

V International Meeting on Plant Breeding

“Integrated data analysis as a tool to revolutionize plant breeding”

PROCEEDINGS



October – 2021

THE INTERNATIONAL MEETING ON PLANT BREEDING

Plant breeding is one of the fundamental strategies for the development of more adapted and productive cultivars, particularly in a world surrounded by uncertainty on food security. Given this scenario, scientists have been putting great efforts into the development of tools that could help to overcome challenges faced every day in the field. Therefore, we feel that discussions around these new tools are important to build next-generation breeders who will make them useful and effective, ensuring its correct application within research and breeding.

The International Meeting on Plant Breeding is one of several events that compose the "Corteva Agriscience Plant Science Symposia Series". In the fifth edition, the topic we intended to address was the integrated data analysis as a tool for advancing plant breeding programs. The importance of data analysis and monitoring of its evolution over the years is evident, to estimate parameters with greater accuracy and thus better support genetic selection. Thus, we intend to deepen this discussion and provide a favorable environment for updates and dissemination of knowledge on the subject.

GVENCK

The Genetics and Plant Breeding Group “Prof. Roland Vencovsky” (GVENCK) is composed by graduate and undergraduate students in Genetics and Plant Breeding at “Luiz de Queiroz” College of Agriculture (ESALQ/USP), under coordination of Professor Dr. José Baldin Pinheiro. Our mission is to integrate academics, professors, and professionals with the goal of improving the training of future breeders and geneticists.

The main activities of the group are:

- Organization of scientific and training events;
- Promotion of discussion on relevant topics in genetic and plant breeding;
- Technical visits to companies and public research institutions;
- Promote the guidance of young talents under training from the “alumni voice”, in which the alumni with consolidated careers will share professional experiences;
- Promote moments and opportunities for interaction between students, professors and researchers outside the university;
- Establishment of partnerships with companies and public institutions.

ORGANIZATION

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PROGRAM

October 5th, 2021 – Tuesday

13:30 - 14:00 → **Jason Rauscher** - Opening session (Corteva Agriscience)

14:00 - 15:00 → **Kevin Hayes** – “Digital Agriculture at Corteva” (Corteva Agriscience)

15:00 - 16:00 → **Guilherme Rosa** – “Combining Big Data Analytics and Omics Techniques to Improve Beef Cattle Selection and Production” (University of Wisconsin-Madison)

16:00 - 16:20 → Research Presentation – “Potential use of prediction for selection of Soybean genotypes with resistance to the stink bug complex” (Maiara Oliveira, PhD student at “Luiz de Queiroz” College of Agriculture/University of São Paulo-ESALQ/USP)

16:20 - 16:40 → Break – Poster presentation

16:40 - 17:40 → **Fernando Correr** – “Unravelling functional genomics of polyploids species through transcriptomics – an application in *Saccharum*” (Montana State University)

17:40 - 18:00 → Research Presentation – “Assessing the genetic diversity and dry matter yield persistence in alfalfa germplasm within Brazil” (Phd student at Federal University of Viçosa-UFV)

October 6th, 2021 - Wednesday

13:30 - 14:30 → **Amy Marshall-Colon** – “Integrative and Multiscale Modeling to Guide Crop Ideotype Design” (University of Illinois)

14:30 - 15:30 → **Carlos Alberto Labate** – “The Genetic Improvement of Plants in the Age of Omics” (ESALQ/USP)

15:30 - 15:50 → Research Presentation – “Genomics insights from the first chromosome-scale genome of the sourgrass smut fungus using oxford nanopore read” (Gustavo Schiavone Crestana, Phd student at ESALQ/USP)

15:50 - 16:20 → Break – Poster presentation

16:20 - 17:20 → **Flavia Winck** - “Advances and Challenges in Plant and Microalgae Systems Biology” (Center for Nuclear Energy in Agriculture/USP)

17:20 - 17:40 → Award “Roland Vencovsky”

17:40 - 18:00 → Closing remarks

SPEAKERS

Dr. Kevin Hayes



Dr. Kevin Hayes is a Biochemistry with Bachelors degree from Boston College (1998) and PhD degree from University of Wisconsin-Madison (2004). He has experience at leader of a computational biology and software development team surrounding genomics data management and analysis. Dr. Kevin have experience in high throughput screening, data mining, experimental analysis, functional genomics, toxicogenomics and circadian rhythms. He is currently working at Corteva as Global Lead, Data Science and Informatics Strategy and Communication.

Dr. Guilherme Rosa



Dr. Guilherme Rosa has a PhD in Statistics and Agricultural Experimentation from the University of São Paulo (USP) - Brazil, and a postdoctoral training in statistical genetics and genomics at the University of Wisconsin-Madison. He is currently an Associate Professor at the Department of Animal Sciences and the Department of Biostatistics & Medical Informatics at the University of Wisconsin-Madison. Dr. Rosa has developed research projects in partnership with several institutions in Brazil, including UNESP, USP, EMBRAPA, UFMG and UFLA.

Dr. Fernando Henrique Correr



Dr. Fernando Henrique Correr has a B.S. degree in Biotechnology from the Federal University of São Carlos - UFSCar (2014), a M.Sc. in Genetics and Plant Breeding from the "Luiz de Queiroz" College of Agriculture - ESALQ/USP (2017) and a PhD from the same program (2021). Dr. Correr has been researching both the impact of orange rust on sugarcane through differential gene expression analysis, and gene expression profiles in contrasting *Saccharum* genotypes for biomass production. He has expertise in Genetics, Bioinformatics and Computational Biology in polyploid species.

Dr. Amy Marshall-Colon



Amy Marshall-Colon has a B.S. degree in biology from Lipscomb University (2000), M.Sc. in Agronomy from University of Florida (2002), and PhD in Horticulture from Purdue University (2009). Currently, Dr. Amy is an Associate Professor of Plant Biology at University of Illinois. She also teaches courses related to genetics, metabolomics and biological networks. Amy's research focuses mainly on integrative models to investigate multi-scale regulation of crop response to genetic and environmental factors.

Dr. Carlos Alberto Labate



Dr. Carlos A. Labate is an Agronomic Engineer from USP (1981), Master in Agronomy (Genetics and Plant Breeding) from USP (1984) and Ph.D. in Biochemistry and Physiology of Plants from the University of Sheffield (1989). He is currently a Full Professor at USP, vice coordinator of the Doctoral Program in Bioenergy at USP, Coordinator of the National Laboratory of Proteomics and Metabolomics Applied to Agriculture, Agroenergy and General Biology and Professor of the Genetics Department at ESALQ / USP.

Dr. Flavia Winck



Dr. Flavia Vischi Winck has a B.S. degree in Biology (2005) and a M.Sc. in Functional and Molecular Biology (2007) from University of Campinas, and PhD in Molecular Biology from Universität Potsdam and Max Planck Institute of Molecular Plant Physiology. Currently, Dr. Winck is a Professor of Biotechnology, Biochemistry and Bioenergy at Center for Nuclear Energy in Agriculture, where she runs the Regulatory Systems Biology Laboratory. Dr. Flavia's research focuses on the investigation of metabolic pathways regulation in microalgae through multiomics integrative approaches, pursuing understand better the environment effect on this peculiar organism and its production of high-interest compounds.

SUMMARY

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IN VITRO SENSITIVITY OF *Colletotrichum spp.* ASSOCIATED WITH *Citrus sinensis* TO TRIAZOIS FUNGICIDES (DMI) AND THEIR COMBINATIONS WITH STROBILURINS (QoI)

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Colletotrichum species coexist in pathogenic, endophytic and saprophytic forms on hundreds of species of fruit, cereal, grain, vegetable and ornamental plants. In citrus plant is responsible for postharvest losses and especially during the flowering of sweet orange trees, which under favorable environment can cause huge yield decreases. In Brazil, *Colletotrichum abscissum* and *C. gloeosporioides* are responsible for the postbloom fruit drop (PFD). There are indications of other species also associated with the disease, especially *C. karstii*. The control of the disease is done by applications of the fungicides tebuconazole and difenoconazole (DMIs), or their combination to strobilurins (QoI), especially trifloxystrobin and azoxystrobin. In this work, the *in vitro* sensitivity of *Colletotrichum* species associated with sweet orange trees in São Paulo State was evaluated. The fungicides evaluated were tebuconazole, difenoconazole, and commercial formulations of these fungicides associated with azoxystrobin and trifloxystrobin, at concentrations of 0.01, 0.1, 1, 10 and 100 µg mL⁻¹. The evaluation consisted in determining the growth inhibition of colonies, from which the percentage of growth inhibition of colonies, and effective inhibitory concentration were determined. Regression analysis of the data was also applied to interpret the results. It was found that all *Colletotrichum* species evaluated were highly sensitive to the fungicides evaluated, proving their efficiency *in vitro*. All *Colletotrichum* species were more sensitive to the combinations of trifloxystrobin and tebuconazole than to the triazoles alone. These results indicate that, despite the recurrent and systematic use of DMI and QoI fungicides in the control of several citrus-associated diseases in São Paulo State, such as PFD and Citrus black spot (*Phyllosticta citricarpa*), their efficiency remains unchanged in the management of *Colletotrichum* species associated with *Citrus sinensis*.

Keywords: Postbloom fruit drop; fungitoxicity; demethylation inhibitors; quinone oxidase inhibitors.

POTENTIAL USE OF PREDICTION FOR SELECTION OF SOYBEAN GENOTYPES WITH RESISTANCE TO THE STINK BUG COMPLEX

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The stink bug complex (*Hemiptera: Pentatomidae*) is one of the main factors that compromise soybean's productivity the most in Brazil. One of the most efficient, economically, and environmentally safe control strategies is the use of resistant cultivars. However, the resistance of soybean to the stink bug complex is considered a quantitative trait and is difficult to be implemented in breeding programs. Our research group is one of the pioneers in this challenging task of revealing the genetic mechanisms related to this trait and selecting superior genotypes using genomic tools that allow the reduction of the time needed to obtain a cultivar. Thus, this work aimed to evaluate the predictive abilities (PA) of genomic selection (GS) targeting at resistance to the stink bug complex and yield in soybean crop and to identify superior genotypes based on genomic estimated breeding values (GEBVs). For GS, a breeding population consisting of 290 genotypes was used. In a period of three crop years, four characteristics associated with resistance to the stink bug complex were considered: weight of healthy seeds (WHS), leaf retention (RF), tolerance (TOL) and grain yield (GY). Genotyping was obtained by genotyping-by-sequencing (GBS), which allowed the identification of 7231 SNPs. The GS models were performed for each trait individually, from GBLUP models (Genomic Best Linear Unbiased Prediction) for the predicting GEBV. The predictive ability was estimated from the correlation between the GEBV and the adjusted means, based on the 5-fold cross-validation procedure. Additive genetic correlations between traits were estimated from GBLUP models. All analyses were performed using the *ASReml-R* package. The PA varied from 0.54 (WHS and GY) to 0.59 (TOL), indicating good potential for using GS for these traits in soybean. Genomic heritability varied from 0.32 for GY to 0.75 for TOL. All genetic correlations between traits were significant and favored the selection of resistant genotypes with high yields. The 20 best genotypes were selected based on the WHS, allowing a selection gain of 304 kg/ha compared to the population mean and, indirectly, allowed an increase of 226 kg/ha in GY. Although the evaluation of other models is indispensable, these results show that the use of genomic selection becomes a promising tool for the selection of superior genotypes. Furthermore, these genotypes can be included in future crosses, aiming to obtain offspring with greater resistance.

Keywords: Genomic selection; *Glycine max*, Plant breeding.

Acknowledgements: CAPES - Finance Code 001 and CNPq.

GAMMA RADIATIONS AND SODIUM AZIDE INDUCED HIGH YIELDING COWPEA MUTANT LINES

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Vigna unguiculata (L.) Walp. (Cowpea) is a warm-season food legume with huge nutritinal importance. Cowpea serves as good source of plant based protien and supplements the cereal based human diet. In addtion it is also used a fodder for livestock and improves the fertility of soil. Cowpea is adapted to dry ecologies of tropics and temperate regions however the yield is low as compared to other legumes. Keeping in view its low yielding potential, two widely grown cowpea varieties were treated with different doses of gamma rays and sodium azide employed individually and in combinations. Mutagenized populations were evaluated for several years under natural field conditions. The results revealed that lower and moderate doses of γ rays and SA induced a statistically significant increase in the mean values of quantitative traits and led to the isolation of high yielding mutant lines in the M₄ generation. These mutant lines serve as genetic resources for the improvement of existing cowpea cultivars.

Keywords: mutation breeding; gamma rays; sodium azide; quantitative traits; yield improvement; food security.

INTRA AND INTERSPECIFIC VARIABILITY OF TOMATO GENOTYPES FOR WATER DEFICIT RESISTANCE

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The tomato crop requires great demand for water, being susceptible to water deficit. With this finite resource increasingly scarce, there is a need to develop cultivars that are more efficient in the use of water. Thus, the objective was to explore the intra and interspecific variability of wild accessions, hybrid and commercial genotypes regarding resistance to water deficit. Seven wild tomato species genotypes were assessed, namely: *S. pimpinellifolium* accession AF 26970, *S. galapagense* accession LA 1401, *S. peruvianum* accession AF 19684, *S. chilense* accession LA 1967, *S. habrochaites* var. *hirsutum* accession PI 127826, *S. habrochaites* var. *glabratum* accession PI 134417, and *S. pennellii* accession LA 716; three *S. lycopersicum* var. *cerasiforme* genotypes, accession RVTC 03, RVTC 20, and RVTC 66; six commercial tomatoes (*S. lycopersicum*), including the four lines Santa Cruz Kada, Santa Clara I-5300, BRS Tospodoro, and Redenção and the two F₁ hybrids, Giuliana and Milagros. The experiment was carried out in a greenhouse with average temperature of 24.80 °C ± 0.78, relative humidity of 77.83% ± 0.98 and 12 h of daily light. A randomized block design was used, containing four replicates with eight plants each. All plants were irrigated until 21 days after transplanting, using micro-drippers. Then, two levels of water supply were imposed, 50% (water deficit) and 100% (control) of optimal water supply. A tensiometer (SoilControl, WC100) was installed 10 cm deep in the pots of the control treatment. Net CO₂ assimilation rate (Anet, μmol CO₂ m⁻² s⁻¹), transpiration rate (Et, mmol H₂O m⁻² s⁻¹), and stomatal conductance (gs, mol m⁻² s⁻¹) were determined using a portable photosynthesis measurement system (IRGA, Infrared Gas Analyzer, Li-COR, LI6400XT), with 1000 μmol photons m⁻² s⁻¹, 400 μmol mol⁻¹ CO₂, and ΔCO₂ + ΔH₂O less than 1%. Water use efficiency [(WUE, μmol CO₂ (mmol H₂O)⁻¹] was estimated by the ratio between Anet and Et. Gas exchange evaluations were performed around midday at eight and 15 days after the imposition of treatments in three completely expanded leaves, from the upper middle third. At 16 days after water stress, plants were evaluated for: leaf area index (LAI) - measured by a leaf area meter (LI-COR, model LI 3100C) (cm²), root dry matter (RDM), stem dry matter (SDM), and leaf dry matter (LDM). The LA 716 access was the least affected by water deficit, with no decrease in Anet, LAI, SDM, LDM, and RDM when subjected to 50% of water supply. Additionally, 'LA 716' showed an increase in water use efficiency at eight and 15 days under water deficit.

Keywords: water stress, plant physiology, genetic resistance, genetic diversity.

CONSOLIDATING 23 YEARS OF HISTORICAL DATA FROM AN IRRIGATED SUBTROPICAL RICE BREEDING PROGRAM

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Rice is one of the major staple foods worldwide. INIA's rice breeding program (IRBP) has been delivering Uruguay's most grown rice cultivars since 1987. The program is currently organized into four components based on germplasm and grain quality types: Tropical Japonica, Indica, Temperate Japonica and Clearfield. Up to date, field trial data was stored separately, hindering the joint analysis of multiple trials and years. The aim of this work is to gather all available information of IRPB's field trials to facilitate joint analysis and thus make a more efficient use of the program's information. Original data consisted of records from 1997 to 2020 of field trials, disease, and grain quality evaluation, of inbred lines in all evaluation stages and its pedigree records, available in separate spreadsheets with a variety of formats. The data processing included merging all available spreadsheets, standardization of missing data and levels of categorical variables, and application of data quality with statistical and agronomic criteria. Agronomic and grain quality traits' distribution and correlation were studied on a per-component basis. A mixed model where genotype was a random effect was applied for each trial and variance components were estimated. Trial's broad-sense heritability (H^2) and coefficient of variation (CV) were calculated. To partition variance per component, a model where all sources of variation were set as random effects was fit. The final unified database consisted of 1,526,415 data points corresponding to 1,007 trials, 12 locations, 23 years, 92,541 records, and 19,447 lines under evaluation, of which 965 had genotypic information. The most represented component is Tropical Japonica (49.8%), followed by Indica (38.8%), Clearfield (9%) and Temperate Japonica (2.5%). Most information corresponds to one location, UEPL, and advanced evaluation stages are present in three locations. Grain yield correlated significantly with all variables, and negatively with some disease and quality variables. Trial's heritability ranged from 0 to 1 with a mean of 0.62. CV ranged from 6.59 to 45.44, with mean 15.84. Trials with lower H^2 also had low genetic variance and CV. All components showed a similar pattern of variation partition where most of the variance was explained by environment related effects (trial, year, location) and genotype by environment effects. The consolidated dataset generated in this work is enabling joint analyses with higher genetic value prediction accuracy, contributing to improve the genetic gain and efficiency of IRBP.

Keywords: *Oryza sativa*; plant breeding; joint analysis.

SELECTION OF VEGETATION INDICES TO ESTIMATE THE LEAF NITROGEN CONTENT IN CORN

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Vegetation indices (VIs) provide information about the crop, assisting in management decisions in the *Zea mays* L. corn, especially in fertilizing crop treatments. Therefore, the objective of this work was to determine the best VIs in the estimation of leaf nitrogen content in corn. In the crop seasons 2017/2018 and 2018/2019, two experiments were carried out with maize cultivation in the experimental field of the Federal University of Mato Grosso do Sul, Chapadão do Sul Campus. The design used in the experiment was a randomized block design with three repetitions in a factorial scheme. The first factor was composed of 11 open-pollinated maize cultivars and the second factor was composed of two contrasting levels of Nitrogen (N) (60 kg ha⁻¹ and 180 kg ha⁻¹). At 50 days after emergence, when the crop was in full flowering, samples from the middle third of five diagnostic leaves were collected to obtain the N content. The wavelengths evaluated were green (550 nm), red (660 nm), Rededge (near infrared; 735 nm) and NIR (infrared wavelength; 790 nm). Through the evaluated lengths, the vegetation indices were calculated: NDVI, NDRE, GNDVI and SAVI. The statistical analyzes evaluated were the path analysis, considering the Nleaf content as the main dependent variable and the wavelengths and IVs as explanatory. Subsequently, a multiple regression analysis was performed, evaluating the relationship of selected indices with leaf nitrogen content. The path analysis showed a high coefficient of determination ($R^2=0.7573$) and a residual effect of medium magnitude (0.4926). The vegetation indices that had high magnitude correlation with leaf nitrogen were Rededge, NIR and SAVI, the first showing a positive correlation and the other a negative correlation. After selecting these IVs, a multiple regression analysis was performed, evaluating the relationship of the IVs with the Nleaf. The multiple regression coefficients between the main variable Nleaf and the vegetation index NIR were expressed in a negative and moderate way (-31.59). Between NF and Rededge, the coefficient was positive and high (73.07). The coefficient between Nleaf and SAVI were positive, with low magnitude (9.24). The spectral variables NIR, Rededge and SAVI proved to be better than the others in the determination of leaf nitrogen, especially Rededge.

Keywords: Index vegetation; leaf nitrogen; NIR; Rededge; SAVI; *Zea mays*.

Acknowledgments: CAPES (Coordination for the Improvement of Higher Education Personnel) for the granting of the scholarship.

ACCESSING THE GENETIC DIVERSITY AND DRY MATTER YIELD PERSISTENCE IN ALFALFA GERMPLASM WITHIN BRAZIL

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Alfalfa (*Medicago sativa* L.) is considered “the queen of forages” and plays a key role in highly specialized dairy herds. Alfalfa has the potential to be grown in different edaphoclimatic regions, though its cultivation in tropical regions is still limited. Because yield persistence is one of the bottlenecks of alfalfa breeding in tropical regions, efforts should be done to overcome this problem. This study aimed to investigate whether the alfalfa germplasm held by Embrapa Southeast Livestock has satisfactory genetic diversity regarding bromatological and agronomic traits. The investigation also looked into yield persistence, how to access it, and how to select persistent accessions based on random regression models and artificial neural networks (ANN). Best linear unbiased predictors (BLUPs) of nine traits of seventy-seven alfalfa accessions from a temperate genetic background evaluated in eight harvests were used to estimate the phenotypic diversity. Microsatellite markers assessed the molecular diversity. Self-organizing maps clustered and organized the accessions accordingly with their scores with regards to the phenotypic and molecular diversity. Dry matter yield taken from 24 harvests was used to assess persistence. A random regression model based on Legendre polynomials with a diagonal residual variance structure was used to fit persistence curves for each accession. The scores of the curves were clustered using the k-means method and persistence groups were established. An ANN was adjusted to classify accessions based on the persistence groups established by the k-means algorithm. Self-organizing maps revealed the presence of genetic diversity for both phenotypic and molecular data. The genetic variability indicated the potential of the germplasm for developing base populations adapted to tropical conditions. The fitted curves showed a great amplitude regarding dry matter yield over time, which suggested a high variability regarding persistence. The three-step method for accessing persistence presented in this study included (1) a random regression model to obtain persistence trends, (2) a k-means method to define different persistence clusters, as well as (3) an ANN to perform classification of persistent accessions in an automated way. The upside of this method is to evaluate different alfalfa accessions using the same ANN. Basically, when new accessions are evaluated, they will be classified according to their genetic value scores using the same ANN previously fitted, with no need for a new clustering step. The persistence method jumps down from three to two steps and can help alfalfa breeders in the decision-making process.

Keywords: *Medicago sativa*; genetic trajectory; artificial neural network, self-organizing maps.

Acknowledgements: The authors would like to thank the National Council for Scientific and Technological Development (CNPq), and Embrapa Livestock Southeast for supporting this work.

GENOMICS INSIGHTS FROM THE FIRST CHROMOSOME-SCALE GENOME OF THE SOURGRASS SMUT FUNGUS USING OXFORD NANOPORE READS

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Commonly called sourgrass, *Digitaria insularis* (L.) Fedde is a perennial weed with invasive behavior and has gained relevance in recent years due to its high tolerance to Glyphosate, generating high production cost for farmers. Sourgrass is also a host to the smut fungi *Sporisorium panici-leucophaei* that infects seedlings of *Digitaria insularis*, responsible for the sourgrass smut disease. Symptomatically, the disease resembles another one caused by *S. scitamineum* in sugarcane, producing a whip-like structure from the apex of the plants where sporogenesis takes place. Despite similarities with sugarcane smut, genomic information is scarce about this pathosystem. The objective of our project was to sequence, for the first time, the complete genome of *S. panici-leucophaei* using Nanopore long reads and predict the fungi effector repertoire. *S. panici-leucophaei* spores were isolated from infected sourgrass plants developing a whip-like structure and a sequence analysis of the PCR-amplified internal transcribed spacer (ITS) region revealed >99% identity with sequences of the fungi available in GenBank (accession numbers AY344986, AY998102, and AY740035). High-molecular weight DNA was extracted from yeast-like haploid cells (SPL10A) and a MinION library was prepared and loaded to the MinION flow cell device for sequencing. Using the Canu v1.8 assembler and combining Nanopore long and Illumina paired-end short reads, we generated a final chromosome-level assembly composed of 23 chromosomes (22 nuclear and one mitochondrial) with 18,915,934 bp (N50 969,070 bp) and a 97.7 BUSCO genome completeness (using the Basidiomycota database). Gene prediction, accomplished using extrinsic evidence from *S. scitamineum*, originated a total of 6,402 protein-encoding genes. Effector P 2.0 was used to predict the candidate effectors repertoire from the secretome (388 proteins, 6% in total), where approximately 17.5% (68 proteins) of all secreted proteins were considered candidate effectors. To the best of our knowledge, this is the first smut and also *S. panici-leucophaei* genome sequence assembled with nanopore reads. The complete telomere-to-telomere chromosome sequence, available in GenBank (BioProject: PRJNA648134; BioSample: SAMN15629615, Long Read Archive: SRR12314149/SRR12314150), of this poorly studied fungus, will provide a valuable resource for future studies as a biocontrol agent against *D. insularis*.

Keywords: Genomics; Nanopore sequencing; Plant pathogen-interaction; Smut disease.

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TOLERANCE OF INTRA AND INTERSPECIFIC TOMATO HYBRIDS TO WATER DEFICIT

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The tomato is a plant that needs a constant supply of water, whether by rain or irrigation. With global warming this important resource tends to become scarce. To get around this, the selection of genotypes that remain productive even in the absence of water is essential. In this context, the objective was to evaluate the tolerance of intra and interspecific hybrids of tomato plants for water deficit. The genotypes included in this experiment were: Santa Clara I-5300, Redenção, LA 716, and RVTC 66, along with five hybrids, F₁(Santa Clara × RVTC 66), F₁(Santa Clara × LA 716), F₁(Redenção × RVTC 66), F₁(Redenção × LA 716), and F₁(RVTC 66 × LA 716). The experiment was setup in a randomized block design, with five replicates containing six plants each. The plants were irrigated until 21 days after transplanting, using micro-drippers. Then, plants were subjected to five levels of irrigation, 0, 20, 40, 60, 80, and 100% (control) of optimal water supply. CO₂ assimilation rate (A_{net}), transpiration rate (E_t), stomatal conductance (g_s), and water use efficiency (WUE) were evaluated at 15 days and leaf area index (LAI), root dry matter (RDM), stem dry matter (SDM), and leaf dry matter (LDM) at 16 days after treatment imposition. Additionally, the leaf relative water content (RWC) was measured at 16 days after treatment. The leaf RWC was calculated as $RWC = [(FW - DW)/(SW - DW)] \times 100$, where FW is the fresh weight, SW is the saturated weight after rehydrating the leaf discs in water for 24 hours, and DW is the dry weight after oven drying the discs. With less water supply (0, 25, and 50% of the water required), the LA 716 accession performed best for A_{net} and RWC, followed by the progenies F₁(Redenção × LA 716) and F₁(RVTC 66 × LA 716). Whereas, under no water supply, the hybrid F₁(Redenção × LA 716) had the highest E_t, and the hybrid F₁(Santa Clara × LA 716) and the LA 716 accession had the greatest g_s values. For WUE, in the lowest percentages of water availability, LA 716-accession stood out, followed by the hybrid F₁(RVTC 66 × LA 716). In general, based on the physiological and growth parameters, the LA 716 accession and its progenies had greater tolerance to reduced water supply. In contrast, the Santa Clara, Redenção, RVTC 66, F₁(Santa Clara × RVTC 66), and F₁(Redenção × RVTC 66) genotypes suffered more as the percentage of water supply decreased. Thus, access LA716 and its descendants proved to be the most tolerant of water shortages.

Keywords: *Solanum lycopersicum*; interspecific variability; water stress; genetic resistance.

FABACEAE ANCESTRAL KARYOTYPE RECONSTRUCTION AS A TOOL FOR GENETIC IMPROVEMENT AND AGRICULTURE

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Fabaceae is a family composed of several economically important species, most of them with karyotype, genetic information, and assembled genome. However, it is essential to show the evolutionary genomic relationships among these species through the ancestral karyotype reconstruction, mapping the chromosome rearrangements that originated the diversity observed. Therefore, this work aims to reconstruct ancestral karyotype and map the chromosomal rearrangements in an evolutionary context, analyzing the information contained in the sequenced and assembled genome of all species available at the NCBI database. Using *Medicago truncatula* as a reference, a chromosome by chromosome comparative analysis was carried out, generating DotPlot graphs by D-genies software. Chromosome maps of each species were also built with their respective structural rearrangements compared to the *M. truncatula* genome, using Circos software. Regions with no homologies with the *M. truncatula* genome were treated as blank regions, demonstrating the lack of information among the chromosomes. Chromosomal rearrangement mapping resulted in a collection of translocations, inversions, deficiencies, duplications, and polyploidy events. Thereby, a connection of the accepted evolutionary tree for the Fabaceae species was assembled with the chromosomal rearrangement mapping. The results produced the first evolutionary overview of the species from the common ancestor to the current species through the computational tools and the localization of conserved genomic regions. Further, conserved regions identified in this stage of the project will be used as probes for the FISH experiments to confirm the existence of the chromosomal rearrangements identified. The results of this work will contribute to the most modern methodologies used for genetic improvement, tracing the origins and localization of regions containing genes of agronomic importance among Fabaceae species. Besides, the results are an essential contribution to the legume genetic improvement market and the area of genetics.

Keywords: *Fabaceae*; genome; chromosome rearrangement; legumes; karyotype.

PRECISION OF EARLY SELECTION USING MIXED MODELS IN INIA'S RICE BREEDING PROGRAM

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Selecting genotypes in their first field evaluation (E1) has a great impact in breeding program's efficiency, as its precision determines the suitable selection intensity. It is also challenging, due to a poor representation of environments that hinders the estimation of environment and genotype by environment effects and variances. Joint analysis of multiple trials and years and the use of mixed models can lead to higher selection precision. The objective of this work is to evaluate the precision of estimations and predictions of the genetic value (GV) from joint analysis of multiple trials and years. Data consisted of 23 years of field evaluation available in INIA's Rice Breeding Program (IRBP) database. Different data availability scenarios (DAS) for GV estimation at E1 selection time were recreated using partial datasets: (T) one trial per dataset, (Y) all trials of the same year, (F) all trials in the previous four and in the year when evaluation occurs, and (A) data from all 23 available years. A model accounting for every source of variation available in each dataset was fitted for each DAS: for models in T genotype and block were modelled as fixed effects; for model Y genotype, block (nested in trial), and trial were modelled as random effects; and for models F and A genotype, block (nested in trial), trial and year were modelled as random effects. Reference GV was defined as the BLUP obtained with model A for those genotypes evaluated in at least 3 years. Indicators for the accuracy of the GV prediction were: r , the Pearson's correlation between reference GV and the GV estimated or predicted for each DAS; and p , the percentage of genotypes selected based on each DAS that match those with best reference GV. Results show that as models accounts for more sources of variation, r and p values increase. The variability attributable to environmental effects such as trial and year accounted for a standard deviation of 2 ton/ha, and to genotype by environment effects was around 1 ton/ha. Thus, the improvement in the precision of GV estimation achieved corresponds to a better modeling of these environment and genotype by environment effects. Forthcoming use of models allowing variance and covariance structures among genotypes and environments is anticipated to enable even higher GV prediction accuracies.

Keywords: BLUP; BLUE; genetic value; genotype-by-environment.

QUALITY OF THE FRUIT OF PASSION FRUIT CULTIVARS PRODUCED IN THE NORTHEAST OF GOIÁS

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The cultivation of passion fruit (*Passiflora edulis*) is considered an agricultural alternative of interest for small properties, as it offers a quick economic return. The objective of this work was to evaluate the quality of the fruits of ten commercial cultivars of *P. edulis*, cultivated under the edaphoclimatic conditions of the Northeast of Goiás. The experiment was carried out at the UEG school farm - Posse Unit, located 6 km from the urban perimeter, at an altitude of 815 m. The used design was that of randomized blocks, with 10 treatments and four replications. The commercial passion fruit cultivars used were the following: IAC 275, IAC 273, F200, F300, UENF Rio Dourado, BRS Rubi do Cerrado, BRS Sol do Cerrado, BRS Gigante Amarelo, Redondo Amarelo, and a variety of Livramento de Nossa Senhora - BA. The harvest was started in the seventh month after planting the seedlings in the field. For the physicochemical evaluations, 6 fruits per plant were utilized. The evaluated parameters of the fruits were its width, its diameter; its weight; its pulp weight; its shell thickness; and its soluble solids content (° Brix). The data were submitted to analysis of variance, and a comparison of means was performed, using the Scott-Knott test, at 5% probability, through the Genes software. Relevant differences were observed for all variables evaluated. The three highest average fruit widths were observed for the BRS Rubi do cerrado with 89.09 mm, the BRS Sol do Cerrado with 88.15 mm, and the BRS Gigante Amarelo with 87.37 mm; while the cultivar IAC 273 had the lowest average, 37.43 mm. As for the diameter of the fruit, the variety of Livramento emerged with the highest value, 77.46 mm. As for the fruit weight, the variety of Livramento and the BRS Rubi of the cerrado presented the highest averages, with 153.46 g and 128.37 g, respectively. The cultivars FB300 and BRS Rubi do cerrado resulted in the highest values for pulp weight, 61.56 and 58.05 g, respectively; and the smallest average pulp weight was verified for the IAC 273, with 19.01 g. As for the °Brix, the FB 300 and the BRS Rubi do Cerrado produced the highest values, 13.70 and 13.47, respectively. Considering that larger, heavier fruits, with higher pulp content, and lower acidity would represent better characteristics for the consumer market, the results obtained show that the cultivars F300 and BRS Rubi do Cerrado presented the best fruit quality when cultivated under the edaphoclimatic conditions of the Northeast of Goiás.

Keywords: *P. edulis*; Passion fruit; Production; fruit characteristics.

AUTOINCOMPATIBILIDADE GENÉTICA E EVIDÊNCIAS DE RELAÇÃO DE DOMINÂNCIA ENTRE OS S-ALELOS EM MARACUJAZEIRO AZEDO

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O maracujazeiro azedo é uma frutífera de clima tropical, com grande importância socioeconômica. Grandes desafios são enfrentados na produção de maracujazeiro, e os esforços de pesquisadores, principalmente na área do melhoramento genético, tem proporcionado grandes avanços para a cultura. O maracujazeiro exibe autoincompatibilidade do tipo esporofítica, o que leva a várias implicações nas estratégias de melhoramento da cultura. A autoincompatibilidade é um mecanismo amplamente conhecido em plantas superiores, que leva ao impedimento da autofecundação e o cruzamento entre plantas relacionadas, com implicações diretas sobre algumas estratégias de melhoramento genético. Este trabalho teve como objetivo avaliar a compatibilidade genética entre acessos elite do Programa de Melhoramento de Maracujazeiro Azedo da Universidade Federal de Viçosa. Treze genótipos superiores do programa foram usados no estudo. As plantas foram cultivadas em casa de vegetação até a fase reprodutiva para realização dos cruzamentos e avaliação da compatibilidade genética. Os cruzamentos foram realizados de forma controlada, em um dialelo completo. Para cada combinação genotípica, o cruzamento foi repetido pelo menos cinco vezes, em cinco flores distintas. Para a polinização, as flores foram emasculadas e protegidas com sacos de papel pela manhã, na pré-antese, e os grãos de pólen coletados e armazenado a 4 °C em geladeira, até a tarde para realização dos respectivos cruzamentos. Após os cruzamentos, novamente as flores foram protegidas com sacos de papel para evitar contaminação dos cruzamentos com pólen indesejado advindo de outras plantas. A avaliação dos cruzamentos foi realizada 10 dias após a polinização, onde cruzamentos cujo ovário ainda se apresentava vivo e o fruto em desenvolvimento foi considerado compatível. Das 156 combinações avaliadas, 40 foram compatíveis produzindo frutos e 55 foram incompatíveis. As demais foram parcialmente compatíveis, onde apenas parte dos cruzamentos geraram frutos. Diferenças de compatibilidade entre híbrido e recíproco foi observada para 16 combinações genéticas, sendo esta, uma característica marcante do sistema de autoincompatibilidade esporofítica, indicando a presença de relações de dominância entre os S-alelos de autoincompatibilidade. As informações de compatibilidade entre os genótipos e o entendimento das relações alélicas obtidas possibilitarão melhor estabelecimento das estratégias de cruzamentos entre estes genótipos.

Keywords: Autoincompatibilidade; S-locus; Fecundação cruzada.

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TRANSLOCAÇÃO 2NS/AS EM PAINEL DE CULTIVARES DE TRIGO DA BIBLIOTECA DA UFV

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A brusone de trigo é causada pelo fungo *Magnaporthe oryzae*, que causa grande impacto na produtividade e qualidade dos grãos de trigo. A doença foi detectada pela primeira vez no Paraná, em 1985 e posteriormente foi encontrada no Rio Grande do Sul, em Goiás, regiões do Brasil Central e Mato Grosso do Sul. Existe um segmento cromossômico que confere resistência a brusone, chamado de translocação 2NS/AS, oriundo do *Triticum ventricosum* (2NS) que foi translocado para o cromossomo 2AS da linhagem de trigo comum VPM1. Objetiva-se identificar a presença da translocação 2NS/AS em um painel de 10 cultivares da biblioteca do Programa Trigo UFV. Foram extraídos o DNA de 10 genótipos. Para identificar a translocação foram utilizados os primers VENTRIUP e LN2. A amplificação foi realizada em termociclador Veriti™, com 60 ng de DNA; tampão 1X; 2,0 mM de MgCl₂; 0,25 μM de cada dNTP; 0,35 μM de primer; 1 U de Taq DNA polymerase (*Invitrogen*). O produto de amplificação foi analisado em gel de agarose 2%. Todos os genótipos testados apresentaram a amplificação do fragmento de 259 pares de base indicando a presença do segmento cromossômico 2NS/AS no seu genoma. Entretanto, apesar da maioria dos programas de melhoramento utilizar a translocação como fonte de resistência, ela tem apresentado suscetibilidade em determinados ambientes. Devido a isso, é necessário, o melhoramento ampliar o mapeamento buscando por novas fontes de resistência, pois a durabilidade da resistência da translocação 2NS/2AS não é totalmente eficaz uma vez que a agressividade do fungo se torna cada vez maior com o decorrer dos anos.

Palavras-chave: Brusone; *Magnaporthe oryzae*; Resistência; Segmento cromossômico.

SELECTION OF GENOTYPES F₂BC₁ TOLERANT TO WATER DEFICIT

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Water is essential for the good development and productivity of tomato plants, so its scarcity is increasingly worrying. In its absence, productivity is compromised, thus more efficient plants in the use of this resource are desirable in an uncertain future. In breeding programs to obtain drought-tolerant plants, wild accessions are crossed with commercial plants. Thus, the objective was to perform the selection of F₂BC₁ segregating genotypes tolerant to water deficit. The experiment was carried out in a greenhouse with average temperature of 24.80 °C ± 0.78, relative humidity of 77.83% ± 0.98 and 12 h of daily light. The F₁ hybrids Santa Clara × LA 716 and Redenção × RVTC 66 were backcrossed with the parents Santa Clara and Redenção, respectively, in order to obtain two populations F₁BC₁ [Santa Clara × (Santa Clara × LA 716)] and [Redenção × (Redenção × LA 716)]. The second-generation genotypes from the first backcrossing (F₂BC₁) were obtained from the self-fertilization of F₁BC₁ plants. From both segregating populations, 60 genotypes were evaluated using Federer's augmented block design, in which the controls were equivalent to the common treatments and the segregating genotypes to the regular treatments. The controls were the LA 716, Santa Clara, and Redenção genotypes. As for irrigation, all the plants were irrigated until 21 days after transplanting, using micro-drippers, then, irrigation was suspended. Relative water content was evaluated at 21 days after treatment imposition. Additionally, the plant wilt was evaluated based on the leaf aspect using a rating scale: 5 – 0% wilted leaves; 4 – 0 to 30% wilted leaves; 3 – > 30% wilted green leaves; 2 – > 30% wilted leaves beginning to dry; and 1 – completely dried leaves. When evaluating these parameters, the water tension (SoilControl tensiometer, WC100) in the commercial substrate of the pots was greater than 80 kPa for all genotypes. In both F₂BC₁ populations explored, the first two components accounted for 100% of the variation. In the two principal component analyses, the F₂BC₁ genotypes were divided into four groups. Regarding characteristics for fresh consumption, the genotype FS02 stood out, whereas for characteristics for industrial processing the genotypes IP16 and IP29 were the most promising, which were grouped together with the LA 716 accession. The characteristics of plant wilt and RWC were inversely proportional, since a higher water content in the leaf results in less leaf wilt.

Keywords: *Solanum lycopersicum*, *Solanum pennellii*, Drought Tolerance, Water stress.

VARIATION OF TEMPERATURE AND RADIATION RESPONSE AT FLOWERING IN RICE

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To provide stability in Uruguay's subtropical rice production, INIA's rice breeding program (IRBP) aims to develop varieties with high yields and tolerance to low temperature and radiation at reproductive stage. This work aims to study the genetic parameters of these traits under a controlled environment and at the experimental field in IRBP's advanced germplasm. A population of 965 inbred lines and cultivars (395 *indica* and 470 *japonica*) was genotyped by sequencing with 50854 and 23614 SNP respectively. For a subset of 655 lines, grain yield (GY) and mean temperature and radiation at flowering stage was retrieved from historical records of yield trials with variable sowing date at El Paso de la Laguna Experimental Unit (33.27 E, 54.17 S), and grain weight (GW) after a treatment with cold stress (5 °C for 24 h at flowering stage) and without cold stress (24 °C) was measured. For both GY and GW a single-step analysis was performed fitting a mixed random regression model accounting for line, temperature and radiation (for GY) effects. Line effect was modelled with the H matrix, combining the numerator relationship matrix for 13205 phenotyped lines accounting for self-breeding generations with the genotypic relationship matrix of the genotyped ones. Genetic variance and covariance for all effects was estimated. For both GY and GW genetic variance captured by the line effect was the highest (87,990,000 kg² and 95,705,000 kg² for GY and 1.23 g² y 0.97 g² for GW for *indica* and *japonica* respectively). The general response effect in GY per °C at flowering represented a variance of 137,760 kg² for *indica* and 151,600 kg² for *japonica*, while the variance of the response at each hour of sun was 157.23 kg² for *indica* and 171.56 kg² for *japonica*. The variance in GW per °C at flowering was 0.002 g² for both subspecies. The line effect covaried negatively both with the response to temperature (-3,323,900 kg² for GY and -0.04 g² for GW) and to radiation (-97,133 kg² and -105,280 kg² for GY). This suggests that lines with the highest general performance are also more stable against changes in temperature and radiation. The genetic covariance between the response to changes in temperature and radiation is positive (2,945.6 kg² for *indica* and 3,191 kg² for *japonica*), which implies that lines with sensitivity to one factor are also sensitive to the other. The correlation between line and response to temperature effects for GY and GW was low (-0.17 and -0.28 for *indica* and -0.04 and -0.12 for *japonica* respectively) which suggests that within the genetic variability of locally adapted germplasm, the response to low temperature in the controlled environment was not a good predictor of the response to low temperatures under field conditions.

Keywords: random regression; single-step; low temperature and radiation tolerance at reproductive stage

ORGANIZATION



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