e-ISSN 3086-0067

Eventos Técnicos
& Científicos

4

Setembro, 2025

IFTBC | II Conferência Internacional de Melhoramento de Forrageiras e Gramados

Abstract

Melhoramento genético de plantas forrageiras,
gramados e culturas agroenergéticas

16 a 18 de outubro, 2024

Brasília, DF

Embrapa
Cerrados

Empresa Brasileira de Pesquisa Agropecuária
Embrapa Cerrados
Ministério da Agricultura e Pecuária

e-ISSN 3086-0067

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Setembro, 2025

Abstract

II Conferência Internacional de Melhoramento de Forrageiras e Gramados

The International Forage &
Turfgrass Breeding Conference

16 a 18 de outubro, 2024

Brasília, DF

Embrapa Cerrados
Planaltina, DF
2025

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www.embrapa.br/fale-conosco/sac

Edição executiva e
e diagramação
Jussara Flores O. Arbues

1ª edição
Publicação digital (2025): PDF

Dados Internacionais de Catalogação na Publicação (CIP)
Embrapa Cerrados

C748 Conferência Internacional de Melhoramento de Forrageiras e Gramados (2. : 2024 : Brasília, DF).
Abstract – Planaltina, DF : Embrapa Cerrados, 2025.

PDF (133 p.) : il. color. – (Eventos técnicos & científicos / Embrapa Cerrados, e-ISSN 3036-0067 ; 4).

1. Pastagem . 2. Forragicultura. I. Título. II. Série.

CDD (23 ed.) 633.2

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Apresentação

O Simpósio Internacional de Melhoramento de Forrageiras (SIMF) foi organizado anteriormente pela Embrapa Gado de Corte, tendo suas primeiras edições no Brasil em 2007, 2009 e 2011. Duas outras edições aconteceram na Austrália e na Argentina, em 2013 e 2015, respectivamente. Paralelamente, o Simpósio de Melhoramento Molecular de Forrageiras e Gramados (Molecular Breeding of Forage and Turf, MBFT) teve uma dezena de edições nos Estados Unidos, Japão, China, Turquia e País de Gales. Os dois eventos se uniram para compor a Conferência Internacional de Melhoramento de Forrageiras e Gramados, que teve sua primeira edição nesse formato em 2019, em Orlando, Flórida, Estados Unidos. Naquela ocasião, o Brasil apresentou sua candidatura para a segunda edição da Conferência, prevista para ocorrer em Brasília em 2021. Entretanto, a pandemia de COVID19 e suas consequências impediram a realização do evento, que só ocorreu em 2024, entre os dias 16 e 18 de outubro.

O público do evento incluiu de estudantes de graduação e pós-graduação de Instituições de Ensino e Pesquisa nacionais e internacionais; geneticistas, melhoristas, profissionais de forragicultura, pastagens, fisiologia, entomologia e fitopatologia do setor público e privado, além de empresas de desenvolvimento de cultivares e produção e comercialização de sementes forrageiras, gramados, plantas de cobertura e culturas bioenergéticas. Estiveram em Brasília representantes de dez países, em três dias de apresentações de trabalhos técnicos na Embrapa Recursos Genéticos e Biotecnologia e um dia de campo na Embrapa Cerrados. No total, 52 trabalhos foram apresentados, reunidos nesta publicação.

O evento reforçou a interação entre estudantes e profissionais de instituições de diferentes países, tornando possível a articulação de projetos em cooperação, a capacitação de recursos humanos e a interação com atores do setor produtivo. A Conferência proporcionou um fórum de discussão, aprendizado, capacitação e compartilhamento de informações sobre a aplicação de tecnologias de genética e melhoramento convencionais e moleculares, biotecnologia, fenômica, genômica e estatística, no desenvolvimento de cultivares de forrageiras, gramados e culturas bioenergéticas no Brasil e no mundo, apresentando desafios e perspectivas da pesquisa na área.

A Embrapa é protagonista mundial no desenvolvimento de cultivares forrageiras, com materiais que ocupam milhões de hectares em sistemas de produção de carne e leite, e como componentes agrícolas de sistemas integrados para produção de palhada, feno, cobertura e melhoria da estrutura física do solo, além de fornecimento e ciclagem de nutrientes. A realização da segunda edição da Conferência Internacional de Melhoramento de Forrageiras e Gramados reforça a importância do papel da equipe técnica da empresa no tema, trazendo de volta ao Brasil um encontro com o DNA da Embrapa.

Sebastião Pedro da Silva Neto
Chefe-Geral da Embrapa Cerrados

Marco Pessoa-Filho
Presidente da Comissão Organizadora

Presentation

The International Symposium on Forage Breeding (SIMF) was originally organized by Embrapa Gado de Corte, with its first editions held in Brazil in 2007, 2009, and 2011. Two additional editions took place in Australia and Argentina in 2013 and 2015, respectively. In parallel, the Molecular Breeding Symposium for Forage and Turf (MBFT) held about a dozen editions in the United States, Japan, China, Turkey, and Wales. The two events merged to form the International Conference on Forage and Turf Breeding, which held its first edition in this format in 2019 in Orlando, Florida, United States.

On that occasion, Brazil submitted its candidacy for the second edition of the Conference, which was scheduled to take place in Brasília in 2021. However, the COVID-19 pandemic and its consequences prevented the event from being held, and it eventually took place in 2024, from October 16 to 18.

The event's audience included undergraduate and graduate students from national and international educational and research institutions; geneticists, breeders, and professionals in forage production, pastures, physiology, entomology, and phytopathology from both the public and private sectors; as well as companies involved in cultivar development and in the production and marketing of forage seeds, turf, cover crops, and bioenergy crops. Representatives from ten countries were present in Brasília during three days of technical presentations at Embrapa Recursos Genéticos e Biotecnologia and one field day at Embrapa Cerrados. In total, 52 papers were presented and compiled in this publication.

The event reinforced the interaction among students and professionals from institutions in different countries, enabling the coordination of cooperative projects, the training of human resources, and engagement with stakeholders in the production sector. The Conference provided a forum for discussion, learning, training, and the sharing of information regarding the application of conventional and molecular genetics and breeding technologies, biotechnology, phenomics, genomics, and statistics in the development of forage cultivars, turf, and bioenergy crops in Brazil and around the world, presenting both the challenges and future perspectives of research in the field.

Embrapa is a global leader in the development of forage cultivars, with materials covering millions of hectares in meat and milk production systems, as well as serving as agricultural components in integrated systems for producing straw, hay, and cover crops, and for improving soil physical structure in addition to nutrient supply and cycling. The successful realization of the second edition of the International Conference on Forage and Turf Breeding reinforces the importance of the company's technical team in this field, bringing back to Brazil an event that embodies Embrapa's DNA.

Sebastião Pedro da Silva Neto
General Chief of Embrapa Cerrados

Marco Pessoa-Filho
Chair of Organizing Committee

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Abiotic Stresses

Abiotic Stresses

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GENETIC RESOURCES
Oral presentations

The ILRI genebank: a window to the global tropical forage biodiversity available for breeding programs(1)

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Abstract – Supported by breeding schemes and the use of modern tools, the genetic resources held in genebanks have huge potential to play multiple roles in feeding livestock and addressing challenges such as climate change impacts, land degradation, food insecurity, poverty, and inequality. Established in 1983, the International Livestock Research Institute (ILRI) forage genebank has been conserving and making available tropical and subtropical forage genetic resources. The genebank holds over 18,000 accessions of nearly 2,000 forage species sourced from 159 countries worldwide and contains one of the most diverse collection of forage species conserved in any genebank globally. Over the last four decades, the forage genebank has been making these vital public goods available to users globally. The large proportion of the seed requests are made by researchers who evaluate the material, select and release the best performing lines as new varieties. However, about 90% of the collection is characterized as wild, or as crop wild relatives and underutilized crops, and the diversity held in the collection has not been fully exploited through breeding schemes. Often resources are limited to screen/evaluate the whole collection of materials in the genebank. To address this gap and enhance the uses of the rich diversity maintained in the genebank, efforts have been ongoing to generate information on agronomic performance, feed quality, and to establish genomics resources. To this end, the generated data have been used for the development of subsets and core collections. Accordingly, several cores/subsets have been developed for the most widely used forage species such as *Cenchrus purpureus*

(Napier grass), *Cenchrus ciliaris* (buffel grass), *Chloris gayana* (Rhodes grass), *Urochloa* spp., *Megathyrsus maximus* (Guinea grass), *Lablab purpureus* (lablab), *Vigna unguiculata* (cowpea), *Sesbania sesban*, etc based on phenotypic and/or genotypic data. In addition, there are also developed subsets that include accessions selected for the tropical highlands and drylands, sources of resistance to diseases as well as accessions historically known as the best performing and distributed for the last several years. The developed cores/subsets can be used as an entry point by breeders and researchers to the full diversity of the forages. In general, the cores/subsets, best bets and the collection maintained in the genebank are useful tools as a gateway into the global diversity available for the different forage species to be used by breeders to develop improved varieties.

Index terms: genebank, subset, best bet, forages, genetic resources, breeding scheme.

Genetic relationships among a global collection of annual ryegrass cultivars

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Abstract – Annual ryegrass (*Lolium multiflorum* Lam.) is an important forage grass in all temperate regions of the world. Breeding programs develop improved varieties at both the diploid and tetraploid levels, and in both the biennial (*italicum*) and annual (*westerwoldicum*) subspecies. Cultivars are often commercialized outside of their country of origin, and breeders also introduce materials from different geographical regions into their breeding programs. Thus, cultivars bred in different regions may be genetically distant or related. The aim of this work was to determine the genetic relationship among commercial cultivars bred in different ryegrass production regions. A total of 84 cultivars contributed by different breeding programs were used, including diploids, tetraploids, *italicum* and *westerwoldicum* accessions (31 *italicum*, 47 *westerwoldicum* and 6 other *Lolium* species and hybrids; 43 diploids and 41 tetraploids; 27 from the Americas, 33 from Oceania, 20 from Europe, and 4 from other regions). To account for the heterogeneous nature of annual ryegrass, genotyping was performed on bulks of 25–30 plants for each variety using the DArTseq platform. The SNPs obtained were filtered in R (call rate > 0.75, PIC > 0.09, and RepAvg > 0.98) and 1642 SNPs were used for the analysis. Dissimilarity matrix between all pairs of genotypes was obtained in DARwin software. Euclidean distances were used in principal coordinates analysis (PCoA) and dendrograms were constructed using different hierarchical clustering analyzes. The average dissimilarity index was 0.167 ranging from 0.061 to 0.306. The first and second coordinates of the PCoA explained 38.4% and 8.6% of the variation, separating the germplasm into at least three major groups of cultivars. The first cluster of the dendrogram included mostly the outgroup cultivars of *L. perenne*, *L. rigidum* and *L. hybridum*. A second cluster included mostly South and North American cultivars, with majority of them identified as *westerwoldicum*. The third cluster included cultivars from Oceania, Europe and other regions, both *westerwoldicum* and *italicum*. Within this cluster, at a lower level of probability, two subgroups were detected: one dominated by cultivars from Oceania, and one mostly of European origin, but with some admixture. Both ploidy levels were represented in the clusters identified, and an independent analysis within both ploidy levels generated similar groupings. We conclude that there is still a broad differentiation between cultivars according to their region of origin which is not explained by the subspecies alone. Nevertheless, germplasm flow between regions is evident as some cultivars were clustered outside their a priori group, as well as in the lower differentiation between cultivars from Europe and Oceania.

Index terms: annual ryegrass, genetic relationship, *Lolium multiflorum*, diversity.

Development of a new *Stylosanthes guianensis* cultivar for subtropical regions(1)

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Abstract – *Stylosanthes guianensis* is an economically significant legume due to the extensive number of cultivars used as forage in the tropics. Its high potential as a forage crop in tropical areas is primarily attributed to its substantial yield of quality forage on infertile soils. However, in humid subtropical zones, the species exhibits low persistence due to the anthracnose disease caused by *Colletotrichum gloeosporioides*, which affects a significant portion of the cultivars. In addition, the low temperatures during winter in subtropical regions impact the species' persistence. The breeding program within the genetics and plant breeding division of the Institute of Botany of the Northeast (IBONE), Faculty of Agricultural Sciences (FCA), National University of the Northeast (UNNE), aims to develop a cultivar of *S. guianensis* that is resistant to anthracnose and cold tolerance, suitable for cultivation in the humid subtropics. Crosses were made between cultivars and a native ecotype of *S. guianensis* from northeastern Argentina. The hybridization was confirmed through the use of male-specific molecular markers. F2 progeny (378 plants) from 10 hybrids and their parents were evaluated in the field for two years for tolerance to anthracnose and low temperatures. Seeds from the best-performing plants were sown and evaluated. This same procedure was conducted over five selection cycles, additionally including forage production and seed yield. Subsequently, the best-performing lines from each selection cycle were evaluated under different defoliation frequencies (clipping and grazing). Finally, the performance of selected lines was evaluated in four contrasting environments in northeastern Argentina. The results indicated that in the first selection cycle, only 8.8% of the population survived the cold and disease. During

the third, fourth, and fifth selection cycles, five lines were identified with cold tolerance, resistance to anthracnose, high biomass production during the initial growth period (6900 kg/ha), and seed production (290 kg/ha). Additionally, the evaluations of defoliation frequency showed that the leaf-to-stem ratio tended to increase with higher frequency. However, no differences were observed in the nutritional quality (average of 16.3% CP and 69.75% TDN) or forage yield. Furthermore, grazing did not adversely affect nodulation, and their number increased over time. One of the lines outperformed the others in two of the evaluated environments and showed no significant differences in the other locations. Based on this data, one of the lines was selected and registered as a new cultivar under the name Pionera UNNE.

Index terms: legume, breeding, new cultivar.

Origin of the *Arachis pintoi* and *A. repens* germplasm and potential for shared research and use[1]

Valls, J. F. M.[2]

[1]Funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq 310766/2022-2). [2]Embrapa Genetic Resources and Biotechnology, Brasília, DF. jose.valls@embrapa.br

Abstract – The legume genus *Arachis* comprises 83 species, all of which are available with germplasm. Among the most common perennial species, the rhizomatous *A. glabrata* and the stoloniferous *A. pintoi* and *A. repens* show special adaptation for the establishment of sustainable grass/legume pastures, as their vegetative organs, with good forage quality, allow continuous propagation, while keeping most of the growing points protected below or near the soil surface, thus withstanding grazing and trampling. While the natural range of *A. glabrata* is shared by Argentina, Brazil and Paraguay, *A. pintoi* and *A. repens* are endemic to Brazil. Arachis glabrata and *A. repens* rarely produce seeds, while there is great diversity in seed production in the germplasm collected from wild populations of *A. pintoi*. A survey conducted in 1992 reported 45 accessions of *A. pintoi* and 16 of *A. repens* then available. Thirty-two years have passed, and the germplasm numbers of both species have steadily increased. The ongoing collection effort has resulted in a total of 173 accessions of *A. pintoi* and 45 of *A. repens*, and a Forage Arachis Genebank has been established in the Amazon region with the aim of developing new options to increase the sustainability and quality of grass/legume pastures, to restore the productivity of large areas taken over by degraded monospecific grass pastures, whose loss of productivity is often used as an excuse to increase deforestation. Institutional and academic research also explored crossing experiments, and 40 hybrids were obtained, including intraspecific crosses of *A. pintoi* accessions, and interspecific crosses *A. pintoi* x *A. repens*, as well as crosses with non-stoloniferous species, such as *A. appressipila*, A. paraguariensis and *A. vallsii*. In all crosses with non-stoloniferous species, *A. pintoi* or *A. repens* served as male parents, and each F1 produced normal stolons, allowing their use as additional diversity for vegetative propagation, a routine in the establishment of pastures of *A. glabrata*, *A. repens*, and even for some released cultivars of *A. pintoi*. The 21st century has witnessed a drastic reduction in germplasm exchange, and Brazilian and international regulations do not favor a different outlook in the short term with regard to endemic Brazilian species. However, at a time when germplasm sharing was a normal practice, especially when field collection was conducted in collaboration with foreign researchers, 92 accessions of *A. pintoi*, 10 of *A. repens* and 11 distinct hybrids were made available abroad, most of which were provided to CIAT and, through Texas A&M Agrilife Research, to the USDA. Mainly from these two partners, 20 distinct accessions of *A. pintoi* have already been deposited for the future in the Svalbard Global Seed Vault.

Index terms: forage legume, diversity, natural populations, vegetative propagation, exchange.

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GENETIC RESOURCES
Poster presentations

Multi trait and multienvironment North Carolina II analysis for *Megathyrsus maximus* breeding(1)

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Abstract – Genetic studies in guinea grass (*Megathyrsus maximus* (Jacq.) B. K. Simon & S. W. L. Jacobs) are crucial for understanding the genetic variability, parental and genetic effects, and their relationship with the environment. The North Carolina II mating design is frequently employed to identify superior parental lines and optimal crosses. Consequently, this study aimed to achieve two objectives: (1) identify the best apomictic tester(s) to be used as male parent in a recurrent selection based on specific combining ability breeding scheme, and (2) select the best hybrids for cultivar development. This was accomplished by analyzing a North Carolina II genetic design using a mixed model methodology and factor analytic analysis. Nine apomictic genotypes were crossed with 24 tetraploid and sexual genotypes to obtain 1995 apomictic hybrids. Parents, hybrids, and checks ('Mombasa', 'Tanzania-1', and 'Tanzania-2') were evaluated four times in a period of 12 months in three mega-environments (Quilichao, Palmira, Llanos). Traits related to forage yield and nutritive value were evaluated. For all variables in all environments, broad sense heritability ranged from 0.3 to 0.8, being greater than 0.5 in 60% of the evaluations conducted, indicating that in most environments, a substantial portion of the phenotypic variation observed is explained by genetic variability. Genetic correlation between each pair of environments varied according to the trait evaluated and ranged from 0.3 to 1. Factor analytic analysis revealed two distinct clusters of environments, one cluster consists of all evaluations conducted in Quilichao and Palmira, and another with all evaluations conducted in Llanos. This suggests that the hybrid performance is similar in Palmira and Quilichao but different to the hybrid performance in Llanos. Heterosis and specific combining ability of forage yield and nutritive value variables clearly reveals differences in performance among all genetic combinations, offering insights into the selection of best apomictic testers. Male genotypes CIAT 6962 and CIAT 16031 are parents that exhibit higher values of heterosis and general combining ability and are the most promising parent options in terms of forage yield and nutritive value. Finally, based on selection indices from BLUPs, 10% of hybrids were selected for cultivar development. According to these results, the first cycle of recurrent selection based on specific combining ability was initiated crossing the apomictic tester CIAT 6962 and a tetraploid and sexual population synthetized from 93 genotypes from Future Seeds GenBank.

Index terms: Panicum, mating designs, factor analytic, combining ability, heterosis.

BRS Oquira: a new forage peanut cultivar for mixed pastures and intensive livestock production systems

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Abstract – Forage peanut (*Arachis pintoi* Krapov. & W.C.Greg.) is an herbaceous perennial forage legume used as animal feed, mainly planted in pastures intercropped with forage grasses. This work introduces ‘BRS Oquira’, a newly released cultivar developed by Embrapa. Several forage peanut genotypes were evaluated based on agronomic traits in different Brazilian environmental conditions (2005–2013), covering regions in the states of Acre, Pará, São Paulo, Mato Grosso do Sul and the Federal District. Subsequently (2016–2019), field trials were established to evaluate the selected genotypes in mixed pastures under grazing, resulting in the validation of a new cultivar. ‘BRS Oquira’ demonstrated high annual dry matter (DM) yield in cutting trials. Performance varied based on the biome: 10–13 tons annual DM per hectare in the Cerrado (prolonged dry season around five months); 13–16 tons annual DM per hectare in the Amazon (high rainfall, short dry season), with tolerance to temporary waterlogging; and 15–20 tons annual DM per hectare under intensive management with irrigation and fertilization (Atlantic Forest-Cerrado transition zone). ‘BRS Oquira’ exhibited excellent nutritive value with an average of 22% crude protein, exceeding alfalfa by 15% in intensive systems while maintaining similar digestibility. Additional fiber fractions (35% acid detergent fiber, 43% neutral detergent fiber) and high in vitro dry matter digestibility (68%) further confirmed its suitability as a high-quality animal feed. Under grazing, it showed high compatibility with forage grasses of *Brachiaria*/*Urochloa*, *Cynodon* and *Panicum*/*Megathyrsus* genera and good capacity for lateral expansion of stolons, with annual growth of 1.0 meter. Three years after establishment, ‘BRS Oquira’ was present in 28% of the pasture botanical composition intercropped with *Cynodon nlemfuensis*, a proportion capable of generating significant benefits from biological nitrogen fixation. Based on the results obtained in the agronomic and in mixed pasture evaluations, ‘BRS Oquira’ was registered and released by Embrapa in 2022. This cultivar should be planted through vegetative propagation, due to its low seed productivity (135 kilograms per hectare). ‘BRS Oquira’ propagules are available for farmers in the Brazilian market through seedlings, sold by companies licensed by Embrapa. This drought-tolerant cultivar (relative to other forage peanut cultivars) with high nutritive value offers a valuable addition to sustainable livestock production systems in Brazil, performing well in both grazing and intensive production settings. ‘BRS Oquira’ is therefore an excellent option to increase biodiversity, resiliency and sustainability of pasture-based livestock systems.

Index terms: *Arachis pintoi*, forage breeding, forage legume, mixed pastures.

Molecular identification of *Urochloa humidicola* cultivars(1)

Azevedo, A. L. S.(2), Da Silva, J. M. A.(2), Magalhães, R. L. O.(2), Lima, L. L.(2), Martins, M. F.(2), Domingues, R.(2), Campos, F. G.(2), Barrios, S. C. L.(3) and Vigna, B. B. Z.(4)

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Abstract – *Urochloa humidicola* (Rendle) Morrone & Zuloaga (syn. *Brachiaria humidicola* (Rendle) Schweick) is a warm-season grass commonly used as forage in tropical regions. This polyploid species exhibits variable ploidy (6X–9X) and facultative apomixis. Known for its tolerance to seasonal flooding and high phenotypic plasticity, this forage provides numerous benefits for tropical dairy farmers. Its adaptability to hot climates, good forage quality, and potential to improve animal comfort make it a valuable asset for sustainable dairy farming in the tropics. Several cultivars are currently available for producers and Embrapa is working on developing new ones to meet the increasing demand. Accurate identification of *Urochloa humidicola* cultivars is crucial for ensuring seed quality and preventing misrepresentation. Existing methods often lack accuracy or are time-consuming. This study aimed to develop a reliable and efficient molecular panel using microsatellite markers to distinguish between three commercially important cultivars: ‘Llanero’, ‘humidicola’ (“comum”), and ‘BRS Tupi’. A total of 27 microsatellite markers was screened against the three U. humidicola cultivars and germplasm samples from Embrapa. DNA was extracted from the leaves of each sample (three biological replicates were sampled for each cultivar); multiplex PCR reactions were performed with 5–7 markers per reaction and fragment analysis was conducted using the capillary electrophorus in the SeqStudio (Thermo Fisher). Ten informative markers that could effectively differentiate between the three cultivars were identified. Specifically, eleven exclusive alleles were found for the cultivar ‘Llanero’, 14 exclusive alleles for humidicola, and four for ‘BRS Tupi’. To ensure the robustness

of the panel, all cultivars were compared against each other and germplasm bank samples to confirm the absence of these exclusive alleles in other accessions. This novel panel offers a reliable and efficient method for cultivar identification compared to traditional techniques. It holds significant value for seed quality control, preventing the inadvertent distribution of misidentified cultivars. Additionally, the panel can be employed to address issues of seed piracy by providing a definitive method for cultivar verification and lays the groundwork for the development of a commercially available test kit, facilitating cultivar identification by stakeholders in the agricultural industry.

Index terms: *Brachiaria*, fingerprint, koronivia grass, SSR.

Productivity and bromatological characteristics of *Paspalum* species from the virgata group(1)

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Abstract – The genus *Paspalum* includes the largest number of native grasses in Brazil, with approximately 220 species, recognized for their high forage potential. Among these, the Virgata group comprises sexual and tetraploid species utilized in the *Paspalum* Breeding Program at Embrapa Pecuária Sudeste. This study aimed to identify accessions with superior forage potential for crossing programs by evaluating dry matter productivity and bromatological variables. Twenty-eight *Paspalum* accessions distributed across three Virgata species (8 *P. conspersum*, 14 *P. regnellii*, and 6 *P. virgatum*) were transplanted in the field using a randomized complete block design with six replications. Each plot consisted of five plants spaced 50 cm apart. Whole plants were harvested 10 cm from the ground, oven-dried, grounded, and analyzed bromatologically using Near-Infrared Spectroscopy (NIRS). The following variables were assessed: plant height (cm), dry matter productivity (kg/ha.month), crude protein (CP) content (%), neutral detergent fiber (NDF) content (%), acid detergent fiber (ADF) content (%), hemicellulose (HEMI) content (%), lignin (LIG) content (%), ether extract (EE) content (%), mineral matter (MM) content (%), and in vitro digestibility (DIV) (%). Genetic variability was observed for all variables. Multivariate analyses, based on the Ward method and Euclidean distances, allowed for the classification of genotypes into four groups: i) exclusively composed of *P. regnellii* accessions, characterized by higher CP content (12.47%), lower NDF (71.72%) and ADF (39.37%) contents, high HEMI content (32.36%), and superior productivity (3694.85 kg/ha.month), making them excellent candidates for breeding programs; ii) Comprised of *P. virgatum* accessions, exhibiting high productivity (4683.86 kg/ha.month) but lower CP

(9.56%) and MM (4.87%) contents, while NDF (75.93%) and ADF (45.01%) contents were higher, rendering them less promising; iii) Composed of *P. virgatum* and *P. conspersum* accessions, also displaying higher NDF (75.87%) and ADF (46.76%) contents, along with elevated LIG (6.06%) content and lower CP (9.99%) and DIV (45.71%) contents, representing the group with the lowest nutritional quality; iv) Formed by *P. regnellii* and *P. conspersum* accessions, presenting DIV (56.25%), MM (5.76%), LIG (2.81%), HEMI (30.04%), and ADF (44.56%) contents, but less satisfactory productivity (2612.83 kg/ha.month). These results demonstrate intra- and interspecific variability and identify *P. regnellii* as the most suitable and advantageous species for crossing programs.

Index terms: forage, germplasm, genetic improvement, natural variation, accessions.

Characterization of seed production related aspects in *Paspalum* species of the virgata group(1)

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Abstract – In Brazil, the genus *Paspalum* presents the largest number of native grasses, considered the second largest genus in the Poaceae family, with approximately 220 species. These species are widely recognized for their high forage potential and genetic variability. Within this genus, the informal Virgata group stands out, encompassing tetraploid and sexual species, making them potential female parents in crosses for breeding programs, such as the one conducted by Embrapa Pecuária Sudeste. Aiming to characterize 28 accessions from the Virgata group maintained in the *Paspalum* Active Germplasm Bank, the following variables were evaluated in 8 *P. conspersum*, 14 *P. regnellii*, and 6 *P. virgatum* accessions: average number of flowering stems per clump, average length of flowering stems (m), number of racemes, raceme length in each third of the inflorescence (cm), and number of spikelets. The accessions were transplanted to the field in a randomized complete block design with six replications. Each plot consisted of five clumps spaced 50 cm apart. During the reproductive period, after the emergence of inflorescences in the tillers, 10 flowering stems were collected per plot, from which data for each variable were obtained. Univariate statistical analysis revealed genetic variability for all variables. Multivariate analyses using Ward's method and Euclidean distances generated a dendrogram, allowing the classification of the materials into five groups: i) composed of 5 *P. regnellii* accessions, characterized by shorter flowering stems (1.13 m) compared to the others, with elongated racemes (12.09 cm), although less numerous (10.56), and an intermediate number of spikelets (1303.03); ii) formed by 3 *P. conspersum* accessions, with tall flowering stems

(1.91 m), a large number of racemes (18.11), and spikelets (2046.11); iii) composed of 6 *P. virgatum* accessions and 1 *P. regnellii*, which, although having shorter and fewer stems (1.46 m and 82.15, respectively), stand out for the number of racemes (14.59) and spikelets (1537.34); iv) formed by 5 *P. conspersum* accessions, with tall and numerous stems (1.86 m and 141.66, respectively), a large number of racemes (12.96), but short (8.48 cm) and with intermediate spikelet production (1174.03); and v) composed of 8 *P. regnellii* accessions, with smaller racemes (9.65 cm), more sparsely distributed (9.46 per stem), and low spikelet production (994.70). The results indicate intra and interspecific variability among the accessions, which can be explored by the genetic breeding program.

Index terms: forage, germplasm, genetic improvement, natural variation, accessions.

Morphological characterization of *Stylosanthes scabra* Vogel germplasm accessions(1)

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Abstract – The *Stylosanthes scabra* Vogel presents a great extent of occurrence in natural environments. Its presence has been reported in sand banks, sand dunes, and on the shores of ponds or bordering deciduous seasonal forests from the northeastern to northwest Brazil, from seashores to the Cerrado of São Paulo state, and, in the state of Mato Grosso do Sul in savannah (cerrado), forested savannah (cerradão) and woody steppe savannah (campo sujo). This work had as an objective to characterize and determine the genetic variability of 80 *Stylosanthes sabra* Vogel germplasm accessions stored at the Germplasm Bank of Embrapa Cerrados using 24 morphological descriptors. Seeds were sowed in trays and plants were maintained in a greenhouse for 90 days. After this period they were transplanted to the field in plots with single rows, without repetitions and seven plants per plot. Data from plants stems, leaves, flowers, fruits and seeds were collected and comparisons among accessions were made. Simpson and Shannon-Weaver diversity indexes were calculated for each descriptor to access the genetic diversity among the accessions for individual descriptors. Principal component analysis was performed, and a cluster analysis to group the germplasm, using the minimum variance method (Ward's). The germplasm presented great morphological variability with most of the descriptors showing polymorphism. The differences among groups were estimated utilizing Tukey's test with 5% probability. The first two principal components explained 50.83 % of the total variation (CP1 = 36.4% and CP2 = 14.4). The cluster analysis differentiated four distinct groups. Groups 1, 2 and 3 represented short plants with large number of ramifications, differing from each other in plant diameter, main stem diameter and length, upper article length. Group 4 presented taller plants and less ramified, with larger leaflets. Groups 1 and 2 were formed primarily by accessions collected in the Cerrado region. Group 3 was formed by accessions collected at the Caatinga and Group 4 primarily by accessions collected in the Mata Atlantica. The morphological descriptors used in this work were efficient in discriminating *S. scabra* germplasm accessions.

Index terms: forage legume, ACP, germplasm.

Genetic variability for thousand-seed weight in the germoplasm bank of *Megathyrsus maximus* of Embrapa(1)

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Abstract – Thousand-seed weight (TSW) is a trait related to seed mass that allows the calculation of sowing density, number of seeds present in a sample and prediction of seed size. The objective of this study was to estimate the magnitude of genetic variability for TSW in a collection of *Megathyrsus maximus* from Embrapa Beef Cattle. For this, 320 genotypes from the Germplasm Bank were evaluated in a partially repeated design with two replications at Embrapa Beef Cattle in Campo Grande, MS. The experimental plots were composed of two rows of five plants with a spacing of 0.5 m between plants and rows. Each plot was harvested one or more times during the seed production period (between March and May) in the years 2022 and 2023. The harvested seeds were processed to obtain pure seeds. Subsequently, 100 pure seeds from each plot were counted and weighed to obtain the hundred seed weight (HSW). The TSW was calculated by multiplying the HSW by 10. Statistical analysis were performed based on mixed models using the ASREML package of the R software. The year effect was considered fixed and the genotype effect and genotype x year interaction were considered random. The restricted maximum likelihood methodology was used to estimate the model's variance components. Heritability was obtained based on the variance of the prediction error and the predicted means were based on the BLUP. The Wald test was not significant, indicating that the year did not affect TSW. In fact, mean TSW were 1.103 and 1.099 grams in 2022 and 2023, respectively. The Likelihood-Ratio Test was highly significant for the genotype variance component in both years, indicating the presence of significant genetic variance for TSW in the species' germplasm. The heritability was 0.96, indicating that the predicted means are highly accurate. The genetic correlation between years was 0.91, indicating that the ranking of genotypes was not changed by the year of evaluation and the genotype x year interaction was low. The TSW average varied from 0.72 to 1.79 grams among the accessions evaluated, showing that there is a high variation for this trait in the germplasm of the species. Among the main cultivars of the species, the TSW varied from 0.76 grams ('Gatton Panic') to 1.43 grams ('Tobiatã'). The results of this study show that TSW presents high genetic variation in *M. maximus* germplasm.

Index terms: *Megathyrsus maximus*, genetic variability, thousand-seed weight.

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GENETIC AND GENOMIC TOOLS
Oral presentations

Developing genomic tools for key underutilized forage species in Africa(1)

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(1)Funding: The Royal society grant (FLR\R1\201095 & FCG\R1\211019), Sustainable Animal Productivity for Livelihoods, Nutrition and Gender inclusion, Department of Foreign Affairs Better World Awards 2020 (COALESCE/2021/84) and Genebanks Initiatives.
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Abstract – Purpose: Despite the heavy density of livestock herd in Sub Sahara Africa (SSA), livestock productivity (milk and meat) in the region, is well below the global average. Furthermore, it has been forecast that the demand for meat and milk in SSA will be up to 150% greater in 2030 when compared to 2005, which offers a golden opportunity for livestock producers in the region. However, limited access to quality feeds is one of the major reasons behind the below par animal performance in the region. Traditionally crop residues and natural pasture were the main feed sources in the region, particularly among pastoralist communities. However, crop residues are poor in quality and bulky that hinder voluntary intake and grazing lands are dwindling due to climate change, as more land being allotted for food crops and urbanization, leading to dire consequences. Scope: Here, we will present on the development of a range of genomic tools and technologies that can be applied to enhance and accelerate the selection of new, high quality, more productive and resilient, forage grass and legume varieties that are important to boost livestock production and minimize greenhouse emissions from small holder livestock production systems in SSA. Methods: In the present study, genomic technologies (via both GBS and WGS approaches) were developed for key tropical species including Napier/Elephant grass, Rhodes grass, oats, Urochloa spp, lablab and cowpea, in order to facilitate the application of genomic based breeding programs. Results: the genomic technologies developed in the present study were so far used for genetic diversity and association mapping studies and will ultimately be utilized for genomic prediction strategies, which have been highly successful in reducing costs of crop breeding programs. Using these tools, a greater understanding of population dynamics, including population divergence and differentiation was noted and QTL linked with target traits such as biomass yield, water use efficiency and feed quality traits were identified. Conclusions: These resources will be placed in the public domain so that interested parties can make use of them to accelerate tropical forage breeding in order to support sustainable livestock systems in SSA.

Index terms: tropical forages, genomics tools, genetic diversity and marker trait associations.

Developing genomic prediction capabilities for underutilized tropical forage species maintained in the CGIAR genebanks(1)

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(1)Funding: 'Improved fodder crops and forage grasses for Africa' of the Crops to End Hungerinitiative. CtEH is a CGIAR initiative to accelerate and modernize the development, delivery and widescale use of a steady stream of new crop varieties. Some of the genotyping were supported by the Genebank and SAPLING initiatives. (2)Feed and Forage Development, International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia.
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Abstract – CGIAR genebanks maintain about 40,000 accessions from nearly 2,000 tropical forage species at ILRI and, the Alliance of Bioversity International and CIAT. The collections represent the largest assembly of tropical forage species, composed of a variety of annual and perennial grasses, dual-purpose legumes, and multipurpose trees and shrubs. The forage species are an important source of livestock-feed in the tropics and subtropics and, as such, have made a substantial contribution to the world's food security. Some of the legume species serve as a protein source for both humans and animals, while certain species of grasses, like Napier grass, are used in various industries such as the production of biofuels and papers. Despite their importance, neither conventional breeding nor the current rapidly advancing molecular technologies have been widely applied mainly because of the reproductive mode or the complexity of the genomes. The majority of the species are in their wild state and there has been limited selection through conventional breeding, with marker-assisted selection (MAS) and genomic selection (GS) not yet visible. The CGIAR institutes, ILRI and CIAT, have made certain improvement efforts on some species. While CIAT has been conducting an ongoing breeding program with the goal of developing hybrids, focusing mainly on *Urochloa* and *Megathyrsus* species, ILRI has been working on the deployment of genomic tools like genome-wide association studies (GWAS), GS

and MAS in CGIAR and CGIAR-NARS (National agricultural research system) breeding programs. Both with the aim to deliver the highest possible rate of genetic gains in the form of productive, high-quality, and climate-resilient forage cultivars in farmers' fields. There have also been collaboration efforts between the two institutes to develop genomic prediction capabilities for the underutilized species by using cheaper genotyping platforms, field phenotyping, and by employing various genomic prediction models accessible in R-packages and machine learning approaches. Here, we present our findings of genomic prediction work on *Urochloa* spp., V*igna unguiculata* and *Lablab purpureus* using GWAS, MAS, and GS. Several SNPs associated with important agro-morphological and feed quality traits per species have been identified by GWAS. The prediction accuracy using the ridge regression best linear unbiased prediction (rrBLUP) on various traits ranged from 0.56 to 0.75 in Urochloa spp., from 0.40 to 0.83 in *V. unguiculata*, and from 0.43 to 0.75 in *L. purpureus*. The results suggested the potential application of genomic prediction approaches in tropical forage breeding programs to improve the efficiency and precision of selection, which would facilitate the development of improved forage varieties.

Index terms: CGIAR, cowpea, genomic prediction, lablab, Urochloa.

Advances in the application of predictive breeding tools in forage and cover crops

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Abstract – Forage and cover crop breeding for complex traits, such as yield, quality, and persistence, requires extensive phenotyping efforts, which is time-consuming and expensive for large breeding populations. The application of remote sensing is becoming a routine method in plant breeding for fast and non-destructive high-throughput phenotyping (HTP) for complex traits, which has enabled the estimation of yield in alfalfa without compromising genetic gain in our breeding program. Advances in genomic tools, such as the availability of chromosome-scale haplotype-phased genome assemblies and next-generation sequencing technologies have offered the possibility to genotype breeding populations in various forage and cover crop species. The goal for the studies presented here was to build genomic prediction models to increase genetic gain for complex traits. Exemplary illustrations will be provided for genomic prediction models in alfalfa (*Medicago sativa* L.), annual ryegrass (*Lolium multiflorum* Lam.), and cowpea (*Vigna unguiculata* Walp.) under monoculture cropping systems, and for crimson clover (*Trifolium incarnatum* L.) and oats (*Avena sativa* L.) under intercropping systems. Predictive abilities for each species and cropping system will be presented for complex traits. In alfalfa, the inclusion of enviromics data in prediction models resulted in greater predictive ability by accounting for G x E for yield and persistence. The preliminary implementation of phenomic selection using near-infrared spectroscopy (NIRS) and hyperspectral sensors mounted to unmanned aerial vehicles resulted in greater predictive ability compared to genomic-based models for yield in most scenarios tested in alfalfa and annual ryegrass. Integrating multi-omics approaches could increase prediction ability of models and ultimately increase genetic gain for complex traits in forage and cover crop species adapted to subtropical and tropical agroecosystems.

Index terms: genomic prediction, phenomic prediction, enviromics.

Development of universal DaRTag markers for alfalfa (*Medicago sativa*) and use in mapping resistance to Aphanomyces root rot

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Abstract – Alfalfa (*Medicago sativa*) is the engine that drives dairy and beef production in the United States and alfalfa is unparalleled for providing environmental services. However, developing genomic resources for alfalfa improvement has been slow due to its large complex genome and the heterogeneity within cultivars. Breeding Insight, a USDA-Agricultural Research Service and Cornell University collaboration, is supporting breeding projects that have not benefited from the genomics and informatics revolution of molecular breeding. Through this collaboration a 3,000 SNP marker panel using the DArTag technology was created from whole-genome skim sequencing of 40 elite alfalfa lines used in North America. DaRTag is an amplicon-based genotyping platform targeting known genetic variants that provides microhaplotypes in addition to the target SNP within 81 bp sequences. Markers were selected for their genome-wide distribution and location within genic regions and can be used on any alfalfa population for molecular breeding and genomic insight. The marker panel was used to identify QTLs for resistance to Aphanomyces root rot (ARR), one of the most important diseases of alfalfa in North America. Two races of the pathogen causing ARR, Aphanomyces euteiches, are distinguished by differential cultivars. Resistant and susceptible plants were identified from the commercial cultivar 53V52 and the check cultivar WAPH-5 and were used as parents to produce F1 mapping populations. Plants were phenotyped with several race 1 and race 2 strains. Race-specific resistance involves a hypersensitive response of individual epidermal or cortical cells upon zoospore penetration and is highly

heritable, suggesting that resistance is conditioned by a small number of genes, most likely of the NBS-LRR resistance genes. Markers significantly associated with resistance to race 1 were identified on chromosome 1 from both populations while resistance to race 2 was identified on chromosome 2 or 4 depending on the parental germplasm. Transcript profiling was done to gain a better understanding of the compatible and incompatible interactions and mapped to the QTLs for resistance to identify candidate genes. Markers associated with race 2 resistance can be used to identify the resistance QTL in diverse germplasm and to follow introgression of the trait into elite parents to increase resistance to the disease. Identification of two different sources of race 2 resistance will enable breeders to stack genes to improve plant health and stand life. The use of DaRTag makers to map other agronomic traits and characterize crop genetic diversity will also be presented.

Index terms: SNP markers, disease resistance, alfalfa.

Genetic linkage mapping in *Megathyrsus maximus* (Jacq.) with multiple dosage markers(1)

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Abstract – Guinea grass [*Megathyrsus maximus* (Jacq.)] is a forage crop widely used as pasture to feed livestock in tropical and subtropical regions. The species stands out for presenting high yield and high nutritional quality, and the ability to be clonally propagated by seeds through apomixis. The majority of *Guinea grass* cultivars are autopolyploids and as such, genetic studies and genomic resources are very limited due to its inherent genetic complexity. In this study, we constructed the densest and most informative genetic linkage map for *M. maximus* to date using multiple dosage markers. We collected leaf samples, extracted and sequenced the DNA of 224 full-sib individuals originated from a biparental cross between S12, a sexual accession used as female parent, and Miyagui, an apomictic cultivar used as male parent. We utilized the reference genomes of five related species to analyze the raw sequencing data, find variants, and call dosage-based genotypes for both parents and all full-sib individuals in the population. The initial set of variants was filtered according to read depth, allele frequency, and amount of missing data, and the remaining set was used to calculate the pairwise recombination frequencies between markers. Using the information from the recombination matrix, markers were grouped into eight linkage groups that correspond to the eight chromosomes in the M. maximus genome and ordered according to the multi-dimensional scale (MDS) algorithm. Using a Hidden Markov Model (HMM), we re-estimated linkage phases and recombination frequencies between all markers based on a multipoint multi-dosage approach. The linkage analysis yielded a fully phased genetic linkage map with 7095 markers distributed across the eight linkage groups, spanning

1573.31 cM of the *M. maximus* genome. There was no evidence of double-reduction or preferential pairing in the studied population. The linkage analysis and the resulting genetic map provide a significant progress on the genetic knowledge of the species, bring new information to the evolutionary relationship between *M. maximus* and closely related species, and serve as a basis to downstream processes, such as the assembly of a reference genome, QTL mapping studies and marker assisted selection in breeding programs.

Index terms: linkage map, polyploid, autotetraploid, Guinea grass.

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GENETIC AND GENOMIC TOOLS
Poster presentations

Genomic prediction for green matter yield in *Urochloa ruziziensis* tetraploid using family bulks(1)

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Abstract – Three species of the Urochloa genus are among the most widely cultivated forage grasses in tropical and subtropical regions. These species are predominantly apomictic and tetraploid, underscoring the importance of *U. ruziziensis*, which is sexual and tetraploidized, for use in interspecific crosses with apomictic species. To support breeding programs, this study examines the feasibility of genome-wide family prediction in fifty half-sibling *U. ruziziensis* families to predict green matter yield (GMY). Based on the predicted family genomic value, the effectiveness of using the simulated individual best linear unbiased prediction method (BLUPIS) for selection at the individual plant level was evaluated. Genotyping was conducted using a genotyping-by-sequencing approach on DNA samples from family pools. A total of 28,106 filtered SNPs were utilized to predict phenotypic measurements. After testing various models and using a complete dataset, a mean predictive ability of 0.79 for family GMY was achieved. The results indicated a correlation of 0.90 between selection by phenotypic BLUPIS methods and genomic BLUPIS. Genomic BLUPIS selected two fewer families, and the number of individuals selected varied among families. Although this study focused on implementing genomic selection in *U. ruziziensis* families, the bulk methodology and prediction schemes used here could inform future studies in the Urochloa genus and other forage grasses and legumes bred in bulk.

Index terms: forage breeding, predictive ability, tropical grass.

Identifying putative orthologs for developing haploid inducer lines in warm-season turfgrass species(1)

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Abstract – Doubled haploid (DH) technology using haploid inducer lines (HIL) offers significant advantages over traditional crop breeding approaches. Recently, HILs have been developed in maize (*Zea mays*), governed by genes such as ZmMTL/PLA/NLD, ZmDMP, and ZmPLD3, and in rice (*Oryza sativa*) by OsMATL2. In maize haploid induction rates (HIR) achieved ranging from 0.1% to 7.7% when knocked out individually or in different combinations. Subsequently, de novo haploid inducer lines HILs were generated in rice and wheat (*Triticum aestivum*) by knocking out the ZmMTL orthologues OsMATL and TaMATL using gene editing techniques. To develop HILs in important warm-season turfgrass species, we identified putative orthologs of these genes using in silico approaches. Our study included zoysiagrass (*Zoysia* spp.), bermudagrass (*Cynodon* spp.), bahiagrass (*Paspalum notatum*), seashore paspalum (*Paspalum vaginatum*), and St. Augustinegrass (*Stenotaphrum secundatum*). For zoysiagrass, we used the Zoysiagrass Genome Database, while for other grasses, we utilized the NCBI database. Protein sequences of ZmMTL, ZmDMP, ZmPLD3, and OsMATL2 were retrieved and used for tBLASTN to identify conserved sequences. Due to insufficient genomic information, bermudagrass and St. Augustinegrass were excluded from further analysis. Sequences with an E-value of 0 were considered significant. Among the haploid induction genes, ZmPLD3 showed the highest sequence similarity (~90%) in all grasses at the protein level, making it a preferred target for developing HILs. Other genes exhibited varying levels of similarity across different species. For instance, ZmMATL showed 77% and 69% similarity in bahiagrass and zoysiagrass, respectively, but only 47% (non-significant) in seashore paspalum. OsMATL2 demonstrated significant similarity only in bahiagrass (83%), while it was non-significant in zoysiagrass and seashore paspalum. ZmDMP was non-significant in all grasses. Further exploration of bahiagrass genomic information was conducted using nucleotide BLAST for ZmMATL, ZmDMP, ZmPLD3, and OsMATL2, revealing identical exon and intron distribution in all genes. This makes bahiagrass a potential candidate for HIL development using gene editing techniques. The similarity indices at the DNA level were as follows: ZmPLD3 (82.78%), ZmMATL (75.6%), ZmDMP (80%), and OsMATL2 (83%). In vitro analysis should be performed to further validate the tissue-specific expression of these genes. Overall, this study provides insights into the sequence conservation of important haploid induction genes, which can be leveraged to develop HILs using gene editing techniques.

Index terms: doubled haploid, haploid induction, haploid inducer lines, orthologs, knock out.

Data integration from different cassava breeding programs increased the prediction accuracy for different traits in small breeding programs(1)

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Abstract – Cassava (*Manihot esculenta*), a tropical root crop, serves as a significant feed source of energy for livestock production due to its high carbohydrate content and adaptability to various environmental conditions. It is estimated that approximately 25% of global cassava production is used as animal feed. Cassava breeding efforts have traditionally been carried out by small-scale, local programs in different regions and countries; and have primarily relied on conventional breeding approaches based on phenotypic recurrent selection. While these programs have made significant contributions to cassava improvement, their genetic gain can be enhanced through the application of modern breeding strategies such as genomic prediction. In this study, we utilised data collected from three different cassava breeding programs (IITA, 42 field trials; NaCRRI, 5 field trials; and NRCRI, 19 field trials) to investigate the potential of data integration across different breeding programs in improving the prediction accuracy compared to running the same analysis within each breeding program. Collectively, the three breeding programs involved 2,742 cassava landraces and elite germplasm lines, phenotyped for seven agronomic and disease resistance traits that were scored in 38 to 54 field trials across the programs. The population was genotyped by genotype-by-sequencing and imputed to whole genome level. All data was downloaded from the NextGen cassava website (https://cassavabase.org/). While the combined analysis of the three breeding programs did not achieve any prediction advantage for the IITA breeding program, the average prediction accuracy across the seven traits significantly improved for the NRCRI program from 0.21 for the within program analysis to 0.30 for the combined analysis. For the NaCRRI program, the average prediction accuracy was slightly improved for the three scored traits from 0.38 to 0.41. The results demonstrate a significant improvement in the prediction accuracy for various cassava traits, emphasising the potential of data integration in optimising cassava breeding, holding particular promise for small-scale breeding programs.

Index terms: predictive breeding, cassava, agronomy and disease resistance traits, genomic selection, data integration across breeding programs.

Draft genome assembly of forage peanut (*Arachis pintoi*)(1)

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Abstract – Forage peanut (*Arachis pintoi* Krapov. and W.C. Greg.), a forage legume native to Brazil, is widely used as a green cover crop in several countries. Its benefits include soil moisture retention, nutrient cycling, biological nitrogen fixation, recovery of degraded areas, and erosion prevention. Its usage in pastures intercropped with grasses has increased daily weight gain by up to 50% and reduced cattle slaughter time by up to 9 months. However, its adoption is limited by the high costs of seed production, low establishment, decreased yields in dry seasons, and susceptibility to viral diseases. The lack of molecular tools to support cultivar development has been listed as one of the bottlenecks of breeding programs. High-quality genome assemblies are fundamental for the development of genomic resources for crops. This work presents a draft genome assembly of *A. pintoi* based on third-generation HiFi reads. High molecular weight DNA was extracted from young leaves of a single diploid individual. Sequencing was performed on a Sequel II and a Revio system at Maryland Genomics, using two SMRT cells on CCS HiFi mode, with 30-hour and 24-hour runtimes, respectively. Approximately 68 Gbp were obtained in 6.6 million reads, with an average size of 10 kbp, representing 61x genome coverage. Analysis of k-mer frequency spectra indicated a heterozygous and highly repetitive genome with a size of 1.1 Gbp. A partially phased draft assembly was obtained with Hifiasm in HiFi-only mode. The initial draft had 1,186 contigs with a total length of ~1.5 Gbp. Blobtools was used to filter contaminant contigs, and MITOhifi was used to assemble mitochondria and chloroplast genomes and filter organelle contigs. The final draft contains 428 contigs with a total size of ~1.5 Gbp, higher than the

1.1 Gbp genome size previously estimated for the species. Contig N50 was 31.6 Mbp, with 39 contigs longer than 10 Mbp (9.1% of the total), and the longest contig had 106.8 Mbp. The assembled gene space assessment using BUSCO (embryophyta_odb10) showed 99% complete orthologs, with only 0.6% fragmented and 0.4% missing BUSCOs. RepeatModeler and RepeatMasker were used to annotate repetitive regions, and 78.25% of the assembly was masked as repeats. Hi-C will be used to group and orient contigs in chromosome-scale scaffolds. RNAseq data will be used to predict and annotate gene models in the final assembly. This is the first genome assembly in the genus for a species not belonging to the Arachis section, increasing the understanding of the genomic diversity of Arachis species. It will be an invaluable resource for forage peanut breeding and genetics, allowing the development of state-of-the-art genotyping technologies to support the development of new cultivars.

Index terms: forage legume, genomics, genomic resources, third-generation sequencing.

Chromosome scale assembly and annotation of the *Paspalum notatum* cv. Pensacola genome(1)

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Abstract – *Paspalum notatum* cv. Pensacola is a diploid perennial grass (2n = 20) used as forage and turf. Native to Argentina, it is related to five of the 17 commercially released cultivars of the species and is widely adopted in Southeast Florida and Southern Brazil, indicating its agroeconomic importance. Here, we present the chromosomal-scale genome of the Pensacola cultivar. To obtain the PacBio-HiFi sequences, Pensacola seeds were grown in pots in a greenhouse at the University of Florida (UF), and the leaf tissue from a single plant was used to extract high molecular weight DNA. PacBio/HiFi sequencing was performed on a Sequel II system in SMRTcell 8M in CCS mode at Maryland Genomics. Around 31.6Gb were obtained in ~2.4M reads, and adapter removal was performed with HiFiAdapterFilt. Flower, leaf, and rhizome tissues and leaf tissues under drought and cold stresses were collected in the greenhouse at UF and sent to Novogene, where they had their total RNA extracted and sequenced at Illumina NovaSeq platform (2x150bp). Clean HiFi reads were assembled using HiFiasm, and Blobtools was used to remove contaminant sequences from the draft assembly. Ragout was used to group contigs using the *P. notatum* cv. Crowver genome (GCA_022530915.1) as a reference, resulting in 21 scaffolds, 10 of which had chromosome-scale lengths ranging from 42 Mb to 81 Mb, with a total assembly size of 548 Mb. Eleven ungrouped scaffolds had a total size of 14 Mb, and shorter unplaced contigs had a total size of 16 Mb. The scaffold-level assembly had an N50 of 53 Mb and a mean scaffold size of 26 Mb. Assembly completeness was evaluated with BUSCO, resulting in 99% complete BUSCOs. RepeatModeler identified the repetitive elements and LTR

transposons were the most prevalent, representing about a third of the 62% masked regions of the assembly using RepeatMasker. Comparative analysis with D-GENIES showed collinearity between Pensacola and Crowver assemblies, with some inversions in the centromeric regions. Preliminary identification of gene models was performed with LiftOff using the publicly available annotation of *P. vaginatum* with 35,565 genes (GCA_026573395.1), and 30,563 genes were lifted over to the Pensacola assembly. The Comparative Annotation Toolkit (CAT) was used to leverage a multiple genome alignment in HAL format, as well as available proteomes of four Panicoid species, the genome annotation of *P. vaginatum*, and RNAseq and IsoSeq data of different tissues of *P. notatum*. CAT analysis is still in progress. The chromosome-scale genome of *P. notatum* cv. Pensacola is an important genomic resource for the species, assisting in the discovery of markers and genes on a large scale as tools to support breeding programs.

Index terms: bahiagrass, third-generation sequencing, genomic resources, forage grass.

An institutional data repository for tropical forage genomics(1)

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Abstract – Genomic research to support plant breeding is often costly and time-consuming, generating a huge volume of data that must be stored and made available to team members and later to the scientific community. Before publishing and uploading data to public repositories, researchers typically need tools for searching and querying specific genomic information, like SNPs, genes, and QTLs, involved in the biological question of their ongoing research projects. One common approach to this problem is to implement an in-house system using the Generic Model Organism Database (GMOD) biological database schema named CHADO. Many systems exist in this regard, like Tripal, but use programming languages less known to the bioinformatics community, like PHP. One alternative is to use MACHADO, an open-source Python-based system developed by Embrapa, which is a framework to store, query, and analyze diverse biological data. This work describes the use of MACHADO to create a genomics data repository for multiple forage species, named ‘Tropical Forage Genomics Data Repository’. This web-based resource aims to support forage breeding research groups in Embrapa, currently providing storage for assembled genomes and genotyping data. Furthermore, the repository is used as a tool for genomic data browsing and querying, as MACHADO provides an embedded JBROWSE genome browser. It also has data filtering and querying capabilities with a keyword search box, as data is indexed with an ElasticSearch engine. Currently, the repository stores three genome assemblies of two species. One is *Urochloa ruziziensis,* also known as *Congo grass*, with a relatively small genome of ~ 615 Mbp, 41,021 loci, 61,374 transcripts, and 18,582 SNPs, all capable of relational querying by the search box. A database of 10,189,604 SNPs is also provided as a track in the genome browser. *Cenchrus* *purpureus*, or *Elephant grass*, has a genome of ~2Gb and two previously published assemblies are available in our repository: one with 14 scaffolds and the other with 252. These two versions provide, respectively, 77,139 and 65,485 loci with the same number of transcripts, as well as 1,799,154 and 1,586,613 SNPs. We expect our repository to soon host the genomic data of *Paspalum notatum*, a perennial grass also known as bahiagrass and used as forage and turf in tropical and subtropical regions Brazil, and the forage peanut *Arachis pintoi*. The creation of the 'Tropical Forage Genomics Data Repository' delivered the expected requirements for storage, browsing, and analysis of the genomic data produced by our projects. This tool showcases the MACHADO features as a powerful open-source resource for genomic-based research projects.

Index terms: CHADO, MACHADO, database, bioinformatics.

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II Conferência
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Melhoramento de
Forrageiras e
Gramados

BREEDING FOR FORAGE QUALITY AND YIELD
Oral presentations

Persistence and forage yield in a group of advanced breeding lines of *Paspalum notatum* under two grazing frequencies(1)

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Abstract – Livestock production systems are mostly based on the utilization of pastures with low adoption of inputs and grazing management. Bahiagrass (*Paspalum notatum*) is a warm-season perennial species native to America. It is an important component of native rangelands as well as cultivated for forage or turf around the world, and is well adapted to low fertile soils and poor management. The objective of this work was to evaluate the persistence and forage production of advanced breeding lines under contrasting grazing frequencies, identifying those more promising for cultivar release. Plots of five advanced breeding lines together with cv Argentine and cv Boyero-UNNE were evaluated using a randomized complete block design following a split-plot arrangement during two years (2020–2021 and 2021–2022). Genotypes exhibited upright- (cv Boyero and line I7), intermediate- (lines G37 and C14), and prostrated- (cv Argentine, and lines I21 and F44) growing habits. The main plots consisted of two grazing frequencies, 2 and 6, and 4 and 12 weeks for the summer and winter seasons, respectively. Sub-plots consisted of five breeding lines plus two cultivars as checks. A mob stoking grazing was used for the plots. Previous to grazing the plots the forage yield (FY) and tiller density (TD) were measured, additionally, root mass accumulation (RoMAc), rhizome mass accumulation (RzMAc), and ground cover (GC) were measured at the beginning, and end of the summer season. A significant interaction date*frequency was observed for FY, where a greater production was obtained in 5 dates for high and 4 dates for low frequency, whereas the forage accumulation for the 2-year round was greater for high grazing frequency. Lines G37, I7, and cv Boyero exhibited the greatest FY. TD was higher in the high frequency for most evaluated dates, additionally, greater TD was observed for prostrated than upright-genotypes. GC, RoMAc, and RzMAc were not affected by grazing frequency. RoMAc, and RzMAc were greater for prostrated- and intermediate-genotypes than upright ones during the first year, whereas no differences were observed for the second year. The cv Boyero-UNNE exhibited a lower GC during the first year. All the evaluated genotypes exhibited GC greater than 95% under both grazing frequencies. In conclusion, all the evaluated genotypes exhibited high persistence and tolerance to high grazing frequency, in addition, lines G37, I7, and C14 outperformed in persistence and forage production, therefore, are promising lines for cultivar release.

Index terms: Warm season grasses, grazing tolerance, forage breeding.

Plant molecular farming of designer feedstocks for animal production(1)

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Abstract – Recent advances in plant, animal and microbial systems biology – from genome to phenome – and associated innovations are finding applications in pastoral and livestock agriculture, managing impact of climate change through adaptation and mitigation, and delivering agriculture productivity, environmental and societal outcomes. Methane production from enteric fermentation in ruminant livestock accounts for approximately 60% of emissions from agriculture. Antimicrobial resistance, associated with the emergence of bacteria and other microbes that are resistant to antibiotics, is considered one of the most significant threats to human and animal health. To contribute to addressing these challenges, we have established a platform for plant molecular farming for the production of designer feedstocks to enable the in planta delivery of target bioactives. An initial target, RNase5, has been discovered through a milk systems biology approach based on functional proteomics. It shows potential as a cost-effective feed additive to increase meat production in cattle, sheep, pork and poultry. The commercial value of RNase 5 and other milk bioactives – including novel potent antimicrobial peptides discovered based on comparative genomics of ancient genomes from extant mammalian lineages - in animal production and health might be realised through plant-based delivery using transgenic and/or transplastomic target crops (i.e. safflower, alfalfa), and other plant cell-based expression systems via designer feedstocks. Proof of concept for in planta expression of RNase5 accounting for ca. 10% of total soluble leaf protein was demonstrated in white clover. Efficient methods for in vitro plant regeneration and Agrobacterium-mediated transformation in commercial varieties of target crops, such as safflower, were developed. Associated platforms for predictive breeding based on genomic selection, complemented with speed breeding protocols, were also established for the key target forage crops to accelerate varietal development. Designer feedstocks could reduce industry reliance on antibiotics, improve animal muscle growth and health, and reduce methane emissions in ruminant livestock.

Index terms: designer feedstocks, plant molecular farming, milk bioactives, alfalfa, safflower.

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II Conferência Internacional de Melhoramento de Forrageiras e Gramados

BREEDING FOR FORAGE QUALITY AND YIELD

Poster presentations

Forage yield in velvet grass progenies(1)

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Abstract – Velvet grass is a temperate forage species that is grown in the coldest regions of Southern Brazil. It belongs to the Poaceae family. In Brazil, it tends to perenize in fresh climates with rainy summer. When in a different condition, it perenizes via natural reseeding. Until now, there are only two cultivars of this species in the National Cultivar Register. As an alogamous species, the most used method of selection is half-sib progeny selection. The aim of this work was to select high productive progenies in one cycle of selection in the Breeding Program at Embrapa. In the 2023 winter season, at Capão do Leão municipality (Rio Grande do Sul State, Brazil) 70 half-sib progenies from the population BRS Adelino were assessed in an incomplete block design. Each experimental unit consisted of one hollow with fifteen seeds. The experiment was sowed in 23/05 and two cuts were performed. The evaluated traits were: vigor, tiller number, fresh forage yield, dry matter yield, dry leaf yield. In the first cut, there was significant difference among progenies for vigor and dry matter yield. Fresh forage yield was significantly different among progenies in the second cut and in the sum of the two cuts. Fresh forage yield varied from 8,207 kg/ha to 19,731 kg/ha. The 20% progenies with more accumulated yield were selected.

Index terms: *Holcus lanatus*, forage yield, half sib progenies.

Modelling genotype by environment interaction improved the prediction accuracy of alfalfa growth traits(1)

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Abstract – Alfalfa (*Medicago sativa*) plays an important role as animal feed due to its high nutritional value being rich in protein. Its multiple cuttings per year make it a sustainable and economical feed option. Moreover, its deep root system allows it to thrive in various environmental conditions. Advancements in predicting and enhancing dry matter yield and other growth characteristics are main objectives in predictive breeding of alfalfa. This study investigated the growth characteristics of alfalfa by incorporating genotype by environment (GxE) interactions into the predictive model through the reproducing kernel Hilbert space machine learning algorithm. We used publicly available data of 400 global alfalfa accessions genotyped with 122,763 genotyping-by-sequencing single nucleotides polymorphisms, and phenotyped in four and five field trials (two locations) for dry matter yield and plant height; respectively. Our results showed that the GxE model demonstrated a significant improvement in prediction accuracy for dry matter yield compared to the standard model that does not consider GxE. The average prediction accuracy increased from 0.50 to 0.56 by modelling GxE, and this improvement was consistent across different field trials ranging from 0.03 to 0.10 per trial. On the other hand, the GxE model had slight improvement in prediction accuracy for plant height increasing to 0.57 compared to 0.55 for the standard model. However, this improvement was not statistically significant, as expected given that plant height is usually controlled by a small number of genes that have low interaction with the environment. These results highlight the potential of GxE modelling in enhancing our understanding of alfalfa growth dynamics and improving biomass yield in alfalfa breeding programs. Further research is required to validate and extend these findings across different traits, germplasm sources, and environmental conditions.

Index terms: predictive breeding, alfalfa, growth and biomass yield traits, genomic selection, GxE modelling.

Multi-trait genomic prediction improved the accuracy of predicting energy and fibre traits in perennial ryegrass(1)

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Abstract – Perennial ryegrass (*Lolium perenne* L.) is a key pasture species of temperate pastoral agriculture worldwide. It serves as a primary source of forage for livestock production. Ongoing improvements in dry matter yield and herbage quality and energy traits are important objectives in perennial ryegrass breeding programs. Accurately predicting these traits in perennial ryegrass through advanced genomic models can significantly enhance genetic gain in predictive breeding of perennial ryegrass. Reliable predictions to improve these traits require overcoming limitations in the availability of proper reference populations. Statistical models that simultaneously analyse multiple traits together have the potential to mitigate these constraints. This study explored the application of multi-trait genomic prediction in enhancing the accuracy of predicting energy (digestible organic matter, metabolizable energy, as well as low, high and total molecular weight carbohydrates) and fibre (acid and neutral detergent) traits in perennial ryegrass. The population used involved 517 publicly available half-sib families genotyped with 1,023,011 genotype-by-sequencing single nucleotide polymorphisms and phenotyped in two locations. The research leverages advanced reproducing kernel Hilbert space machine learning models that simultaneously consider multiple traits, thereby capturing the genetic relations between them. Compared to the single trait analysis, the multi-trait analysis improved the prediction accuracy of the five energy traits from 0.27 to 0.39 (41.8%), while the improvement for both fibre traits was from 0.31 to 0.34 (8.3%). These findings highlight the potential of multi-trait genomic prediction in optimising predictive breeding of perennial ryegrass. Further research is encouraged to validate these results across diverse perennial ryegrass genotypes and environmental conditions.

Index terms: predictive breeding, perennial ryegrass, herbage quality traits, genomic selection, multi-trait genomic prediction.

Seeding *Stylosanthes* cultivars in *Andropogon* pastures and its effect on forage production(1)

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Abstract – The use of forage legumes enhance protein of the ruminant diet and sustain pasture productivity via biological fixation of nitrogen. It could be a promising alternative for low-productivity pastures of central Brazil. The objective of the study was to evaluate dry matter yield (DMY) of *Stylosanthes* cultivars mixed with Andropogon grass. The experiment was conducted in a very clayey Red Oxisol in Planaltina, FD, Brazil, from December 2021 to January 2024. The experimental design was randomized blocks with three replications in plots of 3.5 × 8 m. The treatments were cultivars of the *Stylosanthes guianensis* – BRS Nuno, BRS Bion, BRS Bela and an equal part mix of seeds of BRS Nuno and BRS Bion (Nuno+Bion). The seeding of stylo was carried out on December 9, 2020, using a no-till seeder (rows spaced 0.5 m) in a defoliated pasture of *Andropogon gayanus* cv. Planaltina (~20 cm). The seeding rate was 3 kg/ha of pure viable seeds along with 50 kg of P2O5/ha (simple superphosphate). Cuts were made in the first (5/4/2021; 12/22/2021), second (3/30/2022; 1/10/2023) and third (3/30/2023; 7/12/2023; 1/19/2024) years after seeding, and forage was harvested 40 cm from the ground. Forage samples were separated manually as legume or grass to estimate the botanical composition of the DMY. The legume DMY was affected by Treatment × Cut ($P<0.05$). Contrasting the non-effect of Treatment in the first two cuts (means of 124 and 58 kg/ha), Bela presented greater legume DMY in 3/30/2022 (902 kg/ha), followed in descending order by Bion (672 kg/ha), Bion+Nuno (383 kg/ha) and Nuno (235 kg/ha). In January and March 2023 cuts, legume DMY was greater for cv. Bion (220 and 506 kg/ha, respectively) compared to Bion+Nuno (40 and 172 kg/ha), Bela (8.9 and 68 kg/ha) and Nuno (0.6 and 23 kg/ha). There was no effect of Treatment ($P>0.05$) on legume DMY in the last two cuts (means of 28 and 15 kg/ha). For grass and grass+legume DMY there was no effect of Treatment (P>0.05) (means of 749 and 897 kg/ha/cut, respectively). In the first and second year after seeding, the contribution of legume in the botanical composition was 3 and 7% for Nuno, 13 and 36% for Bion, 16 and 21% for Bela, and 18 and 16% for Bion+Nuno. In the third year, the contribution of legume decreased to 3, 18, 3 and 9% for Nuno, Bion, Bela and Bion + Nuno, respectively. In mixed Andropogon-stylo pastures, Bela and Bion cultivars reveal their greater productive capacity in the second year after introduction, but only cv. Bion persists growing in the third year.

Index terms: BRS Bela, BRS Nuno, BRS Bion, legume, dry matter yield.

Forage yield of *Stylosanthes* cultivars aiming their use in dry season as protein bank⁽¹⁾

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Abstract – *Stylosanthes* protein bank can be established in the rainy season for later use in the dry season, overcoming the seasonal forage production from grasslands. However, the quantity and quality of the forage are sensible to defoliation frequency and stylo cultivars. The trial was conducted in Planaltina, FD, Brazil, aiming to evaluate dry matter yield (DMY) and morphological composition of stylo cultivars in response to defoliation management. The experimental design was completely randomized block in a split plot arrangement with three repetitions, and *Management* factor was allocated to the plots and genotype to the subplots (2 x 2 m). Genotype treatments were *Stylosanthes guianensis* cultivars (BRS Bion, BRS Nuno and BRS Bela), and Management treatments were cutting or not cutting in the rainy season (February) combined with dates of use in the dry season (May, June, July or Flowering). The effect of Management × Genotype was not significant (P>0.05). The total DMY (stem plus leaf) for BRS Bion (5.128 kg/ha) and BRS Nuno (12.967 kg/ha) was inferior to DMY for BRS Bela (15.030 kg/ha). Since plants flowered in May, delaying 15 days when cut in February, there were no differences of DMY in dry season for dates of use, except for July - 6.479, 7.804 and 11.298 kg/ha for May, June and July, respectively. In the same way, DMY of the total rainy and dry season was 9.046, 10.436 and 14.553 kg/ha for May, June and July, respectively. The percentage of DMY from rainy season (~80%) did not differ for Genotype (P>0.05). The lower canopy height for BRS Bion (57 cm in the rainy season and 76 cm in the dry season) was related to their lower leaf and stem accumulations. The Genotype effect on DMY happened due to the accumulation of stems, mostly for later dates of use. BRS Nuno had lower DMY due to influence of stems, which was higher for BRS Bela, both for rainy and dry season. There is no effect of the previously cut in the rainy season on forage yield when the use of the stylo protein bank occurs at the flowering, regardless of Genotype.

Index terms: BRS Bela, BRS Bion, BRS Nuno, dry matter yield, legume.

Genetic variation and correlations of forage yield and quality traits in ruzigrass (*Urochloa ruziensis*) half-sib families(1)

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Abstract – Ruzigrass breeding has targeted superior families or individuals for dry matter yield and forage quality. Knowledge of the available genetic variability and understanding of the correlation magnitud between traits can guide strategies to achieve significant genetic gains. The objective of this study was to estimate genetic and phenotypic parameters, trait heritabilities and their correlations, selection accuracy and expected genetic gain from selection for forage yield and nutritional quality traits on a population of half-sib families of ruzigrass, representative of the available genetic diversity for the species existing in germplasm bank of Embrapa. Eight traits in 178 half-sib families were evaluated. Forage nutritional quality traits were estimated via NIRS. Data were analyzed with mixed models and clustering analysis. Significant differences between progenies were found for all traits. Narrow-sense heritability ranged between 0.26 and 0.42, and selection accuracy ranged between 0.51 and 0.65 among traits. Genetic coefficients of variation between progenies were lower for nutritional quality traits (CVgp% range 1,31–4,34%) when compared to dry matter yield (CVgp% 12,83). Dry matter yield had positive genetic correlations with neutral and acid detergent fiber, with cellulose, and was negatively correlated with crude protein and hemicellulose. Cluster analysis showed two groups of half-sib families, the first being correlated with in vitro dry matter digestibility (IVDMD) and crude protein, and the second with the remaining measured traits. Selection for dry matter yield may have a negative impact on crude protein content but no impact on

IVDMD. In contrast, selecting low fiber and/or high crude protein content may improve forage quality.

Index terms: forages, genetic correlation, spectroscopy, plant breeding.

Adaptability and stability of *Megathyrsus maximus* genotypes under a multi-harvest trial in Campo Grande, MS, Brazil(1)

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Abstract – Selection in perennial plants involves evaluating genotypes over time in different seasons and different years. Thus, the selection of genotypes that are more adapted and stable to environmental variations over time is one of the main objectives of breeding. The objective of this study was to estimate the genotypic x harvest interactions and the adaptability and stability of hybrids pre-selected by Embrapa's *Megathyrsus maximus* (*Panicum maximum*) breeding program evaluated under the Cerrado Biome in Brazil. For this, 40 genotypes composed of 37 pre-selected hybrids, one accession from the germplasm bank and the commercial checks cv. Mombaça and cv. Massai were evaluated for leaf dry matter yield (LDMY, t/ha) in an experiment in a randomized block design with two replications at Embrapa Beef Cattle in Campo Grande, MS The evaluations began in 2020 and ended in 2022, in a total of eight harvests in two dry periods, two dry-wet transition periods and two wet periods. Statistical analyses based on mixed models for each harvest were performed to obtain estimated means (BLUES). Subsequently, estimated means by harvests were used for analysis using the random regression approach for longitudinal data. The adaptability of each genotype was estimated based on the area under the leaf dry matter yield trajectory curve, which reflects accumulated production over time. Genotype stability was calculated based on the coefficient of variation of the trajectory curve, which reflects the stability of the genotypes, where the genotype is stable if there is a small variation between harvests. The genetic correlation between harvests ranged from 0.51 to 0.99, showing the presence of genotype x harvest interaction which varied from moderate to low magnitudes, depending on the combination of harvests. The lowest

correlation was between the first and last harvest. There was a high variation in adaptability and stability among the genotypes over time for LDMY. Ten genotypes, including the cv. Mombaça, showed the highest adaptability and stability values. Of these, four genotypes showed higher adaptability than cv. Mombaça, and all showed superior stability to this cultivar. The results of this study showed the presence of genotype x harvest interaction and genetic variability for adaptability and stability. Four hybrids showed greater adaptability and stability for LDMY than Mombaça, and can follow to a the new phase of evaluation in the breeding program.

Index terms: Breeding, forage grass, Guineagrass.

Persistence of leaf dry matter yield under two levels of soil fertility in *Megathyrsus maximus*(1)

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Abstract – Persistence of leaf dry matter yield (LDMY) is a complex trait that is expressed over time and is influenced by several abiotic and biotic factors. Besides showing a higher LDMY a more persistence genotype also shows lower losses over time due to environments stresses, such as water deficit, lower fertility and under disease attacks. The goals of this study were to evaluate the persistence of LDMY of genotypes of *M. maximus* and to estimate the effects of selection for persistence in two levels of phosphorus and base saturation in a clay oxisol of Cerrado of Campo Grande, MS For this, 10 sexual and 10 apomictic genitors, 86 full-sib families along with four commercial checks were evaluated in an 11 x 10 alpha-lattice design with three replications in two levels of phosphorus and base saturation levels. The plots were two rows of five plants with a spacing of 0.5 m between plants and between rows. LDMY was evaluated under nine harvests from February 2017 to January 2019, which represents 783 days of experimental evaluation. Statistical analyzes were performed based on mixed model, were genotypes were considered random. The effects of the model were used to calculate the REML means. The genotype persistence was obtained by the distance of each genotype to the ideotype (most productive genotypes in each harvest), considering all harvests. There was genetic variation for the persistence among genotypes. There were apomictic and sexual genitors and full-sib families superior to the best commercial check (cv. Mombaça) in both soils. 28 and 34% of full-sib families were superior to the cv. Mombaça in low and high fertility soils, respectively. But, as there is genetic variation within full-sib families, hybrids selected within families can lead to a greater genetic superiority over checks. Four of the nine best selected families in each level of fertility were coincident in both soils, which means that five of the best families were specific for each level of fertility. The results showed that the persistence varied among genotypes, highlighting the importance of the trait to the selection in *M. maximus*, in order to increase the sustainability of the pastures of the species. Phosphorus and base saturation contents affect the selection for persistence in *M. maximus* in clay oxisols.

Index terms: *Panicum maximum*, forage yield, genetic variation, persistence.

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BREEDING FOR SEED QUALITY AND YIELD
Oral presentations

Flowering periods, seed yield components, seed quality and patterns of seed shattering in *Paspalum*: effect of taxonomy and nitrogen fertilization(1)

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Abstract – Seed yield is crucial for the commercialization and establishment of new forage cultivars. Perennial warm-season grasses typically have reduced seed yield, and the ecophysiological factors involved are not well understood. This research aimed to estimate seed yield components in *Paspalum*, evaluate nitrogen fertilization effects on the reproductive phase, seed yield components, and seed quality, and establish the pattern of seed shattering over time. Ecotypes and hybrids covering different reproductive periods were used. The experimental design was a ran-domized complete block design in a split-plot arrangement with three replications. Main plots had two nitrogen levels (0 and 150 kg/ha N), and sub-plots contained different genotypes. Seed yield variation was mainly related to reproductive tiller density among germplasm with different flowering periods. Early flowering germplasm showed an extended flowering period (159%), greater tiller density (27.7%), greater reproductive tiller density (157%), and higher seed yield (302%) in response to nitrogen fertilization. Seed quality traits and seed retention were not affected by nitrogen fertilization. Although there was marked variation among taxonomic groups, an inverted sigmoid response was observed for seed retention over time. Seed yield in *Paspalum* is mainly influenced by the number of reproductive tillers per m^2 and seed retention.

Index terms: Warm-season grasses, seed yield components, seed retention.

Exploring seed yield components in interspecific *Urochloa* spp. hybrids through multi-environment trials(1)

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Abstract – In Brazil, brachiaria grasses (*Urochloa* spp.) serve as the primary forage crop for ruminant livestock, with 90,000 hectares of seed fields of *U. brizantha, U. decumbens, U. ruziziensis*, and interspecific *Urochloa* spp. hybrids registered in 2023/2024 on MAPA. New brachiaria varieties underscores the growing demand for improved forage options. Unlike grain crops, forage breeding prioritizes nutritional and forage traits over seed quality and yield, although these are crucial for varietal success. During 2022–2023, multi-environment trials were conducted to develop interspecific Urochloa hybrids with superior nutritional value, forage and seed performance. Trials took place in three locations in Brazil — Chapada Gaúcha (MG), Paraúna (GO), and Primavera do Leste (MT) —with early and late seeding in the season. Trials included elite hybrids alongside *U. brizantha* cv. Marandu and *U. ruziziensis* cv. Kennedy plotted in a randomized complete block design with four replications. Plots were fertilized and sprayed with pesticides according to the company's seed production protocols. Traits assessed included seed yield, seed set, inflorescence density, raceme length and number, 1000 seed weight, and hay production. Results showed high variability in seed yield components and hay production across different environments and seeding dates. Early seeding resulted in better seed yield in all locations, with a more significant effect in Chapada Gaúcha, where the rain period and total volume were lower. In Chapada Gaúcha, hay production was lower but did not affect seed yield. Some hybrids performed better in this environment. Additionally, for early seeding, Paraúna and Primavera do Leste had a high correlation for seed yield, suggesting most hybrids would perform similarly in both locations. Our results indicate that seed yield is moderately correlated with the number of caryopses per area, a product of inflorescence density, racemes per inflorescence, and caryopses per raceme. Seed yield component interactions were hybrid-specific; in some cases, seed set had a higher correlation with seed yield. Understanding the influence of each component on seed yield can improve seed production management, as they are defined at different phenological stages. Comprehending the relationship between seed yield components and seed yield helps to define target traits for breeding, improving genetic gains. This research facilitated the selection of superior hybrids for seed yield and identified the optimal locations for seed production for each hybrid. Ongoing efforts focus on selecting seed yield and characterizing seed yield components in second-year crops, with preliminary results indicating interspecific hybrids can outperform standard varieties.

Index terms: brachiaria, hybrids, forage seed production.

KNOX4-KCS12 play important roles in seed physical dormancy formation

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Abstract – Physical dormancy, often called hardseededness, exists widely in legume species. This adaptive trait allows plants to maintain a seed bank in soil and thus survive unfavorable environmental conditions. The molecular mechanism of physical dormancy is largely elusive. We utilized the model legume plant, *Medicago truncatula*, to study this trait because this species produces seeds with typical physical dormancy. By screening a large *M. truncatula* population tagged with a retrotransposon, we isolated different mutant seeds that lost physical dormancy. Genetic and molecular analyses revealed that a class II KNOX gene, KNOX4, controls hardseededness by regulating seed coat cuticle development. Further investigation showed that the seed coat specific β-ketoacyl-CoA synthase, KCS12, is a novel KCS enzyme controlling the production of very long chain lipid species; it is also associated with seed physical dormancy. ChIP assay demonstrated that the expression of KCS12 in seed coat is directly regulated by the KNOX4 transcription factor. These findings define a new molecular mechanism by which KNOX4 and KCS12 control seed physical dormancy formation.

Index terms: hardseededness, *Medicago truncatula*, ChIP.

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BREEDING FOR SEED QUALITY AND YIELD

Poster presentations

Phenotypic variability of *Urochloa ruziziensis* genotypes for seed yield and quality(1)

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Abstract – The objective was to evaluate the phenotypic variability of *Urochloa ruziziensis* genotypes regarding seed yield, quality, and seed dormancy, aiming at selecting promising individuals for use in breeding programs. Twenty-four outstanding genotypes were selected (higher forage yield and quality) from a population established from a seed mix of all accessions available in the Embrapa genetic base collection. The number of inflorescences per plant, the number of racemes per inflorescence, the number of seeds in the median raceme were counted, and the average length of the raceme were measured. After manual seed harvest and threshing, the spikelets were pre-cleaned using sieves. The seeds were homogenized, and those containing caryopsis were separated from the empty ones using a seed blower. The mass and proportion of filled seeds (pure lived) were determined. In five repetitions of 100 seeds, the percentage, in number, of filled and empty seeds was estimated, as well as the mass of a thousand seeds. The viability of filled seeds was determined by the tetrazolium test. Germination was tested under two conditions: at 30°C, in the dark, in a germination box with distilled water (GTC), and at 20/30°C (12/12 hours), with light, in potassium nitrate (0.2%). Seed dormancy was estimated by the difference in the average of the two germination conditions and viability. The number of inflorescences per plant (average 544 and range 96–904), mass of filled seeds in weight (average 29,5g and range 15,7–353,6), and mass of filled seeds in percentage, average 73 and range 46–89, were measured from the absolute values of the measurements per plant and thus did not undergo analysis of variance. Analysis of variance was performed for yield components: mass of a thousand seeds average, number of seeds in the median raceme, raceme length, number of racemes per inflorescence, and index of filled seeds, as well as for viability and germination, and in case of significance, the means were grouped using the Scott-Knott test ($p \leq 0.05$). There was a significant difference for mass of a thousand seeds, mean 8,5g, average raceme length 5cm, index of filled seeds 32%, germination at a constant temperature 37%, germination at alternating temperature 31%, and germination average 34% ($p < 0.001$), number of seeds in the median raceme was 32 seeds, number of racemes per inflorescence 4 seeds, and average dormancy was 46% ($p < 0.01$) and average viability 80% ($p < 0.05$). There is variability in yield, quality, and seed dormancy among the evaluated genotypes, allowing the use of these variables as additional criteria for selecting plants for the species breeding program.

Index terms: seed, tetrazolium, germination, grass, forage.

Evaluation of the sensitivity of *Panicum maximum* primers for identification of mixtures in seed lots(1)

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Abstract – The commercialization of forage seeds accounts for about 20% of all seed trade in Brazil. It is estimated that around 30% of this industry is affected by illegal seed production and commercialization practices, which drives initiatives for origin certification and product quality. Additionally, “seed mixes” have become popular among producers. In both cases, monitoring the purity, identity, and/or mixing percentage of the breed is essential to ensure that the pasture meets the desired characteristics for which the seeds are commercialized. The morphological similarity between some seeds and plants of *Panicum maximum* ease unintentional mixing, piracy, and complicates breed identification. Fortunately, with advances in molecular techniques, it is now possible to accurately identify breeds, at genomic level, using specific DNA parts for each genotype. In this context, the aim of this study was to evaluate the minimum percentage for detecting genotype mix using *P. maximum* breed-specific primers. To achieve this, different percentages of mixing between two P. maximum breeds were tested. A count of 100 seeds per sample was standardized, and the mixtures were applied in triplicate at the following proportions 1, 5, 10, 20, 30, 40, 50% of interest breed and one sample per genotype, with 100% of identical seeds. The samples were frozen in liquid nitrogen, ground using a vibrating mill and was used the DNA extraction protocol. The samples were quantified in 0.8% agarose gel. PCR was performed with a final volume of 15 uL and 30 ng of DNA per sample, using exclusive primers for one of the breeds. For visualization of amplifications, PCR products were subjected to electrophoresis on a 1.5% agarose gel, stained with GelRed. The primers tested in this study were able to detect the presence of specific *P. maximum* breed from 1% of seed mixture in the sample, demonstrating their high sensitivity and efficiency. Although preliminary, this result demonstrates that the use of breed-specific primers has great potential for evaluating mixture in forage seed lots.

Index terms: forage seeds, purity, molecular markers.

Seed retention in *Megathyrsus maximus*(1)

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Abstract – Seed shattering is a natural dispersal mechanism in perennial grasses that, although it benefits the perpetuation of the species, causes significant harvest losses. Identifying plants with reduced shattering is crucial for enabling direct panicle harvesting, thereby reducing production costs and the price of seeds. The Miyagui cultivar of *Megathyrsus maximus* (Guineagrass), discovered in a Mombasa field in Brazil and registered in 2017, stands out due to its more compact panicles and high seed retention. Despite its positive impact on the forage seed market, data on the shattering dynamics of this cultivar is lacking. This study aimed to compare seed retention between the Miyagui and Mombasa cultivars. The genotypes were evaluated in a block experiment during the 2019 and 2020 growing seasons. Shattering was monitored weekly using tulle protection on a representative inflorescence during anthesis. Harvesting took place weekly for four weeks, and the inflorescences with retained seeds were harvested, threshed, and processed at the Embrapa Beef Cattle Seed Laboratory in Campo Grande, MS, Brazil, where the pure seeds were weighed. Seed retention was calculated as the proportion of the weight of retained seeds relative to the total seeds produced. The data was analyzed using Generalized Estimating Equations (GEE), considering the experimental design and the effects of harvest times, genotypes, and their interactions. The results showed that the retention of pure seeds varied significantly between the Miyagui and Mombasa genotypes over the harvest period. The Miyagui cultivar exhibited significantly higher retention, with 92% of the seeds retained 7 days after anthesis, 86% after 14 days, 76% after 21 days, and 63% after 28 days after anthesis. In contrast, the Mombasa cultivar showed a sharp decline, with 57% retention in the first week, 14% in the second, and nearly zero after

21 days. It can be concluded that the Miyagui cultivar has superior seed retention in the panicle, marking the first report of this trait in the species. This trait enhances its potential use in the Guineagrass breeding program, promoting more efficient harvests and reducing costs.

Index terms: *Panicum maximum*, seed shattering, tropical forages.

Seed productivity of *Megathyrsus maximus* genotypes genetically improved for seed retention capacity[1]

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Abstract – High seed productivity of forage plants is decisive for their lower selling price. In addition, it is one of the success factors for the adoption of new forage cultivars and the market supply of seeds. An extended seed retention period in the inflorescences facilitates the harvesting process and contributes to greater seed productivity. A high seed retention was identified in *Megathyrsus maximus* genotypes and has been explored in this species forage breeding program at Embrapa. After crossings and phenotypic selection for forage attributes, four promising apomictic genotypes (PM411, PM415, PM430, PM431) were identified and seed productivity and their components were evaluated in a small plot trial in Planaltina, DF, Brazil (15º S, 47º W, 1,000 m.a.s.l) to support the selection of superior genotypes for later grazing experiments. The experimental design was randomized complete blocks with four replications. The plot size was 2.5 x 4.0 m and genotypes were established with young plants (4–6 leaves) cultivated from seeds in a greenhouse (November 2022), and transplanted for the field (0,5 m apart) in January 2024, in a corrected and fertilized soil (P, K, S, Micronutrients) for high level fertility. Sporadic irrigation of the plots was carried out until the plants were established in the area. The plants were fertilized (broadcast) with the equivalent of 50 kg N/ha in the vegetative phase. Inflorescences with mature seeds were manually harvested (1–2 times/week; May to June) from the center line of plot. Seeds samples (all harvests) were grouped and cleaned (seed blower) to estimate pure live seed productivity. The harvested inflorescences were counted and, 4 months after harvest period, the aerial biomass of the plants was estimated. The response variables data were subjected to analysis of variance (F test; P = 0.05) and genotypes means compared (t test; P = 0.05). Pure seed productivity was higher (P<0.05) for hybrid genotypes PM411 (1.38 t/ha) and PM430 (1.09 t/ha) compared to PM415 (0.48 t/ha), PM431 (0.34 t/ha), and control treatments (cv. Mombaça, 0.25t/ha; cv. Myiagi, 0.34t/ha). The genotypes with higher seed productivity (PM411, PM430) also had a higher (P<0.05) number of inflorescences per plant (22–26), compared to the others genotypes (8–12). The cv. Mombaça was the treatment with the lowest pure seed weight/inflorescence (599 vs. 1,022–1,470 mg) and the PM431 had the lowest dry biomass in the shoot (196g/plant vs. 306–327 g/plant). The PM411 and PM430 genotypes are the most promising in terms of seed productivity, being mainly influenced by the largest number of inflorescences per plant. Even the genotypes with lower seed productivity (PM415 and PM431) are promising because do not differ from the reference cultivar (cv. Myiagi).

Index terms: Cerrado, Panicum, tropical forage.

Productivity and Physiological quality of seeds of *Urochloa mosambicensis* genotypes in Campo Grande, MS(1)

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Abstract – *Urochloa mosambicensis* (commonly known in Brazil as capim-corrente) is a forage grass with significant potential for regions with water limitations and is less studied compared to other tropical forage species. Despite its high seed production potential, it often produces a large number of empty seeds and exhibits dormancy, which may represent limitations for commercial production. The objective of this study was to evaluate the seed productivity of six superior genotypes from the *U. mosambicensis* breeding program at Embrapa, pre-selected based on their morpho-agronomic performance in a semi-arid region. The experiment was conducted in Campo Grande, MS, during the 2022/2023 growth season (20°25’32”S, 54°40’49”W , 565 m), on a dystrophic Red Latosol with medium texture (25% clay), with correction and fertilization based on chemical analysis. A randomized complete block design was used, with five repetitions and plots of 1 m² (single plant, transplanted on 12/19/2022, at 55 days old). Harvests were performed manually, on two occasions between 2/22/2023 and 4/5/2023; the seeds were bagged and subsequently processed to determine pure seed productivity (SP). The following physiological analyses were conducted: seed viability (tetrazolium test), germination, first count of germination (FCG), and weight of one thousand seeds (WTS), according to the Seed Analysis Rules (Brazil, 2009). Genetic variability among the genotypes was evaluated (Anova F test; $P<0.01$), and the means were compared using the Scott-Knott test (5%). The SP productivity varied from 141 to 811 kg/ha SP, with the highest values recorded for genotypes 1805 and 1813, at 811 and 632 kg/ha SP, respectively. Genotypes 1816, 1810, 1829, and 1802 produced 142, 292, 399 and 401 kg/ha SP,

respectively, and these values did not differ significantly from each other. Regarding the physiological evaluations, genotypes 1805 and 1810 stood out, with tetrazolium values of up to 62%; the others ranged from 45 to 50%. For germination, the maximum value of 34% was recorded for genotype 1805, indicating dormancy or issues with seed formation. Similarly, the FCG, also indicative of vigor, was considered low, with a maximum of 28% for 1805. The WTS values ranged from 1.1216 to 1.3344 g and did not differ among genotypes. Studies on *U. mosambicensis* are scarce and recent, indicating significant variability in seed productivity, allowing for the selection of superior accessions. However, the species requires in-depth studies on seed production and physiology, including the development and application of classification and/or seed preparation methods.

Index terms: mozambique grass, forage improvement, seed germination, Brachiaria.

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TURFGRASS AND COVER CROPS (BREEDING AND GENECTICS)

Oral presentations

Interplanting maize with summer-dormant cool-season grass as perennial groundcover for sustainable crop production(1)

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Abstract – The US Midwestern landscape is one of the most highly altered and intensively managed ecosystems in which natural plant communities have been mostly replaced by monoculture of annual row crops. With this cropping system, many ecosystem services that were once provided by native plant communities have been lost consequently. Reincorporating perennial plants into cropping systems will restore many of the lost ecosystem services. We have demonstrated that intercropping corn with cool-season grasses as perennial groundcover (PGC) without yield reduction is feasible provided interspecific competitions are managed by either an early season growth suppression of PGC with a herbicide or when a summer-dormant cool-season grass was used as PGC. A two-year study investigating the compatibility between two PGC species, Kentucky bluegrass (*Poa pratensis*) and bulbous bluegrass (*P. bulbosa*) and maize was conducted. Measurements of PGC ground coverage, maize plant height, stage and grain yield were taken. Our results show that maize grain yield comparable to the control can be obtained when maize is grown with bulbous bluegrass, which enters summer dormancy in response to increased day length and higher temperatures early summer and resumes growth in the fall. Significant grain yield loss occurred to maize interplanted with Kentucky bluegrass, which persisted throughout the summer without chemical suppression. The yield loss in maize grown with Kentucky bluegrass is likely due to inter-plant competitions for soil available moisture, nutrients or both, or due to maize plants' shade avoidance response triggered by the presence of actively growing Kentucky bluegrass in their vicinity. Deployment of superior winter-active, summer-dormant perennial groundcover in row crop production has tremendous potentials in making corn and soybean cropping systems more sustainable in the US Midwest and beyond.

Index terms: perennial groundcover, summer dormancy, poa bulbosa, poa pratensis, maize.

Assessment of centipedegrass [*Eremochloa ophiuroides* (Munro) Hack] lines in multi-environment trials across North Carolina(1)

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Abstract – Centipedegrass (*Eromochloa ophiuroides*) requires few inputs and is more tolerant to pests than most warm-season turfgrasses. However, limited morphological variation exists in the species, which has hampered breeding efforts and has resulted in only a few cultivars being available in the market. New cultivars that possess improved turfgrass quality in combination with tolerance to diseases, drought, and cold are needed to expand use of centipedegrass in other markets across the southern United States. This study aimed to evaluate advanced centipedegrass breeding lines in multi-environment trials with two main objectives: (1) to select lines exhibiting stable performance across North Carolina and (2) to estimate the expected genetic gains using the additive selection index. From 2019 to 2021, 87 advanced breeding lines and five commercial cultivars were evaluated in replicated trials at three different locations in North Carolina for establishment rate, turfgrass quality, turfgrass density, genetic color, leaf texture, uniformity, winter survival, fall color, drought response, seed head density, and seed yield. Significant genetic variation was observed among entries for all traits. Best linear unbiased predictions were used to calculate the additive selection index to identify elite genotypes across traits. Additionally, relationships among economically important traits were assessed. Positive genetic gains resulted from selection of the top genotypes indicating that the use of the additive selection index is effective in centipedegrass breeding. Lines that outperformed Common, TifBlair, Covington and Santee were identified, and will be advanced to on-farm trials in order to evaluate their suitability for commercial release.

Index terms: Centipedegrass, breeding, genotypes, genetic gains.

Evaluating selection strategies to enhance genetic gains for multiple traits in zoysiagrass breeding⁽¹⁾

Milla-Lewis, S. R.(2), Gouveia, B. T.(2), Kenworthy, K. E.(3), Zhang, J.(4), Schwartz, B. M.(5), Khanal, S.(5), Chandra, A.(6), Miller, G. L.(2), Carbajal, E. M.(2), Raymer, P.(7), Wu, Y.(8), Fontanier, C.(8), Pudzianowska, M.(9), Beard, J. H.(10) and Unruh, J. B.(11)

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Abstract – The use of a selection index has long been identified as an effective strategy when selecting for multiple traits. The turf performance index (TPI), which ranks genotypes based on the number of times they have been in the top statistical group of performance across traits, has been widely used in turfgrass science to identify the best performing lines. Meanwhile, the additive genetic index, which takes into account the effects of genotypes and the importance of a specific trait to select the best ones in order to increase selection accuracy, has found limited application in turfgrass breeding. The objective of this study was to use multi-environment trial data for zoysiagrass breeding lines evaluated for multiple traits across the southern United States to compare expected genetic gains achieved with these two methods incorporating agronomic as well as consumer preference traits. Moderate to high (.50-.75) heritability values were estimated for most traits. While many positive correlations were identified, establishment rate, sod tensile strength and leaf firing were found to be negatively correlated with most traits. The use of either selection index produced more favorable expected genetic gains across traits than direct selection even in the presence of negative correlations.

No clear winner was identified between the two indexes with AI or TPI producing higher expected genetic gains depending on the trait. In general AI produced higher genetic gains for agronomic and drought tolerance traits and TPI for shade and salinity traits. While several breeding lines outperformed the commercial check ‘Diamond’ regardless of the index used, only five of the selected lines with a 20% selection intensity agreed between AI and TPI emphasizing the importance of choosing selection criteria that provides a more nuanced ranking of lines.

Index terms: zoysiagrass, breeding, multi-environment trials, index selection.

Enhancing genetic gain in warm-season turfgrass breeding with high-throughput phenotyping(1)

Gouveia, B. T.(2), Zhang, J.(2), Kenworthy, K. E.(3), Chandra, A.(4), Schwartz, B. M.(5), Raymer, P. L.(6), Pudzianowska, M.(7), Baird J.(8), Unruh, J. B.(9), Wu, Y.(10), Carbajal, E. M.(2), Khanal, S.(5), Vines, P.(5) and Milla-Lewis, S.(2)

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Abstract – In turfgrass breeding, traits assessed through visual ratings are commonly used, but they present limitations. Image analysis has been used for overcoming it, and despite its potential, the application of these technologies in the early breeding stages has been limited by the challenges of efficiently phenotyping the large numbers of plots typically involved. Recently, the integration of small Unmanned Aircraft System (sUAS) imagery into turfgrass evaluations has allowed to improve the phenotyping efficiency. The objective of this study was to estimate genetic gain and heritability for traits assessed visually versus those assessed using sUAS imagery in four warm-season turfgrass species. One nursery and one advanced trial of each species were evaluated for four years in six locations in the Southern USA. Turfgrass quality (TQ) was visually evaluated using 1–9 scale. The sUAS were used to collect red, green and blue images to estimate two traits: percent green/living plot cover (PGC) and average green leaf index (GLI). The traits were assessed under non-drought and drought conditions. In the multi-environment analysis, the TQ presented higher heritability in all trials and species under drought, except zoysiagrass and seashore paspalum advanced trials, and bermudagrass nursery. For non-drought, the heritability estimate for TQ was higher than the imagery-assessed traits PGC and GLI only in zoysiagrass advanced trial and St. Augustinegrass nursery. Genetic gain estimates were higher for PGC and GLI than TQ in all species, environments and trials, except in zoysiagrass advanced trial. Among the imagery-assessed traits, GLI presented higher gains than PGC. These results can be attributed to the higher phenotypic variation for imagery traits when compared to visually rated traits, which clusters phenotypes into classes. In conclusion, while imagery-traits do not improve the accuracy of target traits, they still can significantly contribute to boosting genetic gain in turfgrass breeding.

Index terms: Bermudagrass, Zoysiagrass, Seashore paspalum, St. Augustinegrass.

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ABIOTIC STRESSES
Poster presentations

Impact of intense thinning of upright perennial tropical forages during cold seasons in southern Brazil(1)

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Abstract – Upright perennial forage species from the warm season, when drastically lowered, expose their basic buds, which can result in the death of these plants during the cold seasons in southern Brazil due to the action of frost and, consequently, compromising the stand of plants for later harvests. On the other hand, intense defoliation during the cold seasons allows for greater forage harvesting at strategically important moments in southern Brazil. Therefore, to verify the impact of this greater intensity of defoliation during the cold seasons in southern Brazil, an experiment was conducted at the Terras Baixas Experimental Station – Embrapa Clima Temperado, located in the Municipality of Capão do Leão, Rio Grande do Sul. the factors: Upright tropical perennial forage (*Pennisetum purpureum* – cultivar BRS Kurumi and *Panicum maximum* – cultivar BRS Zuri); Drastic lowering of tropical species during the autumn and winter seasons (10 cm) and recommended lowering for these species (40cm); and productive moments (first harvest – spring-summer 2022–2023; autumn 2023; off-season – autumn and winter 2023; and second harvest – spring-summer 2023–2024). The experimental area was composed of 3 blocks. The plots were 7m x 4m in size. Data were analyzed using analysis of variance and Tukey's test ($p < 0.05$). Soil preparation and cultivar management, except drastic defoliation, occurred in accordance with technical recommendations (Embrapa, 2014 and Embrapa, 2015), with sowing and planting carried out on December 5, 2022. Forage collections for the cultivar Kurumi were in an area of 80 x 160 cm (two plants) and for the cultivar Zuri in an area of 45 x 50 cm. The forage remained until constant weight in forced air ovens (55°C) to determine the mass of harvested forage. Zuri provided a greater forage harvest than Kurumi over two harvests in southern Brazil (34,151 vs 21,602 kg/ha DM). The intense drawdown during the autumn-winter period (off-season) did not change the amount of forage harvested over two seasons, only the moment when a greater amount of forage was harvested, in the autumn-winter (6,006 vs 3,339 kg/ha DM) in favor of intense drawdown or in the following harvest (7,387 vs 10,243 kg/ha DM) in favor of the recommended management. Due to atypical temperatures and precipitation during autumn-winter 2023 and during the second harvest (2023–2024), there is a need to continue studies so that assessments can take place under environmental conditions closer to normality and, especially, in more extreme winters.

Index terms: Forage, tropical, perennial, cold, drawdown.

Root characterization of selected frogfruit breeding lines(1)

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Abstract – Frogfruit (*Phyla nodiflora*) is a herbaceous groundcover that has garnered interest as a native species for use as an alternative to traditional turfgrass lawns due to its drought resistance and benefits to pollinators. This study aims to investigate the rooting parameter of selected frogfruit breeding lines to provide insights into their rooting behavior and differences between lines. The five frogfruit lines were selected, based on their persistence, from a germplasm collection. The lines were arranged in a randomized complete block design with four replications. For establishment, a single stolon from each line was planted into clear acrylic tubes nested into polyvinyl chloride tubes at a slight angle, allowing for visibility of root growth. Two runs of the experiment were conducted, where Run 1 was planted on May 28, 2024, and Run 2 was planted on June 6, 2024. Weekly measurements of rooting depth were recorded starting two weeks after planting and continued for 6 weeks at which point roots were harvested. The rate of root depth development (RRDD) was determined using the weekly root depth measurements. The harvested roots were scanned using WinRHIZO for determination of root length density (RLD), at incremental depths of 10 cm. Differences were observed for RRDD, RLD, and RLD within different rooting depths. These results add insight into the rooting behavior of frogfruit and support its use as an alternative lawn.

Index terms: alternative lawns, groundcover, turfgrass.

Transient and stable gene expression systems in apomictic *Brachiaria hybrids* Ipyporã and 'BRS Integra'(1)

Cabral, G. B.(2), Carnaúba, L. A.(2), Eufrasio, M. S. V.(2), Dusi, D. M. A.(2), Carneiro, V. T. C.(2), Fragoso, R. R.(2) and Aragão, F. J.(2)

(1)Funding: Embrapa. (2)Embrapa Genetic Resources and Biotechnology, Brasília, DF. glaucia.cabral@embrapa.br

Abstract – *Brachiaria brizantha* (syn. *Urochloa brizantha*) and Brachiaria ruziziensis are important forage grasses widely cultivated in Brazil, particularly in the Cerrado regions. Brachiaria spp. are recognized for their apomictic reproduction, which allows for the production of seeds without fertilization, thus maintaining genetic uniformity. However, *B. ruziziensis* is an exception, as it is the only diploid and sexual species in the Genus. These grasses serve as a primary feed source for beef cattle production, playing a crucial role in the livestock industry in Brazil. Traditional breeding methods for Brachiaria species face challenges due to their apomictic nature. Therefore, genetic transformation techniques are being developed to introduce desirable traits into these grasses. The development of drought-resistant cultivars of Brachiaria hybrids is essential for sustaining forage production in Brazil, particularly in the face of climate variability and water scarcity. Understanding the mechanisms of drought resistance and employing genetic transformation strategies can help improve the resilience of these grasses, ensuring a stable supply of forage for the livestock sector. Mahanarva spectabilis is a significant pest affecting forage grasses, making its management essential for sustaining livestock feed supplies. The development of resistant hybrids through genetic transformation could provide an effective strategy to combat this pest. Our work focuses on developing transient and stable gene expression systems for hybrids like BRS Ipyporã (for abiotic stress - drought resistance) and BRS Integra (for biotic stress), particularly resistance to Mahanarva spectabilis. In monocots, in vitro plant regeneration is primarily achieved through somatic embryogenesis.

This process involves using mature seeds as explants to produce embryogenic calli, which can be transformed using methods like biolistics or Agrobacterium-mediated transformation. We are using both methods to genetically transform *Brachiaria*´s hybrids. The use of specific binary plasmids containing the gus marker gene is crucial for tracking successful transformations. Experiments have shown that after cocultivation or biolistic transformation, the transient expression of the gus gene was detected in *Brachiaria* calli. For stable transformation, embryogenic calli were placed on selection media with appropriate concentrations of selection agents (e.g., geneticin) to isolate resistant somatic embryos and plants. The ongoing research into the genetic transformation of Brachiaria species aims to enhance their resilience against environmental stresses and pests, thereby improving their utility as forage crops in Brazil. This approach not only seeks to maintain agricultural productivity but also to ensure the sustainability of livestock farming in the region.

Index terms: overexpression, silencing, genetic transformation.

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BIOTIC STRESSES
Poster presentations

Investigation of genetic basis of defense against spittlebug in *Urochloa decumbens*⁽¹⁾

Diniz J. F.⁽²⁾, Aono A. H.⁽²⁾ and de Souza A. P.⁽²⁾

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Abstract – Brazil has become a major exporter in agriculture and livestock, necessitating productivity enhancements for national development. A critical strategy is improving pasture grasses, particularly *Urochloa decumbens*, the dominant forage species, which is highly susceptible to spittlebug attacks. This study aims to unravel the genetic mechanisms and regulatory networks in the *U. decumbens*-spittlebug interaction by integrating data from *Urochloa* spp. and *Paspalum regnellii* to identify genetic patterns associated with spittlebug resistance. Gene co-expression networks for *U. decumbens* were constructed using publicly available RNA sequencing data, processed through filtering, mapping, transcript assembly, and gene expression quantification. The WGCNA package was used to define co-expressed gene groups. To identify genes potentially associated with spittlebug resistance, an RNA-Seq experiment was conducted on two *P. regnellii* genotypes characterized by different levels of tolerance to attack by *M. spectabilis* nymphs. This RNA-seq dataset underwent similar processes as those applied to Urochloa but was analyzed for differential gene expression. For constructing the linkage map and conducting the QTL analysis, plant material from an intraspecific crossing between the tetraploidized sexual accession D24/27 and the apomictic tetraploid cultivar was employed. The resistance levels of *U. decumbens* to Notozulia entreriana were assessed in greenhouse experiments. Genotyping-by-sequencing libraries were constructed using leaf samples from each hybrid and both parents. The study examined the relationship between *U. decumbens* genes, *P. regnellii* DEGs, the molecular markers linked to resistance identified through machine learning methodologies, and inferred QTLs. This relationship, along with the crucial defense mechanisms

against biotic stresses documented in the literature, was used to select WGCNA groups of *U. decumbens* potentially associated with biological processes related to resistance. Once the set of selected modules was determined, the topGO package was employed to perform enrichment analysis and establish enriched gene ontology categories and modules associated with biological functions of interest were identified. Evaluating modules potentially associated with resistance and defining targets for further studies are key points in understanding the complex and multifactorial nature of resistance in tropical forages, which remains unexplored. The findings provided insights into the regulatory dynamics of resistance offering valuable directions for breeding programs to mitigate pest impacts on tropical forages. This research advances the understanding of resistance in tropical forages and suggests promising avenues for future studies and breeding strategies.

Index terms: machine learning; QTL mapping; RNA-Seq; Tropical forage, biotic stress.

Omic approaches to understand the forage-spittlebug interaction aiming to control *Mahanarva spectabilis* in tropical pastures(1)

Begnami, I. S.(2), Gonçalves, G. F.(3), Malagó-Júnior, W.(4), Matta, F. P.(4), Gusmão, M. R.(4), Souza, A. P.(2) and Vigna, B. B. Z.(4)

(1)Funding: CAPES (88887.600436/2021-00, 88887.924861/2023-00), Embrapa (20.18.01.014.00.00), FAPESP (2023/14813-5), Unipasto (10200.17/0006-5).

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Abstract – Brazilian pasture areas present high productivity resulting from the large cultivation of forages from the *Urochloa genus*, such as *U. brizantha* cv. Marandu. These exotic species are susceptible to Mahanarva spectabilis spittlebugs herbivory and resistance can be found in some native forage species, such as *Paspalum* spp.. The control of this pest is mostly done with chemical insecticides and understanding the molecular mechanisms of plant-herbivore interactions is crucial for developing pest management alternatives. The work objective was to characterize the transcriptome of 1) the roots of *Paspalum regnellii* infested with nymphs of the spittlebug *Mahanarva spectabilis* to understand the molecular process of resistance and 2) the different developmental stages of M. spectabilis to search for the RNA interference (RNAi) mechanism and targets. Roots of the *P. regnellii* resistant genotype BGP 344 were collected in three conditions (without infestation, after 48h of nymph infestation and after 72h). Total RNA was extracted, cDNA libraries were prepared and sequenced on an Illumina platform. FastQC analyzed data quality, reads were filtered in Trimmomatic and SortMeRNA. De novo assembly was carried out with Trinity and quality verified with BUSCO and Bowtie2. Differentially expressed genes (DEG) analysis was performed in edgeR contrasting the conditions and enriched by biological processes of Gene Ontology (GO) terms and KEGG pathways. The assembly of this *P. regnellii* tetraploid accession resulted in 575,219 contigs. The reads were 80.89% mapped with Bowtie2 and BUSCO found 90.4% of the transcripts in Viridiplantae orthologous. DEG analysis generated 407 genes down-regulated and 1 up-regulated between control time and after 72h of infestation. GO terms from biological processes were related to a response to herbivores, chitin catabolism and response to oxidative stress. The main KEGG pathway enriched was glutathione metabolism. The same methodology was performed for eggs, nymphs and adult transcriptome of *M. spectabilis*. The de novo assembly produced 197,003 contigs, with 96.6% matching with Hemiptera orthologous and 90.59% aligning to this reference. Instead of proceeding to a DEG analysis, we searched for the main RNAi machinery genes and we identified over 30 genes involved in five major RNAi pathways. Therefore, it was possible to characterize that the *Paspalum regnellii* molecular resistance processes are complex and to confirm the RNAi machinery presence in *Mahanarva spectabilis,* which allows a gene silencing approach against this important tropical forage pest.

Index terms: herbivory resistance, pest control, RNAi, RNA-Seq.

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PLANT MICROORGANISM INTERACTIONS
Poster presentations

Inoculation with plant growth promoting bacteria in *Megathyrsus maximus* hybrids(1)

Santos, B. V.(2), Santos, M. F.(3), Jank, L.(3), Hungria, M.(4) and Dias, A. M.(5)

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Abstract – Pasture degradation is a gradual process that compromises the pasture´s carrying capacity, affecting their perenniality and natural regeneration. This results in reduced productivity and the inability to meet the nutritional requirements of animals. With the growing concern for the development of sustainable livestock farming, it is essential to explore alternatives that reduce the environmental impact and costs associated with using mineral fertilizers, without compromising the productivity and nutritional quality of forages. Using microorganisms to aid in the growth and maintain the perenniality of pastures helps minimize degradation and improve the productivity and quality of forage. However, their application in pastures is still limited, requiring greater knowledge about the interactions between these microorganisms and host plants. In addition, it is necessary to develop good inoculation practices, including adequate adjustments in doses and application methods. Thus, this study aims to evaluate the effect of Plant Growth Promoting Bacteria (PGPB) on forage production, nutritional value, leaf dry matter production, and seed production in pre-commercial hybrids of *Megathyrsus maximus*. The experiment will be conducted in a randomized blocks design with three replications, totaling 60 experimental units. The plots, with dimensions of 3.0 x 4.0 m and an area of 12 m², will be subdivided into 4 quadrants. In each quadrant, a control and three different types of PGPB will be tested, still to be chosen among the main ones used in forage grasses according to the literature, which are: *Azospirillum brasilense, Pseudomonas fluorescens, Rhizobium, Bacillus, Pantoea ananatis*, *Burkholderia, Bradyrhizobium, Gluconacetobacter* and *Herbaspirillum*, resulting in 240 subplots. Data collection will include measurements of forage production, leaf dry matter production, nutritive value, and seed production. The study is expected to reveal significant interactions between host plants and microbial inoculants, resulting in improvements in forage productivity, in addition to an increase in the efficiency of animal production on pasture. These results could contribute to the modernization of livestock farming, making it more sustainable by promoting practices that increase food production without compromising the environment.

Index terms: PGPB, pastures, *Megathyrsus maximus*, microorganisms.

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PHENOTYPING TECHNOLOGIES
Oral presentations

Developing a phenological scale for seed production management of *Urochloa* spp. in tropical forage systems(1)

Hoppen, S. M.(2), Sampaio, R.(2), Florian-Vargas, D.(3), Pinzon, F. D.(3), Sanches, E. B.(3), Borges, J. G.(2), Alencar, B. R.(2), Madeira, T.(2), Pizarro, E. A.(2), Silva, A. A. and (2) de Souza, C. H. L.(4)

(1)Funding: Grupo Papalotla. (2)Research and Development, Grupo Papalotla. (3)Research and Development, Grupo Papalolta. (4)University of Florida. sarah.hoppen@hotmail.com

Abstract – Seed production management practices are intricately linked to the phenological development of crops. Established phenological stage scales for crops like rice, corn, and soybean guide optimal timing for applying fertilizers and pesticides. In Brazil, Brachiarias (*Urochloa* spp.) pastures cover millions of hectares, making seed production a significant industry. Recently developed interspecific hybrids such as Camello and Cayman offer improved nutritional value, tolerance to spittlebugs, and resilience to abiotic stresses like drought and flooding. However, there is a significant knowledge gap regarding the phenological development of *Urochloa* spp. when managed for seed production. These grasses show non-uniform seed production with multiple consecutive flowering events and seed dehiscence. To address this, we are developing a phenological scale proposal for Brachiarias based on the Rice BBCH scale (Biologische Bundesanstalt, Bundessortenamt and Chemical industry). The scale is divided into nine major stages: germination, leaf development, tillering, stem elongation, booting, inflorescence emergence, flowering, seed development, ripening, and senescence. We regularly evaluate a collection of interspecific *Urochloa* hybrids and check varieties (*Urochloa brizantha* cv. Marandu, *Urochloa ruziziensis*, and *Urochloa decumbens* cv. Basilisk) at three locations in Brazil and Mexico. A key aspect of this study is redefining the term 'flowering' term. *Brachiaria* exhibit non-uniform flowering, mainly due to a prolonged tillering period and higher tillering capability, which affects seed production. Successive flowering cycles occur during the growth season, developing seeds at each cycle, which

accumulate to form the total seed yield, as seeds are swept from the ground at the end of the wet season. We define a flowering cycle when at least 20% of inflorescences on a plant are at the same stage. Each cycle is individually scored, with up to five cycles per growth season. Hybrids exhibit different flowering behaviors, with early-flowering hybrids like those belonging to Camello family showing multiple cycles, while late-flowering hybrids have fewer cycles. Our next steps include studying seed dehiscence and its correlation with hybrid phenology. We also aim to combine climate and soil data with our phenotypic database to model phenological development using thermal time. This approach will help predict the physiological development of commercial varieties in different seed production zones and assist growers in implementing better agronomic practices.

Index terms: Urochloa interespecific, Camello, Cayman, BBCH brachiarias.

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BIONERGY CROPS (BREEDING AND GENETICS)
Poster presentations

Energy potential of elephant grass for biogas production via anaerobic digestion(1)

Coelho, F. F.(2), Silva, G. H.(3), Carneiro, J.C.(4), Otenio, M. H.(4) and Machado, J. C.(4)

(1)Funding: Fundação de Amparo à Pesquisa do Estado de Minas Gerais – Codes APQ-00731-18 and APQ-03630-23, Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Finance Code 001 and Associação para o Fomento à Pesquisa de Melhoramento de Forrageiras.

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Abstract – The need for clean energy alternatives is critical. Bioenergy production from agricultural crops offers a strategic solution for achieving sustainable development goals. Elephant grass [*Cenchrus purpureus* (Schumach.) Morrone] emerges as a promising plant species for energy production through anaerobic digestion, given its outstanding characteristics such as high biomass productivity, short growth cycle allowing for multiple harvests per year, and good adaptability to the climate and soil conditions found in Brazil. This study evaluated ten elephant grass genotypes for their potential in biogas production via anaerobic digestion. Elephant grass samples were collected 103 days after planting and characterized for their chemical composition through analyses of neutral detergent fiber, acid detergent fiber, crude protein, dry matter content, volatile solids, ash, and lignin. Biochemical biogas potential (BBP) tests were conducted using the Nautilus equipment (Anaero Technology) to assess the energy conversion efficiency of each genotype. The substrate was prepared by mixing the samples with an inoculum of bovine manure acclimated for anaerobic digestion. Batch anaerobic digestion tests were carried out for 21 days under mesophilic conditions. Biogas production was measured on days 7, 14, and 21, and methane and carbon dioxide contents were determined using gas chromatography analyses. The initial (7.14) and final (7.88) average pH of the samples indicated stability during the anaerobic digestion process, remaining within the optimal range for the growth of methane-producing methanogenic bacteria. Biogas production ranged between 139.57 and 496.92 NLbiogas.

kgVS-1, achieving methane content above 60%. The highest biogas productions were obtained by genotypes T_23.1 and PCEC, which obtained 8120.29 and 5244.57 Nm3biogas.ha-1, respectively. These findings suggest elephant grass, particularly genotypes T_23.1 and PCEC, hold significant promise for sustainable bioenergy production via anaerobic digestion.

Index terms: *Cenchrus purpureus*, bioenergy, lignocellulosic biomass, methane.

Programação/Schedule

Wednesday, October 16, 2024	
8h am – 8h30 am	Registration open
Opening Plenary Session [8h30 am – 10h am]	
8h30 am – 9h30 am	Welcome and Introductions by Organizing Committee
9h30 am – 10h am	Opening talk – Dr. Cacilda Borges do Valle – Remembering the works of John Miles and Rainer Schultze-Kraft and their contributions to forage breeding Moderator: Dr. Marco Pessoa-Filho, Embrapa Genetic Resources and Biotechnology, Brazil
10h am – 10h30 am	Coffee break
Session 1: Genetic Resources and their Use in Forage Breeding [10h30 am – 12h pm] **Moderator: Dr. Carlos Acuña, UNNE, Argentina**	
10h30 am – 10:50 am	The ILRI genebank: a window to the global tropical forage biodiversity available for breeding programs – Dr. Alemayehu Teressa Negawo, ILRI, Ethiopia
10:50 am – 11:10 am	Genetic relationships among a global collection of annual ryegrass cultivars – Dr. Javier do Canto, INIA, Uruguay
11:10 am – 11h30 am	Development of a new *Stylosanthes guianensis* cultivar for subtropical regions – Dr. Elsa Brugnoli, IBONE (UNNET-CONICET), Argentina
11h30 am – 12h pm	Discussion
12h pm – 1h30 pm	Lunch break
Keynote Presentation	
1h30 pm – 2h30 pm	Environmics in breeding – Dr. Rafael Tassinari Resende, Universidade Federal de Goiás, Brazil Moderator: Juarez Machado, Embrapa Dairy Cattle, Brazil

Session 2: Genetic and Genomic Tools I [2h30 pm – 4h pm] **Moderator: Dr. Rosangela Simeao, Embrapa Beef Cattle, Brazil**	
2h30 pm – 2h50 pm	Development of universal DaRTag markers for alfalfa (*Medicago sativa*) and use in mapping resistance to Aphanomyces root rot – Dr. Deborah Samac, USDA-ARS, USA
2h50 pm – 3h10 pm	Genetic linkage mapping in *Megathyrsus maximus* (Jacq.) with multiple dosage markers – Dr. Gabriel Gesteira, North Carolina State University, USA
3h10 pm – 3h30 pm	Plant molecular farming of designer feedstocks for animal production, Dr. German Spangenberg, Qingdao Agricultural University, China
3h30 pm – 4h pm	Discussion
4h pm – 6h pm	Poster session + Social
Thursday, October 17, 2024 **Keynote Presentation**	
8h30 am – 9h30 am	Applied systems biology in pastures, forage and feedstock crops - Dr. German Spangenberg, Qingdao Agricultural University, China Moderator: Dr. Liana Jank, Embrapa Beef Cattle, Brazil
9h30 am – 10h am	Coffee break
Session 3: Genetic and Genomic Tools II [10h am – 11h30 am] **Moderator: Dr. Andrea Raposo, Embrapa Beef Cattle, Brazil**	
10h am – 10h20 am	Developing genomic tools for key underutilized forage species in Africa – Dr. Abel Teshome Gari, ILRI, Kenya
10h20 am – 10h40 am	Developing genomic prediction capabilities for underutilized tropical forage species maintained in the CGIAR genebanks – Dr. Meki Muktar, ILRI, Kenya

10:40 am – 11h am	Advances in the Application of Predictive Breeding Tools in Forage and Cover Crops – Dr. Esteban Rios, University of Florida, USA
11h am – 11h30 pm	Discussion
11h30 am – 1h30 pm	Lunch break
Keynote presentation	
1h30 pm – 2h30 pm	Advancing Forage Grass Breeding: Harnessing the Power of Multi-Omic Integration and Phenomics Strategies – Dr. Alexandre Aono, Swedish University of Agricultural Sciences, Sweden Moderator: Dr. Bianca Vigna, Embrapa Southeast Livestock, Brazil
Session 4: Phenotyping Technologies Applied to Breeding Programs [2h30 pm – 3h30 pm] **Moderator: Dr. Esteban Rios, University of Florida, USA**	
2h30 pm – 2:50pm	Developing a Phenological Scale for Seed Production Management of Urochloa spp. in Tropical Forage Systems – Dr. Sarah Hoppen, Papalotla Brasil, Brazil
2:50pm – 3:10pm	Enhancing genetic gain in warm-season turfgrass breeding with high-throughput phenotyping – Dr. Beatriz Gouvea, North Carolina State University, USA
3:10pm – 3h30 pm	Discussion
3h30 pm – 4h pm	Coffee break
Session 5: Breeding and Genetics of Turfgrass and Cover Crops [4h pm – 6h pm] **Moderator: Dr. Kevin Kenworty, University of Florida, USA**	
4h pm – 4h20 pm	Origin of the *Arachis pintoi* and *A. repens* germplasm and potential for shared research and use – Dr. José F. M. Valls, Embrapa, Brazil

4:20 pm – 4h40 pm	Interplanting maize with summer-dormant cool-season grass as perennial groundcover for sustainable crop production, Dr. Shui-zhang Fei, Iowa State University, USA
4:40 pm – 5h pm	Assessment of Centipedegrass [*Eremochloa ophiuroides* (Munro) Hack] Lines in Multi-Environment Trials Across North Carolina, Mr. Esdras Carbajal, North Carolina State University, USA
5h pm – 5h20 pm	Evaluating Selection Strategies to Enhance Genetic Gains for multiple traits in Zoysiagrass Breeding – Dr. Susana Milla-Lewis, North Carolina State University, NCSU, USA
5h20 pm – 6h pm	Discussion
.Friday, October 18, 2024 **Field tour Embrapa Cerrados**	
8h am – 8h45 am	Bus transfer from Embrapa Genetic Resources to Embrapa Cerrados
8h45 am – 9h am	Reception and Welcome to Embrapa Cerrados
9h am – 9h30 am	Station 1: *Andropogon gayanus* breeding program – Dr. Marcelo Ayres Carvalho and Dr. Claudio Karia – Embrapa Cerrados
9h30 am – 10h am	Station 2: *Brachiaria breeding* program – Dr. Sanzio Barros, Embrapa Beef Cattle and Dr. Marco Pessoa, Embrapa Genetic Resources and Biotechnology
10h am – 10h30 am	Station 3: Grazing trial of *Andropogon* and *Brachiaria* – Dr. Gustavo Braga and Dr. Allan Ramos, Embrapa Cerrados
10h30 am - 11h am	Station 4: Integrated Crop-Livestock-Forestry Systems, Dr. Kleberson de Souza, Embrapa Cerrados
11h30 am – 12:15 pm	Brunch
12h30 pm – 1:15 pm	Return to Embrapa Genetic Resources

Session 6: Breeding and Genetics for Forage and Seed Quality and Yield [2h pm – 4h pm] **Moderator: Dr. Mateus Santos, Embrapa Beef Cattle, Brazil**	
2h pm – 2h20 pm	Persistence and forage yield in a group of advanced breeding lines of *Paspalum notatum* under two grazing frequencies, Dr. Alex Zilli, IBONE (UNNET-CONICET) Argentina
2h20pm – 2h40pm	Flowering periods, seed yield components, seed quality and patterns of seed shattering in *Paspalum*: effect of taxonomy and nitrogen fertilization – Dr. Carlos Acuña, Universidad Nacional del Nordeste, Argentina
2h40pm – 3h pm	Exploring seed yield components in interspecific *Urochloa* spp. hybrids through multi-environment trials – Dr. Cleber de Souza, University of Florida, USA
3h pm – 3h30 pm	Discussion
Closing session [3h30 pm – 4h pm]	
4h pm	Conference concludes

Patrocinadores

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PESQUISA DE MELHORAMENTO DE FORRAGEIRAS

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