographed under ultraviolet light. Out of the eight *primer* pairs, four generated satisfactory amplification products, however such fragments were monomorphic. This result can be attributed to small differences in size between alleles and less reproducible genotyping of individuals in the polyacrylamide gel. The results indicate the potential use of markers that generated positive amplification for genetic characterization studies of the species in their natural populations.

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ÁREA: MELHORAMENTO DE PLANTAS

GENETIC CONTROL OF NITROGEN USE EFFICIENCY IN POPCORN

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The supply of popcorn in the Brazilian market is still much lower than its demand, especially, due to the reduced number of cultivars registered in the country because of breeding programs are still incipient. One of the objectives of the popcorn breeding program of UENF for the next few years is to improve the use of nitrogen through the development of cultivars with high efficiency in its use (NUE). NUE can be defined as the ratio of grain yield per unit of nitrogen applied in the plants. It is known that nitrogen is an essential element for agricultural production and that the yield of crops cannot be increased without the acquisition of this element by the plants. In this scenario, the objectives of this research will be: (i) identify efficient popcorn lines in the use of nitrogen; and (ii) investigate possible maternal heritability effects related to NUE. Twenty-nine popcorn elite lines belong to 'Viçosa', 'BRS Ângela' and 'Beija-Flor' populations will be evaluated with high and low N. The following traits will be measured: days for male and female flowering (DF); hundred-grain weight; ear weight (EW); grain yield (GY); and expansion rate (ER). After identifying the efficient and inefficient lines in the use of nitrogen, ten lines will be chosen: three efficient in nitrogen use, four inefficient ones and four intermediate ones, aiming to obtain a normal distribution of the genotypic and allelic frequencies. After the ten lines have been chosen, a complete diallel with reciprocals will be performed, considering the maternal effect for the NUE heritability. The F_1 will be evaluated together with the parents and reciprocals. The evaluated traits will be: cycle (Cl) - days from seeding to harvest; plant height (PH) - measured, in meters, from soil level to the insertion of the flag leaf, in ten competitive plants; chlorophyll content (Clor); ear height (EH) - measured, in meters, from soil level to the insertion of the upper ear in ten competitive plants; stem diameter (SD) - measured, in mm, at the lower third of the plant with caliper ruler; hundred-grain weight (W100); expansion rate (ER) - determined by measuring the mass of 30 g of grains and taking it to a microwave oven in a special plastic jar for popping at a power module of 1000 W for one minute and forty-five seconds, and then the popcorn volume will be measured in a 2,000 mL beaker, wherein the quotient of the popped volume is divided by 30 (grain mass), with ER expressed in $mL.g^{-1}$; grain yield (GY) - determined as the total mass of grains in the plot, transformed into $kg.ha^{-1}$; prolificacy (PR) - the average number of ears per plant, evaluated in ten competitive plants; and grain length (GL), width (GW) and height (GH) - measured with a digital caliper ruler. Through this research we aim to characterize the efficient and inefficient lines in the use of nitrogen and determine the heritability patterns in the efficiency of use of this nutrient.

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EVALUATION OF RESISTANCE TO ANTHRACNOSE IN FRUITS OF *Capsicum SPP*. IN TWO HARVEST SEASONS

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Anthracnose is caused by fungi of the *Colletotrichum* genus and can cause serious damage to agriculture. In *Capsicum*, the disease can cause countless damage to fruit production, with important studies of plant breeding for resistance. Therefore, the objective of this study was to evaluate the resistance to anthracnose in Capsicum spp. in two harvest seasons. Twenty-seven accessions of *Capsicum spp.* of the Active Germplasm Bank of UNEMAT were evaluated for resistance to the fungus *Colletotrichum gloeosporioides*. The experimental design was a completely randomized block design with three repetitions, with four unripe fruits and four ripe fruits per repetition. All fruits were disinfected and packed in styrofoam trays covered with transparent plastic bag, and within each tray was placed wet sheets of filter paper to compose a humid chamber. In each fruit was made a tiny wound in medium region of fruit with one sterilized needle and a fungus inoculation was made in three fuits of each type, immature and mature, by dropping 20 µL of spores' suspension (10^6 conidia/ml). One ripe fruit and one immature fruit from each plot have consisted in the attesters, which have received 20 µL of sterile distilled water. The trays were left at room temperature (controlled at 24 ° C ± 2) and every day evaluation of all fruits was made based on the measurement of the diameter and lesion length of each fruit on a period of 11 days. The experiment was conducted in two harvest seasons: April and August 2014. A ratio after 11 days evaluation (lesion size x 100 / fruit size) and data were subjected to analysis of variance 120x2x2 triple factorial (access x fruit ripening x harvest time) was calculated to determine if there significant interaction between the variables. Characteristic analyzed for lesion diameter, the treatment variable was significant at 1% by the F test, being the UNEMAT 113, UNEMAT 38, UNEMAT 110 and UNEMAT 102 accessions with the lowest average so are the group of resistant accessions anthracnose, for the same trait analyzed. Treatment x harvest interaction was also significant, with the 38 UNEMAT access with better mean for the first harvest season and UNEMAT 110 and UNEMAT 113 with the best means in the 2nd harvest season hits. To lesion length, all variables, including the interactions were significant at 1% by F test, being the fruits of the first harvest season and ripe fruits with the best means, thus representing the most resistant to anthracnose fruit. The accesses that presented resistance within all the variables analyzed were the UNEMAT 113, UNEMAT 110, UNEMAT 112, UNEMAT 108 and UNEMAT 116. We conclude that the first harvest season in April and ripe fruit are more resistant to anthracnose, and among the accessions considered to be resistant are UNEMAT 113, UNEMAT 38 and UNEMAT 110.

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EVALUATION OF FAMILIES FROM THE EIGHTH CYCLE OF INTRAPOPULATION RECURRENT SELECTION OF POPCORN

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Popcorn is an excellent alternative culture to minimize socioeconomic problems, as it is highly profitable and has wide popular acceptance. Universidade Estadual do Norte Fluminense Darcy Ribeiro develops a breeding program aiming to release new popcorn cultivars with desirable agronomic traits using the intrapopulation recurrent selection method. The objective of the present study was to obtain and evaluate families of full siblings of popcorn variety UENF 14 referring to eight recurrent selection cycle and analyze its genetic components. The intrapopulation recurrent selection method of full siblings was adopted to obtain 200 families originated from the mixture of seeds of the families selected from the population of popcorn UENF-14 from the seventh cycle. The evaluation of families was carried out in Campos dos Goytacazes and Itaocara, which are municipalities located in the North and Northeast regions of Rio de Janeiro State (Brazil), respectively. The following traits were evaluated: average plant height and height of insertion of the first ear (cm); final stand; tipping; prolificacy; diseased ears; ears attacked by pests; grain yield ($kg.ha^{-1}$); hundred-grain weight (g); and grain expansion rate ($mL.g^{-1}$). Six controls (UENF-14-C4, UENF-14-C5, UENF-14-C6, UENF-14-C7, variety BRS Ângela and hybrid IAC-125) were used for the competition trial. The experimental design was set in randomized blocks with three repetitions in each of the eight sets, wherein each set contained 31 treatments (25 families of full siblings and the 6 controls), totaling 744 plots each environment. An analysis of variance was conducted and subsequently the genetic, phenotypic and environmental components were estimated. There were differences in all sources of variation for most traits. The obtained significances demonstrate that the environments as well as the genetic material were sufficiently distinct to generate differences between the evaluated traits. The genotypic variance had higher values for the traits of greater economic interest, which were grain yield and expansion rate. All traits obtained good variation and heritability values, above 0.6 and 60%, respectively. The results allow us to infer that there is genetic variability, which enables continue the recurrent selection process. Thus, the next steps are: to estimate the genetic gains through the selection indices for the evaluated traits aiming, especially, increasing grain yield and expansion rate; to select the 30 best families that will be part of the next selection cycle; and to compare the grain yield and expansion rate data with the controls.

Financial support: Capes and Faperj.

COMBINING ABILITY FOR ORNAMENTAL TRAITS IN CHILI PEPPER (*Capsicum annuum*)

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Plant size and color of *Capsicum* fruits are peculiar characteristics that give aesthetic value and make these plants attractive for the ornamental market. Obtaining ornamental pepper cultivars adapted to the conditions of the Rio de Janeiro State can stimulate production and attend a growing niche market. The objective of this study was to determine combining ability for ornamental traits in *C. annuum*. Six ornamental chili pepper (*C. annuum*) accessions were crossed in a 6 x 6 complete diallel scheme without reciprocals. Fourteen hybrids, six parents and two commercial genotypes were tested in a greenhouse from march to july 2014, in a randomized block design with ten replications and one plant per plot. Seven quantitative traits (plant height; canopy diameter; days for flowering; days for fruiting; fruit lenght; fruit diameter, and fruit number per plant) were evaluated in hybrids and parents. General combining ability (GCA) and Specific combining ability (SCA) were highly significant for all traits. GCA estimate values were higher than SCA for most traits, but canopy diameter and days for fruiting, indicating that additive effects play an important role in genetic control of the ornamental characters in the genotypes evaluated. According to the values observed for GCA, the parents that contributed most for the reduction in plant height were UENF 1626 (-2.60) and UENF 1632 (-2.49); UENF 1623 (1.04) contributed for larger canopy diameter, flowering (-2.04) and fructification (-2.09) earliness; UENF 1626 and UENF 1750 contributed to reduce the fruit length (-9.24 and -9.71), fruit diameter (-0.85 and -1.58), and also to increase the number of fruits per plant (10.94 and 27.63) in crosses. Hybrid UENF 1627 x UENF 1623 is promising regarding to smaller plants, since SCA estimative was 3.05, while UENF 1626 x UENF 1627 had interesting SCA result for larger plant canopy (2.23). Two accessions (UENF 1626 and UENF 1750), and six hybrids (UENF 1626 x UENF 1623; UENF 1626 x UENF 1632; UENF 1626 x UENF 1750; UENF 1626 x UENF 1627; UENF 1627 x UENF 1623 and UENF 2030 x UENF 1623) have the potential to be released to the farmers and also to be used in breeding program of ornamental pepper.

Financial support: Faperj

PROPOSAL OF IDENTIFICATION OF HETEROTIC GROUPS IN POPCORN LINES

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Due to the fact that popcorn has a reduced genetic base resulting from its evolution from selections of common corn type “flint”, it is relatively important to know about the formation of heterotic groups. Despite it is one of the bases of plant breeding for several cultures, the use of molecular markers in the identification of genetic variability of popcorn germplasm for the composition of heterotic groups is not yet widespread in Brazil. The knowledge of popcorn germplasm hinders the development of superior materials for a large part of productive areas in the country. However, the absence of heterotic groups is an obstacle to the development of cultivars and hybrids adapted to tropical conditions, not only for Brazil, but also for a big part of the productive areas of other countries and/or continents. Given the foregoing scenario, this study was carried out with the following objectives: to make a comparative analysis of the genetic diversity of local popcorn genotypes in relation to those from other countries, testing the varied models to estimate genetic diversity; identify heterotic groups of interest for breeding in tropical conditions; and identify genotypes of interest for the formation of hybrids of varieties developed for use in recurrent-selection programs, as well as materials to obtain lines and future formation of simple, simple-modified, double and triple hybrids. Forty popcorn lines from different genetic constitutions will be used to develop the proposal of formation of heterotic groups, wherein the genetic distances among the lines will be determined by a similarity matrix based on the results found with the aid of SSR markers. As general results we expect to form different heterotic groups of popcorn that will provide greater efficiency of effective gains in the breeding programs for this culture. This proposal of formation of heterotic groups may result in studies aiming to obtain promising popcorn hybrids for the region, with the possibility of tests in more regions of the country, thereby expanding the cultivation of popcorn in Brazil.

Financial support: CNPq, CAPES, FAPERJ and UENF

GENOTYPIC CORRELATION AMONG AGRONOMIC TRAITS AND PHYSICOCHEMICAL FRUIT COMPOSITION IN CHILI PEPPERS

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The genetic correlation coefficient measures the degree of association between the genetic variations of two quantitative traits in a population. In chili pepper, important quantitative traits include agronomic characteristics, as fruit length and fruit diameter, and physicochemical fruit composition. The genetic correlation among traits can assist breeders in optimizing both agronomic traits and physicochemical fruit composition simultaneously, using indirect selection. This study examined the genetic correlation among agronomic traits and physicochemical fruit composition in chili pepper (*Capsicum annuum* var. *annuum*). Two chili peppers genotypes developed by the *Capsicum* breeding program of UENF, identified as L3, L4 and the cultivar Jalapeño M were grown in a greenhouse from January to July 2014, in Campos dos Goytacazes, Rio de Janeiro, Brazil. Fruit length, fruit diameter, pericarp thickness, vitamin C, titratable acidity and soluble solids were measured. Vitamin C content was determined either from immature or mature fruits, and the other traits were measured only in mature fruit. the Pearson correlation coefficients were estimated. Negative genetic correlation (-0,24 to -0,71) was detected between fruit length and all other variables, indicating that an increase in fruit length is correlated with a reduction in all other traits. Nevertheless, a positive genetic correlation among the fruit diameter with all variables was observed, except with the fruit length (-0,76). Such correlations indicated that an increase in fruit diameter is related to an increase in pericarp thickness, titratable acidity, and vitamin C. Negative genetic correlation was also observed for pericarp thickness x titratable acidity, pericarp thickness x vitamin C in immature and mature fruits, and pericarp thickness x fruit diameter indicating that an increase in pericarp thickness results in a reduction of all physicochemical attributes in fruits. Such data support the hypothesis that indirect selection for some important physicochemical traits in chili peppers can be carried out with selection of fruits with larger diameter, since there is a high positive genetic correlation between the fruit diameter and physicochemical attributes such as high soluble solids, and high vitamin C content, in both immature and mature fruits.

Financial support.: Faperj, Capes and CNPq

ESTIMATES OF GENETIC PARAMETERS OF ROBUSTA COFFEE

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Coffee is one of the main commodities of the world and its importance in terms of consumption is smaller only in comparison to fresh water and oil. Brazil is ranked as the major producer and exporter of coffee of the world and regarding to consumption, Brazil stands on second position. The official estimate for Brazilian coffee production in 2014 is about 49.15 million bags with 60kg each. In addition, about 30% of World coffee production is represented by Robusta Coffee (*Coffea canephora* Pierre ex A. Froehner). The present study aimed to estimate genetic parameters and evaluate the yield of clones of *Coffea canephora*, var. conilon using REML/BLUP method. The grain yield of eight coffee clones was measured during an experiment in Randomly Blocks with 4 repetitions and 8 plants per plot, using a plant spacing of 3.0 m × 1.0 m, resulting in 3,333 plants/ha. Thus, the production evaluation was conducted at Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural (Incaper) during the period from 2013 to 2014. High magnitude of genetic values was observed among the evaluated clones, wherein the value of average heritability ($\hat{h}^2_{mc}$) was 0.60. According to literature, high heritability is related to high value of additive genetic variance, low environmental variance and low genotype x environment interaction. The value of selection accuracy of clones (Acclon) was 0.78, proving the selection adequacy for clones. Considering the selection based on yield, the clones of number 6 and 4 have presented better performances.

SELECTION IN PROGENIES OF GUAVA BASED ON UNIVARIATE AND MULTIVARIATE INDEX

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In Brazil, guava play an important role in agribusiness, due to appreciable characteristics of the fruit, such as taste, appearance, nutrients richness and functional elements, besides the possibility of utilization of the fruit for the production of high added value products such as pulp, nectar, juice and jam. The selection of more productive genotypes is of great importance for plant breeding. The objective of the study was to assess the genetic variability in full-sib families of *Psidium guajava* (guava), and estimate those based on the genetic progress of different selection criteria. The experiment was set in a randomized block design with two replications, 10 full-sib families, and 12 plants per plot. The direct and indirect selection and classical index or index of Smith and Hazel was used for the prediction of genetic gain, between and within progenies. Regarding to the selection of the classical index, the vectors of economic weights were established by experimental data, and used the heritability, coefficient of genetic variation, genetic standard deviation and weights for attempts. The top five progenies analyzed and top five plants in these families were selected. Estimates of genetic correlations in some characteristics were higher than phenotypic, suggesting the existence of pleiotropic genes. The genetic correlation of number of fruits and other characteristics have generated negative estimates, being necessary to choose a form of selection to estimate genetic gain for all the evaluated features. The selection criteria obtained different results, even for the same index selection with different economic weights, which shows divergence in progenies studied. The direct and indirect selection provided lower genetic gains. The classic index (Smith and Hazel) was the selection criterion that showed the best results in terms of gains in the number and weight of fruits, being indicated as the most suitable strategy of selection for genetic improvement in the population under study.

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REPEATABILITY ESTIMATE IN CHARACTERS OF FRUITS OF GUAVA

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The estimate of the repeatability coefficient allows the breeder to assess if the selection based on some phenotypic trait will be reliable, in other words, if the selected genotypes maintain their superiority indefinitely. Such analysis enables labor and cost reduction which is a useful tool to guide breeding projects. This study aimed to estimate the repeatability coefficient in fruit characteristics of guava, and determine the number of measurements which must be made for an accurate prediction of the actual value of the genotypes. The experiment consisted by three genotypes of guava (*Psidium guajava* L) from two varieties: Petri, Pedro Sato and a commercial genotype, Roxa. The experimental design adopted was randomized blocks with four replications. Each repetition presented a unit composed by two plants and five fruits per plant were used to estimate repeatability. Features such as fruit mass, mass cored and endocarp thickness were evaluated. The repeatability coefficient was estimated by analysis of variance considering two sources of variation. There were significant differences at 1% of probability between genotypes for fruit mass and endosperm mass, showing the existence of variability, an essential factor for the study of genetic divergence. The experiment has shown good experimental accuracy, with low coefficients of variation presented by the mass characteristics of fruit (8.16%), endocarp thickness (13.63%) and mass of the endosperm (11.83%). The repeatability coefficients ranged from 0.76 to 0.86% for mass cored and fruit weight respectively. The estimate of the repeatability coefficient is classified as high when ≥ 0.6, when mean <0.6 and ≥ 0.3 and low when <0.3. The correlation coefficients obtained for the five measurements the characteristics ranged from 90.20 to 96.39%, for mass cored and fruit respectively, indicating good reliability in the evaluation of characteristics. Fruit mass and endocarp thickness had the highest coefficients of determination and therefore higher repeatability estimates, demonstrating accuracy of the measurements, high regularity of the superiority of the progeny and the expression of characteristics has a good genetic control. Coefficients of determination higher than 90% were obtained for fruit mass, endocarp thickness and mass core from two, three and four steps, respectively, indicating that the number of fruits used in the work is sufficient to predict actual values of the progenies studied. High repeatability coefficients are good indicators in the selection process, since it expresses the total variance that is explained by variations provided by genotypes and changes attributed to the environment, in other words, represents the maximum amount the heritability in the broad sense can achieve. The number of four fruits is shown to predict the actual value of the genotypes for the traits. The characteristics showed high repeatability coefficients, demonstrating high regularity and indicating that they can be used in simple breeding methods of guava.

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ESTIMATION OF AGRONOMIC TRAITS IN PAPAYA USING DIGITAL IMAGES ANALYSIS

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Estimates of agronomic traits in papaya for breeding purposes are manually made, therefore it is a time consuming activity, which requires intensive labor, limits the evaluation of large number of plants and reduces the possibility of identifying superior genotypes. Digital Phenotyping is a methodology which uses analysis and processing of images that has been used on fruit species to measure the characteristics of agronomic importance. This tool allows to automate and accelerate the process of measuring, reducing the labor required to perform this activity. The objective of this investigation was to validate a methodology for the analysis and processing of digital images to estimate the number of commercial fruits per plan-NFCom, number of deformed fruits, length of the fruit bunch-CC (cm), plant height–AP (cm) and stem diameter-DC (mm).Thus, 150 plants of both the hybrid UENF/Caliman-01 and THB variety were randomly selected in two commercial crops of the company Caliman Agricola Linhares/ES. A Sony DSCHX 300 digital camera was used to take three photographs per plant, as follow: a photo of the complete plant to estimate the CC, AP and DC characteristics; one photo perpendicular to the plant (side A) and another obtained by rotating the camera 180° counterclockwise (side B) to estimate NFCom and NFD. The characteristics were also accessed manually to evaluate the efficiency of the digital methodology. Images were processed and analyzed using ImageJ v1.48. The confidence intervals calculated for the digital methodology were similar to those obtained with the manual methodology, for both genotypes in all traits. The confidence intervals were similars for each side, which means that they are statistically equal and correspond to half the number of fruits per plant. Therefore, confidence intervals for each side were estimated for NFCom and NFD by multiplying the number of fruits obtained by two (each side LA*2, LB*2) to estimate the total production of fruits per plant. This result showed that by photographing only one side of the plant it was possible to accurately estimate these characteristics in both genotypes. The precision of the digital methodology when compared to the manual method was high, ranging from 99% in AP to 85% in NFD for both genotypes. When it was considered only one side (side *2) the precision for NFcom was similar, ranging from 97% to 98%. The precision for NFD was lower when considering only one side, ranging from 87.71% in the hybrid UENF/Caliman-01 to 66.19% in the THB variety; suggesting the use of two-sides photographs in order to accurately measure this trait. The sample size was significant for the design of the ideal sample for all traits in both genotypes, except for NFD when considered one only side, in which 267 and 272 plants are needed. For both genotypes, estimates of agronomic traits through the analysis and processing of digital images showed no significant differences when compared to manual estimates, suggesting that this methodology could be used to accurately measure agronomic important traits in a convenient way that requires less labor in the field.

INTRAPOPULATION BREEDING OF SOUR PASSION FRUIT USING MICROSATELLITE MOLECULAR MARKERS TO MONITOR THE GENETIC VARIABILITY OF THE POPULATION.

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Recurrent selection is a cyclical process that basically involves obtaining progenies, evaluation, and recombination of the best ones aiming the increase of the favorable alleles wanted, providing an increasing in predicted genetic gain and the maintenance of genetic variability for future gains. For this last one, it has been employed the assisted selection via molecular markers for monitoring the variability, allowing faster characterization, quality and large scale. So that, this research aims to conduct intrapopulation breeding of sour passion fruit using microsatellite molecular markers to monitor the genetic variability of the population. It will be assessed 150 families of full siblings (FFS), using a randomized block design with three replications, three plants per plot and four additional control (UNEMAT S10, UNEMAT S30, BRS Rubi do Cerrado and and BRS Gigante Amarelo). The planting will take place in October 2014, at the experimental area of Universidade Estadual do Mato Grosso in Tangara da Serra. The characteristics evaluated will be: days to flowering, yield, number of fruits, fruit weight, longitudinal fruit length, transversal diameter of fruits, average peel thickness, pulp percentage, total soluble solids, pulp color, total titratable acidity, potential hydrogen and the total soluble solids / total titratable acidity ratio. It will be performed variance analysis for each characteristic using the software GENES. From the mean square values obtained by variance analysis it will be estimated the variance components associated with environmental and genetic effects. For character simultaneous selection it will be used the Kempthorne and Nordskog index, Pesek and Baker index, James index, Smith and Hazel selection index, and Mock Mulamba index aiming to identify the best one. 40 FFS will be selected according to their importance for industry use and for fresh consumption. The genomic DNA will be extracted from the leaves of the 40 FFS and then amplified. From the numerical matrix it will be calculated the genetic distance between the genotypes assessed, heterozygosity level and the dendrogram constitution. After divergence analysis, the most divergent of 25 FFS will be selected and have their selection gain estimated. So that, this project will contribute to the passion fruit breeding program of Universidade Estadual do Mato Grosso, in order that such institution be the academic and scientific medium for the biotech research corroborates with the growth and development of sustainable agriculture.Thus, the research demands are numerous and can only be met with the joint effort of institutions and the formation of interinstutional and muldisciplinary research networks to ensure the continuity of the research and its role in different phases of conservation programs, germplasm use and breeding of sour passion fruit.

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CIRCULANT DIALLEL AND REPEATABILITY BY MIXED MODELLING IN ELEPHANT GRASS FOR ENERGY PURPOSES

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Elephant grass (*Pennisetum purpureum* Schum.) has a high dry-matter-accumulation ability and also features qualitative traits for energy purposes such as high fiber content, high C:N ratio, high calorific value, and low ash content, which qualify this culture as an alternative energy source. In the evaluation of plants, especially the perennial ones, it is common to take repeated measurements of a given trait from a same individual. This procedure allows us to infer about the genotype's ability to repeat the expression of that character over time. In this sense, the objectives of this study will be: to evaluate the combining ability of ten elephant-grass genotypes; to choose parents and promising combinations for energy purposes; to analyze repeated measures over time; and to estimate the coefficient of repeatability for selection of elephant-grass genotypes. Controlled crossings will be carried out among the ten elephant-grass parents in a circulant diallel system. The hybrids, along with the parents, will be evaluated in a randomized block design with three repetitions. The plot will consist of two 7.5-m rows spaced 1.5 m apart. The following characters will be assessed: flowering onset; number of tillers; stem diameter; plant height; dry matter yield; percentage of cellulose and lignin; percentage of ash; C:N ratio; and calorific value. The obtained data for each character will be subjected to analysis of variance using the GENES computer software. The combining abilities will be analyzed according to Griffing's model, by deploying the effects of treatments into general combining ability (CGA) and specific combining ability (SCA). The data will be analyzed as repeated measures over time, with the use of the mixed models by the PROC MIXED procedure of the SAS software. The variables data will be adjusted by the covariance matrix (CM), by the lowest value of Akaike's information criterion (AIC). Means will be obtained by the adjustment of the fixed effects via the LSMEANS procedure of SAS. Through this research we expected to obtain promising hybrids of elephant grass for energy purposes, environmental benefits through the availability of an alternative energy source, and technical-scientific benefits.

Financial support: CNPq/Capes

COMBINING ABILITY OF POPCORN FOR AGRONOMIC TRAITS AND RESISTANCE TO *Puccinia polysora* BY CIRCULANT DIALLEL

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One of the desirable traits in a good popcorn cultivar is high expandability, as desired by consumers, and grain productivity as desired by producers. In addition, disease resistance is also a trait of interest in breeding programs of this crop. Within the diseases affecting corn, polysora rust is currently one of the most relevant in Brazil. Despite the research progress and the recent development of new popcorn cultivars, there is still a need for cultivars with superior agronomic traits and resistance to diseases. In this sense, the objectives of this study are: to obtain, evaluate and identify superior hybrids obtained in a circulant diallel among 16 lines of popcorn, and to evaluate the potential of the 16 tested lines. For this purpose, 40 hybrids obtained from 16 popcorn lines by circulant diallel will be used. The experimental design will be set in randomized blocks with four repetitions and no competition among the lines and hybrids. Four experiments will be installed: two in the crop season and two others in the off season. The experiments will be carried out at Colégio Estadual Agrícola Antônio Sarlo, located in Campos dos Goytacazes/RJ, North of Rio de Janeiro State (Brazil), and at the Experimental Station of PESAGRO-RIO in Itaocara, Northern of Rio de Janeiro State. Genotypes IAC 125, L70×L54 and L70×P1 will be used as controls for the hybrids. Varieties UENF 14, Barão de Viçosa and Ângela, on the other hand, will be used as control for the lines. After the establish of trials, the severity of *P. Polysora* will be evaluated with a diagrammatic scale. Expansion rate, in $mL.g^{-1}$, and grain productivity, determined by the total mass of grains of the plot and transformed to $kg.ha^{-1}$, will also be evaluated. It is expected to obtain superior hybrids, i.e., hybrids with a high expansion rate and grain yield and that are resistant to polysora rust. It is also expected to know the potential of the lines *per se* and in combination for the evaluated traits.

Financial support: Capes.

GENETIC GAIN ESTIMATES AND SELECTION OF S_1 FAMILIES BASED ON SELECTION INDICES AND REML/BLUP IN SUPER SWEET CORN

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The objectives of this study were to compare four selection indices based on the method of least squares and the additive index through the REML / BLUP multi-traits method in the evaluation of genetic gain and consequently proceed to an early selection of S_1 families evaluated according to the main traits required by the market. Thus, 80 S_1 testcross hybrids, divided proportionally into two distinct groups: the CIMMYT-SH (CSH) population, and the CIMMYT-8HS (C8HS) population were evaluated. The selection indexes Smith & Hazel, Williams, Pesek & Baker, Mulamba & Mock and additive REML/BLUP multi-trait were tested. The estimated gains from selection were performed for each group (CSH and C8HS) aiming to maintain the identity of each population separately. Among the four indices of selection based on the ANOVA, the Mulamba & Mock was the most suitable for the selection of half-sib families in super sweet corn. The additive index REML/BLUP multi-trait showed better predicted genetic gains than Mulamba & Mock, and was efficient for the selection of half-sib families in super sweet corn. The high coincidence between the REML / BLUP multi-trait and Mulamba & Mock indices indicates that for purposes of selection their efficiency was similar.

CORRELATION BETWEEN HETEROSIS AND GENETIC DIVERSITY OF PAPAYA INBREED LINES BY SSR MARKERS

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Papaya is a tropical fruit of great importance in Brazil. Its vitamin C rich fruits are widely used in diets for their digestive and nutritional values. Information on genetic diversity is of great importance because it enables the prediction of the performance of hybrids, facilitating their development. The objective of this work is to verify whether the genetic diversity between inbreed lines obtained via SSR (microsatellite) molecular markers is correlated with heterosis for yield and fruit quality components. For this, 22 lines were selected from a backcross program of UENF and 42 respective hybrids obtained from crossing these lines with the testers 'JS-12' (Formosa Group) and 'SS 72/12' (Group Solo) and then evaluated. We used lattice design 8 x 8 with two controls and six repetitions with four plants per plot. The following characteristics were evaluated: number of nodes without fruit (NNWF), number of deformed fruit (NDF), number of commercial fruit (NCF), mean fruit weight (MFW), fruit length (LF), diameter of the fruit (DF), pulp firmness (PF), fruit firmness (FF), total soluble solids (TSS) and Production (PROD). The extraction of total DNA genomic was made from young leaves following the methodology of Quiagem Kit. Twenty-nine primers were used (9 genics and 20 genomics) and their amplifications followed a specific PCR program. Separation of DNA fragments was performed by a capillary electrophoresis system. Pearson correlation was performed to test the significance of the association between matrices of genetic distances and heterosis. There was significant and positive correlation for the hybrids obtained with JS-12 tester in the following traits: MFW, LF, DF, PROD. On the other hand, there was a significant and negative correlation for NDF and TSS, indicating that the greater the genetic distance smaller the NDF and the TSS. For the hybrid obtained with SS-72/12 tester, the traits MFW, LF, DF, PF showed significant and negative correlation. Genetic distances obtained via SSR showed correlation with heterosis for many traits. These results allow us to infer future steps of the breeding programs facilitating the development of new papaya hybrids.

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ANALYSIS OF COMBINING ABILITY OF S3 FAMILIES OBTAINED FROM POPCORN VARIETY UENF 14

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The development of corn hybrid in a breeding program is based on obtaining and evaluating lines. The stage of obtainment of pure lines is achieved through successive self-pollinations of a genetic material; however, the high number of lines to be conducted in the many generations makes the advance of inbred families an unfeasible process. A widely accepted methodology of evaluation used by many researchers is top cross, which allows the identification of superior genotypes in initial generations of self-pollination. The objective of this study is to discriminate and evaluate the combining ability of 50 partially inbred S_3 families originated from the UENF 14 variety (*Zea mays* L.). The S_3 families were evaluated for their performance *per se* and in their crossings with four testers - two from a broad genetic base (varieties BRS Angela and UENF 14) and two from a narrow genetic base (triple hybrid IAC 125 and line P2). The hybrid seeds were obtained in the off-season of the 2013 crop year, at *Colégio Agrícola Antônio Sarlo*, located in Campos dos Goytacazes/RJ, Brazil. A simple lattice genetic design was used to evaluate the performance *per se* of the S_3 families and their crosses with testers (top crosses). The trials were carried out at *Colégio Agrícola Antônio Sarlo*, in Campos/RJ, and at the Experimental Station at Ilha do Pomba, in Itaocara/RJ, during the 2013/2014 crop year. The evaluated traits were grain yield (kg/ha) and expansion rate (mL/g). Data were collected and are being tabulated for the subsequent analysis of genetic and phenotypic parameters, which will allow for comparisons between the estimates from the top-cross hybrids obtained with each tester and the S_3 families *per se*. The general (GCA) and specific (SCA) combining abilities will be estimated according to the partial diallel model of Griffing (1956), adapted by Geraldi and Miranda Filho (1988). The heterosis of the top cross hybrids in relation to the testers *per se*; the discriminatory ability of the testers compared by the differentiation and performance index proposed by Fasoulas (1983); and the correlations between the performance of the families and their respective top crosses will also be evaluated. According to the analyses to be conducted, it is expected to obtain conclusive results in the indication of the best tester(s) for the partially inbred S_3 families and consequently obtain superior hybrid combinations in relation to the popcorn cultivars tested in the North and Northeast regions of Rio de Janeiro State.

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GENETIC BREEDING OF SNAP BEAN (*Phaseolus vulgaris* L.) WITH DETERMINED GROWTH IN ESPÍRITO SANTO: GENERATION ADVANCE BY SSD AND EVALUATION OF QUANTITATIVE MORPHO-AGRONOMIC CHARACTERS

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The snap bean (*Phaseolus vulgaris L.*) is economically and socially valuable in Brazil. It can be cultivated in mountainous region and lowland as well. The genetic breeding of these plants are performed to reach the yield stabilization with a cost production that allow high profit. Diallel cross is one of the most used methodology for both, increase variability and identify promising segregant population. Fifteen hybrids were obtained using diallel cross allowing analyze of F$_2$ generation. These hybrids were obtained by using 6 progenitors (‘Alessa’, ‘Andra’, ‘Paulista’, ‘Turmalina’, ‘Manteiga baixo’ e ‘UEL’). The goal of this study is to predict the characteristics of F3 segregating population using quantitative characters. The experiment was conducted at Instituto Federal do Espírito Santo-Campus Itapina, located in Colatina-ES, at 71 meters of altitude. The weather of the region is tropical Aw, according to Koppen classifaction of climates. The F$_3$ population was conducted performing SSD method (Single Seed Descent) using 15 hybrids and its respective parents, however, it was analyzed statistically using the randomized blocks design with 3 blocks and 21 treatments. Different quantitative descriptors were analyzed such as: total weight of pod (PV); total number of pod (NV); plant mean height (AP); height of first pod insertion (AIPV); average pod length (CV); pod diameter (DV), for possible early generation test. The data were submitted to a mean test, performing the Tukey’s using the Assistat software Version 7.7 beta (2014). The mean square test for treatments was no meaningful for all meaningful F- test, however, most of the analyzed characters treatments were genetically contrasting. The most valuable characteristics for the farmers (PV) showed average 92.12 g/plant, highlighting T13 treatment reaching 151.21 g/plant. The descriptive NV showed a mean value of 17.56 unit/plant, T14 showed the highest value, 23.7 unit/plant. Once these plants have determined growth behavior, their heights were not over 50 cm, and it was observed in our treatments. For this characteristic the average value was not higher than 36.41 cm, reaching 43cm for T8. The insertion of the first pod in most plants was at the middle part, ranging from 14.28 cm with the lowest value of 9.50 cm in T14. For CV characteristic the mean value was 41.47 mm, highlighting T13 reaching 72.6 mm. Pod diameter is one of the most appreciated characteristic, once consumer choose smaller pod, as observed in T9 (12,5 mm), although the average was 17.61 mm. The F$_3$ hybrids presented a low accomplishment for morpho-agronomic characters, due to several field variation occurred during the experiment. Wherefore, they will not be selected for coming generation. For future snap bean breeding studies, we propose some adjust to minimize the field variation and improve the evaluation of coming generation to equally analyze early generation.

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STARTING A BREEDING PROGRAM FOR *COLLETOTRICHUM* RESISTANCE IN *Capsicum* SPP.

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Pepper fruits ranked at the top of *Agência Nacional de Vigilância Sanitária* list as the most contaminated from pesticides within vegetable crops cultivated in Brazil. Many pathogens can cause diseases in *Capsicum* plants, including *Colletotrichum* spp., the causal agent of anthracnose. Typical anthracnose symptoms on pepper fruit include sunken necrotic tissues, with concentric rings of acervuli. Fruits showing symptoms have reduced marketability. Although the management and control of anthracnose are still being extensively researched, commercial genotypes of sweet and chili pepper that are resistant to the *Colletotrichum* spp. have not yet been developed. Pathogen variability is one of the major constraints in establishing a resistance breeding program and there is little information concerning the interactions between the complexes of species involved in chilli anthracnose. This work describes the efforts to collect *Colletotrichum* spp. isolates from contaminated pepper fruits, in order to establish a collection of the fungus culture. This collection will be characterized and used to screen pepper genotypes seeking anthracnose resistance. Samples of 49 fruits with typical anthracnose symptoms were collected from June to July, 2014 in the local markets and fairs of Campos dos Goytacazes, RJ, Brazil, Açu, Teresópolis, Rua Nova and in a market in Vitória, Espirito Santo, Brazil. Fruits were individually collected, placed in plastic bags to avoid cross contamination, and transported to the Plant Breeding Department of Universidade Estadual do Norte Fluminense where the isolation were performed to obtain fungus cultures. Fungi were isolated by aseptically transfer of the spores from the fruits to the Petri dishes containing potato-dextrose-agar (PDA) with addition of streptomycin in concentration 1:10 (v:v) using inoculation needle to collect the spores. The Petri dishes were kept in a BOD at 27ºC until mycelial growth, for approximately 15 days. After that, mycelium disks were stored in sterile distilled water (Castellani method). The PDA medium favors *Colletotrichum* mycelial growth, when compared to oat-agar medium, which can be observed with the lowest number of conidia produced in PDA. The next steps of the research will be the fungi identification using classical and molecular approaches followed by plant inoculations in *Capsicum* accessions from germplasm collection of Universidade Estadual do Norte Fluminense.

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TOLERANCE TO ASIAN RUST OF SOYBEAN EXPERIMENTAL POPULATIONS BY COMBINING FUNGICIDES, LOCATIONS AND CROP YEARS

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The Asian soybean rust (*Phakopsora pachyrhizi*) is currently the disease that most limits the cultivation of soybean in Brazil. A total of 24 experimental populations obtained by crossing and two checks (BRS - 133 and Monsoy 8001) of soybean were evaluated in eight experiments conducted in two fungicide managements, two locations (ESALQ and Areão) from Piracicaba (SP), and two crop years (2010/11, $F_{4:15}$ generation; 2011/12, $F_{4:16}$). Each experiment was designed as complete randomized blocks with three replications, each one organized in two experimental sets; each set was composed of 14 experimental plots, corresponding to 12 populations and two common checks. An experimental plot consisted of four rows of 5.0 m x 0.5 m. In each location and crop year were installed two neighbor experiments for the fungicide managements: in the first experiment was applied the fungicide Derosal (D) for controlling the late season leaf diseases (LSLD), while in the second experiment was successively applied the fungicides Opera and Native (O & N) for controlling LSLD and Asian rust. In the useful area of each plot (four central meters of two intermediate rows) were evaluated the traits: seed yield (g / plot, transformed to kg/ha), and the seed size (represented by one hundred seed weight, in grams). Then, for each population and check was estimated the rate of reaction to rust (R) through of the difference between the adjusted means of each genotype in the two experiments (D and O & N), divided by the mean in D and multiplied by 100; this estimate of R was made individually for seed yield (RY) and seed size (RS) in each location and crop year. Thus, four estimates of RY and RS were obtained for each genotype. Finally, the arithmetic mean of RY and RS was calculated for each genotype in all environments, and their respective percentage in relation to the mean of the common checks. The analysis of variance detected significant effects among populations, checks, and populations *vs.* checks contrasts, as well as significant interactions among the effects of populations and environments (fungicides, locations and years for seed yield; locations and years for seed size). Based on RY values, 21 populations showed higher tolerance to rust, because their RY estimates were inferior to those of the checks; already for RS, 17 populations were more tolerant than the checks. In terms of rust tolerance, the major highlights were the populations USP 04-17.027 and USP 04-18.063, respectively with 13% and 16% of RY and both with 38% of RS, in relation to the checks; these two populations yielded respectively 88% and 92% relatively to the checks. The major highlight for seed yield was the population USP 04-18.111, with 3273 kg/ha (101% of the checks), but with smaller rust tolerance (RY = 81% and RS = 91%, compared to the checks). The USP 02-16.122 population combined relatively high seed yield (3239 kg/ha or 100% of the checks) and well satisfactory levels of rust tolerance (RY = 35% and RS = 57%, relatively to the checks).

STUDY OF HERITABILITY FOR PHOSPHORUS ABSORPTION EFFICIENCY IN POPCORN

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One of the main essential elements for plant survival is phosphorus. The objective of this research will be to evaluate the study of the heritability for efficiency and traits related to the responsiveness in phosphorus absorption of popcorn. After identifying the five most contrasting lines of the Active Germplasm Bank of UENF for traits of responsiveness and efficiency in the use of phosphorus, a genetic-control study of this trait will be undertaken via complete diallel. The experiment will be conducted in a completely randomized design with six treatments: P1, P2, F1, F2, RC1 and RC2, with two replicates, wherein treatments P1 and P2 will contain 15 plants each; F1, 20 plants; F2, 140 plants; and RC1 and RC2, 50 plants each. A crossing between the P1 and P2 parents most and least tolerant to phosphorus will be performed aiming to obtain generation F1, which will be backcrossed with both parents to obtain generations RC1 and RC2, and it will also be self-pollinated to obtain generation F2. The genetic parameters will be estimated based on two models: by analysis of variance and, on the additive-dominant model, of the means of the generations of the system comprising the six generations. The generations will be cultivated in a greenhouse with plastic pots with 3.0 dm^{-3} capacity filled with a substrate formed by three parts earth and one part washed sand. Approximately 30 days after seedling emergence, the following traits will be evaluated: shoot dry matter yield; root dry matter yield; phosphorus content in shoots and roots; P content in shoots; and P content in roots. Having obtained the dry matter and P contents data, the following efficiency indices will be estimated: rooting efficiency = (g of root dry matter)$^{-2}$/mg of P in the shoots; phosphorus absorption efficiency = mg of P in the shoots/g of root dry matter; phosphorus translocation efficiency = mg of P in the shoots/mg of total P; and efficiency of use of P in the shoots = (g of shoot dry matter)$^{-2}$/mg of P in the shoots. The obtained data will be submitted to analysis of means and variances, using the computational resources of the GENES software. Through this application, the studies of means for each index will be achieved by the resolution of the following matrix system: $\beta = (X'D^{-1}X)^{-1} X'D^{-1}Y$. Thus, it will be possible to quantify the additive, dominance and epistatic effects involved in the expression of the efficiencies for phosphorus. Subsequently, the variances of the efficiencies for phosphorus will be studied on the GENES software, generating the estimates of the average degree of dominance, of the number of genes involved, of the heritabilities in broad and narrow sense, of the prediction of gains per selection, as well as the prediction of the average improved populations.

PREDICTION OF GENETIC GAINS THROUGH SELECTION INDICES IN CORN HYBRIDS FOR SILAGE

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During the dry season, pastures become deficient, requiring the use of an additional roughage source. The corn silage remains one of the best options for supplementation in this period due to its high energy content and high dry matter yield per area unit. Thus, it is of paramount importance that genetic breeding programs in Brazil develop a specific program for production of forage corn. The objective of this study was to compare the predicted gains obtained with simultaneous selection of characters, using several selection indices and several selection criteria, and choose the most appropriate selection index and criterion to select corn hybrids for silage. To conduct this study, 19 genotypes of the "Dent" group were chosen; each group was crossed with one tester, — Piranão 12 — also from the "Dent" group. Later, the trials were installed to evaluate the hybrids in two environments. The experimental design was of randomized blocks with five replicates, with 24 treatments: 19 top-cross hybrids and five controls (BR106, AG 1051, UENF 506-11, L21 and L25). Each plot consisted of one 5-m row, spaced 1.0 m apart, and five seeds per linear meter. Agronomic and chemical characteristics were assessed. The statistical analysis was performed by an analysis of variance for environment and combined. The combined analysis of variance was carried out considering the following statistical model: Yijk = m + Gi + B/Ajk + Aj + GAij + Eijk. In all analysis, Scott-Knott's test was employed at 5% probability for clustering the means of the hybrids. All analyses were performed on the GENES software. The selection indices employed to predict the gains were those suggested by Mulamba and Mock, Willians, and Smith and Hazel. The economic weights adopted were: genetic coefficients of variation (CV_g), variation index (CV_g/CV_e), coefficient of heritability (h^2), genetic standard deviation (DP_g) and values attributed by attempts (PT) (40, 20, 20, 100, 20 and 20), wherein selection was conducted on three characters (productivity, ear weight with and without stover, green mass weight, percentage of grains in the green mass, and total number of ears); Mulamba and Mock's index provided the highest magnitudes of gain predicted for the productivity and green-mass-weight traits, which were 5.76 and 8.44%, respectively, in the use of heritability as economic weight. Thus, it was found that the selection index enables the prediction of simultaneous gains in the two main traits of interest for silage production.

EVALUATION OF RESISTANCE TO *Fusarium solani* AND CHARACTERIZATION OF INTERSPECIFIC HYBRIDS OF *Passiflora*

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The several diseases that affect passion fruit have been provoking a decrease in production and even preventing the cultivation in certain areas. Due to pest problems, it has become necessary the adoption of alternative control measures such as the development of resistant cultivars. This study aimed to characterize and evaluate the resistance to *Fusarium solani* in 10 interspecific hybrid genotypes (*P.edulis* X *P. mucronata*) and their parents. Thus, 10 hybrids and their parental genotypes *P. edulis* (susceptible) and *P. mucronata* (resistant) were used. Nine clones of each genotype were taken to field and conducted in random blocks with three replicates to perform the morphological characterization. Qualitative and quantitative variables were evaluated. And nine clones from each individual were maintained in a greenhouse, inoculated with the fungus *F. solani*, and evaluated 76 days after inoculation, performing the a second isolation of the fungus later. For data evaluation conducted - ANOVA, Scott-Knott test at 5% probability, and using the UPGMA clustering method. The existence of variability among individuals assessed for significance was observed ($p < 0.05$) by the F test for the characteristics related to the floral anatomy and characteristics related to length and width of leaves. In relation to morphological characters of flower, it was observed that the genotypes of *P. edulis* showed no significant differences ($p < 0.05$) by Scott and Knott test, differing from all others for seven of the variables related to the flower. For the characteristic leaf length there was a large variability between genotypes, with mean values ranging from 93.82 to 68.76 mm. In regards to the fruits, hybrid genotypes showed normal fruit without seeds and aborted seeds. The genotypes were grouped into six groups, with Group III and V divided into two subgroups. In the evaluation resistance to two hybrid genotypes and its female parent, *P. mucronata* accessions Ilhéus were considered to be resistant, since 100% of the plants showed no symptoms of the disease. Therefore, the fungus was not re-isolated. However, one of the resistant hybrids produced no flowers and the other produced seedless fruits. For this study, hybrids classified as resistant genotypes are not fertile, however, these can be used as a rootstock because there was no significant difference between these genotypes stem diameter and stem diameter of *P. edulis* species.

EVALUATION OF THE EFFECT OF THE *COLLETOTRICHUM GLOEOSPORIOIDES* ON THE SEED GERMINATION OF *CAPSICUM SPP.*

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Peppers and chilies belong to Solanaceae family and *Capsicum* genus. Currently, there are more than 2000 ha of cultivation areas in Brazil. However, there are several phytosanitary barriers that can lead to losses in quantity and quality of production, such as anthracnose, a disease that attacks the fruit causing necrotic lesions. Pathogens related to seeds can decrease germination percentage and seed vigor. Therefore, the development of pepper cultivars resistant to anthracnose is interesting to breeding programs. Thus, the objective of this study was to evaluate the effect of *Colletotrichum gloeosporioides,* cause of anthracnose, on the germination of *Capsicum spp* seeds that will be inoculated with such pathogen. Seeds of two accessions: UNEMAT 38, which is considered to be resistant and the susceptible accession UNEMAT 81, were submitted to germination test on a completely randomized design (CRD) in a 2x2 factorial (treatment x condition inoculation). The pattern of germination for each treatment was: 10 replicates of 25 seeds for each treatment distributed in petri dishes (acrylic) on a sheet of blotting paper and dampened with distilled water in the proportion of 2.5 times the weight of the paper. The plates were stored in an incubator (BOD) at 20-30 ° C, with a photoperiod of 12 hours, during 15 days. The analyzed variables were: index of germination speed, germination percentage (%), number of plants germinated, number of normal plants, number of abnormal plants, number of dead seeds. Seeds were placed in petri dishes containing PDA medium, and stored in BOD over a period of seven days at 24 ° C ± 2 and 12 h photoperiod in order to verify the presence of *C. gloeosporioides* in seeds. Results were significant at 1% probability by F test for all variables. During germinatiom tests, the acession UNEMAT 81 (*Capsicum annuum)* presented superior means in comparison to UNEMAT 38 (*Capsicum chinense)*. Although, the resistance pattern found in fruits is not the same of seeds because the accession UNEMAT 38 presented resistant fruits to *Colletotrichum gloeosporioides*. Seeds from fruits that were not inoculated with such fungus presented the best germination percentages when compared to those from inoculated fruits, indicating that the presence of the pathogen can result in harm to the quality of seeds. In conclusion, the fungus *Colletotrichum gloeosporioides* interferes on seed germination of the *Capsicum spp.*, causing a loss in the seeds quality, but does not prevent seed germination. The resistance pattern found in fruits of pepper is not the same found in seeds during germination.

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DIALLEL ANALYSIS IN POPCORN FOR RESISTANCE TO SPOT BLOTCH, PRODUCTIVITY, AND EXPANSION RATE

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Popcorn stands out as one of the most appreciated foods by the population, having a commercial value superior to that of common corn. However, the existence of genotypes resistant to diseases and with good yield and expansion rate is still limited. In this scenario, the objectives of this study will be to generate information on the combining ability of eight popcorn parents as well as to obtain estimates of heterosis and genetic and environmental components for resistance to spot blotch (*Cochliobolus heterostrophus* and *Setosphaeria turcica*), yield and expansion capacity. In order to achieve the proposed goals, two experiments will be conducted in randomized blocks at Colégio Estadual Agrícola Antônio Sarlo, located in Campos dos Goytacazes/RJ (Brazil). The trials will be established during the traditional corn crop, from October to March 2014/2015, and in the off-season, from May to September 2015. The genetic material to be used will consist of 56 simple hybrids (28 F1's and 28 reciprocals) with their eight parents and six controls (varieties BRS Ângela, UENF-14 and Barão de viçosa, and hybrids IAC 125, L70×L54, P8×L54). The grain yield will be evaluated as the total grain mass of the plot and transformed into kg.ha^{-1}; for expansion rate (ER), the mass of 30 grains will be measured and taken to a microwave oven in a special plastic jar for popping at a power module of 1,000 W for one minute and forty-five seconds, and then the popcorn volume will be measured in a 2,000 mL beaker, wherein the quotient of the popped volume is divided by 30 (grain mass), with ER expressed in mL.g^{-1}; The evaluations of disease severity will be conducted three times for each of the trials, using a diagrammatic scale to determine the severity of *Setosphaeria turcica* and *Cochliobolus heterostrophus* in five plants per plot. After obtaining the data, the diallel analysis will be performed using methodologies proposed by Gardner and Eberhart and Griffing and Hayman, on the Genes software. The result of the diallel analysis will allow us to make inferences on heterosis, study the genetic control of evaluated quantitative traits, and estimate the general and specific combining abilities of the evaluated genetic material. It is also expected to identify superior hybrids, i.e., those which aggregate high yield values and expansion rates as well as satisfactory levels of resistance to disease caused by *S. turcica* and *C. heterostrophus*. In conclusion, the development of genotypes resistant to disease will reduce the impact that the pathogen exerts on the yield and quality of this culture. Thus, the study to investigate the population of superior genotypes is an effective alternative in disease control.

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MOLECULAR MARKERS APPLIED TO RECIPROCAL RECURRENT SELECTION IN MAIZE

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Maize (*Zea mays* L.) is one of the most important on the national scenario, with a high production of 82 million tons, plays a strategic role in the Brazilian economy, since Brazil stands as the third largest producer and second largest exporter of culture. Therefore, the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) has been conducting a program of genetic breeding of maize via reciprocal recurrent selection of full-sib families (SRRFIC) assisted by markers molecular. The objective of this study was to evaluate the genetic divergence between and within CIMMYT and Piranão populations from the 14th cycle of recurrent selection, seeking individuals with greater genetic diversity in order to compose the 15th cycle of reciprocal recurrent selection. The full-sib families obtained at the 14th cycle were evaluated at the Centro Estadual de Pesquisa em Agroenergia e Aproveitamento de Residuos in Campos dos Goytacazes - RJ. According to the analysis of variance, the characteristic grain yield presented an increase of 402.72Kg. $ha^{-1}.cycle^{-1}$ at 14° cycle in comparison to 12° cycle, which is one of the main characteristics in a maize breeding program. Concerning to the selection of the best families to continue the next cycle, we used the selection index of Mulamba e Mock (1978), allowing the selection of the 40 best families, representing a genetic gain for yield of 9.1% compared to the total mean of the evaluated families. Fourty agronomically superior families of each population, totaling the 80 families S1 superior, was carried to the stage via molecular genotyping microsatellite markers (SSR). Based on the bands revealed by 20 SSR primers, the matrix of genetic distance among individuals was obtained using the arithmetic complement of the Jaccard index and cluster analysis by UPGMA hierarchical method. Considering the results obtained from the genotyping of the 80 families, it was possible to clearly distinguish CIMMYT and Piranão groups, resulting in the identification of the 46 (23 CIMMYT e Piranão 23) more divergent individuals for both intra and inter-population recombination. The dendrogram generated by the UPGMA method from the Jaccard dissimilarity matrix allowed the grouping of genotypes into homogeneous groups according heterotic group. The results showed that the variability among the genotypes ensures continuity of recurrent selection program and the use of SSR markers was an important tool for the identification of genetically divergent individuals.

GENETIC ANALYSIS OF RESISTANCE TO SOUR PASSIONFRUIT TO *Colletotrichum gloeosporioides* UTILIZING THE GENETIC DESIGN II

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Anthracnose is an important disease for passion fruit, causing considerable losses in productivity and fruit quality. Thus, it is necessary to obtain more resistant cultivars and hybrids aiming to reduce production costs, improve product quality, the sustainability of agribusiness and reduced environmental impacts. Within the methods used in the selection of parents in plant breeding programs, the genetic design II informs about the potential of the parents and the existence of heterosis, providing major advances in the selection and formation of progeny. This design is appropriate for the estimation of genetic components of variance in the populations of study and estimates of genetic parameters. The objective of this project is to perform the genetic analysis of passion fruit resistant to the *Colletotrichum gloeosporioides* using genetic design II. Crossings according to the genetic design II will be done in order to obtain the genetic material.Therefore, four plants of *P. alata*, identified as resistant to *C. gloeosporioides* will be used as pollen donor (male parent) and four plants of passion fruit from UNEMAT 01 population will be used as female parent. Thus, 16 crossings will be done. The crosses are performed manually, where ten female parent flowers are pollinated with pollen from each male parent. Seven days after executing the crossings, the fixation will be checked. The completely randomized design will be used with 16 treatments (crosses), five repetitions and 10 plants per plot. The isolate of *C. gloeosporioides* will be obtained from leaves of plants infected by the fungus and placed in petri dishes containing approximately 20 ml of potato dextrose agar (PDA). The inoculation with *C. gloeosporioides* will be performed by small injuries on leaf blade, with the aid of bristle brush and then sprayed the solution containing the pathogen. Inoculations will be held in seedlings of sour passion fruit at 45 days after sowing in greenhouse. The plants will be covered with plastic bags for 12 hours, free of irrigation in this period thus simulating natural environmental conditions for disease transmission. No chemical control will be performed in order to evaluate the behavior of cultivars before the disease. It is expected that this study can estimate genetic variance components and allow the selection of resistant parents to *C. gloeosporioides* in order to help the plant breeding program of passion fruit.

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HISTOLOGICAL ANALYSIS AND AGRONOMIC PERFORMANCE OF GRAFTED SOUR PASSIONFRUIT

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Brazil stands out on the world scenario as a major producer and consumer of passionfruit. However, the high incidence of fusarium have caused significant decreases in the number of fruits and reduced life of this culture. Thus, the use of seedlings grafted on rootstocks resistant to fusarium enables the acquisition and multiplication of productive plants. Therefore, the aim of this work is to evaluate the effect of rootstocks on the quality and productivity of sour passionfruit and describe the histological characteristics of the tissue binding process between passionfruit plants and rootstocks, obtained by the full cleft grafting and *ex vitro* micrografting methods. The experiments will be conducted at the experimental area of the plant breeding laboratory of Universidade Estadual do Mato Grosso, in Tangará da Serra, MT. The field experiment will be set in a randomized block design in a 4x2+4 (genotypes x rootstocks) with three replicates and nine plants per plot. It will be used as graft two genotypes from the UNEMAT passionfruit breeding program called UNEMAT S10 and UNEMAT S30 and the commercial cultivars FB200 and FB300. The rootstocks will be *Passiflora alata* and *Passiflora nitida* and the four controls will be the genotypes without grafting. The seedlings will be produced using propagation by full cleft grafting. The assessed characteristics will be productivity, fruit diameter, fruit weight, fruit length, number of fruit per plant, peel thickness, percentages of pulp, pulp color, total soluble solids, total titratable acidity and hydrogen potential. It will be performed again the full cleft and *ex vitro* micrografting techniques to obtain each combination scion/graft to subsequent histological analysis. For the micrografting, it will be removed the seedlings tops of the genotypes UNEMAT S10 and UNEMAT S30 and the commercial cultivars FB 200 and FB 300 which will be micrografted in the rootstock species *P. alata* and *P. nitida* both obtained by germinating seeds and cultured in commercial substrate in laboratory conditions. The micrografting experiments will be performed on the hypocotyl and tested with application in culture medium at the micrografting point. Finally, it will be performed histological analysis of combinations between the grafts and rootstocks. The regions in which the grafting and the micrografting occurred will be sectioned, fixed in FAA (formaldehyde: acetic acid: ethanol 50%, 5:5:90) for 48 hours and stored in ethanol 70% and sectioned in the microtome. The materials will be stained with astra blue and basic fuchsin and arranged between slide and coverslip with Canada balsam obtaining semi-permanent histological slides. The sections will be observed and analyzed under optical microscope and photomicrographed. It is expected that the species of *P. alata* and *P. nitida* are promising as rootstock resistant to fusarium and that the grafted sour passionfruit may generate fruits within the market standards, presenting a good agronomic performance regarding to quality and productivity.

GENERAL AND SPECIFIC COMBINING ABILITY IN SUPER SWEET CORN

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Maize (Zea Mays L.) presents the largest volume of cereal production in the world. In Brazil, the production reaches 15.12 million hectares and a production of 82 million tons. Thus, Brazil is the major producer of maize and has great potential for the production of sweet corn. At this scenario, the program of genetic improvement of Universidade Estadual do Norte Fluminense Darcy Ribeiro has acted in order to obtain lines and hybrids of maize. Thus, this study aims to estimate the general and specific combining ability among genotypes of super sweet corn in order to obtain superior hybrids. The experiment will be conducted in two locations, at Colégio Estadual Agrícola Antônio Sarlo and Estação Experimental da Ilha Barra do Pomba in Itaocara. A partial diallel (10 x 10) involving the best strains (S7) will be held. The plant material will be selected from populations CIMMYT SH2, CIMMYT SH2-8HS, Piranão SH2-8HS and Piranão SH2, which were obtained from a single ear by successive selfing until the S6 generation in order to increase homozygosity. The materials will be evaluated for all characters related to productivity. A molecular analysis will be held on at an auxiliary basis in order to select superior genotypes. This step will be done with EST-SSR primers obtained by the software SSR Locator and the software Primer Select 6.1. Based on the results of all analyzes, we expect a strong association of quantitative and molecular factors by the use of EST-SSR primers. Thus, a greater genetic gain can be expected due to better conduction of future crossings.

ESTIMATES OF GENETIC PARAMETERS IN FULL-SIB PROGENIES OF GUAVA (*Psidium guajava*)

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The experiment was conducted in a greenhouse at Universidade Estadual do Norte Fluminense Darcy Ribeiro in Campos, Rio de Janeiro, from March to September 2014, aiming to study genetic parameters, such as genetic and phenotypic variances, coefficient of error variation, genetic heritability and variation index related to seedlings quality of full siblings progenies of guava (Psidium guajava L.). The seeds of full-sib progenies of guava were sown in polystyrene trays of 128 cells and placed in a greenhouse with misting. Sixty days after sowing the seedlings were transplanted in polyethylene bags with a capacity of 2 L, filled with commercial substrate (Tropstrato HT®) and allocated in a greenhouse in a randomized block design consisting of nine full-sib progenies of two replications, five plants per plot. One hundred and eighty days after sowing the seedlings were evaluated with analysis of variance and estimated genetic parameters for the following features: Width of leaf (LF); Leaf length (CF); Leaf area (LA), estimated by linear equation involving the product of linear dimensions L x L, using the equation $AF = 1.2312 + 0.7829CXL$ regression; Height of Plants (ALT); Number of Sheets (NF); Stem diameter (DM) and Height / Diameter Relation (AM / DM). The mean squares of the progenies were significant by F test with $p < 0.01$ for the features, CF, NF and ALT; significant at $p < 0.05$ for AF and DM, indicating the existence of genetic variability among the progenies of guava for these characters, which is a favorable situation to practice breeding, except for LF and ALT / DM who did not have significant differences. Variation within broods were detected only for the number of leaves, because it was significant at $p < 0.05$, indicating variability within progenies for this trait. While for other traits, there was no significant variation. Heritability coefficients generally ranged widely, with values from 13.07% (AM / DM) to 71.91% (ALT). Based on the results, higher heritability coefficients were obtained for ALT and NF characters, and they are caused by high genotypic variance of these characters, because the marked superiority of some individuals and some progenies relative to the population mean, that predicts favorable conditions for selection of progenies for these characteristics. Values above 80% and the index of greater than unity variation heritability, selection satisfactory gains can be obtained. This situation was not observed for any trait, indicating that superior progenies can be obtained by the use of more accurate methods of improvement, as the genotypic recurrent selection.

PHOTOCHEMICAL EFFICIENCY IN *Capsicum frutescens* SEEDLINGS CULTIVATED IN DIFFERENT SUCROSE CONCENTRATIONS

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Peppers (*Capsicum spp.)* are used as fresh vegetables, condiments and ornamental plants and therefore, they have great economic importance in the world. The genetic breeding programs of such genus present problems that can be solved with embryo culture. Thus, studies related to photosynthetic capacity *in vitro* are of great importance to optimize the cultivation of seedlings in this environment. So, this study aimed to verify the effect of sucrose concentrations on germination of cotyledonary late embryos of *Capsicum frutescens* and on their photosynthetic capacity. In order to proceed the experiment, mature seeds of *C. frutescens* (UENF 1636) were taken from the germplasm bank of the Universidade Estadual do Norte Fluminense. The seeds were sterilized in 70% alcohol for one minute, in NaClO 0.7% + Tween 20 for 15 minutes, rinsed three times in deionized autoclaved water and soaked for 12 hours. During the germination essay, embryos were isolated and placed in Petri dishes containing ½MS medium with different concentrations of sucrose (0, 10, 20, 30 and 40g L^{-1}) with four replications and five explants in each dishes, and evaluated during 15 days. During experiment of seedling growth, the embryos were isolated and germinated in Petri dishes containing ½MS medium without sucrose. After 15 days, the seedlings were transferred to flasks containing ½MS medium with different concentrations of sucrose (0, 10, 20, 30 and 40g L^{-1}) with four replicates and with five explants each. The evaluations of photochemical efficiency (chlorophyll fluorescence, SPAD reading and potential photosynthesis) were made after 30 days. In the evaluation of potential photosynthesis, 8 intensities of photosynthetic active radiation (PAR): 0; 71; 143; 214; 286; 357; 429 e 500 µmol m^{-2} s^{-1} were used, spending three minutes for each intensity. Treatments with 0 and 10 g sucrose showed the highest germination rate with 100 and 97%, respectively. There was no statistical difference in the values of the fluorescence emission from chlorophyll *a* in that maximum quantum yield of PSII (F_v/F_m) in all treatments. the values of the fluorescence emission from chlorophyll *a* had means between 0.75 and 0.85, indicating that the PSII this in the appropriate activity. In relation to the photosynthetic index (PI), only the treatment with the concentration of 20 g L^{-1} sucrose has differed statistically, presenting value of 2.58, with the highest photochemical efficiency. The SPAD reading treatment without sucrose has not differed statistically from the other treatments, presenting values ranging from 27.68 to 34.88. In conclusion, in PAR values around 400-500 mol m^{-2} s^{-1}, the presence of sucrose in the culture medium enhanced the efficiency of the oxygen evolving complex in PSII. Therefore it turns out that this technique is a good tool for breeding programs obtaining good germination rate and no physiological alteration.

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EVALUATION OF POPCORN GENOTYPES FOR RESISTANCE TO *Cochiobolus heterostrophus* AND *setosphaeria sela*

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Several factors contribute to lower production of a corn crop. Overall, leaf diseases in corn have caused great economic losses to producers, generating reductions up to 40% in grain productivity. Regarding to the cultivation of popcorn, this value can be even higher because of its susceptibility to diseases. These losses result from the restriction of the useful leaf area, which compromises the energy requirement of plants and the development of grains. The objective of the present study was to evaluate the genetic potential of popcorn genotypes contained in the germplasm bank of UENF for their resistance to the *Cochliobolus heterostrophus* and *Setosphaeria sela* fungi, which cause helminthosporium maydis and turcicum leaf blight, respectively. To achieve the proposed objectives, 37 genotypes of popcorn were subjected to resistance tests. The experiment was installed in randomized blocks with four replicates at *Colégio Estadual Agrícola Antônio Sarlo*, located in Campos dos Goytacazes/RJ, Brazil. Each experimental unit consisted of 3m rows containing 16 plants. The natural occurrence of foliar diseases was monitored by quantifying the severity (%) via diagrammatic scale based on the plant and based on the leaf immediately below the first ear in six plants per experimental unit. In order to provide reliability to the levels of resistance and susceptibility observed in the field, the experiment was replicated simultaneously in a greenhouse, installed in randomized blocks with four replicates, totaling 148 experimental units. Fungi *C. heterostrophus* and *S. sela* were inoculated in such pants. For this purpose, a suspension of such fungi was prepared in laboratory at concentration of 10^4 conidia/mL and later, the suspensions were pulverized on the plants to pour point (20 mL suspension, on average). The severity of the diseases was evaluated with the aid of a diagrammatic scale based on the third leaf (leaf showing the highest intensity of the disease). The data were registered and are being tabulated for later analysis (analysis of variance and means test). The results will allow us to identify the level of resistance and susceptibility of the popcorn genotypes to the evaluated diseases. Thus, allowing the development of future studies with the use of potentially resistant genotypes through the popcorn breeding program of UENF.

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RECURRENT SELECTION EFFECT IN UENF-14 POPCORN POPULATION

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Agricultural diversification is an interesting strategy to minimize socioeconomic problems arising from low-profit monocultures as the case of the sugar cane monoculture in the North and Northeast regions of Rio de Janeiro (Brazil). Within the options, the culture of popcorn is an excellent alternative because of its high profitability and popular acceptance. However, the commercial cultivation of popcorn is still rather modest in the country and inexistent in Rio de Janeiro. This is mainly a result of the limitation in the number of available cultivars in the market. Not coincidentally, only three cultivars (RS 20, UFVM2 Barão Viçosa and IAC 125) have been made available for the market in the 2011/2012. In Brazil, one out of the 30 popcorn cultivars registered from 1998 to 2010 in the National Register of Cultivars (*Registro Nacional de Cultivares*, RNC) of Ministry of Agriculture, Livestock and Food Supply (MAPA), was provided by Brazilian public sector. It is not a coincidence that there are few breeding programs with this culture in the country, although it provides an income three times higher than common corn. UENF develops the only popcorn breeding program in Rio de Janeiro, containing activities for hybrid production, evaluation of accessions by molecular markers aiming the use in applied breeding, as well as the use of intrapopulation recurrent selection. The objective of the present study was to investigate the effective genetic gains and the genetic variability of population UNB-2U among seven recurrent-selection cycles of the Popcorn Breeding Program of UENF. Regarding to the different strategies employed to obtain the cycles (mass selection, full-sibling families, S_1 families and half-sibling families), we aim to equate the genetic structures of the cycle through their use as female parents in crossing with the least advanced cycle as a common male tester. The following procedure was adopted to obtain such progenies: rows with a sample of individuals from the recurrent selection cycles (C_0 to C_6) interspaced with rows of the tester (cycle C_0 of population UENF-14) so that the half-sibling families are obtained from the crossing of two recurrent-selection cycles with the tester (C_0). One hundred and eighty families of half-siblings were obtained and evaluated for ten traits of agronomic interest, including grain yield (GY) and expansion rate (ER) in two environments of Rio de Janeiro State, using an incomplete block design with an arrangement of replicates within sets. It is believed that with the results obtained in this experiment we will be able to answer the question whether there is effective variability in the referred population under study, which is crucial to determine the perspectives and the future of the Popcorn Breeding Program of UENF.

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RESPONSE TO VIRAL INFECTION OF THE WOODINESS OF A POPULATION OF PASSION FRUIT COMING FROM BACKCROSS

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Brazil possesses a great diversity of species of passion fruit. Since the Decade of 70, Brazil has been excelling as major world producer of passion fruit (*Passiflora edulis* Sims), but productivity and cultivation of the passion fruit have been seriously affected by phytosanitary problems. In some situations, the incidence of diseases can derail the passion fruit cultivation. Within the diseases that affect the culture of passion fruit, it is highlighted the hardening of fruits that is caused by the *Cowpea aphid-borne mosaic virus* (CABMV). Affected plants reduce leaf area and weight of fruit, with consequent reduction in the number, quality and commercial value of fruits. There is no measure to control such disease properly. It is known that the genetic basis of commercial passion fruit for disease resistance is too narrow, thus, the wild species can contribute to increase the degree of resistance by means of interspecific hybridizations. This study aimed to evaluate the CABMV resistance in a segregating population from backcrossing, continuing the program of genetic improvement of passion fruit to CBMV resistance of Universidade Estadual do Norte Fluminense Darcy Ribeiro. The experiment was conducted in the experimental area of Colégio Agrícola Antonio Sarlo, in Campos dos Goytacazes. The backcrossing were performed between a hybrid (*P. edulis* and *P. setacea*), which is potentially resistant to CBMV and two elite genotypes of *P. edulis*. The plants were inoculated with the virus at the stage of seedlings in greenhouse and subsequently taken to the field. Evaluations proceeded in 177 genotypes, wherein nine genotypes are of the species *P. edulis*, three of *P. setacea* and 165 genotypes derived from backcrossing. The characterization of genotypes was based on severity of foliar symptoms, by means of a scale of notes ranging from 1 to 4 wherein 1 = no, 2 = mild mosaic without deformation leaf; 3 = severe mosaic without leaf deformation and 4 = severe mosaic, leaf deformation and bubbles, the evaluations proceeded during 120 days. The data obtained were used to calculate the area under the disease progress Curve (AACPD). With the results of the AACPD the genotypes were classified in susceptible and resistant. Hybrids H 237, H269, H247 and H58 obtained the greatest value of AACPD (480) equal to some genotypes of commercial species, being that these genotypes showed the most severe symptoms of the disease. In contrast, the genotypes H25, H95, H120 and H62 presented minors values for AACPD, 135, 135, 142.4 and 120 respectively, and the H62 genotype introduced the same performance of *P. setacea*, species considered resistant to the virus. The resistant hybrids can be selected to be used in the next cycle of backcrossing, or in case of presenting good agronomic performance such hybrids can be released as new cultivars.

GUAVA RESISTANCE FOR *Meloidogyne enterolobii*

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Meloidogyne enterolobii is currently the main phytosanitary problem of the culture of guava (*Psidium guajava L*). Its incidence results in decrease in productivity and inevitable death of plants. The most effective method for controlling nematodes is the use of resistant cultivars. In this sense, the objective was to find sources of resistance to *Meloidogyne enterolobii* in guava genotypes collected in the southeastern region: four in Caparaó (Minas Gerais) and six in São Paulo. Seedlings grown from seeds of guava were inoculated with 5,000 eggs and J2 (second stage juveniles) in suspension of *Meloidogyne enterolobii*. The population of nematodes was confirmed as *Meloidogyne enterolobii* by electrophoresis of esterase isozyme technique. The cultivar Paluma was used as control of susceptibility. The roots of the inoculated plants were processed after 180 days of nematode inoculation. The population of juvenile and adult eggs were estimated with Peters counting chamber at stereoscopic microscope. The data obtained constituted the final population and were used in determining the reproduction factor. Plants with reproduction rate below one were considered resistant, while those whose reproduction rate values were bigger than one were considered susceptible to nematode. The evaluated genotypes of *Psidium guajava L.* showed a mean of reproduction factor of 2.4. We conclude that all tested genotypes of *Psidium guajava L*. were susceptible to *Meloidogyne enterolobii* and more research needs to be done in order to search resistance to this nematode.

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ESTIMATES OF GENETIC PARAMETERS IN SWEET SORGHUM

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The cultivation of sweet sorghum is a complementary alternative to sugar cane regarding to ethanol production, because sweet sorghum presents stalks with good sugar yield. Thus, sweet sorghum can be used during the off-season of sugar cane. Sweet sorghum Presents various advantages that make possible the cultivation, such as low cost production, short cycle, mechanical harvesting and its bagasse can be used as an energy source. Within the main objectives of breeding programs of sweet sorghum, the improvement of sugar content and quality and the increase of green biomass productivity are preferred. Therefore, it is important to know the genetic parameters related to such characters in order to assist the selection of genotypes. The objective of the study was to estimate the genetic parameters of agronomic characters of 25 sweet sorghum genotypes in Cáceres-MT. The experiment was conducted in the experimental area of Universidade Estadual do Mato Grosso (UNEMAT). Twenty-five genotypes of sweet sorghum were evaluated in randomized blocks with three replications and the characteristics evaluated were: number of days from planting to flowering (FLOWERING); average plant height (ALTP); average number of stalks (NC); average stem diameter (DC); average volume of broth (VC) and total soluble solids (°BRIX). The data were submitted to analysis of variance and the analysis of genetic parameters using the software Genes. Significant at 1% probability for FLOWERING, ALTP, NC, PMS, NC, DC and ° Brix, and significant at the 5% for the PMV and VC difference was detected, showing genetic variability among the genotypes. The phenotypic and genetic variances among genotypes were of low magnitude for ALTP, NC, PMV, PMS, NC, DC, CV and Brix, except FLOWERING that presented values of 24.98 to 23.06, and phenotypic variance and genotypic respectively, indicating the existence of high degree of genetic variability among genotypes and suggesting the possibility of success for selecting them. The heritability estimates were high for FLOWERING magnitude, and ALTP and NC with 92.33%, 92.26% and 90.45%, respectively. Such index reflects the presence of considerable genetic component in the expression of this character. The index variation presented high estimate for FLOWERING, ALTP, NC and NC with values of 2.00, 1.99, 1.78 and 1.39 respectively, indicating that they are favorable in the selection process. In general, there is significant variability among the evaluated genotypes of sweet sorghum. The genetic parameters indicate great possibilities of success in breeding programs aiming the selection of the characteristics evaluated by the present study.

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POPCORN PLANT SYSTEM *VERSUS* PHOSPHORUS: BIOMETRIC ANALYSIS OF NUTRITIONAL EFFICIENCY

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The expansion of agribusiness in Brazil has allowed the increase of the planted areas of certain crops, such as popcorn. Thus, popcorn has become interesting to producers because its product is highly profitable and greatly appreciated by Brazilian population in general. In order to achieve optimal productivity, phosphorus (P) stands out as the main element for plant survival. In Brazil, most soils are highly weathered, with low phosphorus availability under natural circumstances. Not coincidentally, the agricultural production in the country is mostly based on the use of mineral fertilizers in order to provide P, which significantly elevates the production cost. Despite such scenario, no research has been conducted yet, regarding to the improvement of popcorn associated with the efficiency of P use. Therefore, the objective of this study is to understand the existing relationships between traits related to efficiency and responses to phosphorus in 37 popcorn lines from the Active Germplasm Bank (*Banco Ativo de Germoplasma*, BAG) of UENF (Universidade Estadual do Norte Fluminense Darcy Ribeiro). The evaluated traits will be: shoot dry matter yield; root dry matter yield; phosphorus content in shoots and roots; P content in shoots; P content in roots; rooting efficiency; absorption efficiency; and efficiency of translocation and use of P in the shoots. The experimental design will be completely randomized, with 37 treatments and two levels of P in five repetitions. The experiment was conducted at a greenhouse at UENF using 3.0-dm^{-3} pots filled with substrate. Data will be submitted to Analysis of Variance, Means Test, Multivariate Analysis, and Parameter α, an estimator of the use efficiency of phosphorus. Thus, this study will enable the identification of contrasting parents regarding to phosphorus efficiency, which will be the basic tool to determine the genetic control of this trait in popcorn populations. Then, such study will allow the establishment of the most suitable breeding strategy in order to select superior genotypes in segregating generations.

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SELECTION OF *PENNISETUM PURPUREUM* SCHUM. GENOTYPES FOR ENERGY PURPOSES THROUGH DIFFERENT STABILITY METHODOLOGIES

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The demand of energy is becoming a global concern. Within the possible solutions to such situation is biomass, which stands outs as an opportunity for short and long terms. Within the sources of alternative energy, elephant grass (*Pennisetum purpureum Schum*.) is noteworthy because it is typically tropical, perennial, provides high biomass yield. Because of its large genetic variability, elephant grass can adapt to prevailing climatic conditions in almost all the Brazilian territory. Due to the increased importance of this forage plant in Brazil, the stability of genotype production is a feature that should be considered in the selection of materials for better adaptation to different environmental conditions as well as to generate greater yields and reduce costs. The objective was to obtain a parameter of stability in the selection of elephant grass genotypes for biomass production. The dry matter yield of 40 elephant-grass genotypes was evaluated during four harvests performed from 2009 to 2011, in a randomized-block design. Individual and combined analyses of variance of harvests were performed. The estimate of the parameters of stability of the genotypes was achieved by the methods: Yates & Cochran, Plaisted & Peterson, Wricke, Lin & Binns, Annicchiarico and ecovalence of Kang & Phan. Genotype × harvest interactions were verified, indicating that the relative responses of the genotypes were not the same among different harvests. The Genotypes Mercker Pinda México, Mercker 86-México, P-241-Piracicaba and Guaçu/I Z.2. presented high stability and productivity by the methods of Lin & Binns and Annicchiarico. The evaluation of the genotypes by different stability methods for biomass production allowed a better characterization of the productive response and provided greater reliability to the identification of superior genotypes.

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OBTAINING INTERSPECIFIC HYBRID OF *PSIDIUM* SP. TO STUDY THE INHERITANCE OF RESISTANCE TO *Meloidogyne enterolobii*

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The extermination of guava orchards in Rio de Janeiro (RJ) is caused by a complex disease that was called decline of guava. The best prospects is the development of resistant cultivars or rootstocks. The aim of this study was to obtain and evaluate interspecific hybrids of *Psidium* for nematode resistance *M. enterolobii* and conducting genetic studies, such as mapping sources of resistance in segregating generations of interspecific hybrids. Crosses between species *P. guajava, P. guineense* and *P. cattleyanum* were performed. The crosses were performed when the flower buds had burst the calyx. In the pollination procedure, the flower buds of the maternal plant were emasculated and stamens removed with tweezers and emasculation pollination was held during the same day. Donor flowers were macerated in a blade of glass microscope and pollen from male parent was distributed across the surface of the stigma. After pollination, the buttons were labeled with identification of the parents and protected with paper bags to prevent contamination, either by wind or by pollinators. 1,200 crosses were performed, and the mean percentage of fruit set were 24.13% for the crosses with the parental *P. cattleyanum* (CV1) *X P. guineense* (CV11) and 1 % for the reciprocal crossing *P. guineense* (CV11) *X P. cattleyanum* (CV1); 10 % for *P. cattleyanum* (CV6) X *P. guajava.* (1310 I); 5 % for *P. cattleyanum* (CV6) X *P. guajava.* (97I); 40 % for *P. cattleyanum* (CV8) *X P. guineense* (CV11); 10 % for *P. cattleyanum* (P11) X *P. guajava.* (97I); 3% for *P. cattleyanum* (P11) X *P. guajava.* (99I); 5% for *P. cattleyanum* (P35) X *P. guajava.* (97I); 2 % for *P. guajava.* (99I) X *P. cattleyanum* (P52); 6 % for *P. guajava.* (134 II) X *P. cattleyanum* (P51); 4% for *P. guajava.* (95I) X *P. cattleyanum* (P11); 5 % for *P. guajava.* (132II) X *P. cattleyanum* (CV4). There was no success for the remaining 714 crosses made between different genotypes. Mature fruits were collected, taken to the laboratory for separation of seeds from the pulp and seeds put to dry in the shade for 24 h. After that it was done the counting of seeds, which were placed inside an identified paper bag, properly for cold storage. Subsequently the seeds of each fruit will be germinated and the hybrids will be confirmed with microsatellite genotyping, and then declared as true hybrids and continuing with the study of the inheritance of resistance to *M. enterolobii* with segregating populations.

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EVALUATION OF INBRED FAMILIES OF GUAVA USING MORPHO-AGRONOMIC TRAITS

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Brazil is one of the world's biggest producers of guava (*Psidium guajava L.*), and this crop has great economic importance for the country. There is high variability among cultivated varieties due to the presence of a mixed mating system. This study aimed to estimate genetic parameters of 18 inbred families, based on morpho-agronomic traits. The experiment was conducted in the experimental area of Universidade Estadual do Norte Fluminense Darcy Ribeiro, located in Itaocara / RJ. The experimental design was a randomized complete block with five replicates. Eighteen inbred families obtained from controlled pollination were evaluated. Genetic parameters were estimated based on plant height (PH), stem diameter (DC). Plant height was determined from ground level to the edge of the plant using a ruler (cm) and stem diameter in the middle third of the plant area using a caliper (mm). Analysis of variance were significant for plant height ($p < 0{,}01$) and stem diameter ($p < 0{,}05$) between the families analyzed. The data demonstrate the existence of genetic variability among the evaluated families, which indicates potential for selecting superior plants in the breeding program of guava at UENF. There was no significant difference for the source of variation plant within family. The lower herdability trait was identified in DC (33,66) as well as the variation index (0,66), while for AP estimates were relatively high, 61,60 and 3,34, respectively. These analyzes suggest favorable conditions for the selection gain in families evaluated using the variable plant height.

ÁREA: RECURSOS GENÉTICOS VEGETAIS

GENETIC DIVERSITY AMONG PAPAYA ACCESSES BASED ON TWO MORPHOLOGICAL CHARACTERS

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The genetic diversity study provides fundamental information on the plant breeding programs in relation to the characterization, conservation and utilization of genetic resources. This study aimed to evaluate the genetic divergence of papaya (*Carica papaya* L.), based on morphological characteristics. Two agronomic traits were evaluated in fifty-nine accessions of papaya, belonging to an active gene bank. The experimental design was a randomized block with two replications. The divergence between accessions was estimated by hierarchical clustering technique based on the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). There were significant differences at 1% of probability among accessions regarding to plant height and stem diameter, showing existence of variability. The experiment showed low coefficients of variation for plant height (8.04%) and stem diameter (10.16%), showing good experimental managing. The heritability values were 86.03% and 68.40% for plant height and stem diameter respectively. These results demonstrate low environmental influences on the manifestation of these characteristics, expressing the reliability of the phenotypic value as an indicator of genetic value. Based on the criterion Mojema, the cutting held at the distance dendogram of 12.04% allowed the formation of four groups of dissimilarity. The first group was composed of 42 accessions, the second group presented 14, the third group presented 2 and finally, the fourth group contained only one, totaling 59 accessions under study. Thus, this study shows that the groups 3 and 4, contains the most divergent genotypes. These results may infer that crosses between the most divergent accessions with the accessions of other groups could contribute for the improvement of papaya.

EVALUATION OF MORPHOAGRONOMIC TRAITS IN ELEPHANT GRASS GENOTYPES FOR ENERGY PURPOSES IN NORTH RIO DE JANEIRO STATE

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Elephant grass has a high dry matter yield despite low consumption of nitrogen fertilizer, so it is considered a promising culture for alternative energy sources. For a long time, the objectives of genetic breeding with this species were to identify and generate cultivars aiming at animal feeding. Due to the need to develop genotypes with potential for use as energy sources, the objective of this study was to evaluate morphoagronomic traits of 73 genotypes of elephant grass for energy purposes in Campos dos Goytacazes/RJ, Brazil. The experiment was conducted at the Experimental Station of PESAGRO-RIO, located in the municipality of Campos dos Goytacazes/RJ. The experimental design was of randomized blocks, with two replicates. Each plot was formed by a 5.5-m row spaced 2 m apart, totaling 11 m^2. Planting took place in February 2011. A plot-leveling cut was made in December of the same year, and four evaluation cuts were also made, wherein the following traits were evaluated: dry matter yield (DMY), in t·ha^{-1} cut^{-1}; number of tillers (NT) per linear meter; plant height (HGT), in m; stem diameter (SD), in cm; and leaf blade width (LW), in cm. The first two cuts were made in June and December, 2012, respectively; the third, in August, 2013; and the last cut was in February 2014. The genotypes showed significant differences in all cuts, which allowed the formation of distinct groups by the Scott-Knott's mean clustering test. Except for the second cut, the genotypes showed a significant difference only regarding the height variable, according to the aforementioned test. Regarding to dry matter yield, two groups were formed both in the first two cuts and in the evaluation of the annual production. Most genotypes showed lower productivity in the second and fourth cuts, due to the low precipitation during the evaluation period. Most genotypes showed lower productivity in the second and fourth cuts due to the low precipitation during the evaluation period. Based on the mean values of dry matter yield in all cuts, genotypes King Grass and Gigante de Pinda stood out among the others, and were always present in the elite group, with mean values of approximately 28 t·ha^{-1} cut^{-1} in both DMY cycles.

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PRE-BREEDING OF *Heliconia* spp. WITH ORNAMENTAL POTENTIAL IN MATO GROSSO

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Heliconias are known as herbaceous plants, with different sizes, reaching up to 12 meters of height. Its propagation is done by rhizomes, comprising pseudostem, leaves and inflorescences. Such Tropical genus stands out in ornamental plant market, competing with the main species considered traditional as anthuriums, roses, chrysanthemums. Its appeal for commercialization in the world market is due to the exotic appearance of the inflorescence variation of colors, shapes, continuous production of flowers and postharvest longevity. Thus, the cultivation of Heliconia genus must be considered a viable activity especially for smallholders, because of countless reasons. In this context, the objective of the study is to characterize the morphological and genetic divergence among accessions of Heliconia genus collected in different regions Mato Grosso. Therefore, it will be used the randomized block design with 28 accessions and 10 repetitions with one plant per plot. The plant spacing is 1.5 m x 3.0 m under unshaded systems. For morphological characterization, 37 descriptors will be evaluated, with 14 qualitative descriptors and 23 quantitative descriptors. The field evaluations will be performed at 90, 150 and 240 days after planting. From the morphological data, the estimation of genetic divergence among accessions will be held and then, the cluster analysis by UPGMA method. It is expected that the study describes the morphological characteristics and estimate the genetic diversity of Heliconia spp. accessions aiming at the possible use as parents for the development of a breeding program for obtaining genotypes of interest.

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CRYOPRESERVATION OF *PASSIFLORA Mucronata* LAM.

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Cryopreservation is a technique for germplasm conservation, which allows for long-term storage at ultra-low temperatures (-196 ° C) in liquid nitrogen (NL_2), so it is important to safeguard the genetic diversity of species with potential for use in breeding programs. Brazil is considered the main center of diversity of the genus *Passiflora* spp., however, genetic erosion associated with other factors such as poor knowledge about the species, low germination and difficulty in cultivation for some wild species, have complicate their use for commercial purposes. The objective of this study was to evaluate efficiency of cryopreservation of seeds of *Passiflora mucronata* Lam. For this, was held initially a test to determine the low moisture content that seeds tolerate without losing their physiological quality. Based on this evaluation, the moisture content more appropriate for cryopreservation was determined, and the best results obtained with the content of 12% (w.b.). After that, the seeds were subjected to four treatments: (7% DMSO; 0,3 M sucrose; without cryoprotectors and control), wherein the control consisted of seeds that were not submitted to NL_2, with five replications of 50 seeds, in a complete randomized design. The variables analyzed were: IVG, germination percentage (%), IVE, emergence percentage (%), shoot length (cm / seedling), radicle length (cm / seedling) and dry weight (g). The data were analyzed by SISVAR program, performing the analysis of variance (F test) and the Tukey test (probability of 5%). The results were significant for almost all variables, except the IVG and the germination percentage. The best means were obtained for the seeds used as control (without cryoprotectants and immersion in NL_2) and those treated with 0.3 M sucrose. Comparing them, they have showed the same statistical performance as the shoot length (6.384 and 5.950 cm) and dry weight (0.052 and 0.066 g). The lowest means were observed in the treatment with DMSO, followed group seeds cryopreserved without cryoprotector, except for the variable radical length, where the best means was the DMSO and without cryoprotectors. This result may be due to a lower emergence percentage of seedlings these two treatments (8,800 and 15,200 respectively) to evaluate the radicle length of a few individuals within each repetition. As for the IVE and emergence percentage, the best averages were the control (1,766 and 57,200) followed by treatment with sucrose (0,938 and 36,400). Given these results, it was concluded that cryopreservation causes damage in seeds of Passiflora mucronata, and thus required the use of cryoprotectors, such as sucrose, which showed satisfactory results, reducing injury in seeds caused by exposure to low temperatures. The DMSO presented the worst results, indicating possible toxicity or inefficacy as the concentration used. Other tests should be performed to determine the best concentrations of cryoprotectors, such as sucrose and others cryoprotectors were not included in this study. Furthermore, the cryopreservation is promising for *Passiflora mucronata*.

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CRYOCONSERVATION OF SEEDS OF *Passiflora suberosa* L.

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The passion fruit is a species of high economic value, ornamental and medicinal and is in relation to tropical fruit for the ex situ conservation, due to the existence of great genetic variability intra and interspecific of *Passiflora*. An interesting alternative for conservation of this germplasm is the cryoconservation, conservation in liquid nitrogen (-196ºC). Seeds of the access of *Passiflora suberosa* L. from germplasm bank of Universidade do Estado de Mato Grosso in Cáceres were used. A part of the seed was used for standardization of water content to 9.5 % using the method of dehydration in silica gel. Subsequently, the seeds were submitted to four distinct treatments, being: T1 - 7% DMSO; T2 - 0.3M sucrose; T3 - without cryoprotection + storage in NL_2; and T4 (control) – without cryoprotection and storage in NL_2. The experimental design was completely randomized. Each treatment was composed of 450 seeds in five repetitions of 50 units each. After 3 days, the seeds frozen in NL_2 were removed from the cryogenic tank and thawed in water bath at a temperature of 37 ºC for 20 minutes. The seeds were evaluated by standard germination test and by the following tests of vigor: index of germination speed, percentage emergence, index of emergence speed, shoot length (cm/seedling) and dry weight (g) to 30 days. For germination test, seeds were placed on blotting-paper in plastic boxes (Gerbox®), kept in a germinator type BOD at 25 ºC and photoperiod of 12h. The substrate was moistened with distilled water in the proportion of 2.5 times the weight of the paper. For vigor tests, new plastic boxes (Gerbox®) were filled with vermiculite moistened with distilled water and distributed on laboratory bench, with temperature and relative humidity variables and without monitoring. The data obtained were submitted to analysis of variance by Sisvar program, being the averages compared by the Tukey test, with probability of 5%. It was found that the cryoconservation did not significantly affect the quality of the seeds. The germination was similar for all treatments, keeping general average of 52.3% (cv. = 22.92%). In relation to the vigor test, the passion fruit seeds showed the same index for index of germination speed (2.74; cv. = 23.95%), percentage emergence (33.60%; cv. = 31%), index of emergence speed (1,48; cv. = 29,06%) and dry weight (0,02 g; cv. = 35,18%), i.e., there not was significant change between treatments during the conservation. The use of DMSO, sucrose and without cryoprotectors has fostered the growth of shoot length of the seedlings, with average above 4.20 cm, being statistically higher than the mean value of the experiment, equal to 4.19 cm (cv. = 7.25%). The seeds of *P. suberosa* L. can be previously dehydrated at low water content (9,5%) and, subsequently, treated with cryoprotectors for their conservation in liquid nitrogen.

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GENETIC DIVERGENCE BETWEEN GENOTYPES OF SWEET SORGHUM BASED ON AGRONOMIC AND MORPHOLOGICAL CHARACTERISTICS

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Due to the energy crisis in the 1970s, Brazil has begun to invest in alternative sources of fuel, such as sweet sorghum (*Sorghum bicolor L. Moench)*. In order to achieve success in the use sweet sorghum as an alternative source of fuel, it is important to consider a plant breeding program for it. In this context, it is necessary to be careful during the choice of parents in order to obtain superior cultivars. In the choice of parents, the mean of genetic divergence is considered are measure of performance. The more divergent are parents more heterosis is achieved. Genetic divergence was evaluated by multivariate analysis, which is the evaluation of morphological, physiological and agronomic traits of the parents. Thus, the aim of the present study was to evaluate the genetic divergence of 16 cultivars of sweet sorghum based on agronomic and morphological characteristics applying multivariate analysis. The experiment was carried out at the experimental area of Universidade Estadual do Mato Grosso (UNEMAT) in Cáceres - MT, which is located in Southwest Mato Grosso at 176m, 16 4´ 16´´ SI and 57 40´ 44´´ W, with temperature and average rainfall of 24C and 1.500mm, respectively. The planting occurred in December 2013. The cultivation was carried out based on the agronomic recommendations for the culture. 16 cultivars (BRS 511, CV 198, V82393, V82392, CMSXS629, CMSXS647, CMSXS646, CMSXS644, CMSXS630, BRS509, CMSXS643, V82391, BRS 508, BRS 506, Sugargraze, CV 568) of sweet sorghum from EMBRAPA Milho e Sorgo were assessed. The experiment was installed in randomized blocks design, with three repetitions, and plots were composed of four 5 m rows, 0.7 m distant. The two center lines were considered as useful plot. The following characters were evaluated: number of days to flowering; plant height (m); diameter of stem (mm); weight of dry matter (kg); weight wet (Kg); total soluble solids content (Brix, % Broth); weight of broth (Kg) and volume of broth (ml). It was estimated the genetic divergence between genotypes based on the distance of Mahalanobis, and the clustering was performed using the method of Tocher. The statistical analyzes were performed with the aid of the computer program GENES. There was significant difference in at 1% of probability for plant height and diameter of stem. There was significant difference in at 5% of probability for number of days to flowering, weight of broth, total soluble solids content and volume of broth. Such F test results demonstrate genetic distance between cultivars. The CV ranged from 5 to 20.9% for significant characteristics, indicating appropriate experimental accuracy. The Cluster analysis allowed the distribution of cultivars in three distinct groups that diverged mainly because of total soluble solids content (37%) and number of days to flowering (33%), which are important features related to plants with higher ethanol production capacity and lower vegetative cycle, therefore with high potential for exploitation of culture in the region of Cáceres-MT.

PRODUCTIVE BEHAVIOR OF BIOMASS SORGHUM HYBRIDS (*Sorghum bicolor*) FOR ENERGY PRODUCTION IN SINOP-MT

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The demand for renewable energy sources is a matter of global concern. The burning of vegetal biomass has becoming an alternative for the production of electricity in thermoelectric. In this context, the cultivation of grasses has tried to attend this demand, because they have a short cycle and simple treatments. Among the grasses cultivated with this purpose, there are different species of the genus Sorghum Pennisetum sp., and more recently the biomass sorghum. Biomass sorghum stands out in this scenario, because it is a crop that allows mechanization from sowing to harvesting, is propagated by seed, with ability to produce large amounts of biomass per hectare in a cycle of, approximately, six months. This work aimed to evaluate agronomic characteristics of experimental biomass sorghum hybrids, giving focus those related to energy production, ie, dry matter production (DMP) and superior calorific value (SCV). For this purpose, an experiment was conducted with 14 biomass sorghum hybrids in a randomized block design with three replications. The experimental plot had four rows of 5 m, 0.7 m spaced. Were evaluated: flowering (FLO), plant height (PH), green matter production (GMP), percentage of dry matter (% DM), DMP and SCV. The experiment was carried out at Embrapa Agrossilvipastoril in Sinop-MT. The planting occurred in 11/19/2013, and the harvest happened six months later. The data obtained were applied to analysis of variance and the minimum significant differences between the means were calculated by (DMS-t) t test. Differences were observed among the hybrids for all the characteristics evaluated except to SCV, whose mean value was 4.423kcal kg-1. These results show that exist genetic variability among the hybrids and that is possible to choose those showing the best characteristics. The FLO occurred 113-136 days after planting, ALT ranged from 4.49 to 5.35 m, the PMV 60-111 t ha-1 with MS between 32% and 49% in average. The mean value of DMP was 36 t ha-1, with the most productive genotype reaching the mean value of 47.35 t ha-1. Thus, it is possible to state, that in the experiment, the potential for energy production was 185.17 ha-1 Gcal, and using a conversion rate of 0.001163 kcal KW-1, resulting in a production of 215.35 MW energy. This result is similar to that is found for eucalyptus, that has generally dry matter production of 30 t ha-1 per year and calorific value around 4600 kcal kg-1, generating 138 Gcal ha-1. Based on energy production and studies of cost of production of biomass sorghum, it is possible to conclude that the co-generation of electricity by the burning of biomass sorghum becomes economically viable, without mention to the industrial costs, with sales values above R$ 15.76 per MW. However, more experiments are necessary, but with proper care, biomass sorghum becomes an interesting and promising alternative for the energy production.

GENETIC DIVERGENCE OF FORAGE SORGHUM GENOTYPES BY THE METHOD OF TOCHER

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The forage sorghum [*Sorghum bicolor* (L.) Moench] is a C4 plant of tropical origin, which in addition to photosynthetic advantage, can adapt to various environmental conditions, and it is more tolerant than corn at high temperatures and there is no water deficit type. Sorghum is the fifth most produced cereal in the world, culture has been used in silage, green cut, feed and hay process. Although little spread in the region of Cáceres MT sorghum is presented as an alternative to livestock producers during drought in the region. This research was conducted to evaluate the genetic diversity of forage sorghum genotypes through multicategoric variables by Tocher optimization method. Twenty five forage sorghum genotypes were evaluated in the region of Cáceres MT, implemented in the experimental area of the Laboratory of Genetic Resources & Biotechnology of Universidade Estadual de Mato Grosso (UNEMAT) in a randomized block design with three replications. These characteristics were: number of days from planting to flowering; mean of plant height; Green pigmentation blade of revelry; Pigmentation of the midrib; Cerosity the sheath; Curl in blade margin of revelry; panicle density; Tillering capacity; Synchronization of tiller flowering the mother plant; Anthocyanin pigmentation of the coleoptile; Pigmentation of the dorsal part of the anthocyanin and anthocyanin pigmentation sheath. Data were submitted to multivariate analysis using computational resource Genes. The optimization method of Tocher genotypes divided the genotypes into six groups putting more similar in the same group and separating dissimilar. The group I was the most numerous, allocating 64.0% of the genotypes (12F38006, 12F39006, 12F40006, 12F38005, 12F40019, 12F39005, 12F39019, 12F40007, 12F40007, 12F37005, 12F38007, 12F38009, 12F40005, 12F38014, and 12F37014 12F40014.) Group II was the second largest with 12.0% of the genotypes (12F39014, 1F305, 12F37016) already in group III and IV (BRS655 and BRS610) (12F38019 and 12F37007) respectively, had the same number of genotypes with 8.0% and the latter two groups V and VI (12F39007) and (VOLUMAX) had 4.0%, respectively. The Tocher optimization method permitted the estimate of intragroup and intergroup dissimilarity, wherein the highest average intragroup distance was observed in group VI (DIII = 0.25), while lower intragroup was observed in Group III (IBD = 0.17). Intragroup distances were less than any distance intergroups, according to the criteria established for the Tocher optimization method. The largest intergroup distances were observed between V and VI (dII V = 0.50) groups, II and VI (dII; VII = 0.47) and I and III (DIII V = 0.46), representing the largest differences between groups and possibly be indicating the best combinations for crossing. On the other hand the smallest intergroup distances were obtained between groups I and II (dI; VIII = 0.31), IV and V (dI; VII = 0.29) and I and II (dV; VII = 0.31). The results obtained from the Tocher method demonstrated the existence of genetic variability among genotypes, with genotypes and 12F39007 Volumax showing greater divergence among the rest.

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EVALUATION OF GENETIC DIVERSITY AMONG 85 ELEPHANT GRASS ACCESSIONS BASED ON CONTINUOUS AND DISCRETE DESCRIPTORS

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The knowledge of genetic diversity among accessions in germoplasm banks is important for conservation of genetic resources and for breeding programs. Therefore, the objective of this study was to evaluate the genetic diversity among 85 elephant grass accessions, using ten morphological decriptors of continuous variation, and twelve morfophenological descriptors for two years. The quantitative characteristics were: number of tillers per meter (NP), height (ALT), stem diameter (DC), width and length of the leaf (LL and CL), and the multicategoric were the remaining tussock format (FT), the color of the plant portion (CP), bristle intensity on the leaves (IPF), angle of leaves (AF), number of days to 10% emergence of the flag leaf, flowering percentage at the end of the reproductive period. All characters were evaluated in the years 2012 and 2013. For both kinds of characteristics, quantitative and qualitative, it was used the clustering method of Tocher based on the Euclidean Distance Mean, the UPGMA, and the correlation of quantitative and qualitative matrices using the Mantel´s test. All these analyzes were performed using the GENES software. By Tocher´s method, 17 groups were formed indicating that there is a great genetic diversity among the accessions of this collection. This result was validated by UPGMA method that grouped the 85 accessions into 13 distinct groups. By multicategoric characters, it was possible to group the 85 accessions into 10 distinct groups by Tocher optimization. The estimated Mantel´s correlation was high (0.41) and significant at 1% of probability, indicating that diversity from a set of data can be extrapolated to another set of data of different nature. These data show that there is genetic dissimilarity among accessions of *P. purpureum* studied, and this can be exploited to compose blocks of crosses in breeding aiming to develop various types of genotypes programs for biomass production as well as for fodder. The characterization based on quantitative and qualitative descriptors provide data that can be used for a better interpretation of genetic dissimilarity and can be used for indicating accessions for crossings in the elephant grass breeding programs.

MEIOSIS, POLLEN VIABILITY AND MEIOTIC INDEX OF AN INTERSPECIFIC HYBRID OBTAINED BETWEEN *C. FRUTESCENS* AND *C. CHINENSE*

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The objective of this study was to analyze the meiosis and estimate pollen grain viability and meiotic index (MI) of an interspecific hybrid developed from crosses between C. frutescens (UENF 1636) and C. chinense (UENF 1785). For meiotic analysis as well as for the meiotic index, floral buds were collected and fixed in a solution of ethanol: acetic acid (3: 1) for 24 hours and then, they were transferred to 70% ethanol and stored in freezer. For slides preparation for meiosis and meiotic index, anthers were squashed in a drop of 1% acetic carmine solution. The meiotic phases as well as meiotic abnormalities were registered per slide. For MI estimation, anthers were squashed in acetic carmine solution and it was counted the number of normal and abnormal post-meiotic products. It was considered normal post-meiotic products, the tetrads and abnormal the triads, dyads, monads, and polyads. The MI is estimated by the relation between the total of tetrads by the total of post-meiotic products. In order to determine the pollen grain viability, flower buds were collected at anthesis and immersed in 70% ethanol and the anthers were squashed in drops of the Alexander's triple solution. The viable pollen grains were detected by the presence of red or purple color in the protoplasm, while unviable pollen grains were identified by the green color. It was counted 250 pollen grains per slide and it was prepared 5 slides. The meiosis was normal when 12 bivalents were counted in diacinesis, suggesting that the parental species are genetically close. A few anomalies were considered as lack of synchrony in the second meiotic division and precocious chromosome segregation. The MI was 85% and therefore considered satisfactory. Among the abnormal post-meiotic products, the triads were the most common, which are resulting from abnormal cytokinesis. The pollen grain viability was also satisfactory with a mean value of 72.5%. It can be concluded that the interspecific hybrid had a normal meiosis resulting in reduced and a few unreduced gametes. The normal chromosome pairing at diakinesis suggests that the species are genetically close since there was chromosome homology resulting in perfect chromosome pairing.

ASSESSMENT OF THE GENETIC DIVERSITY IN A SEGREGATING POPULATION OF GUAVA (*PSIDIUM GUAJAVA* L.)

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The guava *Psidium guajava* L. is a tropical fruit that has been showing the greatest increase in planting areas in the last years. The study of genetic diversity is important in defining populations and serves as the basis for selection and identification of parents to obtain different hybrid combinations which present greater heterosis and also, provide greater segregation in recombinations. Thus, the present study aimed to evaluate the genetic diversity of 90 seedlings of guava genotypes of the breeding program at Universidade Estadual do Norte Fluminense by means of multivariate techniques. The seeds of such genotypes were sown in polystyrene trays containing 128 cells and placed in a greenhouse with misting. Sixty days after sowing the seedlings were transplanted in polyethylene bags filled with commercial substrate Tropstrato HT® and allocated in a greenhouse. One hundred and eighty days after sowing, the seedlings of 90 genotypes were evaluated. Multivariate analysis was performed in order to obtain the genetic dissimilarity matrix based on the Euclidean distance mean, which was used in the formation of the cluster dendrogram by The Unweighted Pair Group Method with Arithmetic mean (UPGMA) method. The following characteristics were analyzed: leaf width (LF); Leaf length (CF); Leaf area (LA), estimated by linear equation involving the product of linear dimensions L x L, using the equation AF = 1.2312 + 0.7829CXL regression; Height of Plants (ALT); Number of Sheets (NF); Stem diameter (DM) and Height / Diameter Relation (AM / DM). Cluster analysis of the 90 genotypes by UPGMA method led to the formation of two distinct groups. The first group presented two subgroups and, the second group presented five subgroups. Groups I and II were composed by 41 and 49 genotypes, respectively. Within the group I, the two subgroups presented similar values based on the harmonic mean of the variables, indicating low variation between these materials allocated to that group and lower than the overall mean. The greatest variation is in the group II, which consists of five subgroups, whose harmonic mean reveals differences between genotypes, especially the genotypes of subgroups I and III that showed a mean of 8.29 and 8.10, respectively. Thus we observe a large genetic variability in seedlings of study population, and in the future it's possible obtain great genetic gain in those genotypes.

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MATURITY CURVE OF SWEET SORGHUM IN FUNCTION OF TOTAL SOLUBLE SOLIDS CONCENTRATION

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Sweet sorghum (*Sorghum bicolor* (L.) Moench) has been standing out as a source of feedstock for ethanol production in Brazil from January to April (period characterized as off-season of sugarcane). The aim of this study was to construct a maturity curve of two sweet sorghum cultivars, BRS 508 and BRS 511, in order to identify the ideal point of harvest for each material and estimate the maximum of total soluble solids (TSS) reached by the cultivars. For this purpose, an experiment was carried out at Embrapa Agrossilvipastoril, located in Sinop-MT. The seeds of each cultivar were mechanically sown in contiguous lines, spaced 0.7m, aiming to establish a population 140,000 plants ha^{-1}. Fifteen days after flowering (DAF), plants were harvested weekly during nine weeks (71 DAF), aiming to evaluate TSS of each cultivar along this period of time. The TSS was measured by digital refractometer (°Brix scale) using syrup from stems of each cultivar by an electric milling. The maturity curves of each cultivar were constructed by values of TSS measured during nine weeks and the regression equations were obtained for each cultivar. In order to estimate the optimal harvest moment, the maximum point was calculated by derivation of the original equation. By deriving such equations, it was possible to estimate the number of DAF of each cultivar in order to know the highest TSS concentrations, which can be considered as the point of maximum maturity. In addition, the maximum TSS concentrations were estimated for each cultivar. The results showed that the cultivar BRS 508 obtained maximum concentration of 20.4 °Brix at 51 DAF. On the other hand, the cultivar BRS 511 presented a TSS peak value of 17.6 °Brix at 50 DAF. It was noted that BRS 508 obtained a higher content of TSS than BRS 511, with a magnitude approximately of 2 °Brix. However, the maturity cycles of both cultivars were similar, 50 and 51 DAF (around 130 days after sowing). After this period, the TSS concentrations tended to decrease for both genotypes, decreasing, consequently, the yield of ethanol per volume of syrup. The next stage of this work will be the evaluation of TSS and the volume of syrup produced, such characteristics are better correlated to the ethanol production and will help in the identification of the cultivar with better performance.

EVALUATION OF SOYBEAN GENOTYPES REGARDING RESISTANCE TO THE SOYBEAN MOSAIC VIRUS BY RGA MARKERS

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Soybean, *Glycine max* (L) Merril, is one of legume species with the highest economical and nutritional importance. Despite this fact, the quality of grains and the productivity is constantly threatened by several diseases, such as soybean mosaic virus, caused by the virus SMV. One of the strategies used to avoid infection by such virus is the use of resistant cultivars containing R genes. The identification of such genes may be performed by using RGA markers (Resistance Gene Analog), based on conserved domains present in resistance genes, which allows the amplification of fragments related to resistance. The identification of resistant cultivars to such disease is useful to breeding programs, contributing to crossings and genotype recommendation. The objective of this work was to evaluate 16 soybean genotypes regarding the resistance to soybean mosaic virus using RGA markers. The genomic DNA was extracted and amplified by 11 RGAs primers combinations (P-Loop1, P-Loop2, P-Loop5, P-Loop6, GLPL1, GLPL3, S2, As1,As2, As3, LM637, and F1) described on literature. The PCR products were separated by eletroforesis in agarose gel. The dissimilarity matrix was obtained by the simple coincidence index and the cluster was performed by UPGMA. Seventy-eight amplicons were obtained with a mean of seven amplicons per primer combination. The dissimilarity observed among the genotypes varied from 0.18 (BRS 256 RR and BRSGO Raissa) to 0.32 (BRS 263 Diferente and BRS Favorita). It was observed the development of seven groups with a cutting point of 60%. The first of them was compounded by the cultivars TMG 117, TMG 121 and BRS 256 RR, all of them were resistant to the mosaic virus. The second group allocated the susceptible cultivars Iara and BRS 263 Diferente. The third, fourth and fifth group were compounded by resistant and susceptible cultivars. The third group was constituted by BRS BRSGO Paraíso (susceptible), TMG115 (resistant) and BRSGO Chapadões (susceptible). The fourth group allocated the genotypes BRS Valiosa (resistant) and BRSGO Raissa (susceptible). The fifth group allocated the cultivars BRS Invernada (susceptible), BRS Favorita (resistant), Luziânia (susceptible) and BRS Jiripoca (resistant). The sixth group was compounded by the genotype BRS Raimunda and the seventh group by the genotype BRS 211. The amplifications results showed that the RGA markers reached genomic regions related to resistance, wherein it was possible to separate two groups regarding to resistance to soybean mosaic virus (group one, compounded by resistant genotypes and group two containing only susceptible genotypes). It is deduced that groups three, four and five should be evaluated by other primer combinations aiming to distinguish the genotypes which remained in mixed groups. The RGA markers allowed distinguishing some genotypes according to the resistance to soybean mosaic virus. However, it is necessary the use of a bigger set of markers for the complete distinction of such cultivars.

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MORPHOLOGICAL CHARACTERIZATION OF GERMPLASM OF SWEET POTATO (*IPOMOEA BATATAS* L. LAM) OF UNIVERSIDADE ESTADUAL DO NORTE FLUMINENSE DARCY RIBEIRO

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Morphological characterization of a germplasm is usually the most accessible manner to quantify the genetic diversity and has been widely used, due to several advantages such as lower cost and the easy handling of data. The value of germplasm increases as it becomes known and documented. Such studies are of great importance to avoid planting genetically similar plants and consequently, genetic narrowing of species. Furthermore, the characterization of germplasm allows the identification of duplicates and quite similar genetic material. Thus, it indicates more genetically distant genotypes, which may be recommended for future breeding programs. Genetic divergence can be evaluated from morphological, molecular, biochemical, physiological, and agronomic characteristics. The present study aimed to characterize 30 accessions of sweet potatoes belonging to the germplasm bank of sweet potatoes at UENF, by means of morphological descriptors of specific shoots to sweet potatoes. Data concerning to the characteristics of leaves and petioles were obtained from the central part of branches (mature leaves), using three leaves per plant and three plants of each accession. Seven qualitative descriptors were used to leaf: general outline, lobe type, lobe number, shape of central lobe, immature leaf color, leaf size and petiole pigmentation. Variation was observed for all qualitative characters studied. Leaf formats were observed for: triangular (53.5%), lobed (43.5%) and cordate (3.0%). The lobe type was a feature with great variability among accessions, being found five variations: no lateral lobes (36.5%), very slight (teeth) (17.0%), slight (3.0%), moderate (26.5%) and deep (17.0%). Three categories were observed for the number of lobes: only one lobe (45.0%), three lobed (17.0%) and five lobed (38.0%). The shape of central lobe was characterized as: toothed (13.0%), triangular (47.0%), semi-elliptic (30.0%) and elliptic (10.0%). Two classes were observed for leaf size: small (37.0%) and medium (63.0%). For color of immature leaf, green leaves were prevalent (70.0%), follow by green with purple edge (23.0%) and with purple veins on upper surface (7.0%). Regarding to the variable petiole pigmentation were found the following types: green (33.5%), green with purple near leaf (43.5%), green with purple at both ends (20.0%) and green with purple spots throughout petiole (3.0%). The cophenetic correlation presented by data of the distance matrix and clustering was 0.82. Values over 0.80 indicated good representation of the real distances among the genotypes by means of graphic representation of the dendrogram. Thus, the UPGMA method was effective in adjusting these distances for the qualitative variables. Concerning to the characterization of shoots, three possible duplicates were detected, and presented high phenotypic variability for the descriptors, indicating perspectives for the breeding program of this culture.

Financial support: Capes

SELECTION OF SUPERIOR LINES IN PAPAYA (*Carica papaya* L.) WITH ADEQUATE SPECIFIC COMBINING ABILITY

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Brazil is the second biggest producer of papaya, only after India. Bahia is the largest producer in Brazil, followed by Espírito Santo, Rio Grande do Norte and Ceará. Espírito Santo is responsible for 50% of national exportation of papaya. Regarding to plant breeding the combined selection is more selective, preserving the favorable characteristics. Besides productivity, it is possible to take into account qualitative aspects of the fruit for the consumer market. The selected genotypes can be tested in Top-cross with known testers and thereby obtain good hybrid combinations. Thus, the objective was to apply the selection index combined for seven morphoagronomic characteristics to identify and select agronomically superior lines and test the specific ability of these genotypes with known testers. The experiment was installed in the company Caliman Agrícola S.A, in Linhares, ES. Twenty-two lines were selected from a backcross program of UENF/CALIMAN and 42 hybrids obtained from crossing these lines with the testers SS-72/12 group 'Solo' and JS-12 group 'Formosa'. The cultivar Golden and Tainung were used as controls. The experimental design was an 8 x 8 lattice, unbalanced, with six repetitions and four plants per plot. The characteristics evaluated were: Height of insertion of the first fruit - AIPF (cm); Number of commercial fruits - NFC; (uni.); Fruit weight - PMFr (g); Production per plant - Prod/Plt (ton.ha^{-1}); Firmness of fruits external - FEFr (N); Firmness of fruits Internal - FIFr (N) and Total soluble solids - TSS (Brix). These characteristics were attributed weights associated with the agronomic values and obtained the index, as follows: AIPF (-10), NFC (100), PMFr (1), Prod/plant (100), FEFr (100), FIFr (100) and TSS (100). The weights were attributed considering the importance of the characteristics evaluated. After obtaining the individual genetic values for the characteristics in each individual, such values were multiplied by weights of index and the sum value of the characteristics in each individual, constituted the ultimate value of selection index. Based on the ranking, the index was done a simultaneous selection of 11 lines superior (01, 04, 06, 10, 13, 16, 17, 18, 20, 21 and 22) to all the characteristics, applying an intensity of selection of 18%. These lines showed good performances both per se as crossed with genotypes to the group 'Solo' and 'Formosa'. The same lines will be crossed with four testers of known characteristics, which are parents of hybrids registered at Ministério da Agricultura, Pecuária e Abastecimento - MAPA. The hybrids obtained will be evaluated in Top-Cross and/or partial diallel and the characteristics will be evaluated as the same that led to the choice of 11 lines. It is expected to obtain hybrid combinations that can meet the consumer market.

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ÁREA: OUTRAS

EFFECT OF PHENOL IN DISINFESTATION OF SEEDS OF AÇAÍ (*Euterpe oleracea Mart.*) AND *IN VITRO* GERMINATION OF ZYGOTIC EMBRYOS

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Açaizeiro stands out due to the great socioeconomic potential of the exploration of its fruits, which present a high nutritional value. It is also used in the manufacture of cellulose, medicines, biojewels and production of palm heart, which is leading açaizeiro to the risk of extinction. One technique that has been helping to solve this problem is the *in vitro* culture of zygotic embryos, an alternative frequently used in the production and conservation in medium and long term, as a source of genetic variability. The objective was to evaluate the effect of phenol in disinfestation of seeds and germination *in vitro* of Açaí (*Euterpe oleracea)* zygotic embryos. Açaí seeds were collected in the municipality of Vila Bela da Santíssima Trindade/MT and sent to the Laboratory of Plant Tissue Culture - CPEDA, *Campus* of Tangará da Serra - MT. Initially, the seeds were disinfested in pre immersion in 5% phenol for 5' and rinsed in running water. Subsequently, the pulp was manually removed rubbed in a sieve, the seeds were disinfested under immersion in sodium hypochlorite at 2.5% for 20 and 4 rinses in sterile water and dried on paper towel for 24 h. Tegument was removed with the aid of a vise and embryos were isolated from regions of the cotyledon petiole and haustoria, using a scalpel. The disinfestation was performed in a chamber laminar flow, using 70% ethanol (v/v) 2', followed by immersion in commercial sodium hypochlorite at 2.5% and 2 drops of Tween -20° for 5' and 4 rinses in distilled water and autoclaved. The culture medium used full force MS and MS ½, 30 g L-1 sucrose plus 1% activated charcoal, solidified with 9 g L-1 agar and pH 5.7 ± 0.1. The experimental design was CRD, with nine replications and ten embryos per flask. The embryos were grown in the dark in culture room at a temperature of 26 ± 2 °C. 10 days after inoculation, the intumescence of developing embryos and calluses were observed. After 20 days of culture, embryo germination began with the development of primary roots and cotyledonary petiole. At 30 days, there was an increase in thickness of the germinal button, and the elongation of the cotyledon petiole and subsequently the development of primordial leaves. The use of phenol in the disinfestation of seeds showed the reduction of contamination by bacteria at 70%, because there was activity of coagulation proteins of these micro-organisms. About 24% of zygotic embryos germinated when cultured on MS with total concentrations of basic salts and 73% grew in MS ½.

MOLECULAR CLONING OF PROTEASE INHIBITORS KUNITZ TYPE INVOLVED IN THE PASSION FRUIT DEFENSE MECHANISM

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Plants respond to attacks by predators by activating a signaling cascade that leads to production of jasmonic acid. Such phytohormone and its derivatives are strong inducers of the expression of genes that encode proteins with defensive function and plays a central role in the activation of plant defense response. Brazil is a major producer of passion fruit, with most of the production for the juice industry. Due to its importance, the culture was studied regarding its defense mechanisms dependent on jasmonates. Our studies have assessed molecular Kunitz inhibitors in response induced by elicitation methyl jasmonate. Passion fruit after 4 weeks were exposed to methyl jasmonate vapors for 12 h. Total leaves RNA was extracted using TRIzol . 5μg of total RNA was used for cDNA synthesis. The 1st cDNA strand was submitted will polymerase chain reaction for obtaining the 2nd cDNA strand. For the efficiency of amplification, the sample was undergone to electrophoresis on agarose gel. After we check the existence of the fragments of interest (600 bp - 750 bp), we proceeded to link the fragments to the vector cloning and subsequent transformation of Escherichia coli DH5α . The selection of colonies that possessed the recombinant vectors was performed by analyzing the resistance to the antibiotic ampicillin and functionality of the LacZ gene. Selected colonies were grown and plasmid DNA was extracted and digested with the enzyme *Eco*RI. Clones which had the fragments of interest were sequenced. 5 different clones obtained together from two 5 'primers used. Analysis of the deduced amino acid sequences revealed sequence similarity to protease inhibitors Kunitz described. The sequences obtained in this study may be useful for future experiments, like super expression of these proteins *in vitro*.

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PROTEOMIC ANALYSIS OF SOYBEAN ROOTS IN RESPONSE TO INOCULATION WITH ROOT KNOT NEMATODES

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The expansion of soybean cultivation in Brazil has been accompanied by increases in occurrence of diseases and pests related to this species, therefore these factors are now limiting the obtainment of higher crop yields. Amongst the pathogens that attack soybean root, knot nematodes are notable for occurring throughout the country and causing serious crop damage. Studies aiming to improve our understanding of plant-nematode interactions have been carried out but it still remains a lack of information in this area. The analysis of proteins by 2D-electrophoresis associated with mass spectrometry is a well established and refined technique that can be used to investigate the molecular aspects of plant-pathogen interactions. The objective of this work was therefore to identify proteins in soybean roots that are differentially expressed in response to inoculation with root knot nematodes (*Meloidogyne javanica* and *Meloidogyne incognita*). Samples of roots from the resistant variety "Conquista" were evaluated, which had been collected 12, 24 and 48 hours after inoculation and roots from non-inoculated plants were used as a control. Proteins were extracted using the phenol-SDS method and separated by 2D electrophoresis. Differentially expressed proteins were then detected by comparative analysis of the gels and identified using mass spectrometry (MS/MS). Various proteins/enzymes associated with cell signalling (annexin), metabolism of reactive oxygen species (ascorbate peroxidase, glutathione transferase), production of the plant hormones ethylene and jasmonic acid (protein related to maturation, the precursor of the 31kDa glycoprotein stem), lignin biosynthesis (Caffeoyl-CoA methyltransferase), amino acid metabolism (glutamine synthase, glutamate dehydrogenase, methionine synthase), redox processes (flavoprotein WrbA, isoflavone reductase) and energy metabolism (triose phosphate isomerase, enolase, UGPase, aconitate hydratase, transketolase, 6-phosphogluconate dehydrogenase, phosphoglycerate kinase, phosphoglucomutase, ATP synthase alpha subunit). These results will help to clarify the mechanisms of soybean defense against root knot nematodes and identify candidate genes that may be used in the development of transgenic plants resistant to nematodes.

CLONING, HETEROLOGOUS EXPRESSION AND ACTION OF PEPTIDES FROM SEEDS OF *Coffea canephora* ON THE DEVELOPMENT OF PATHOGENIC FUNGI MECHANISM

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Coffee, one of the most widely traded commodities in international markets, is an agricultural crop of significant economic importance. During the last few years, a growing number of antimicrobial peptides (AMPs) have been isolated from plants and particularly from seeds that act in plant defense. Some defense proteins and AMPs have been identified in *C. canephora* seeds, as cyclotides, chitinase and lipid transfer proteins (LTPs). In recent years, due to the selection of an increasing number of resistant pathogen the AMPs have attracted the attention of many researchers trying to develop new agents to control plant diseases cause by fungi and bacteria. The aim of this project is to clone and overexpress a glycine rich protein from *Coffea canephora* (*Cc*-GRP) seeds, purify other AMPs and study their antimicrobial activity and their mechanisms of action against phytopathogenic fungi. Initially, the proteins from the powder of *C. canephora* seeds were extracted in acid buffer. The extract was submitted to DEAE chromatography, which initially were obtained two fractions called D1 and D2. D1 fraction was then subjected to the next purification step on reversed-phase C8C18 column in a HPLC system into eleven different fractions (H1 - H11). The entire purification process was monitored by electrophoresis in tricine gel. The H10, which correspond to *Cc*-GRP, and H11 fractions were tested for inhibition of spore germination of phytopathogenic fungi such as *Fusarium solani*, *Rhizoctonia solani* and *Colletotrichum gloeosporioides*. Our results showed that these fractions were not able to inhibit spore germination at the tested concentration. However they were able to permeabilize the plasma membranes of phytopathogenic fungi, as verified by fluorescence microscopy. For molecular cloning of *Cc*-GRP, initially total RNA extraction from *C. canephora* beans was made using the RNeasy Plant Mini Kit. RNAm was converted to cDNA directly of total RNA by the Reverse Transcription System GoScript Kit. The N-terminus amino acid sequence of *Cc*-GRP was used to design a degenerate primer which allowed amplification of the fragment of interest by multiple polymerase chain reactions (PCR) done at different temperatures. New experiments will be performed to further evaluate the antimicrobial activity and determination of the mechanisms of action of the peptides isolated from *C. canephora* seeds over different phytopathogenic fungi, and additionally it will be give continuity to the process of cloning and overexpression of *Cc*-GRP.

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EVALUATION OF FLORAL BIOLOGY IN SOUR PASSIONFRUIT GENOTYPES GROWN IN TANGARA DA SERRA, MT

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In passionfruit, flowering can be affected by several factors such as changes in temperature, photoperiod, solar radiation and precipitation. This work aimed to evaluate the floral biology of sour passionfruit genotypes at different times. It was used a randomized block experimental design in a factorial 2x8 (eight passionfruit genotypes x two evaluation times), with 4 replicates and 20 flowers per plot, totaling 640 flowers at each assessed time. The genotypes were cultivars 'BRS Sol do Cerrado', 'BRS Gigante Amarelo', 'BRS Rubi do Cerrado', 'FB 200', 'IAC 275' and the genotypes obtained from the UNEMAT breeding program called 'UNEMAT S5', 'UNEMAT S10' and 'UNEMAT C5'. The floral morphometric evaluations were performed as follows: sepals and petals length; corona diameter and length; anthers length and height; androgynophore length; stylet height; stigmatic surface length; distance from the nectariferous chamber to the anthers surface and taking the flowers with fully curved stylet. The obtained data were submitted to variance analysis and the means were compared by the Scott Knott test at 5% significance level using the statistical software Sisvar. The results showed a significant interaction between the time factor and the cultivar only for the characteristic diameter of the corona. In the rainy season the highest means were observed for the genotypes 'UNEMAT S5' (70,1mm), 'UNEMAT S10' (71,2mm), 'UNEMAT C5' (74,9mm). However, in the dry season, the 'BRS sun Cerrado' (73,25mm), 'BRS Rubi Cerrado' (70,6mm) and the 'UNEMAT S5' (74,8mm) stood out among the others. The function of the corona is to attract pollinators. In sour passionfruit, it acts as a landing platform and it is a visual attractive. For the time factor only the characteristics corona diameter, anther height and distance from the nectariferous chamber to the anthers surface were not significant. For the cultivar factor there was no significant difference between stigma height, stigmatic surface length, and fully curved stylet. Regarding the evaluation period, the floral characteristics evaluated showed higher means during the rainy season, except for the stylet curvature, which showed significantly better performance in the dry season. This may have been influenced by the climatic conditions of the evaluation period. However, there are no reports in the literature about the photoperiod influence on the stylet deflection. In general, the rainy period provided the genotypes significantly better performance regarding the evaluated characteristics.

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CHARACTERIZATION OF YEASTS ISOLATED FROM SUGAR CANE *SACCHARUM SPP*.

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Agricultural productivity has been severely affected by the occurrence of acidic soils in tropical and subtropical areas over the world. Sugar cane is a major agricultural product of many tropical countries and, especially in Brazil, it is highly relevant for economy. Within the factors which limit crop production on the acid soils is aluminum toxicity. The improvement of plant productivity at this condition could be achieved by the use of biofertilizers. Several studies have shown the efficiency of diazotrophic bacteria and arbuscular mycorrhizal fungi for purpose of the promotion growth, but the potential of yeasts remains poorly accessed. Also, the control of phytopathogenic molds by yeasts could help in the production process. The present study describes the isolation and characterization of yeasts from sugar cane with potential to promote plant growth and to control plant pathogens. A total of twenty one isolates were obtained from three varieties of sugar cane CB56155, RB867515 and SP803280. To identify the isolated yeast species the molecular identification is performed based on the amplification and sequencing of the 5.8S-ITS rDNA region and D1/D2 domains of the 26S rRNA gene. The isolated strains are tested for indole production, and towards resistance to aluminum and acidic pH, phosphate and zinc solubilization. In addition, the capacity for secretion of lipase was evaluated as well as biocontrol antagonism tests with fungi *Fusarium oxysporum*. The most promising yeast in promoting plant growth are being evaluated to promote growth in maize. Most isolates were resistant to low pH and aluminum, however only a few exhibited high levels of indole production. The phosphate and zinc solubilization was also a restricted characteristic among isolates. Sixteen isolates were endowed with production of lipase and only 8 isolates exhibited antagonistic activity towards *Fusarium oxysporum*. Two isolates, namely CBA106-19 and SPA106-12, have been selected for further investigation as bioinoculants in tests using sugar cane and other plants.

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ANTIMICROBIAL PEPTIDES OF LEAVES AND ROOTS FROM *Capsicum annuum*: CHARACTERIZATION AND INHIBITORY ACTIVITY AGAINST PHYTOPATHOGENIC FUNGI

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Plants are continually exposed to a large number of pathogenic organisms. As a result they had developed several defense mechanisms. Among them is the production of antimicrobial peptides or AMPs. AMPs have a great biological interest because of their ability to interact with certain cell membranes, giving them potent antimicrobial activity. In plants, AMPs have a role in defense against the invasion of microorganism, insect attack, or even environmental stress. The aim of this work is to identify and purify AMPs from leaves and roots of *Capsicum annuum* and evaluate their inhibitory effect against fungi of agronomic interest, such as *Colletotrichum lindemuthianum*, *Colletotrichum gloeosporioides* and *Fusarium oxysporum*. Two methodologies were used for the extraction of AMPs: an acid extraction and an extraction in etanol 50%. AMPs-rich extracts were subjected to C18 reversed-phase column on HPLC system. The process of extraction and purification was monitored by electrophoresis in tricine gel. AMPs-rich fractions purified by reversed-phase column and the crude extracts were evaluated for their ability to inhibit the fungi: *C. lindemuthianum, F. oxysporum* and *C. glolosporioides*. Our results show the presence of AMPs in various fractions obtained from leaves and roots of *C. annuum* as well as inhibition of fungi for all the crude extracts tested. However the alcoholic extract of the roots was the extract that showed strongest growth inhibition. Thus, this work are expected to contribute to the possible use of these AMPs in cultures to control pests and pathogens that cause severe damage to agriculture.

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EFFECT OF CYTOKININ KINETIN IN *REGENERATION IN VITRO Ananas comosus* CV. IAC FANTASTIC.

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In Brazil, pineapple is very exploited commercially and has become a profitable business in recent years, acting as the main crop for various regions in which the species is cultivated. Pineapples of the variety 'IAC Fantastic' consist of very vigorous plants with resistance to fusarium gene. The propagation by tissue culture accelerates the development and multiplication of pineapple. Techniques of *in vitro* multiplication allow the production of seedlings with high phytosanitary quality and the development of various seedlings using a single explant in a short period of time. The study aimed to evaluate different concentrations of cytokinin kinetin on *in vitro* multiplication of pineapple 'IAC Fantastic'. The concentrations of 0, 0.5, 1.0, 1.5 and 2.0 mg L-1 kinetin are added to the MS medium with 9.5 g L agar and 30 g of sucrose and L autoclaved for 20 minutes (121 ° C and 1.1 atm pressure). Explants of ± 3 cm were inoculated in culture medium and cultived at 27 ° C, with a photoperiod of 16 h under irradiance of 36 µmol m-2 s-1 provided by fluorescent lamps and photoperiod of 12 h light and 12 h dark. The evaluation was performed at 30 days and the variables analyzed were the mean number of shoots and average shoot length. The experimental design was a randomized block consisting of 5 repetitions per treatment, each repetition consisting of one vial with 5 explants, totaling 25 explants per treatment. Data were subjected to analysis of variance and means were compared by Sisvar program using regression and the Scott-Knott test. After 50 days, it was verified by the results that different concentrations of Kinetin influenced significantly ($p < 0.05$) in the average number of shoots. The control treatment was in the absence of regulatory low production of shoots with a mean value of 4.6 shoots per flask, the treatment 2 and 3 with the presence of regulator respectively at concentrations of 0.5 mg L^{-1} and 1.0 mg L $^{-1}$, the mean value was 25, 20 and 28 shoots per flask, respectively. The major number of shoots was observed in treatment 4 in the presence of kinetin regulator concentration 1.5 mg L resulting in a mean value of 168 shoots per flask. In treatment with 2.0 mg L-1 kinetin had a slight drop in the production of shoots with a mean of 136 shoots. Thus, we can infer that the optimal concentration of kinetin in these cultive conditions is 1.5 mg L-1 *for in vitro* cultivation of 'IAC Fantastic'. However, stature in both treatments of shoots had a mean of 1.2 cm.

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GENOTYPING BY SEQUENCING IN POPULATIONS OF DWARF COCONUT (*COCOS NUCIFERA L.*)

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The advent of next-generation sequencing (NGS) technologies enabled the genotyping via sequencing in order to detect not thousands of polymorphic markers from single nucleotide (SNPs) in almost the whole genome. Thus, such technique allows the detection variability with highly accuracy and, in other words, the discrimination of individuals or populations in order to characterize them genotypically. This paper proposes the genotyping via sequencing of four individuals from twelve populations of dwarf coconut, such as: seven Brazilian green dwarf coconut populations (BGD-BA; BGD PARAIPABA-RN; BGD FIGUEIREDO SOUZA-PB; BGD JIQUI-RN, BGD SOUSA DANTAS-PB; BGD TRAIRÍ-CE and BGD PARÁ-PA); three red Dwarf populations (MRD-SE, RD-GRAM-CE e CRD-CE) and two yellow Dwarf populations (MYD-SE e YD-GRAM-CE) using DNA sequencing associated with restriction sites (RAD sequencing). The genotyping of such populations are in progress yet. DNA extraction was performed using the DNeasy Plant Mini Kit (QIAGEN) kit. Using the DNA of BGD JIQUI-RN was performed the next-generation sequencing (next-generation) via HiSeq2000 Illumina-platform by two lanes running paired-end (2x100pb) at UNICAMP-LACTAD. This procedure resulted in obtaining 730,232,854 sequenced fragments with a mean of 89% of ≥ Q30 bases in order to obtain the assembly of a "genomic draft" of coconut, which will be used as the reference genome sequences for aligning the RAD generated from other genotypes via Illumina MiSeq-platform UENF-LMGV. Considering the size of coconut genome to be 2.5GB, it can be concluded that the sequences generated will be sufficient to ensure the coverage of the genome of coconut at about 58X, disregarding the repetitive regions. A new method called Short Oligonucleotide Analysis Package (SOAPdenovo2) was used for the assembling. The SOAPdenovo2 uses an algorithm that reduces the memory consumption during building and avoiding the problems of repetitive regions along the genome, optimizing the coverage and building drafts. The RAD sequences generated will be submitted to the alignment following the procedure novoalign which will be overlaid and compared with the reference genome and obtained by the detected single nucleotide polymorphisms (SNPs). Note that the alignment of these RAD sequences will be processed by Perl Scripting (E.A.J.) in order to optimize the number of readings and reduce artifacts in the data group. After obtaining the SNPs of different individuals within the 12 populations of dwarf coconut, we can infer the intra and inter-diversity as well as capture the presence of rare alleles within each population. Also, it is planned a visit to CIRAD (Center of Research for Agriculture Development) in France in 2015, in order to perform analyzes in the area of bioinformatics that will allow annotations of genes and a possible work of comparative genomics between related species and checking their similarity.

MICROPROPAGATION OF MUSA (VAR. GRAND NINE GROUP AAA) AND EVALUATION OF SOMACLONAL VARIATIONS IN THE CICLES OF CULTIVE

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The present study aims to the micropropagation from shoot tip of Musa sp. var. Grand nine AAA group and evaluation of somaclonal variations through DNA content and morphological characteristics of plants to third subcultive. The plant materials will be obtained from matrices in private collections in Tangará da Serra/MT. Seedlings with approximately 2 kg will be collected, and after, external sheaths will be extracted in order to reduce the weight of the materials. Lately, stem apexes will be pre-disinfected. During 20 days, the materials will be inoculated on MS medium without growth regulator and with the addition of 300 mg L-1 Timentin antibiotic for controling bacterial contamination. Apexes free of contaminants will be grown in culture medium of MS and supplemented by 0-3 mg L-1 growth regulator BA (benzyladenine) for induction of adventitious shoots. Shoots will be produced individually and subsequently multiplied and distributed with repetitions for each treatment (concentrations of BA). The occurrence of plants that visually shows variegation will be assessed later by flow cytometry analysis. Such assessments will be carried out until the third subcultive. The determination of ploidy level will be conducted according to the methodology described by Dolezel et al. (2007). The characteristics to be evaluated in each subcultive will be: the number of oxidized plants, number of shoots per subculture of each apex, number of plants with the occurrence of somaclonal variations, number of dead plants in the course of acclimatization. The morphogenic events will photodocumented by Electronic Scanning Microscopy (SEM) and Stereomicroscopy. The experimental design is a Completely Randomized Design (CRD) and data will be submitted to analysis of variance and regression and means will be compared by Tukey test. Plants will be acclimatized under laboratory conditions, and later, in the greenhouse.

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SEED PRODUCTION OF SYNTHETIC *ADENIUM OBESUM* (var. *Yellow sweet*)

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The production of synthetic seeds is one technique of plant tissue culture consisting in artificial encapsulation of somatic embryos, or any other type of propagule. This technique enables species conservation by the method of cryopreservation. In this study, we aimed to product Sixty (60) synthetic seeds of *Adenium obesum* (var. *Yelow sweet*). This one were submited to aseptic conditions, sterilized in 70% ethanol for 1 minute, commercial sodium hypochlorite at 2.5% and two drops of Tween-20 for 6 minutes, and finally, submitted to four rinses in distilled and autoclaved water. We used sodium alginate (Sigma Chemical Company®, USA) 2.5% (v/v) for seeds encapsulation. Thirty seeds were encapsulated in alginate with artificial endosperm, supplemented with basic MS salts in half its concentration and other thirty seeds were encapsulated with sodium alginate only. Seeds were immersed into $CaCl2.2H_2O$ (1 mM) solution for 20 minutes for complexation. Subsequently, we washed capsules in distilled and autoclaved water, separating them in four treatments: (T1) 15 seeds without artificial endosperm growing in agar + water, (T2) 15 seeds with artificial endosperm growing in water + agar, (T3) 15 seeds without artificial endosperm growing on substrate (T4) 15 seeds with artificial endosperm growing on substrate. We sterilized culture medium and substrate in a vertical autoclave for 15 minutes at 121°C. All treatments were stored at a culture room at ± 25°C with photoperiod of 16 hours and 36 μmol m^{-2} s^{-1} irradiance. The *ex vitro* cultivation was carried out in plastic trays with substrate, washed sand + black earthenware + triturated charcoal in 1:1:1 ratio. *In vitro* culture was separated in test tubes sealed with plastic wrap. We consider germinated seeds those that showed disruption of the sodium alginate matrix and primary root. Data were evaluated via frequency of seed germination. After 30 days of culture *in vitro*, we evaluated the percentage of emergence. The experimental design was completely randomized, submitted to variance analysis (ANOVA) and Tukey test at 5% probability. Seeds asepsis was 100%. Polymerization in the presence of sodium alginate $CaCl2.2H_2O$ (1 mM) resulted in the formation of well-defined hydrogel capsules, which completely enveloped the propagule. In all treatments, germination occurred after five days. During the process, we verified that it is not necessary artificial endosperm because seed already possess reservation content, which feeds the seedling development. Therefore, synthetic seeds production of such species is promising because it provides the prospect of cryopreservation as well as eases transport and germoplasm exchange and serves as an alternative for genotypes storage in *in vitro* conditions.

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EFFECT OF 2,4-D ON *IN VITRO* INDUCTION OF CALLUS IN *Carica papaya*

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Carica papaya L. is a fruit of economic importance in many countries. However, papaya faces problems derived from seed propagation. A lot of research has been carried out aiming to define methodologies to improve micropropagation for such species. Regeneration *in vitro* by growth of plants from callus can be an alternative to propagate quality material. Callus formation from an explant, a process called callogenesis, is a basic step in the propagation of plants by organogenesis or somatic embryogenesis systems. It can also be useful to produce cells for genetic manipulation, such as somatic hybridization, polyploidization and transformations. It has been suggested that auxins are required for the formation of embryogenic aggregates from individual cells expressing the totipotency of competent cells. The agent 2,4-dichlorophenoxyacetic acid (2,4-D) is the most commonly used synthetic auxin for callus induction. It is also the most active auxin, and may thus replace the natural auxin indole acetic acid (IAA) in culture media, since the latter is rapidly oxidized. The aim of this study was to induce callus formation in leaves of hermaphrodite *C. papaya* plants. Leaf fragments were sterilized and inoculated in ½MS culture medium containing five different concentrations of 2,4-D (1.0, 2.0, 3.0, 4.0 and 5.0 mg L-1. By the adopted disinfestation protocol, the percentage of contamination was of 7.4%. Considering this value, young leaves represent an adequate source of explants from adult *C. papaya* plants for induction of somatic embryogenesis. After 15 days, friable calli were induced in all culture media. In general, the calli showed whitish coloration and originated in the rib area, morphological features that suggest their being friable. Moreover, the occurrence of calli around the rib shows that the embryogenic competence is limited to this area. Based on statistical analysis, the number of responsive explants determined for each of the culture media did not differ significantly. Independently of concentration, 2,4-D enabled the induction of friable calli formation. According to this result, it is suggested that induction of friable calli from leaf explant is possible in the three sexual types of *C. papaya* if using lower concentrations of the synthetic auxin 2,4-D. Other authors have reported that high concentrations of 2,4-D favor the occurrence of somaclonal variation, in addition to the toxic effects, interfering to the development and proliferation of cells. One of the most important factors for inducing callus formation from explants is the choice of these sources, since the morphogenetic potential of calli generally varies with the origin of the plant material. In this context, the results indicate that leaves of hermaphrodite papaya plants were appropriate for the ability of callus formation. Because of the problems related to seed propagation of *C. papaya*, the results of the present study may contribute to the improvement of technical protocols for *in vitro* cultivation of this species.

ESTABLISHING OF PROTOCOL FOR DISINFESTATION OF PINEAPPLE SHOOTS

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Pineapple (*Ananas comosus* (L.) Merrill) belongs to Bromeliaceae family and is original from South America, where is consumed *in natura and also* is widely used in food industry. There are many breeding researches for selection of superior and resistant genotypes, since this culture is annually damaged due to the occurrence of Fusarium. In order to avoid microbial contamination *in vitro*, there are several explants disinfestation protocols based on chlorine, such as sodium hypochlorite, household bleach of easy access. Some protocols use sodium hypochlorite and ethanol 70% as the most effective in controlling microorganisms. The use of biotechnology techniques such as tissue culture, focused on plant breeding, allows the development of new varieties. The aim of this work was to develop an efficient protocol for asepsis of pineapple shoots for propagation *in vitro* of seedlings free of pathogens. The work was performed at Universidade Estadual do Mato Grosso in Tangará da Serra, MT. Pineapple shoots from the University Germplasm Bank were collected with size of 10 cm and washed under tap water with soap, and then immersed in water with fungicide for 2 hours. In a laminar flow chamber the material was separated into 5 treatments, 10 explants each. Subsequently, such shoots were submitted to disinfestation phases: T1 immersed in 70% ethanol for 2', and commercial sodium hypochlorite solution 2.5% by 10', T2 20' and T3 30' with 0.5g of fungicide and 4x rinsed in distilled and autoclaved water; T4 ethyl alcohol 70% (v/v) for 5' with 0.5g of fungicide and 4x rinsed in distilled and autoclaved water; T5 commercial sodium hypochlorite solution 2.5% for 5' and 0.5 g of fungicide and 4x rinsed in distilled water and autoclaved. The material was inoculated in a medium with semi-solid MS basic salts, 3.0% sucrose, 100 mg L^{-1} of inositol, 10 ml L^{-1} of MS vitamin and 7 g L^{-1} of agar with adjusted pH at 5.7 before autoclaving. Cultures were maintained in a growth room at 27°C, with photoperiod of 16h. The experimental design was completely randomized factorial with 10 replications. After 10 days of culture, it was assessed the percentage of contaminated shoots. In T1 and T4, 9 explants contaminated by bacteria, being the shorter exposure time to hypochlorite and ethyl alcohol which does not completely eliminated microorganisms, the T2, one explant contaminated by bacteria and T3 no contaminated explants, however, the exposure time of 30' injured the explants, T5, 8 explants contaminated by bacteria, because with only sodium hypochlorite exposure at 5' it was not enough to eliminate the microorganisms present. It can be say that, for disinfestation of pineapple shoots, the best result was those presented by T2 with one contaminated explant, and this treatment are the most feasible to establish disinfestation protocol. Therefore at this concentration the sodium hypochlorite had eliminated the microorganisms without damaging the material, while in other treatments the explants had injuries and further contaminations.

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