



*Improving Plants, Improving
Livelihoods and Economies*

**3rd INTERNATIONAL CONFERENCE
OF
THE NIGERIAN PLANT BREEDERS ASSOCIATION (NPBA)**
The Affiliate of African Plant Breeders Association (APBA)

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Preface

By 2050, Nigeria's population is projected to approach 400 million, making our nation the third most populous in the world. This demographic reality presents both an immense challenge and an extraordinary opportunity: how do we ensure that every plate is filled with nutritious food, produced in ways that are sustainable, resilient, and future-focused? At the very heart of this mission are plant breeders—tasked with innovating to feed a rapidly growing nation and a changing world.

The Nigerian Plant Breeders Association (NPBA), as the national affiliate of the African Plant Breeders Association (APBA), has in just three years of its international annual conference become a vital platform for scientists, innovators, and policymakers to converge, share insights, and shape the future of agriculture. The theme of this year's gathering—"Crop Improvement for Food Security, Sustainable Agricultural Systems and Environment"—could not be more fitting. From accelerating genetic gains to unlocking plant genomes and deploying biotechnology, the sub-themes of this conference reflect the full spectrum of tools and creativity required to secure the future of food.

As an Association, NPBA stands firmly committed to supporting the Federal Government of Nigeria and global partners in delivering a food-secure and climate-resilient future. Our work centers on fostering innovation, strengthening seed systems, and advancing sustainable crop improvement strategies. Through these efforts, we continue to position plant breeding as a catalyst for achieving Nigeria's Agenda 2050 as well as the United Nations Sustainable Development Goals.

This volume proudly presents 90 accepted abstracts—each representing a distinct contribution to the science and practice of breeding better crops. Collectively, they embody the dedication, ingenuity, and collaborative spirit of our community, all directed toward one common goal: ensuring food security for generations to come.

As NPBA, we reaffirm our commitment to driving Nigeria's agricultural transformation—one improved variety at a time. To all conference participants: we encourage you to engage deeply, collaborate widely, and embrace the conversations that will shape our shared future. Feeding 400 million people is no small task, but together—with innovation, resilience, and even a smile—we can rise to the challenge.

Professor Chiedozie Egesi

President, Nigerian Plant Breeders Association (NPBA)

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Sub-Theme 1

**Accelerating Genetic Gains for Increased Crop
Productivity**

(AGICP)

AGICP 001

Genetic Variability for Yield and Secondary Traits in Tropical Yellow Maize Hybrids (*Zea Mays* L.)

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Abstract

Maize is a critical staple food security crop in sub-Saharan Africa, but its productivity is low due to genetic and environmental limitations. Addressing these challenges requires the identification of superior genotypes and knowledge of inherent variability among available genotypes. In this study, the performance and genetic variability of 21 recently developed yellow maize hybrids and three checks (Oba Super-2, Ife Hybrid-3, and Ife Hybrid-4) were investigated. The hybrids were evaluated in two years in Ibadan, Nigeria, in a randomized complete block design with three replicates. Significant genotypic differences were found for all the traits, except plant height, ear height, plant aspect, and ear aspect. Genotype environment interaction was significant for all the traits. Grain yield (GY) ranged from 4.20 (LY1501-9) to 6.77 t/ha (LY2201) with a mean of 5.17 t/ha. LY2201, LY2301-3, LY2301-2, LY2301-4 had GY above 6.00 t/ha with LY2201 (6.77 t/ha) and LY2301-3 (6.35 t/ha) significantly out-yielding the dominant check (Oba Super-2; 5.80 t/ha). Genotypic variance was significant for GY, Days to silk (DS), and Anthesis-silking interval (ASI), whereas environmental variance was significant for all the traits, except Days to anthesis (DA). Estimates of phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the traits, ranging from 2.99 (DA) to 88.99 (ASI) and from 1.55 (DA) to 74.11 (ASI), respectively. Broad-sense heritability ranged from low to high. Genetic advance was high (108.3%) for ASI, medium (12.3%) for GY, and low for other traits. Variability exists among the maize hybrids. The identified hybrids could be exploited to improve maize productivity.

Keywords: *Genotypic variance, Broad-sense heritability, phenotypic coefficient of variation, Genetic advance, Yellow maize,*

AGICP 002

Comparative Efficiency of Chemical and Physical Mutagens on Growth of Tomato (*Solanum lycopersicum* L.)

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Abstract

Maize is a critical staple food security crop in sub-Saharan Africa, but its productivity is low due to genetic and environmental limitations. Addressing these challenges requires the identification of superior genotypes and knowledge of inherent variability among available genotypes. In this study, the performance and genetic variability of 21 recently developed yellow maize hybrids and three checks (Oba Super-2, Ife Hybrid-3, and Ife Hybrid-4) were investigated. The hybrids were evaluated in two years in Ibadan, Nigeria, in a randomized complete block design with three replicates. Significant genotypic differences were found for all the traits, except plant height, ear height, plant aspect, and ear aspect. Genotype environment interaction was significant for all the traits. Grain yield (GY) ranged from 4.20 (LY1501-9) to 6.77 t/ha (LY2201) with a mean of 5.17 t/ha. LY2201, LY2301-3, LY2301-2, LY2301-4 had GY above 6.00 t/ha with LY2201 (6.77 t/ha) and LY2301-3 (6.35 t/ha) significantly out-yielding the dominant check (Oba Super-2; 5.80 t/ha). Genotypic variance was significant for GY, Days to silk (DS), and Anthesis-silking interval (ASI), whereas environmental variance was significant for all the traits, except Days to anthesis (DA). Estimates of phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the traits, ranging from 2.99 (DA) to 88.99 (ASI) and from 1.55 (DA) to 74.11 (ASI), respectively. Broad-sense heritability ranged from low to high. Genetic advance was high (108.3%) for ASI, medium (12.3%) for GY, and low for other traits. Variability exists among the maize hybrids. The identified hybrids could be exploited to improve maize productivity.

Keywords: *Mutagens, Genotypic variance, Broad-sense heritability, phenotypic coefficient of variation, Genetic advance, Yellow maize,*

AGICP 003

Molecular Marker Assisted Identification of Suitable Testers for Hybrid Breeding Across Striga-Infested and Optimum Environments

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Abstract

The success of sustainable maize hybrid production is largely dependent on identifying suitable testers. Molecular markers can enhance this process by predicting promising parent candidates for field evaluation. This study used molecular-based SNP markers to predict parent candidates and identify both inbred and hybrid testers for the development of *Striga*-resistant hybrids. Using a Diallel design IV, 300 crosses were generated from 21 inbred lines and 4 standard testers. The crosses, along with six checks, were evaluated in an 18 × 17 alpha lattice design with two replications at two locations under artificial *Striga* infestation and *Striga*-free environments. In addition, the 25 inbreds were genotyped using 3,305 DArTtag SNP markers. Phenotypic and genotypic data were analyzed using R. Analysis of variance revealed significant effects for hybrid, general combining ability (GCA), specific combining ability (SCA), and their interactions with environment. The analysis of molecular variance also showed substantial genetic differences within and between clusters. Significant positive and negative GCA and SCA effects were detected for grain yield and other measured traits. The SNP-based and heterotic group based on GCA effects of multiple traits (HGCAMT) approaches classified the inbred lines into two and three heterotic groups, respectively, confirming the potential to identify appropriate testers. The study successfully identified two new inbred testers and validated the four standard testers. These testers demonstrated high genetic divergence and average genetic distance from other inbred lines. Furthermore, four hybrid testers were identified among crosses whose parents showed consistent genetic dissimilarity with other lines. The information is valuable for predicting parental candidate testers to enhance future breeding programs.

Keywords: Combining ability, genetic divergence, heterotic group, maize hybrid production, *Striga*-resistant

AGICP 004

Identification of sources of resistance to cowpea aphid (*aphis craccivora* koch) in cowpea genotypes (*vigna unguiculata* (L.) Walp.) Through phenotypic screening

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Abstract

Cowpea (*Vigna unguiculata* (L.) Walp.) is a vital leguminous crop cultivated by smallholder farmers in sub-Saharan Africa. Its productivity is threatened by biotic stresses, particularly the cowpea aphid (*Aphis craccivora* Koch), which causes significant yield losses. This study aimed to evaluate 120 cowpea genotypes for resistance to *A. craccivora* through phenotypic screening. The experiment employed a 12 × 10 alpha lattice design with two replications. Five seeds of each genotype were sown in wooden trays filled with sterilized sandy loam soil. Seven days after sowing, seedlings were infested with five fourth-instar nymphs of *A. craccivora* per plant and maintained in insect-proof cages to prevent external interference. Data on aphid population and plant damage were recorded at 7, 14, and 21 days after infestation (DAI) using a 1–5 rating scale. Results showed progressive increases in both aphid population and damage scores across time points. Mean aphid population and damage scores were 2.2 and 1.5 at 7 DAI, 3.5 and 2.5 at 14 DAI, and 4.0 and 3.2 at 21 DAI. Six genotypes showed maximum damage symptoms, while 12 genotypes displayed no visible symptoms throughout the assessment period. 'Dan Misra' and 'Aloka Local' were highly susceptible, whereas 'SAC20KTE-11' and 'Sampea 14' demonstrated strong resistance, exhibiting low aphid populations and minimal damage. These resistant genotypes represent valuable sources of aphid resistance and could be utilized in breeding programs to develop improved aphid-resistant cowpea varieties in Nigeria.

Keywords: *Aphis craccivora*, cowpea, resistance, genotypes, phenotypic screening

AGICP 005

The influence of alpha spin nanoparticles on the growth and yield of finger millet (*eleusine corocana*) in riyom local government area of plateau state, nigeria.

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Abstract

The growing interest in nanotechnology present new opportunities for enhancing crop performance, this study assessed the influence of alpha spin nanoparticles on the growth and yield attributes of five finger millets accessions (*Eleusine corocana*) under varying exposure times in National Cereals Research Institute sub-station in riyom local Government Area of Plateau state, Nigeria. A Randomized complete block design (RCBD) was used with three replications. The treatments included three exposure times of alpha spin nanoparticles (20, 40 and 60minutes) with one control (0) and five accessions of finger millets. Data was collected on germination%, plant height, tiller number, leaf length, leaf width, number of spikes, panicle length and grain yield. The analysis of variance (ANOVA) revealed a highly significant difference ($p=0.05$) among varieties for most of the parameters particularly germination%, plant height, tiller number, number of spikes and grain yield. Treatment was significant only for germination % with v4 at 40minutes exposure (T2) producing the highest germination % (92.0%) while v5 showed the best yield performance (1410.00kg/ha) at 20minutes exposure time (T1). Correlation analysis indicated strong positive relationships between plant height, number of spikes and grain yield, with a moderate negative correlation observed between tiller number and grain yield. Principal components analysis (PCA) revealed that PC1, dominated by plant height and grain yield, explained 37.48% of total variation. The study has demonstrated that alpha spin nanoparticles can significantly improve early growth and productivity in finger millet depending on accession and exposure time. The current results seem to suggest that 20-40minutes exposure time is the optimal and identifies (Redlocal) V5 as the most responsive variety in terms of enhanced yield. These results are further dissembled in elucidating the potential of finger millet in promoting sustainable food and security in Nigeria.

Keywords: *Finger millet, Alpha spin, Nanoparticle, Nanotechnology Accessions.*

AGICP 006**Genetic Underpinnings Of Morphological, B-Carotene, Tryptophan, And Agronomic Traits In Extra-Early Biofortified Maize Under Southern Leaf Blight Pressure**Bashir, O. B.¹, Musa, S.¹, Alafe, H. A.², Zainab, A.A.¹¹Department of Agronomy, Faculty of Agriculture, University of Abuja, Nigeria.²Department of Crop, Soil and Pest Management, Federal University of Technology, Akure, Nigeria.

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Abstract

Developing extra-early maturing, nutrient-dense, and disease-resistant maize is essential for enhancing food and nutrition security in sub-Saharan Africa, where erratic rainfall and Southern Leaf Blight (SLB) limit productivity. This study evaluated 20 extra-early biofortified SAMMAZ quality protein maize inbred lines, including two checks, under natural SLB infestation across two rainfed seasons. There was significant phenotypic variation among genotypes for major agronomic, nutritional, and disease resistance traits. Grain yield ranged from 4.7 to 8.8 t ha⁻¹, with SAMMAZ 58, 63, and 62 emerging as top performers, also exhibiting favourable plant architecture and synchrony in flowering. Nutritional quality varied markedly, with β -carotene ranging from 4.7 to 9.0 μ g/g and tryptophan from 0.070% to 0.090%, exceeding biofortification thresholds in several genotypes. Disease severity scores ranged from 1.6 to 3.5, and area under the disease progress curve from 110.7 to 178.9, with genotypes SAMMAZ 59, 62, 55, and 34 showing strong SLB tolerance. High heritability estimates and genetic advance for most traits indicate the predominance of additive genetic effects and strong potential for genetic gains. These findings highlight promising inbred lines combining early maturity, high yield, nutritional quality, and SLB resistance for integration into climate-resilient maize improvement programmes.

Keywords: *Agronomic traits, heritability, genetic advance, nutritional quality, disease severity*

AGICP 007

Genetic variation in maize (*zea mays* L.) Inbred lines for yield and yield related traits

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Abstract

The presence of genetic variability in Maize (*Zea mays* L.) inbred lines is vital in making significant progress through selection. A total of 52 maize inbred lines were evaluated at the Institute for Agricultural Research farm, Zaria, during 2024 rainy season to assess the levels of genetic variability in the inbred lines. The experiment was laid out in randomized complete block design with two replications. Data collected on grain yield and other agronomic traits were analyzed using appropriate statistical software. Results of the analysis of variance revealed significant ($p \leq 0.5$) differences among the inbred lines, indicating high levels of genetic variability. Grain yield ranged from 39.8 kg/ha for SMLP-48 to 894.7kg/ha for SMLW-93 with a mean of 346.33kg/ha. Rank summation index identified genotype SMLW-134 as the best performer with a score of 39, followed by SMLW78 with 50, and SMLW93 with 58. Genetic and phenotypic components of variation for yield were the highest 60.5 and 63.7 while days to silking had the lowest values of 5.90 and 6.22, respectively. Repeatability estimates ranged from 93% for days to silking to 99% for ear height, plant height, and Anthesis-silking interval. Grain yield had highly significant positive correlation with plant height ($r = 0.38^{**}$), ear height ($r = 0.38^{**}$) and ear length ($r = 0.43^{**}$). Three identified inbred lines SMLW134, SMLW78 and SMLW93 could be used as parents in maize breeding programme for yield improvement.

Keywords: *Inbred lines, Genetic variation, Maize improvement, Yield.*

AGICP 008**Evaluating Inbreeding Depression And Genomic Selection For Enhancing Genetic Gains And Stability In Cassava (*Manihot Esculenta* Crantz)**¹Nwaogu, A.S., ²Eluwa, U. K and ³Nwanguma, F. C.*sanhereonly@yahoo.com*^{1,2,3}National Root Crops Research Institute, UmudikeCorresponding author: *sanhereonly@yahoo.com*

Abstract

Cassava is a vital staple crop in tropical regions, especially in sub-Saharan Africa, Asia, and Latin America, where it supports food security. Despite its importance, cassava breeding is hindered by issues like inbreeding depression, low genetic gains, and vulnerability to pests and diseases. This study evaluates the impact of inbreeding depression and assesses how effectively genomic selection can reduce genetic load and boost genetic improvement in cassava. The research was conducted across four agroecologically distinct locations in Nigeria: Ubijaja (Edo State), Umudike (Abia State), Otobi (Benue State), and Minjibir (Kano State). The study focused on selfed progenies (S1) from elite S0 genotypes (IBA-TMS070337 and IBA-TMS980581), which were evaluated for key traits such as yield, disease resistance, and starch content. DNA analysis using 44,930 SNP markers was conducted to calculate genomic estimated breeding values (GEBVs), which were used to identify superior genotypes. The study found significant inbreeding depression in S1 progenies, evidenced by reductions in plant vigor, root yield, and disease resistance. The study demonstrates that genomic selection effectively identified high-performing cassava genotypes with lower genetic load and strong traits across various environments. It highlights the power of genomic tools to speed up genetic improvement, enhancing traits like drought tolerance, disease resistance, and starch content—offering key insights for advancing cassava breeding to meet increasing demand.

AGICP 009

Estimation of Genotypic and Phenotypic Coefficient of Variation, Heritability and Genetic Advance in Okra (*abelmoschus esculentus* (linnaeus) moench)

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Abstract

Okra genotypes were evaluated for their genetic variability, heritability, and genetic advance for two cropping seasons. The investigation was carried out at the research field of Plant Science Department of Olabisi Onabanjo University, Ago-Iwoye, Ogun State, Nigeria. The experimental material comprised thirty genotypes of okra collected from different agro-ecological zones of Nigeria. Evaluation of the genotypes was carried out by Randomized Complete Block Design (RCBD) with three replications for yield-contributing traits in okra during the early and late rainy seasons. The Analysis of Variance (ANOVA) revealed that the mean sum of squares due to genotypes are highly significant for all the traits indicating the existence of substantial genetic variation in the genotypes for the characters studied. The high values of genotypic and phenotypic coefficient of variation were observed for all the yield-contributing traits (plant height, number of branches, number of fruits per plant, and yield per plot). The high heritability values as well as high genetic advance were exhibited by all yield traits. The findings have implications for breeding for improvement, industrial-scale production, and utilization of okra to meet specific demand by end users. Based on genotype performance, genotypes Ogt3 and NH47-4 can be further purified and effectively used for the improvement of early flowering and high-yielding okra hybrid through the process of hybridization.

Keywords: *Okra, Heritability, Genotype, Genetic advance, Crop improvement*

AGICP 010

Classifying Accessions Of *Corchorus Olitorius* (Jute Mallow) Using Agronomic Characteristics And Mineral Profile: An Implication For Conservation And Improvement

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Abstract

Jute mallow (*Corchorus olitorius* L.) is an important leafy vegetable in West Africa, valued for its nutrient-rich leaves and fibrous stems. Despite its dietary and economic significance, its genetic resources remain underutilised. This study evaluated 34 *C. olitorius* accessions from the National Horticultural Research Institute genebank, Ibadan, Nigeria, to identify genotypes exhibiting superior agronomic performance and mineral composition. Field trial was conducted in a randomised complete block design with three replications. Data were collected on key agronomic traits and leaf mineral concentrations (Ca, Fe, Zn, Na, Mg, K) using atomic absorption spectrophotometry. Highly significant accession effects ($p < 0.001$) were observed for most traits, indicating substantial phenotypic diversity within the collection. These findings provide a foundation for the selection of superior jute mallow accessions for agronomic and nutritional improvement. Correlation analyses revealed both strong positive (Ca and Mg; $r = 1.00^{***}$) and negative (Zn and leaf number; $r = -0.36^*$) relationships among traits. Principal component analysis revealed five components accounting for 80.8% of total trait variance and identified the key traits underlying variation among jute mallow accessions. Hierarchical cluster analysis categorized the accessions into five distinct groups. This multi-variate approach revealed underlying patterns of trait diversity and highlighted groups of accessions with similar agronomic and nutritional profiles. Based on the Rank Summation Index, NHJM0522, NHJM0500, and NHJM0538 were identified as the top-performing accessions, exhibiting both high leaf mineral content, particularly iron and calcium, and desirable leaf yield. Conversely, NHJM0517, NHJM0519, and NHJM0516 recorded the lowest overall performance across these traits. The top-performing accessions identified in this study offer valuable resources for breeding nutrient-dense, high-yielding jute mallow cultivars to enhance both household nutrition and farmer livelihoods.

Keywords: *Agronomic traits, Jute mallow, Leaf yield, Mineral content, Phenotypic diversity*

AGICP 011

Character Association Studies And Path Coefficient Analysis In Cucumber (*Cucumis Sativus* L.)

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Abstract

knowledge of the relationship between yield and its components, obtained through correlation and path analysis, helps a great deal to formulate selection programme. This research was carried out at the Eastern farms of Michael Okpara University of Agriculture Umudike. Four genetically distinct genotypes were evaluated for yield and yield attributes using a randomized complete block design with three replicates. Data collected was subjected to statistical analysis to study the character association and path coefficient analysis. According to correlation studies, fruit weight per hectare was significantly and positively correlated with number of leaves ($r = 0.766^{**}$), fruit length ($r = 0.858^{**}$), fruit diameter ($r = 0.842^{**}$) and fruit weight per plant ($r = 1.000^{**}$). Direct selection for these characters would increase yield. Path-coefficient analysis was studied considering fruit yield as dependent character and other yield attributes as independent characters. Results obtained shows that the highest positive and direct effect was found for fruit diameter (0.92) and leaf area (0.92). This was followed by number of leaves (0.14), number of branches (0.13) and number of fruits per plant (0.07). Thus, selection for the parent with more number of branches, fruit diameter and many number of fruits per plant is a pre-requisite for attaining improvement in fruit yield using the present material and should be given high weightage in any selection process aimed at improving fruit yield in cucumber. The effect of residual factor (0.9) on fruit yield was negligible, suggesting that no other yield components was captured in the analysis and an indication of appropriateness of characters chosen.

Keywords: *Correlation, Path coefficient analysis, Cucumber.*

AGICP 012

The Role Of Private Sector In Gendered Seed Demand And Distribution: A Case Study Of Iita GoSeed And Umudike Seeds

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Abstract

Since 2015, Nigeria's public cassava breeding program, led by the International Institute of Tropical Agriculture (IITA) in partnership with the National Root Crops Research Institute (NRCRI), has prioritized developing new cassava varieties that meet the diverse needs of users across the value chain. A crucial component of this initiative understands gender-specific trait preferences that motivate cassava seed distribution and exchange. A recent study reveals that commercial seed companies like IITA GoSeed and Umudike Seeds are emerging as vital sources of insights on gender-specific trait preferences in cassava, complementing traditional research methods. By engaging with farmers selling improved seeds, these companies gather valuable feedback, validating earlier research findings and providing breeders with real-time market intelligence to inform future investments. A key informant interviews with IITA GoSeed and Umudike Seeds staff, seed producers, buyers of improved varieties and the review of company reports, and sales data, confirmed the importance of previously identified traits like high yield, root size, early maturity, dry matter content and processing suitability are highly valued traits; while ratooning ability and sweet, mealy cassava roots and plant architecture are new gender-preferred traits. Both seed companies observed distinct gender differences in seed demand, with newly bred varieties gaining traction over older ones like TME419. However, women and men had different priorities: men emphasized agronomic traits, while women focused on processing and food quality. Notably, women in Village Seed Entrepreneurs (VSE) showed a strong preference for Game Changer and Farmers' Pride, exceeding demand from men. This highlights the value of market demand for seed and integrated action research in capturing emerging trends and informing breeding programs to meet the needs of diverse users.

Keywords: *Breeding program, Gender, IITA GoSeed, Umudike Seeds, Cassava*

AGICP 013

Generation Mean Analysis For Grain Yield And Nutritional Traits In Carotenoid-Biofortified
Maize GenotypesShuaibu, M¹ and Bello, O. B^{1*},¹Department of Agronomy, Faculty of Agriculture, University of Abuja, Nigeria.Corresponding author: obbello2002@yahoo.com; +2348035618020

Abstract

Developing biofortified maize with improved nutritional quality and stable performance across diverse environments is essential for combating malnutrition and achieving sustainable food security. This study elucidated the inheritance patterns, genetic parameters, and genotype-environment interactions (GEI) of grain yield, tryptophan, and carotenoid contents in maize genotypes. Two maize inbred lines that exhibited contrasting genetic parameters (TZEEIORQ 10 and TZEEI-4) were crossed to produce six generations (P₁, P₂, F₁, F₂, BC₁P₁, and BC₁P₂) and evaluated at two locations over two years. The generation mean analysis revealed that additive gene action predominantly controlled these traits, with some influence from dominance and epistasis. The TZEEIORQ 10 **line exhibited** superior agronomic and nutritional properties compared to TZEEI-4. Heterosis was observed in the F₁ hybrids, followed by **moderate reductions** in the F₂ generations due to genetic recombination. The **backcross BC₁ (F₁ × TZEEIORQ 10) retained** higher trait values highlighting additive contributions through genetic inheritance. GEI contributed 14–16% to the total phenotypic variance, underscoring the substantial influence of genetic background and environmental conditions on trait expression. The Which-Won-Where analysis identified high-performing, adaptable genotypes. The additive main effects and multiplicative interaction analysis revealed significant genotypic effects, with genotype accounting for 45.2% of the observed variation in grain yield. The prevalence of additive gene action underscores the potential of recurrent selection and targeted crosses to improve grain yield and nutritional composition, thereby facilitating the accelerated development of biofortified maize lines tailored to specific agroecological zones.

Keywords: *gene action, additive, backcrosses, dominance and epistasis*

AGICP 014

High-Throughput Phenotyping Using Uav Technology For Enhanced Cassava Breeding

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Abstract

Cassava (*Manihot esculenta*) is a key staple crop in sub-Saharan Africa, providing food security and economic stability for millions. Traditional field phenotyping methods are time-consuming and labor-intensive, limiting the speed of cassava breeding programs. Unmanned Aerial Vehicles (UAVs) offer a rapid, non-destructive solution for high-throughput phenotyping, enabling breeders to capture detailed imagery across large fields efficiently. By utilizing advanced drone technology and multispectral sensors, this study aims to assess cassava traits such as plant height, canopy cover, vigor, and disease symptoms, providing precise phenotypic data to enhance breeding decisions. Monthly UAV flights with a DJI Mavic 3M drone provided high-resolution RGB and multispectral imagery for cassava phenotyping. Using tools like AGISOFT-MetaShape®, R and QGIS involving many steps. Processed DEMs enabled estimation of plant height, canopy volume, biomass, and relative growth rate, while orthomosaics enabled vegetation indices (GRVI, GRA, VGE, VARI) canopy cover area, sprout, and vigor. The approach revealed clear growth trends across time and enhanced objective phenotyping, supporting yield-related trait assessment in cassava breeding. In conclusion, the data from UAV aids in building predictive models, allowing breeders to make more informed selections based on yield traits, resilience, and quality.

AGICP 015

Genetic variance and gains in maize (*zea mays* L.) Population following s_1 recurrent selection for grain yield and drought tolerance

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Abstract

Drought stress causes substantial grain yield losses of 15–30% annually in sub-Saharan Africa, necessitating the need for effective breeding strategies. This study evaluated genetic variability and realized gains in a maize population subjected to S_1 recurrent selection for grain yield and drought tolerance. Two cycles (C3 and C4) of the IARTZI-Y-Pop population were selfed to generate 60 S_1 families per cycle. A total of 120 S_1 families were evaluated under drought and well-watered conditions across Samaru and Minjibir during the 2024 dry and wet seasons, using a 10×12 alpha lattice design with two replications. Significant genotypic differences ($p < 0.05$) were observed for grain yield and agronomic traits under both conditions, revealing a substantial residual genetic variability. Under drought stress, grain yield ranged from 571.8 kg/ha (C4) to 801.0 kg/ha (C3), while under well-watered conditions, yield ranged from 1148.1 kg/ha (C3) to 1200.0 kg/ha (C4). Realized genetic gain for grain yield under drought was -229.3 kg/ha (-28.62%), whereas under well-watered conditions, it was 51.9 kg/ha (4.52%). Other realized gains under drought included: 3.21 days for days to 50% anthesis, 2.95 days to silking, 1.85 cm for plant height, 3.90 cm for ear height, 0.66 for anthesis-silking interval, ear aspect 0.37, plant aspect 0.11 and stay green character 0.46 under-drought. The higher grain yield observed in C3 over C4 under drought implies that S_1 recurrent selection was effective in improving the population for drought tolerance to C3 and may not be necessary to advance, or further introgression of drought tolerance genes in C4 is needed before advancing to the next cycle.

Keywords: *Drought stress, Realized gain, Recurrent selection, S_1 family, Well-watered.*

AGICP 016**Regression analysis of some cassava genotypes in Nigeria**

Njoku, D.N., Onyeka, J and C.N. Egesi (NPBA Conference Preceeding: ORAL
PRESENTATION)

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Abstract

In a cassava study involving nine F1 populations, 2,411 botanical seeds were harvested, sown in pots, and nurtured in a screenhouse for 40 days. In May 2022, the emerging seedlings were transplanted into the field alongside their parent plants sourced from stem cuttings, done family by family. Ultimately, 529 progenies were successfully harvested. Data collected from both field and laboratory settings were analysed to assess key metrics, including total carotene content (TCC), dry matter content (DMC), fresh root yield (FRY), dry root yield (DRY), and other quality traits of the roots. The seed germination rates varied significantly among the different populations, ranging from 20.4% to 90.6%, with an average of 52.44%. Notably, phenotypic variation in DMC, TCC, FRY, DRY, biomass, root number, harvest index, and reaction to cassava mosaic disease (CMD) was observed across all family lines. For the populations examined, the average metrics were as follows: TCC at $10.84 \mu\text{g ha}^{-1}$, DMC at 37.29%, FRY at 23.68 t ha^{-1} , and DRY at 16.24 t ha^{-1} . Heritability estimates were calculated through midparent-offspring regression analysis, revealing genetic gains for TCC, DMC, FRY, DRY, and the response to CMD. The TCC, DMC, and CMD traits exhibited high heritability estimates of 0.82, 0.89, and 0.94, respectively, while FRY had a low estimate of 0.17. A negative correlation between TCC and DMC was noted throughout all evaluation phases and locations. Significant variation was identified within the segregating F1 progenies for each trait examined. The narrow-sense heritability estimates indicated that genetic factors were more influential than environmental factors for TCC, DMC, and CMD. This suggests that employing simple recurrent phenotypic selection could lead to successful and reliable advancements in these traits.

Keywords: *Cassava, Heritability, Regression, Clone*

AGICP017

Assessment of genetic variation in groundnut (*arachis hypogaea* L.) Accessions from togo and south sudan based on seed yield using dartseq snp markers

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Abstract

Groundnut (*Arachis hypogaea* L.) production in Nigeria is constrained by pests, diseases, poor soil fertility, drought, and climate change. Assessing the genetic diversity of groundnut germplasm is critical for breeding resilient, high-yielding varieties. This study evaluated 39 accessions from Togo and South Sudan based on seed yield, agronomic traits, and single nucleotide polymorphism (SNP) markers. Accessions were obtained from the Genetic Resources Center of the International Institute of Tropical Agriculture, Ibadan, Nigeria, and tested at Ibadan, Ikenne, and Kano in 2022 using a randomized complete block design with three replications. Data on seed yield, pod weight, hundred seed weight, and other traits were analyzed with ANOVA in R (version 4.1). A total of 4,488 SNPs were generated, of which 2,586 high-quality DArTseq SNPs were retained. Significant ($P < 0.05$ – 0.001) differences were observed among accessions for all traits except days to first flowering, while location effects were significant for all traits except seed length. Accession $\times$ location interaction was significant only for seed yield. Principal component analysis identified hundred seed weight, pod weight, and seed yield as major contributors to diversity, and cluster analysis grouped the accessions into three heterogeneous clusters. Molecular variance showed that 47.7% of total variation was explained by the first five principal components, with heterozygosity ranging from 0–50% across loci. Considerable genetic variation was detected, with accession TGO-AH2021-026 emerging as a promising candidate for breeding and cultivation in Nigeria.

Keywords: Groundnut, Genetic variation, Agronomic traits, SNP markers, Breeding

AGICP018

Screening Of Cassava Plantlets From Semi-Autotrophic Hydroponic (SAH) Under Different Weather Conditions For Effective Survival Rate

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Abstracts

This study evaluated the performance of Semi-Autotrophic Hydroponic (SAH)-derived cassava plantlets (*Manihotesculenta* Crantz) under varying weather conditions at the National Root Crops Research Institute (NRCRI), Umudike, Nigeria. Five cassava varieties (Dixon, TMEB419, Obasanjo2, Fineface, and Sunshine) were assessed in a Randomized Complete Block Design (RCBD) to determine their survival and growth traits. Data on net sprout count, total sprout count, and plant height were collected at 1–12 weeks after planting (WAP) across early, peak, and end rainy seasons. Results revealed significant genotypic differences in sprouting and growth responses. Sunshine consistently exhibited the highest sprout counts during early and peak rainy seasons, demonstrating adaptability to high moisture, while Dixon, Fineface, and Obasanjo2 maintained stable performance across rainfall intensities. TMEB419 showed rapid early height growth but lagged in late-season sprouting. Plant height varied with weather phases, with Dixon excelling during peak rainfall and Sunshine showing prolonged vegetative growth toward the season's end. The study highlights genotype-environment interactions in SAH systems, emphasizing the importance of varietal selection for climate-resilient cassava production in tropical regions. Sunshine and Dixon emerged as promising candidates for rainfed systems due to their consistent establishment and vigor under fluctuating moisture conditions. These findings support optimizing SAH techniques for sustainable cassava cultivation in Nigeria and similar agroecologies.

Keywords: *Cassava, Semi-Autotrophic Hydroponics (SAH), sprouting, plant height, weather adaptability, Umudike.*

AGICP019

Multi-Location and On-Farm Evaluation of White Maize Hybrids for Yield, Agronomic Traits, and Stability in Nigeria

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Abstract

The development of stable and high-yielding maize hybrids is critical for improving food security in sub-Saharan Africa. In Nigeria, hybrid maize adoption is expanding, but there remains a need for improved cultivars with greater adaptability, agronomic desirability, and resistance to production constraints. This study evaluated the performance and stability of newly introduced experimental white maize hybrids relative to a commercial check and a farmer-preferred variety across contrasting environments. Five experimental hybrids (EXP WHITE 3W TH9, TH10; EXP WHITE SINGLE TH11, TH12, TH13) and a commercial check (Oba Super 11) were tested in on-station trials at Kura during the 2021/22 dry season using a randomized complete block design. Based on performance, four hybrids were subsequently evaluated in multi-location trials across six sites in 2022 and eight sites in 2023. On-farm evaluations in 2023 included two hybrids, the check, and a local farmer's variety across six states. Trials used uniform agronomic management with 120 kg N/ha applied, and data were collected on phenology, plant and ear traits, disease severity, and grain yield. Statistical analysis included ANOVA and genotype plus genotype $\times$ environment (GGE) biplot to assess yield stability. On-station evaluation revealed significant variation for plant height, stem and cob borer incidence, and ears per plant, with mean hybrid yields ranging from 3.8 to 5.8 t ha⁻¹. All experimental hybrids showed reduced pest incidence and superior ear traits relative to the check. Across environments, EXP WHITE SINGLE TH11–13 out-yielded Oba Super 11 by 0.9–1.3 t ha⁻¹, with TH11 reaching 10.4 t ha⁻¹ at Chiromawa and TH13 achieving ~10 t ha⁻¹ at Lafia. GGE biplot identified TH13 as both high-yielding and stable across locations. On-farm trials confirmed its superiority (7.5 t ha⁻¹), with a 6.5% yield advantage over Oba Super 11. EXP WHITE SINGLE TH13 demonstrated high yield potential, desirable agronomic characteristics, and broad stability, making it a strong candidate for release and adoption in Nigeria's diverse maize production systems.

Keywords: Maize hybrids, yield stability, Multi-location trials, GGE biplot analysis, On-farm evaluation

Sub-Theme 2

.Plant Genetic Diversity and Resilience

(PGDR)

PGDR 001**Phytochemical Profiling and Molecular Characterization of *Jatropha* Species Cultivated in Nigeria**

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Abstract

Jatropha, a well-known medicinal plant in Nigeria, has considerable untapped potential for both medicinal and agricultural applications. Despite extensive global studies, limited research has focused on *Jatropha* landraces' genetic diversity and phytochemical composition in Nigeria. In this study, traditional farmers collected forty *Jatropha* landraces across the country using local nomenclature and morphological identification. Six representative landraces from Nigeria's six geopolitical zones were analyzed for phytochemical composition via Gas Chromatography-Mass Spectrometry (GC-MS) and subjected to Principal Component Analysis (PCA). The *rbcL* gene was used to genotype all forty landraces, followed by sequencing and analyses, including Analysis of Molecular Variance (AMOVA) with GenALEX 6.5, phylogenetic analysis using the Neighbor-Joining method, and SNP identification with DnaSP software. GC-MS analysis identified 122 phytochemicals, with compositions varying geographically. Linoelaidic acid was prominent in landraces from northern Nigeria (Borno, Nasarawa, and Kano). PCA revealed that the Borno landrace had the highest loading value (0.521 on PC1) for phytochemical variation. Phylogenetic analysis grouped landraces into three major clusters, with no correlation to geographic origin, indicating high genetic variability. DNA polymorphism analysis detected 685 mutations, 39 unique haplotypes, and a diversity rate of 0.999, suggesting mutation and recombination as drivers of diversity. Significant nucleotide diversity (0.70410) confirmed this variation. AMOVA indicated 1% variation among populations and 99% within populations. These results highlight the extensive genetic and phytochemical diversity in Nigerian *Jatropha* landraces. This variability offers valuable insights for selecting parent lines in breeding programs to enhance *Jatropha*'s agricultural and medicinal value.

Keywords: *Jatropha*, Genetic Diversity, *rbcL* Gene, Phytochemical Analysis, GC-MS.

PGDR 002

Agronomic performance of plantain (*Musa* spp.) genotypes in the rainforest agroecological zone of Nigeria

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Abstract

Plantain is an important staple foods and sources of rural income in most parts of sub-Saharan Africa particularly for the smallholders who grow them in home gardens. Objective of this study was to investigate the fruit yield of four plantain cultivars comprising of two hybrids (PITA 3 and PITA 24) and two landraces (Orishele and O' Ntanga GM) with the aim of promoting improved hybrids for increased production and commercial utilization. The plantain cultivars were evaluated using a randomized complete block design with two replications. Each plot was 48 m² in size giving a total of 12 plants per plot at a spacing of 2 m x 2 m. Data on agronomic and yield-related parameters were collected on six middle plants in each plot for 2 production cycles. Significant variation was observed for suckering ability, bunch weight, number of hands and number of fruits. Orishele (landrace) had the highest number of suckers (6) while PITA 24 had the heaviest bunch (15.9 kg), highest number of hands per bunch (9) and highest number of hands per bunch (148). Positive and significant relationship ($p < 0.05$) was observed between bunch weight and plant girth ($r = 0.98$); fruit pedicel length and each of bunch weight (0.99) and number of hands ($r = 0.96$). This study confirmed that other plantain hybrids can be grown profitably and considered for processing other plantain food products such as chips, roasted and boiled plantain in the face of increasing cost of landrace cultivars.

Keywords: *Bunch weight, Hands per bunch, Musa* spp., *Suckering ability,*

Physical: *Oral*

PGDR 003

Effects Of *Aspergillus Flavus* And *Fusarium Verticillioides* Infestations On Agronomic Traits And Mycotoxin Accumulation In Provitamin-A Maize Inbred LinesIseghohi, Innocent^{a*}, Ajayi. Bisola^a and Mboup, Mamadou^b^aDepartment of Crop Science and Horticulture, Federal University Oye-Ekiti, Ekiti State, Nigeria^bInternational Institute of Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria*Corresponding author: innocent.iseghohi@fuoye.edu.ng, +234-8038147675**Presentation type: Physical Oral**

Abstract

Maize, an essential crop, is often affected by fungal pathogens, *Aspergillus flavus* and *Fusarium verticillioides*, which cause ear rots, contaminate grains with carcinogenic mycotoxins, aflatoxin and fumonisin, and reduce agronomic performance. Developing host-resistant varieties can help mitigate these effects. Evaluating maize inbred lines (ILs) under artificial infestation can assist in identifying tolerant lines. The study aimed to (i) assess the agronomic and yield performance, along with mycotoxin levels of ILs, and (ii) examine the impact of ear rots on grain yield (GY), aflatoxin, and fumonisin levels in the ILs. Twenty-one ILs, including two checks, were tested under artificially-infested *A. flavus* and *F. verticillioides* in a split-plot design. Data on GY (t/ha), ear rot (%), and mycotoxins (ppm) were collected following standard procedures. Analysis involved ANOVA, descriptive statistics, and regression at $\alpha=0.05$. Infestation and genotype effects varied across all traits. The average GY (2.32), ear rot (8.98), and mycotoxin levels (20.71) were significantly higher under *F. verticillioides* infestation compared to *A. flavus*. Ear rot did not significantly affect GY. However, the regression model indicated a significant increase of 0.14 ppm in aflatoxin and 1.22 ppm in fumonisin when ear rot increased by 1%. Four ILs (IITATZI2142-1, IITATZI2116-3, IITATZI2028, and IITATZI2065) maintained comparable GY to the best check under both infestations and were tolerant to *Aspergillus* ear rot and aflatoxin. Nonetheless, most ILs exhibited undesirably high fumonisin levels, except IITATZI2116-3, which is recommended for further breeding programmes.

Keywords: *Aflatoxin, Ear rot, Fumonisin, Grain yield, Mycotoxin contamination*

PGDR 004

Testcross performance and genetic variability in tropical *shrunk-2* super sweetcorn (*zea mays* L. Var *saccharata*)

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Sub-Theme: Accelerating Genetic Gains for Increased Crop Productivity

Presentation mode: Oral

Abstract

Enhancing the production of super sweetcorn in Nigeria requires the development of superior hybrids and knowledge of the extent of variability for desirable traits in available genotypes. In this study, the performance and genetic variability among 24 testcross hybrids developed from 11 tropical *shrunk-2* super sweetcorn inbred lines, three of which were selected as testers due to their overall agronomic performance was investigated. The testcrosses were evaluated under rain-fed conditions for two years using a randomized complete block design with three replicates. Data were collected on 15 agronomic and yield-contributing traits. Highly significant differences were found among the testcross hybrids for the traits. The yield of marketable ears (YME) ranged from 6.95 - 11.98 t/ha. Eleven of the testcrosses (45.8%) had higher YME than the mean (8.66 t/ha). On average, number of marketable ears (NME) was 80.5% of the total number of ears (NE) harvested. Estimates of phenotypic coefficient of variation (PCV) were marginally higher than the corresponding genotypic coefficient of variation (GCV) for the traits. The PCV and GCV were moderate to high for yield of ears, YME, NME, NE, anthesis-silking interval, ear aspect, plant aspect and husk cover, but low for other traits. Broad-sense heritability ranged from medium to very high. Genetic advance was moderate to high for the traits, except days to anthesis and silking. Variability exists among the *shrunk-2* super sweetcorn testcross hybrids which could be exploited for the improvement of the crop. The superior hybrids identified should be further evaluated for possible release and commercialization.

Keywords: Super sweetcorn, Broad-sense heritability, Genotypic coefficient of variation, Genetic advance

PGDR 005

Phenotypic Characterization and Evaluation of *Hevea Brasiliensis* for Genetic Diversity and Improvement of Latex Quality Attributes.

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Presentation Type: Oral

Abstract

Experiment on phenotypic characterization of 16 natural rubber (*Hevea brasiliensis*) genotypes was conducted during the 2023 cropping season and evaluation of latex quality was done for two seasons (2023 and 2024), at the clonal garden of Rubber Research Institute of Nigeria (RRIN) Iyanomo, Benin City. The objective of this study was to characterize available natural rubber genotypes with a view to classifying them into distinct similarity groups using the RRII and IPGRI natural rubber descriptor manual at mature stage. The two parts of the natural rubber trees characterized include the trunk and branches. Yield evaluation was also done using the half spiral alternate day system donated as S/2d/2 without yield stimulation and the dry rubber yield data collected were subjected to analysis of variance to determine the variability that existed among the genotypes. The principal component analysis showed that most of the traits measured significantly contributed to the total observed variability among the genotypes. Combined analysis of variance (ANOVA) indicated highly significant genotypic differences among the genotypes for the agronomic character (latex yield) measured. This work showed considerable genetic variability in agro-morphological attributes of natural rubber genotypes. Genotypes with highly similar traits and high-yielding potentials were identified and characterized.

Keywords: *Characterization, Genetic Diversity, Latex Quality, Genotypes, Descriptortraits.*

PGDR 006

Morphological Characterization and Evaluation of some soybean breeding lines.

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Presentation Type: Physical Oral

Abstract

The advancement of plant genetics and genomics plays a critical role in unlocking superior crop varieties for sustainable agriculture. This study evaluated 45 soybean (*Glycine max* L.) breeding lines using a 5 × 9 alpha lattice design, replicated thrice at the Teaching and Research Farm of the Federal University Oye-Ekiti, to investigate the underlying genetic diversity for key agronomic traits. Seven traits were analyzed: days to 50% and 100% flowering, lodging score, 100-seed weight, shattering score, nodule weight, and net plot yield.

Analysis of variance revealed highly significant ($p < 0.05$) differences among genotypes for all traits, confirming the presence of exploitable genetic variation. Correlation analysis indicated strong positive relationships between flowering traits and yield ($r = 0.225$), while lodging and shattering scores were negatively associated with yield performance. Principal Component Analysis showed that the first principal component (PC1) accounted for 99.23% of total variation, predominantly influenced by net plot yield and flowering traits, signifying their critical contribution to genotypic variability.

Ward's hierarchical cluster analysis, visualized through a dendrogram, classified the genotypes into distinct groups, reflecting their phenotypic similarities and differences. This stratification supports the identification of complementary parental lines for crossing programs.

The integration of lattice design with multivariate statistical approaches provides robust insights into trait associations and diversity, reinforcing the potential of genomics-led breeding for developing next-generation soybean cultivars with enhanced yield and adaptability.

PGDR 007

Genetics of Nitrogen Use Efficiency in Cassava

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Abstract

Cassava is an important food security crop; it is a reliable food source and highly resistant to drought, ensuring a stable food supply even when other crops fail due to climate variability. Low nitrogen (N) stress remains a significant constraint to cassava production. Enhancing nitrogen use efficiency (NUE) in cassava is essential for improving system resilience, promoting sustainable intensification, and mitigating the economic and environmental costs associated with N fertilisation in cassava-based production systems. This study aimed to develop cassava varieties with enhanced nitrogen use efficiency (NUE) by identifying genomic regions and candidate genes associated with NUE. A genome-wide association study (GWAS) was conducted using the Genome Association and Prediction Integrated Tool (GAPIT) on a panel of 265 diverse cassava genotypes. These genotypes were phenotyped for 10 physiological and agronomic traits under both optimum and low-nitrogen conditions. Whole-genome genotyping was performed using the Diversity Arrays Technology sequencing platform (DArTseq), yielding 68,814 single-nucleotide polymorphisms (SNPs) distributed across the 18 cassava chromosomes. Fifty-two SNPs were significantly associated with NUE and yield-related traits. The putative genes identified through GWAS, particularly those with significantly associated SNP markers, represent valuable targets for marker-assisted selection to develop cassava varieties with enhanced nitrogen use efficiency (NUE). Such improvements can potentially reduce reliance on exogenous nitrogen inputs, thereby mitigating their adverse environmental impacts and promoting sustainability.

Keywords: *Cassava, GWAS, SNPs, Nitrogen use efficiency (NUE).*

PGDR 008**Growth and Yield Responses of Cowpea to Plant Densities in Two Agro-Ecologies in Northern Nigeria: A Yield Compensation Mechanism**

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Abstract

Low plant stands at early crop establishment contribute to yield reduction in legumes. Gap-filling is considered to mitigate these losses. There is, however, limited understanding of yield-compensation mechanism in cowpea. This study was aimed to investigate the mechanism of yield-compensation in some accessions of cowpea at Minjibir and Shika in Northern Nigeria. The experiment was laid out in split plot fitted into a randomised complete block design in three replicates. The main plot consisted of four plant densities (33,333; 66,666; 99,999; 133,333 plants ha⁻¹) while the subplots consisted of six cowpea accessions (IT89KD-288, IT93K-452-1, IT99K-537-1-1, IT98K-205-8, IT08K-150-27 and DANILA). Results showed that plant density and environment affected grain yield. Total grain yield increased with increasing plant density and was higher at Minjibir than at Shika. The highest total grain yield of 1793.3 kg ha⁻¹ was observed in the accession DANILA at 99,999 plants ha⁻¹, while the lowest (1100 kg ha⁻¹) was observed in the accession IT98K-205-8 at 33,333 plants ha⁻¹. Leaf area index, stand count at harvest and intercepted photosynthetically active radiation were positively correlated with total grain yield at both locations, suggesting that these traits could be considered for cowpea improvement. Cowpea growers and breeders could consider the erect (IT93K-452-1 and IT98K-205-8) and semi-erect accessions (IT99K-573-1-1 and IT08K-150-27) for cultivation at 133,333 plants ha⁻¹. Prostrate accessions (IT89KD-288 and DANILA) could be planted at 99,999 plants ha⁻¹ at Minjibir. The accessions IT93K-452-1-1, IT98-205-8, IT99K-573-1-1 and IT08K-150-27 could be considered for cultivation at Shika irrespective of plant density.

Keywords: *growth; yield compensation; cowpea; missing stand; plant density; Fabaceae.*

PGDR 009

Genome Diversity of Bambara Groundnut (*Vigna subterranea* (L.) Verdc.) in Nigeria Using SNP Markers

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Abstract

Bambara groundnut (*Vigna subterranea* [L.] Verdc.) is an important leguminous crop within tropical agricultural systems, offering substantial economic value. While Nigeria harbors considerable genetic variation in Bambara groundnut populations, comprehensive characterization of these genetic resources remains incomplete. This research aimed to elucidate the genetic diversity patterns within Bambara groundnut collections from Northern guinea savanna of Nigeria using advanced molecular techniques. Field evaluation of germplasm was conducted alongside DArTseq-GBS technology for genomic characterization. Genetic analysis employed single nucleotide polymorphisms (SNPs) processed through R-programming environment, Mega software, Plink, and TASSEL version 5.2.23 for comprehensive diversity evaluation. Genomic sequencing yielded 11,821 SNPs, with 4,526 markers (45.13%) meeting quality standards. Major allele frequencies ranged between 0.50-0.98, contrasted with minor allele frequencies of 0.2-0.50. SNP distribution demonstrated right-skewed patterns toward major alleles, SNP density peaked at 2,500 markers at allele 3, while allele 1 contained 200 SNPs. Principal component analysis revealed four distinct genetic clusters: three main population groups plus one outlier. Similarly, clustering algorithms identified three subpopulations alongside the distinct TVSu-838 accession from Kaduna state as an outlier group. These findings confirm the effectiveness of SNP markers for genetic diversity studies and variability assessment in Bambara groundnut. The unique genetic signature of outlier TVSu-838 suggests potential value for identifying novel allelic variants and candidate genes for crop enhancement programs.

Keywords: *Bambara groundnut, Genetic improvement, Genetic diversity, DArTseq technology, SNP-based markers.*

PGDR 010**Comparative Performance of Nigrescens and Virescens Oil Palm Fruit Types: Opportunities for Breeding and Commercial Production**Okereke, A. C.¹ Okoye, M. N.¹ Imasuen, J. A. and Ahanon, M. J¹Plant Breeding Division, Nigerian Institute for Oil Palm Research (NIFOR), Benin City, NigeriaCorrespondence: chiomaabu@yahoo.com 07069183755

Abstract

Oil palm (*Elaeis guineensis* Jacq.) is the world's highest-yielding oil crop, and fruit type differences play a major role in harvest efficiency, processing quality, and profitability. This study compared the nigrescens and virescens fruit types, focusing on agronomic performance, fruit colour, and harvesting convenience. Mature palms were evaluated in the field using standardized agronomic measurements, and fruit and bunch quality were assessed in the laboratory. Data were analysed using standard statistical tests, including ANOVA and mean separation.

Nigrescens palms produced slightly fewer bunches (12.8) but heavier average bunch weights (7.1 kg), giving yields comparable to virescens (14.0 bunches; 6.7 kg). Nigrescens also outperformed virescens in oil yield traits, including mesocarp content (65.2% vs. 60.5%), oil-to-bunch ratio (50.8% vs. 47.5%), and oil extraction ratio (43.4% vs. 40.6%). By contrast, virescens showed greater stability in fruit-to-bunch ratio and kernel content, supporting consistent field performance. A key advantage of virescens is its clear visual ripening signal: bunches turn bright orange before harvest, facilitating timely harvest, reducing reliance on skilled labour, and minimizing losses from unripe or overripe fruit.

Vegetative traits were similar between fruit types, suggesting compatibility in breeding programmes. Overall, the complementary strengths of both types indicate that introgression of virescens into NIFOR's breeding programme could enhance harvesting efficiency and operational precision while maintaining yield potential. This offers a promising pathway for sustainable and profitable oil palm production in Nigeria.

Keywords: *Oil palm, breeding, fruit type, virescens, nigrescens, harvest efficiency.*

PGDR 011

Assessment of Stem Borer Resistant Sorghum Genotypes Lines for Resistance to Fall Armyworm (*Spodoptera frugiperda* J.E. SMITH) Artificial Infestation.

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Abstract

Fall armyworm (FAW) is an economic pest affecting sorghum when susceptible cultivars are grown and environmental conditions are supportive. Resistance breeding to FAW is, therefore, of crucial importance to offer effective, sustainable, and environmentally friendly management options. Having varieties that combined resistant to stem borer and FAW would enhance and stabilize sorghum productivity in SSA. This study was performed to assess some stem borer resistant sorghum genotypes for FAW resistance under artificial infestations. The study was carried out in the screen house and open field of ABU/IAR Zaria. 19 sorghum stem borer resistant lines were sourced and arranged in a randomized block design in two replications and were assessed based on the fall armyworm leaf damage score on a scale of 1 to 9, as specified by Davis and Williams (1992). Each treatment stands were infested twice using camel hair brush at days 14 and 21 after seedling emergence with 5 FAW first instar larvae. Observations of foliar leave damage started 4th days after the first infestation and subsequently six days interval for 5 weeks after the second infestations. The results revealed significant differences (0.01 and 0.5%) among the genotypes for all the agronomic traits evaluated and foliar leaf damage scores. The best promising genotypes from the results obtained were 73.69% which recorded lower leaf damage score of 4-5 and were classified as moderately resistant genotypes. These genotypes could be exploited as a resistance source in breeding for resistance to FAW.

Keywords: *Sorghum genotypes, Fall armyworm, Artificial infestation, Leaf damage*

PGDR 012

Genetic and Morphological Diversity of Lima bean Conserved at the Genetic Resource Center, IITA

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Abstract

Phaseolus lunatus (Lima bean) is an important underutilized crop with the potential of alleviating food and nutritional insecurity as it contains a high amount of protein and is climate resilient. Breeding advancement which is important for crop improvement is dependent on genetic diversity and phenotypic assessment. Hence, the objectives of this study were to evaluate the genetic kinship and assess the morphological characters of 51 lima bean accessions from the International Institute of Tropical Agriculture (IITA), Genetic Resources Centre. Morphological data was taken on plant height, days to first flowering, number of seeds per pod, and total seed weight. The Analysis of Variance (ANOVA) revealed significant differences ($p < 0.01$) for all of these traits. Cluster analyses identified two distinct clusters based on morphological traits with cluster I having the highest number of accessions, reflecting patterns of phenotypic variation largely influenced by total seed weight. Principal Component Analysis (PCA) revealed that the first three components explained 98.90% of the total variation among accessions. DArTseq Genotype-by-Sequencing approach generated 10,014 high-quality SNPs. Both cluster analysis and PCA identified three distinct genetic groups within the lima bean populations, indicating diversity. DArTseq was effective in analyzing the genetic diversity within and between populations. This information could aid in the improvement of lima bean.

Keywords: *DArTseq, Morphology, Diversity, Breeding*

PGDR 013

Multi-Trait Selection for Drought-Tolerant Soybean Genotypes Under Contrasting Water Regimes

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Abstract

Soybean, a crucial source of protein and oil, faces significant yield reductions due to drought stress, particularly at the flowering and pod-filling stages. This study evaluated 150 genotypes from the Soybean Breeding Program of the International Institute of Tropical Agriculture (IITA) in Ibadan, Nigeria, using a multi-trait selection approach under both well-watered and water-stressed conditions across two growing seasons. The drought stress treatment was applied intermittently in two phases: 14 days at 35 days after sowing (DAS) and 7 days at 63 DAS, targeting critical reproductive stages. The results revealed significant variation ($p < 0.001$) among soybean genotypes for all traits under both water-stressed and well-watered conditions. Broad-sense heritability estimates under both conditions ranged from 21.56 % to 86.56%, with the highest values observed for lodging score and days to 50% flowering. Based on the drought tolerance indices and a 20% selection intensity, high-yielding and drought-tolerant genotypes were selected. Pearson correlation analysis revealed that yields under stress and non-stress conditions showed a moderate positive correlation ($r = 0.38$), supporting stability across environments. A similar positive correlation was observed between hundred-seed weight and yield under both water regimes. The multi-trait genotype-ideotype distance index (MGIDI) identified 30 outstanding genotypes under each water condition, with 8 genotypes consistently performing well in both. The Venn diagram plot highlighted genotype SY150 as the most stable across all three selection methods applied. Drought tolerance indices enabled a comprehensive assessment of genotype resilience under stress. Together with the MGIDI approach, these tools provide insights for identifying drought-tolerant genotypes in soybean breeding programs.

Keywords: *drought stress, drought tolerance indices, MGIDI, Glycine ma*

PGDR 014

Genotypic Variability in Morphological and Proximate Traits of Onion (*Allium cepa* L.) under Iron Oxide Nanoparticle Applications in Lafia, Nigeria

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Abstract

This study evaluated the morphological and proximate responses of five onion (*Allium cepa* L.) genotypes Wade, Prema, Mara Kara, Super Yali, and Me Kara exposed to varying concentrations (0, 20, 40, 60, and 80 rpm) of iron oxide nanoparticles in Lafia, Nigeria, during the 2025 planting season. The experiment assessed establishment count, plant height, number of leaves, neck thickness, final stand count, bulb biomass, bulb diameter, bulb length, dry weight, and proximate composition. Results revealed significant ($p \leq 0.05$) genotype by treatment interactions across most morphological traits. Me Kara consistently showed superior performance in key parameters such as dry weight (6.81 g), bulb biomass (28.27 g), and final stand count (14.07), particularly under 20 and 60 rpm treatments. Notably, plant height and leaf number peaked under 80 rpm (30.55 cm and 9.20, respectively), while bulb characteristics such as length and diameter varied significantly across genotypes and treatments, with Mara Kara and Prema responding favourably at higher nanoparticle concentrations. Proximate analysis indicated minimal variation in moisture content (90.2–92.2%) and crude fat (0.20–0.35%), but moderate differences in crude fibre, protein, and carbohydrate levels among treatments. Pearson correlation analysis demonstrated strong positive associations between dry weight and bulb weight ($r = 0.928^{**}$), bulb biomass ($r = 0.663^{**}$), and fresh plant weight ($r = 0.838^{**}$), suggesting these are reliable indicators of yield potential. Conversely, carbohydrate content showed significant negative correlations with moisture ($r = -0.770^{**}$) and bulb length ($r = -0.402^*$). The finding shows the potential of iron oxide nanoparticles, particularly at 40–60 rpm, in enhancing onion growth and nutritional value, with Me Kara and Super Yali emerging as promising genotypes for nanoparticle based agronomic interventions in similar agroecologies.

Keywords: *Onion genotypes, Iron oxide nanoparticle, Morphological traits, Proximate composition, Correlation analysis.*

PGDR 015

Profiling of Some Nigerian Yam (*Dioscorea rotundata* Poir) Accessions Towards an Improved Yam Breeding System in Umudike, Southeastern, Nigeria.

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Abstract

A two-year field experiment was carried out at National Root Crops Research Institute, Umudike, in Southeastern Nigeria. The study aimed to profile 36 selected *D. rotundata* landraces traits in order to establish minimum standards and bench mark to be considered by yam breeders. Field establishment was done using a lattice design replicated three times for two cropping seasons. Planting sett was 200g with a plot dimension of 10m². The result suggested that for an improved variety to be released by Nigeria yam breeders, it should have a minimum yield of 20 t/ha, minimum yield of 7.9kg/plot, minimum yield of 5.0kg of big tuber per plot, minimum yield of 3.8kg of medium tuber per plot, minimum yield of 2.7kg of small tuber per plot, average tuber length of 31.8cm per plot and a minimum diameter of 5.8mm per plot. The improved variety must also have a minimum average severity score of 1.2 for yam mosaic virus disease, 1.5 for anthracnose and 1.1 for nematodes. It also revealed that improved varieties must have a minimum of 30.5% of dry matter composition, a minimum of 28.5% of starch yield and a minimum of 20.4% of flour yield. Punch, Yandu, Ogoja, Myamiyo, Mumuye, Mekaccusa, Fakesta, Danacha, Ame, Alumaco, Nwopoko, Ojuiyawo, Adaka, Asangwu, Gwagwa, Afiemine, Didiya, Agboiyo, should all be classified as standard for yield, dry matter, starch, flour and tolerance to pest and diseases.

Keywords: Bench mark, Yield, Pest and disease, Dry matter, Landraces

PGDR016

Assessment of Genetic Variation and Yield Performance of Groundnut (*Arachis hypogaea* L.) Accessions from South Sudan and Togo.

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Abstract

Groundnut (*Arachis hypogaea* L.) is a drought-tolerant crop widely cultivated in Sub-Saharan Africa. This study assessed the genetic diversity and yield performance of 39 groundnut accessions collected from IITA's Genetic Resources Centre. The experiments were conducted across three agroecological zones in Ibadan, Ikenne, and Kano, Nigeria, using a Randomized Complete Block Design with three replicates. Traits were evaluated and analyzed using ANOVA, PCA, correlation, and cluster analysis. ANOVA showed significant variation among accessions for most traits, except plant width, pod weight, number of pods per plant, total pod weight, total seed weight, seed weight, shelling percentage, and hundred seed weight. Genotype $\times$ environment interactions were significant for traits such as flowering time, pod width, seed width, and biomass weight. PCA (PC1 – PC5) explained 89.3% of the total variation, with pod weight per plant and total pod weight dominating PC1. Accession TAh-146 was the first to flower with the mean of (29.78) days after planting. Seed yield showed strong positive correlations with total pod weight ($r = 0.93$), number of pods per plant ($r = 0.93$), pod weight per plant ($r = 0.92$), and seed weight ($r = 1.00$). Late-flowering accessions TAh-179 and TAh-152 could be improved for early maturity, while TAh-143 and TAh-176 are promising high-yielding lines for further breeding program. Accession TAh-143 which has the highest pod and seed yield of 8433.49 kg/ha can inform seed and pod based selection for groundnut improvement.

Keywords: groundnut accessions, genetic diversity, genotype $\times$ environment interaction, multivariate analysis, variation.

PGDR017

Characterization of of *Parkia biglobosa* (Benth) accessions collected across Nigeria

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Abstract

The African locust bean (*Parkia biglobosa*) is one of 34 species of *Parkia* an important multipurpose tree of West African Savannah, Africa. It is considered to be endangered as a result of over- exploitation, negative impact of human's activities on the plant's habitat, non - cultivation of *Parkia* and lack of established plantations. Twenty-eight *Parkia biglobosa* accessions' matured fruit pods handpicked from their parent plants in Benue, Ekiti, Kogi, Gombe, Oyo, Plateau and Kano states in Nigeria were assessed for their fruit and seed traits. For seed colour, two accessions were light brown, four accessions were brown, twelve accessions were dark brown and ten were black. For seed shape, twenty-one accessions were oval, three were round and four were oblong. A two-way analysis of variance (ANOVA) at $p < 0.05$ probability level was used to test the differences in morphological characteristics of the pods and seeds of the accessions. Results from means separation using Duncan Multiple Range Test (DMRT) among the accessions showed highly significant difference for fruits per bunch (NF/B); accession 28 (ACC28) had the highest mean number of 44 fruits per bunch and the highest number of seeds per bunch (NS/B) (671.00). Highly significant difference was observed for fruit weight per bunch (FW/B). ACC18 had the highest FWB (707g) while ACC40 had the least FW/B (7.75g). High significant difference among the parkia accessions for 100 seed weight (100SW) was observed. ACC30 had highest 100SW (34.00g). Significant morphological variations observed among the *P. biglobosa* accessions suggest their usefulness in making selection towards their domestication, conservation and establishment of plantations based on desired traits for commercial purposes.

Keywords: Traits; Accessions, fruit pod; seed traits *Parkia biglobosa*

PGDR018

Morphological Diversity and Trait Associations for Yield and Agronomic Characteristics in *Phaseolus vulgaris* (Common bean).

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Abstract

Phaseolus vulgaris (Common bean) is a globally cultivated annual plant primarily grown for its edible dry seeds and unripe green pods. Understanding the correlations between different traits and their effects on yield and other characteristics is vital for identifying key selection objectives. The objective of this study is to assess morphological diversity and trait associations for yield and agronomic characteristics in common bean. One hundred and twenty-six accessions of common bean were evaluated using alpha lattice design. The accessions exhibited significant ($p < 0.01$) differences for all (25) studied traits. The PCA result showed that the first three eigenvalues (PRIN1 to PRIN3 71%) contributed largely to the number of plants per accession, pod weight per plant, seed width and pod width. The genotype by traits biplot revealed that most accessions had a good performance for most of the trait measured with TPv-952, TPv-834 and TPv-882 outperforming with good seed quality traits. Hierarchical clustering based on Gower's distance using the evaluated agronomic traits produced five clusters which were based on different agronomic traits. Traits such as days to maturity ($r = 0.33$, $p < 0.001$), days to 50% flowering ($r = 0.42$, $p < 0.001$) and pod weight per plant ($r = 0.41$, $p < 0.001$) had strong and positive correlation thus, showing their potentials for yield improvement and selection. The findings revealed genetic diversity among common bean accessions, which provides a good basis for selecting superior lines for future breeding.

Keywords: Morphological diversity, Correlation, PCA, Common bean

PGDR019**Maximum Yield Potential of Some IAR Released Sunflower (*Helianthus annuus* L.) Varieties in two agro-ecological zones of Nigeria.**

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Abstract

Sunflower (*Helianthus annuus* L.) belongs to the family Asteraceae/Compositae. It is a diploid species ($2n = 2x = 34$). Sunflower is an important oilseed crop and is the preferred source of oil for use in domestic consumption and industries. Information on the recommended agronomic practices and yield stability of newly release IAR sunflower varieties is crucial for development of parental and new cultivars. The study was conducted to optimize the existing recommended production practices for yield potential of some released Sunflower varieties and to develop contents for the promotion and dissemination of the potential of some released Sunflower varieties. The experiment was conducted in Kaduna (Samaru) and Kano (Minjibir). Four sunflower released varieties (SAMSUN 1, SAMSUN 2, SAMSUN 3, and SAMSUN 4) were planted under three inter row spacing levels (20cm, 25cm and 30cm), three fertilizer levels (50:25:25, 100:50:50 and 150:75:75 of NPK 15:15:15) and three level of sprays for foliar diseases (one, twice and thrice). The experiment in each location (Samaru and Minjibir) was laid out in a split plot randomized as an RCBD with factorial main plot: Combinations of levels of Factors A (Fertilizer) and B (Spray) are assigned to main plots, levels of Factor C (Variety) and Factor D (Spacing) to subplots within each main plot. The analysis of variance revealed significant differences ($P < 0.05$) for the interaction observed for grain yield (kg/ha) Samaru. The yield value ranged from 2317.4 kg/ha for SAMSUN 3 to 150.7 kg/ha for SAMSUN 1 with an average of 1230.4 kg/ha. The highest grain yield of 2498.5 kg/ha was observed for SAMSUN 3 when fertilizer 1 (NPK 50:25:25) was applied and spaced at 30cm with two sprays under Samaru. However, the head diameter ranged from 14.9 for SAMSUN 1 to 6.4 for SAMSUN 4 with an average of 10.2. The highest head diameter was observed for SAMSUN 1 when fertilizer 1 (NPK 50:25:25) was applied and spaced at 25cm with two sprays under Samaru. The positive and highly significantly correlation ($p < 0.05$) was observed between yield with head diameter ($r = 0.47^{**}$). Similarly, plant height has positive and highly significance correlation with leaf area index ($r = 0.33^{**}$) while negatively and significance correlated with relative growth rate ($r = -0.27$) under Samaru indicates their usefulness as reliable secondary traits which could be included in base index for selection of superior sunflower genotypes across locations.

Keywords: Fertilizer rate; Spacing; Spray; Asteraceae.

PGDR020

Diversity Assessment of Yam Accessions Conserved at IITA Genetic Resources Center Using Sensory and Field Evaluation.

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Abstract

The Genetic Resources Center of the International Institute of Tropical Agriculture (IITA) maintains in *ex situ*, over 5,000 yam accessions representing eight species. This collection serves as a critical safeguard against genetic erosion and supports global food and nutritional security initiatives. While Genetic diversity and morphological characterization have been employed to assess diversity within yam species, comprehensive sensory evaluation remains limited. In this study, 100 white yam accessions, including one elite variety as a control, were evaluated to identify accessions with superior quality traits that could accelerate trait introgression into breeding programs while preserving genetic integrity. This experiment was conducted at IITA yam breeding laboratory. Descriptive traits including taste, quality, stretchability, aroma of boiled yam, and mouldability of pounded yam were assessed. Field-based evaluations were done following the International Board for Plant Genetic Resources descriptors to assess flower characteristics, sex expression, oxidation susceptibility, and flesh coloration. Data were analyzed using divergence plots and descriptive statistics using R software. Results revealed significant variation in trait performance across accessions. Cluster analysis grouped accessions into four distinct clusters based on similarity indices. Notably, 8% of evaluated accessions exhibited excellent appearance after pounding, while 13% demonstrated superior pounding quality. Four accessions were identified as particularly promising, displaying exceptional boiling and pounding characteristics. This preliminary investigation highlights exceptional accessions from the IITA-GRC yam collection with potentials for use as parental stock in crop improvement initiatives. These findings provide valuable information for yam genetic resource utilization and support evidence-based breeding strategies.

Keywords: *Genetic erosion, Sensory evaluation, Genetic diversity, yam breeding.*

PGDR021

Phenotypic and biochemical characterization of selected pearl millet (*pennisetum glaucum* L.) Seed accessions from plateau state, nigeria

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Abstract

Despite its nutritional and agronomic importance, pearl millet remains underutilized in Plateau State due to limited characterization of local seed accessions. This study aimed to address this gap by assessing the morphometric, physical, phytochemical, and proximate characteristics of three pearl millet (*Pennisetum glaucum* L.) accessions—Zhi, Imar, and Ghai—collected from different locations in Plateau State, Nigeria. Significant variation was observed among the accessions, with Imar exhibiting the greatest seed length (3.36 ± 0.02 mm) and geometric mean diameter (17.31 ± 7.25 mm), while Zhi recorded the highest bulk density (830 ± 20 kg/m³) and thousand seed weight (9.71 ± 0.25 g). Phytochemical screening showed diverse profiles, with flavonoids being most abundant in Imar, while the presence of alkaloids, saponins, and phenols varied across accessions. Proximate analysis revealed Ghai to have the highest protein content ($10.00 \pm 0.20\%$), Imar the highest crude fat ($6.87 \pm 0.09\%$) and fiber ($12.11 \pm 0.11\%$), and Zhi the highest ash content ($5.8 \pm 0.20\%$). The findings highlight the genetic and nutritional potential of local pearl millet accessions and underscore their value for future crop improvement and food security initiatives in Nigeria's semi-arid regions.

Keywords: *Phenotypic, Biochemical, Characterization, Morphometric and Alkaloid.*

PGDR022

Diversity And Character Association Of Bean Biochemical Traits Of Cocoa (*Theobroma Cacao*) Accessions In Farmers Fields From Cross Rive State, Nigeria

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Abstract

Variability in nutritional value of food crops is essential to complement agro-morphological characteristics for an overall quality improvement. This study evaluated the diversity and character association of bean biochemical traits in forty-two cacao accessions collected from farmers' fields in Cross River State, Nigeria. Using well fermented and dried bean samples, nineteen biochemical traits (proximate, minerals and phytochemicals) were analyzed following standard protocols. Results revealed significant variation ($p < 0.001$) among accessions for most biochemical traits, excluding moisture, phenolics, anthocyanins, and soluble carbohydrates. Crude fat ranged from 23% to 39%, with caloric values spanning 421.14 to 508.08 kcal/g. Alkaloid content varied widely, with the highest at 29.84 mg/g. Pearson correlation analysis revealed strong relationships among key traits, such as a positive correlation between crude fat and caloric value ($r = 0.989$), and a negative correlation between carbohydrate and caloric value ($r = -0.944$). Principal component analysis indicated that eight components explained 74.2% of the total variation, with proximate traits loading heavily on the first axis, and phytochemicals and minerals dominating subsequent axes. accessions NDE-IKO-SC, IKO-IKO-SC and AEB-BOK-TLB showed superiority in crude fat and caloric value. The 42 cacao accessions formed two major clusters with ten groups, revealing distinct genetic relationships between farmers' accessions and elite CRIN accessions across clusters. This study reveals significant biochemical diversity in Nigerian cacao, influenced by genotype and environment, supporting the selection of superior parental lines for breeding. It provides a baseline for future research and underscores the value of conserving on-farm genetic diversity.

Keywords: *Cocoa; Farmers' field; Genetic diversity; Minerals; Proximate; Phytochemicals*

PGDR023

Enhancing Agronomic Performance and Seed Quality of Snake Tomato (*Trichosanthes cucumerina* L.) through Soil Amendments

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Abstract

Snake tomato (*Trichosanthes cucumerina* L.) is an underutilized crop with significant nutritional and medicinal value, particularly in tropical regions. Despite its potential, its cultivation is limited by climate change and lack of agronomic optimizations. This study investigates the effects of different soil amendments—biochar, poultry manure, and NPK fertilizer—on the growth, yield, and seed physiological traits of snake tomato grown in a degraded Alfisol. A randomized complete block design was employed with six treatment groups, including combinations of organic and inorganic inputs. Key parameters assessed included vine length, leaf number, fruit weight, seed germination rate, and seedling vigour index. Data were analyzed using ANOVA, Fisher's LSD, and Spearman's correlation. Results revealed that poultry manure significantly enhanced vegetative growth and fruit yield compared to other treatments. Seeds from poultry manure-treated plants also exhibited superior germination and vigour, indicating improved physiological quality. The combination of biochar and poultry manure showed synergistic effects, further boosting performance metrics. Correlation analysis demonstrated strong positive relationships between fruit yield and seed vigour traits, suggesting that agronomic improvements directly influence reproductive success. These findings highlight the efficacy of organic amendments, particularly poultry manure, in revitalizing degraded soils and enhancing the productivity of snake tomato. The study supports the adoption of sustainable soil management practices as climate change mitigating approach to promote the commercial viability of this crop, contributing to food security and agricultural diversification in tropical regions.

Keywords: Biochar, seed vigour, snake tomato, soil amendment, sustainable agriculture.

PGDR024

Characterizing Retting Ability in Cassava Germplasm: Unlocking Diversity for Breeding Improvement

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Abstract

Cassava (*Manihot esculenta*) is a key crop for food security in tropical regions, where efficient processing is crucial for household and industrial use. One important step in cassava processing is retting, a fermentation process that softens the roots and affects the quality of end products like fufu. However, the variation in retting ability (especially retting time) across different cassava types remains poorly understood, limiting breeding efforts to improve processing traits. Using a single-row trial design, this study evaluated 600 cassava genotypes over two cropping seasons (2021/2022 and 2022/2023) in Ibadan, Nigeria. For each genotype, 5 kg of roots were fermented in water for 5 days, and the softness of the roots was scored on a 5-point scale (1 = hard, 5 = extremely soft). After fermentation, the retted mash was sieved to remove fibers, dewatered, pressed, oven-dried, and weighed for further analysis. Significant differences ($P < 0.05$) were observed among genotypes for traits such as fresh root yield, retting time, pH, fufu dried weight, and fiber content. Moderate heritability was found for fufu pressed weight (0.33), dried weight (0.35), and fiber weight (0.39), suggesting potential for genetic improvement. Positive correlations were observed between starch weight and fufu pressed weight ($r = 0.35$), and between retting time and foaming ability ($r = 0.22$), while retting time was negatively correlated with fufu fiber weight ($r = -0.18$). Five genotypes TMS21F1204P0026, TMS21F1915P0001, TMS21F1674P0008, TMS21F1383P0037, and TMS21F1502P0007 showed superior retting ability, high fufu yield, and low fiber content, making them strong candidates for breeding programs targeting improved fufu processing efficiency.

Keywords: Retting, Fufu, Fibre content, Softness scale, Retting time

PGDR025

Genetic Variability, Heritability, and Inter-Traits Correlation for Yield and Agronomic Traits in Winged Bean

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Abstract

The Winged bean (*Psophocarpustetragonolobus*(L.) DC.) is a multipurpose, valuable, nutritious crop that can help alleviate nutritional and food insecurity, yet remains underutilized due to the lack of high-yielding varieties. Evaluating genetic variability and understanding inter-traits relationships is essential for breeding high-yielding winged bean varieties. This study aimed to assess genetic variability, heritability, and inter-traits correlation for yield and agronomic traits in the winged bean. One hundred and ten accessions of winged bean were evaluated over two years using an 11 by 10 alpha lattice design with three replications in four locations. Significant variation ($P < .001$) was observed for all studied traits. Higher values of the genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and environmental coefficient of variability (ECV) were recorded for total seed weight (TSW) (kg) (12.33%, 72.33% and 71.13%), as well as the total pod weight (TPDW) (kg) (9.93%, 68% and 67.27%), and number of seeds per plant (NSPP) (9.38%, 54.45%, and 53.63%). Higher broad-sense heritability (h^2) estimates were observed for the pod length (PL) (87.56%), fifty percent flower (FPF) (84.98%), and pod weight (PW) (78.86%). Traits such as seed weight per plant, pod weight per plant, number of seeds per pod, and number of pods per plant showed strong positive correlations, indicating their importance as selection criteria for yield improvement. These results indicate substantial genetic variability among the accessions, highlighting the potential for selecting promising lines for future winged bean breeding programs.

Keywords: Genetic variability, Heritability, Correlation, Winged bean

PGDR026

Genetic Profiling in Tuber Quality Evaluation of Breeding Lines and Market Variety of White Guinea Yam (*Dioscorea rotundata*)

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Abstract

White Guinea yam (*Dioscorea rotundata*) is a staple crop highly contributing to food security across the tropical zone especially in West Africa. A gap exists in connecting genetic diversity to tuber quality traits, which this study aimed to address using SNP-based genetic profiling combined with nutritional evaluation. In this study, we evaluated the performance of 16 white Guinea yam genotypes from IITA, Ibadan based on sensory, tuber quality with genomic data integrated. Tuber quality evaluation included physical traits such as Lightness(L*), Red-Green axis(a*), Yellowness(b*), whiteness index, oxidative browning index, tuber shape, surface cracking, texture, tuber surface hairiness), agronomic traits (yield, virus severity, anthracnose incidence, and fresh tuber weight), proximate traits (moisture, ash, protein, and dry matter), and functional traits (water and oil absorption capacity, swelling power). Additionally, sensory attributes (taste, aroma, mealiness, texture) of boiled and pounded yam were assessed by a trained panel. Significant genotype effects ($p < 0.01$) were found for most colour and functional traits, indicating strong genetic influence. Protein and dry matter varied significantly ($p < 0.05$), supporting their use in selection for processing. Hierarchical clustering grouped the genotypes into three clusters based on genetic and nutritional data. The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) identified TDr1756023 (MGIDI=3.42) and TDr1756057 (MGIDI=4.26) as the most ideal genotypes for breeding advancement. These findings provide a practical framework for breeders to select superior yam genotypes with enhanced nutritional and agronomic traits, supporting efforts to improve food security and market value in West Africa.

Keywords: Yam breeding, Tuber quality, Genetic diversity, Sensory evaluation, MGIDI index

PGDR027

Uncovering Indigenous Diversity in Pigeon pea (*Cajanuscajan*): Insights from Germplasm Exploration and Digital Phenotyping for Climate-Smart Breeding

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Abstract

Pigeon pea (*Cajanuscajan*) remains one of Africa's underutilized legumes, despite its significant potential for climate resilience, food diversification, and nutritional security. A national germplasm exploration was conducted between February and June 2025 across 18 Nigerian states, representing the agro-ecological zones. The goal was to collect, document, characterize, and conserve indigenous cultivars along with associated ethnobotanical knowledge. One hundred seventy-three (173) accessions were collected from farmers' fields and local markets, supplemented by 100 accessions from the IITA genebank, as well as from Ghana, the Benin Republic, and the Gambia. Capturing agro-ecological and morphological diversity, farmers shared insights on planting seasons, intercropping practices, vernacular names (e.g., *Otili*, *Fiofio*, *Waken Gwari*), and important culinary and medicinal uses. Evidence of transboundary seed exchange was detected in border communities in Ogun State, reflecting historical ties with the Benin Republic and contributing to regional genetic diversity. All 273 accessions were characterized using seed morphometric data obtained from the VideometerLab4 multispectral imaging device. The analysis revealed significant variation in seed shape, size, and surface features. Traits such as seed area (14.91–39.89 mm²), length (4.23–7.92 mm), and perimeter (13.60–21.70 mm) revealed moderate phenotypic variability. Additionally, shape descriptors such as compactness (0.79–0.98) and eccentricity (0.16–0.78) reflected both rounded and elongated seed types, while color component (CIELab_A) values ranged from –6.02 to 39.45, highlighting pigmentation differences. The principal component analysis (PCA) showed that the first two components explained 67.1% of the total variation, primarily driven by seed size and shape. Cluster analysis grouped the accessions into four distinct morphotypes. This study provides a foundational dataset for pigeon pea improvement, supporting selection for seed quality, market preferences, and climate-smart adaptation, suitable for diverse market segments across sub-Saharan Africa.

Keywords: pigeon pea, underutilized legume, germplasm, exploration, diversity

PGDR028

Genetic variability for agronomic traits of groundnut (*arachis hypogaea* L.) Genotypes in keffi, nasarawa state north central nigeria

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Abstract

Groundnut (*Arachis hypogaea* L.) is one of the most important legume crops worldwide, in terms of production and consumption. Farmers in Nigeria grow groundnut primarily as cash crop and for consumption, also as plant protein components of their diets. For a breeding program to be productive and successful, genetic variety is a requirement, with the intention to enhance the crop plants yield, adaptation to stresses and peculiarity in a farming system. The trial of this study, evaluating the genetic variability in groundnut genotypes, was conducted in Keffi, Nasarawa state. Five (5) improved varieties were sourced from Institutes of Agricultural Research (IAR) Zaria, and two land races from Keffi. Twenty-four (24) pots, each having a radius of 30cm, and height of 40 cm were used for the experiment. Data collected was subjected to Analysis of Variance (ANOVA) and mean calculated using least significant difference (LSD). The study looked at plant growth, measured by variability in height, number of leaves, leaf area, and number of days to flowering. It also looked at plant yield measured by variability in number of pods, pod yield, kernel yield and 100 kernel weight. Measurements and readings were taken at 3 weeks, 6 weeks and 9 weeks after sowing. Results showed that Samnut 23, 24 and 26 performed well and showed significant relationship to all the variables at 5 percent level. The two local varieties, Jamar and Roko showed no significant correlation with the plant growth and yield parameters. The study is of the view that breeding programs to improve the traits in the local varieties be instituted by the relevant institutions, universities and research institutes. It further recommended introducing the Samnut 23, 24 and 26 to farmers and other users for increased production and income in the area of study. The study also holds the opinion that the local names of the local varieties whose trait are to be improved upon, be maintained for easy identification by farmers.

Keywords: *Genetic variability, Groundnut (*Arachis hypogaea* L.), Agronomic traits*



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**Innovative and Sustainable Food Systems for a Safe:
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ISFSSE 001

Phenotypic and biochemical characterization of selected pearl millet (*pennisetum glaucum* L.) Seed accessions from plateau state, Nigeria

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Abstract

Despite its nutritional and agronomic importance, pearl millet remains underutilized in Plateau State due to limited characterization of local seed accessions. This study aimed to address this gap by assessing the morphometric, physical, phytochemical, and proximate characteristics of three pearl millet (*Pennisetum glaucum* L.) accessions—Zhi, Imar, and Ghai—collected from different locations in Plateau State, Nigeria. Significant variation was observed among the accessions, with Imar exhibiting the greatest seed length (3.36 ± 0.02 mm) and geometric mean diameter (17.31 ± 7.25 mm), while Zhi recorded the highest bulk density (830 ± 20 kg/m³) and thousand seed weight (9.71 ± 0.25 g). Phytochemical screening showed diverse profiles, with flavonoids being most abundant in Imar, while the presence of alkaloids, saponins, and phenols varied across accessions. Proximate analysis revealed Ghai to have the highest protein content ($10.00 \pm 0.20\%$), Imar the highest crude fat ($6.87 \pm 0.09\%$) and fiber ($12.11 \pm 0.11\%$), and Zhi the highest ash content ($5.8 \pm 0.20\%$). The findings highlight the genetic and nutritional potential of local pearl millet accessions and underscore their value for future crop improvement and food security initiatives in Nigeria's semi-arid regions.

ISFSSE 002

Computational Screening of Plant-Based Ligands Targeting *Fusarium* Pathogenic Enzymes: Supporting Breeding Strategies for *Fusarium* Resistance in Wheat

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Abstract

Fusarium graminearum, an aggressive and highly virulent phytopathogen, poses a significant threat to wheat production by infecting spikes during anthesis, culminating in grain deterioration and the biosynthesis of hazardous trichothecene mycotoxins. This study employed a structure-based virtual screening approach to identify plant-derived bioactive compounds capable of inhibiting critical virulence-associated proteins of *Fusarium*. Twenty-one phytochemicals were docked against three validated molecular targets, Tri5 (trichodiene synthase), Tri4 (cytochrome P450 monooxygenase), and CAMK1 (calmodulin-dependent kinase), using PyRx with AutoDock Vina scoring. Top-performing ligands, including solanine (−9.7 kcal/mol), sanguinarine (−9.7 kcal/mol), and quercetin (−7.4 kcal/mol), demonstrated high binding affinities and stable interactions with active site residues. In silico ADMET profiling indicated favorable absorption, low toxicity, and pharmacokinetic viability for several compounds, while phylogenetic analysis revealed strong evolutionary conservation of the target proteins across *Fusarium* species, reinforcing their suitability as broad-spectrum antifungal targets. The results highlight the effectiveness of integrative computational approaches in identifying potent antifungal candidates and provide molecular evidence to support the development of *Fusarium*-resistant wheat through targeted breeding strategies.

Keywords: *Fusarium graminearum*, Molecular docking, Natural antifungal compounds, ADMET profiling, Phylogenetic analysis.

ISFSSE 003

Public Perception and Acceptance of Genetically Modified (GM) Crops in Plateau State

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Abstract

Amid global efforts to enhance food security and agricultural resilience, genetically modified (GM) crops have gained prominence as a potential solution. However, their acceptance remains subject to public perception, influenced by a complex interplay of sociocultural, religion believes, educational, and informational factors. This study assessed public perception and acceptance of GM crops in Plateau State, Nigeria, through a well-structured, anonymous online survey distributed via Google Forms. Findings revealed that 73.2% of respondents had prior awareness of GM crops, yet knowledge levels varied, with only 28.8% self-identifying as very knowledgeable. While 44.8% perceived GM crops as safe, a substantial proportion expressed ambivalence or concern, largely driven by perceived health and environmental risks. Factors such as scientific evidence, government regulation, and endorsement by trusted organizations were identified as critical influences on acceptance. Media was regarded as a significant driver of public opinion (59.6% rated it as influential), while nearly half of the respondents (48.8%) indicated that educational resources on GM crops were insufficient. Although a cross-tabulation between education level and acceptance did not yield statistically significant differences. The findings stress the critical need for targeted public education, transparent regulatory communication, inclusive policy development, and sustained stakeholder engagement to bridge the gap between scientific innovation and public trust in the adoption of genetically modified crops in Nigeria.

ISFSSE 004

Evaluation of Farmers' Preferred Traits Across Gender in Nigeria: Implications for Yam Breeding

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Abstract

Understanding gender-specific preferences in yam traits is essential for developing varieties that meet the diverse needs of Nigerian farmers. This study evaluates the traits prioritized by male and female yam farmers across multiple agro-ecological zones in Nigeria and explores how these preferences can inform demand-led breeding strategies. A total of three hundred and twenty (320) yam farmers from eight states in Nigeria, were randomly selected using a multi-stage random sampling approach. A 5-point Likert scale was utilized to evaluate the data and identify the main traits that farmers consider when selecting yam varieties. The findings reveal significant gender-based differences in trait prioritization, which have implications for varietal adoption, food security, and inclusive agricultural development. Specifically, male farmers tended to prefer yam varieties with good pounding quality, high germination rates, and large tuber sizes. In contrast, female farmers favored varieties that have high tuber yields, good storage quality, and early maturity. The primary constraints limiting yam production in Nigeria include pest and disease attacks, climate change, the high cost of seed yams, expensive staking, and weed infestation. To enhance acceptance and improve food security in Nigeria, there must be a concerted effort to consider these farmers' desired yam traits and incorporate them into the development of improved yam varieties.

Keywords: *Farmers, Yam, Preferred traits, Gender, breeding*

ISFSSE 005

Effect Of Drying Methods On The Nutrient And Phytochemical Composition Of Bitter Leaf (*Vernonia Amygdalina* Del)

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Physical oral

Abstract

Vegetables are normally obtained as the fresh parts of plants which when consumed as raw, cooked, or processed in some other ways, provide suitable human nutrition. One of the most efficient ways to preserve vegetables is by drying. The study investigated the effects of three different drying methods on nutrient and phytochemical compositions of *Vernonia amygdalina* harvested from farms within Umudike Oboro, in Ikwuano L.G.A Abia State. The leaves were washed and air dried for 1 hour to reduce excess water and were divided into 3 parts and subjected to 3 different drying methods (sun, oven and microwave). The dried leaves were ground to powdered form and used for analysis. Proximate, mineral, vitamin and phytochemical composition analysis were carried out on the leaves. The result obtained showed that the moisture, ash, fat, fibre, protein and carbohydrate content of the leaves ranged from 10.35 - 12.10%, 10.40 - 11.20%, 1.60 - 2.40%, 15.55 - 18.20%, 19.45 - 21.93 and 36.08 - 39.83% respectively. The result of the mineral content of the microwave-dried leaf was found to be higher than that of sun-drying and oven-drying. Values obtained for calcium ranged from 31.45 - 42.05 mg/100g, for magnesium it ranged from 31.67 - 40.79 mg/100g, sodium, potassium and phosphorus ranged from 16.39 - 20.13 mg/100g, 28.93 - 34.78 mg/100g and 41.39 - 49.13 mg/100g respectively. The vitamin B₁, B₂, B₃ and C content recorded ranged from 0.17 - 0.27 mg/100g, 0.27 - 0.48 mg/100g, 0.31 - 0.74 mg/100g and 10.76 - 15.10 mg/100g respectively. The phytochemical content of the dried leaves differed significantly as a result of the difference in the drying methods employed. Values obtained for tannin ranged 6.76 - 9.33 mg/g, for phenol, it ranged from 1.78 - 3.59 mg/g, alkaloid, flavonoid and saponin content ranged from 5.24 - 8.14 mg/g, 5.21 - 7.90 mg/g and 1.34 - 2.42 mg/g respectively. Oven dried and microwave dried had the highest and least value respectively in all the phytochemical constituents. From the result obtained from this study, it was observed that drying bitter leaf with microwave enhanced the nutritional, but reduced the phytochemical quality more than the other methods investigated, hence the study recommends microwave drying as the suitable method to be employed in the drying of bitter leaf and other vegetables.

Keywords: Drying techniques, Phytochemical composition, Proximate analysis, Nutritional profile, *Vernonia amygdalina*

ISFSSE 006

Improving Cassava Food Product Quality through Genetic Trait Selection

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Abstract

Integrating end-user quality traits into breeding programs, particularly sensory characteristics, is important for enhancing the adoption of improved crop varieties. This study focused on cassava food products, evaluating 254 progenies from six families of a nested association mapping population and seven parental lines for five key sensory traits of gari, a popular cassava product. Sensory attributes such as mouldability, hardness, smoothness, stickiness, stretchability, and color influence consumer acceptability. Using the quantitative descriptive analysis (QDA) for sensory evaluation and the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) analysis, this research assessed sensory traits interrelationship and identified superior genotypes. The results showed high genetic variances for color, hardness, stickiness, and mouldability, indicating strong potential for genetic improvement. Positive correlations were observed between mouldability and hardness, and between stickiness and smoothness. On the other hand, negative correlations were found between gari/eba colour and stretchability, and between mouldability and stickiness/stretchability. Among the top 25 selected accessions, TMS23F1018P0068 and TMS23F1020P0095 emerged as the best genotypes, associated with different traits. TMS23F1018P0068 correlated with textural properties (smoothness, stretchability, hardness), while TMS23F1020P0095 was linked to gari/eba color. This highlights the importance of integrating multiple sensory attributes in cassava breeding to meet diverse consumer preferences.

Keywords: *Gari quality, Multi-trait selection, Genetic improvement*

ISFSSE 007

Comparison of the Performance of Biotech Potatoes and Their Near-Isogenic Lines in Different Environments in Nigeria

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Abstract

This study was part of a regulatory trial evaluating the agronomic performance of biotech potato events carrying a 3 R-gene stack for late blight resistance, compared to their near-isogenic lines, under environments with low or no late blight pressure. The objective was to determine whether the insertion of resistance genes compromised tuber yield in the absence of disease. Trials were conducted across six environments in three locations (Bokkos, Kuru, and Kusuku) during the 2024 rainy and 2024/2025 dry season. Weekly fungicide applications during the rainy season effectively suppressed late blight, while dry-season trials benefited from naturally low disease pressure due to low relative humidity. Genotypes included biotech events DIA MSU-015, DIA MSU-255, Sha 105, and Vic 185; their near-isogenic lines (Diamant, Shangi, Victoria); and a check variety (Marabel). ANOVA revealed highly significant effects of genotype, environment, and genotype $\times$ environment interaction on tuber yield ($p < 0.01$). Mean yields showed that DIA MSU-015 (20.68 t/ha) and Vic 185 (21.44 t/ha) significantly outyielded their near-isogenic lines Diamant (18.14 t/ha) and Victoria (18.86 t/ha), respectively ($p < 0.05$). Sha 105 (20.13 t/ha) and DIA MSU-255 (18.23 t/ha) yielded comparably to Shangi (19.43 t/ha) and Diamant, with no significant differences. Marabel had the highest mean yield (22.17 t/ha) but displayed greater environmental sensitivity. PCA and GGE biplot analyses confirmed the yield stability and adaptability of several biotech events. These findings suggest that biotech potatoes maintain competitive yields under minimal late blight pressure, supporting their biosafety and suitability for release in Nigeria.

Keywords: *biotech potato, regulatory trial, late blight, yield stability, near-isogenic lines*

ISFSSE 008

Phenotypic Performance of Cowpea (*Vigna unguiculata* L. Walp) Cultivars under Different Insect Pest Control Methods

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Abstract

Cowpea production in Nigeria's derived savanna is constrained by photoperiod sensitivity and severe insect pest infestations, particularly during the rainy season. This study sought to identify a photoperiod-insensitive cowpea cultivar, evaluate genetic variability, assess the effects of different insect pest control methods (IPCMs) on phenotypic traits of cowpea cultivars, and analyze the relationships among these traits. Four (4) cowpea cultivars were evaluated under synthetic and botanical (neem, bitter leaf + pepper extracts) pest control methods from April to July, 2025 at Landmark University, Omu-Aran, Kwara State. The treatment combinations were assessed using a split-plot arrangement in a randomized complete block design with three replications. None of the cultivars flowered during the study, indicating photoperiod sensitivity. However, significant differences ($P < 0.01$) were observed among cultivars for plant height, number of leaves, and number of branches, though pest control methods did not significantly affect these traits. Sampea 14 consistently recorded the highest values for the three traits across IPCMs, showing superior vegetative performance. Both synthetic insecticide and neem extract had the most positive effect on plant traits, with neem extract performing comparably to the synthetic chemical, suggesting its potential as a sustainable alternative. Equally, strong positive correlations ($r = 0.83\text{--}0.87$, $P < 0.001$) among the three traits indicate they can be used interchangeably in selection. Although no photoperiod-insensitive cultivar was found, Sampea 14 and neem extract are recommended for further studies under shorter photoperiods to assess the effect of neem extract on the cowpea grain yield in this agroecology.

Keywords: cowpea cultivars, phenotypic performance, synthetic insecticide, neem extract, derived savanna agroecology of Nigeria.

ISFSSE 009

Kinetic analysis of heavy metal removal by sunflower (*helianthus annuus* L.) and African spinach (*amaranthus hybridus* L.) From Contaminated SoilSaidu Haruna¹, Mohammed Jibrin Ndejiko², Abubakar Raliya Babayo¹, Muhammed Kabiru¹¹Department of Biological Sciences, Faculty of Science, Gombe State University, Gombe, Nigeria;²Department of Microbiology, Ibrahim. Badamasi Babangida University, Lapai Niger State, Nigeria;Corresponding author's email address: saiduharunn@gmail.com; 07065440943

Abstract

Soil located in industrialized regions is more prone to heavy metal pollution. Long term application of heavy metals in soil causes decline in soil microbial activity, and groundwater contamination. This study was aimed at determining the heavy metal removal potential of *Helianthus annuus* L. and *Amaranthus hybridus* L. plants from the soil. The soil was collected via pretreatment and sorting method. Phyto-removal of three heavy metals namely lead, copper and chromium were assessed at different concentrations of 1.5, 2.0 and 2.5 g/dm³ respectively. The percentage removal efficiency of Cu, Cr, and Pb in leaves, stem and root were found to be highest in 2.5 concentration accounting for 91, 82, 99% (leaves), followed by 94, 89 and 94% (stem) and 99, 99 and 94% (root) respectively. Similarly, for *Amaranthus* plant, 2.5 Concentration gave the highest removal efficiency of 98, 93 and 99% (leaves), 92, 36, and 96 (stem) and 91, 85 and 95% (root) removal respectively. Results of the Venn diagram showed that both plants intersect, while accumulating lead in root and leaves of the plants. It was observed that both plants absorbed more chromium than copper and lead. Results of translocation factor suggested that these plants could transport metals actively via root to stem than root to leaves, thereby proposing *Helianthus annuus* L and *Amaranthus hybridus* plants for phytoremediation because of its efficiency to remove heavy metals.

Keywords: Heavy metal, Venn diagram, plants, translocation factor, pollution

ISFSSE 010

Comparative Analysis of Local and Imported Substrate in Semi-autotrophic Hydroponics System for Seed Yam Production

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Abstract

Yam production is hindered by low multiplication rates, compounded by the dual use of tubers as both food and seed. While semi-autotrophic hydroponics has shown promise in rapidly multiplying true-to-type disease-free yam plantlets, the substrates used in existing systems are often imported. This study aims to evaluate the effectiveness of locally sourced commercial substrates in semi-autotrophic hydroponics for yam production. Single-node cuttings of three varieties of white yams (Favourite, Asiedu, and Super) were cultured in three substrates (Cocopeat, Klasmann, and Cocogro) and fertigated with Miracle-Gro for 9 weeks. The experiment was a 3 (varieties) × 3 (substrates) factorial arranged in a completely randomized design and replicated three times. Data was taken on plant height (PH), number of nodes (NoN), and number of roots (NoR). All data were analysed using ANOVA, and means were separated using LSD (0.05). The PH, NoN, and NoR differed significantly among the varieties, and ranged from 3.10±0.44 (Super) to 10.84±0.44 (Asiedu), 1.56±0.20 (Super) to 5.93±0.20 (Asiedu), and 2.90±0.13 (Super) to 8.48±0.44 (Asiedu). The PH, NoN, and NoR differed significantly among the substrates and ranged from 6.82±0.44 (Cocopeat) to 7.71±0.44 (Cocogro), 3.37±0.20 (Cocopeat) to 4.36±0.20 (Cocogro), and 4.03±0.13 (Cocogro) to 4.78±0.13 (Klasmann). The interaction between variety and substrate was significant on the NoR, ranging from 2.60±2.42 (Super, Cocogro) to 6.78±1.33 (Favourite, Klasmann). Asiedu produced higher multiplication rate compared to other varieties, while Cocogro supported the growth of the varieties better than the imported substrate.

Keywords: *Semi-autotrophic hydroponics system; Dioscorea rotundata; Micropropagation; Subculturing.*

ISFSSE011

Evaluation of agronomic performance of fall armyworm (*Spodoptera frugiperda*) resistant maize hybrids in the Derived savanna agro-ecology of Nigeria

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Abstract

Maize production in Nigeria has increased since 2010, yet significant challenges persist due to biotic and abiotic stresses, notably the fall armyworm (FAW) insect pest. Fall armyworm-resistant (FAWR) maize hybrids have been developed across Africa, but their performance and adaptability require evaluation across Nigeria's agro-ecological zones. This study assessed the agronomic performance of FAWR maize hybrids, relationships between grain yield and agronomic traits, and the selection of superior hybrids adapted to the derived savanna agroecology of Nigeria based on genotype by yield×trait analysis. Twenty-six FAWR maize hybrids and six commercial checks were obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, and evaluated using an 8 × 4 α -lattice design with three replications at the teaching and research farms of Ladoké Akintola University of Technology, Ogbomoso, and Ajayi Crowther University, Oyo, Nigeria. Agronomic data were collected at key growth stages and analyzed using R statistical software v4.4.2. Significant ($p < 0.001$) phenotypic differences were observed among hybrids for grain yield, ear height, plant aspect, ear aspect, southern corn leaf blight, and FAW damage at 8 and 12 weeks after planting. Notably, FAWSYN-1/(TZLComp. 1 C6-W-39-1-1)-B-B), Oba Super 11, FAWSYN-2/(TZLComp. 1 C6-W-39-1-1)-B-B, FAWSYN-1/IITATZI2305, and FAWSYN-1/TZISTR1121 exhibited superior performance, combining high yield with desirable agronomic traits and low FAW damage. Across the environments, FAWSYN-1/(TZLComp. 1 C6-W-39-1-1)-B-B) followed closely by FAWSYN-2/(TZLComp. 1 C6-W-39-1-1)-B-B and FAWSYN-1/IITATZI2305 recorded the highest grain yield. These superior hybrids are recommended for further multi-location testing across diverse agro-ecologies in Nigeria before their release to farmers.

Keywords: Fall armyworm resistance, maize hybrids, trait selection, variation, Genotype by yield×trait biplot

ISFSSE012

Soil assessment of selected communities in okitipupa local government area of ondo state nigeria, to determine efficiency for commercial cassava production.

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Abstract

The soil is polluted as a result of different human activities. Farming activities could also lead to soil disruption, degradation and change of soil properties due to nutrient loss/imbalance by erosion and crop removal resulting to a decline in soil fertility. Soil analysis was carried out to assess the physico-chemical qualities of the soils and identify the microbial presence in the study areas. Twelve composite soil samples were taken from 0 - 15cm (top soil) and 15 - 30cm (sub soil), homogenized and analysed in a laboratory. The soil pH values ranged from 5.5 (IGBS1) to 6.5 (IGBS7) in Igbotako, and 6.0 (ODSS11) to 6.7 (ODSS10) in Ode-Aye. The least soil porosity was observed at Igbotako Site 3 (IGBS3) with porosity of 9% and highest (40%) at Igbotako Site1 (IGBS1). Moisture content ranged from 5.8% (IGBS4) to 6.8% (IGBS1) in Igbotako and 5.9% (ODSS9) to 7.0% (ODSS11&ODSS12) in Ode-Aye. Soil Anions were moderate with sulphate (SO_4^{2-}) highest (47.1 mg/kg) at IGB S6. Soil Cations were low to moderate with potassium (K^{2+}) highest (72.5 mg/kg) at IGB S1. Heavy Metals (Pb^{2+} , Ni, As and Cd) were not detected in all samples from both locations. Zinc (Zn^{2+}) concentration in the soils ranged between 0.99 – 3.5mg/kg, with the least value (0.99mg/kg) at IGB S2 and the highest value (3.5mg/kg) at ODS S8. Organic matter was found in small amounts. Samples showed presence of Total Heterotrophic Bacteria (THB), its count ranged from 1.0×10^2 cfu/ml to 4.0×10^6 cfu/ml, with other soil microbes present. E. coli was not detected in all samples across various sites. The soils in both locations are healthy ie., contain nutrients that support crop growth but will require extra enhancement through fertilizer application for increased cassava production.

Keywords: Soil Analysis, Physico-chemical, Heterotrophic Bacteria, Coliform, Cassava production

ISFSSE013

Genetic variability of finger millet (*eleusine coracana*) accessions.

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Abstract

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important cereal crop widely cultivated in arid and semi-arid regions of Africa and Asia. Understanding its genetic variability is crucial for breeding programs aimed at improving yield, stress tolerance, and nutritional quality. This study assessed the genetic diversity of 25 finger millet accessions obtained from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, and Plateau State, Nigeria. Field evaluations were conducted at the National Cereal Research Institute, Riyom substation, during the 2022 and 2023 cropping seasons, using a Randomized Complete Block Design (RCBD) with three replicates. Data were collected on 12 agro-morphological traits, and phenotypic variation was analyzed using analysis of variance and principal component analysis (PCA). Significant differences ($p < 0.05$) were observed among accessions for all traits measured. Accession LV1 consistently exhibited superior performance, recording the tallest plant height (102.35 cm), highest plant height at maturity (131.10 cm), and strong performance in yield-related traits. Conversely, accessions such as GULUE and ETIYO BROWN displayed shorter statures, likely reflecting early maturity. PCA revealed that the first six principal component axes accounted for 77.30% of the total variation. The findings indicate substantial genetic variability among the tested accessions, providing opportunities for crop improvement. Promising genotypes, particularly those with high yield potential, should be advanced to multilocal and advanced yield trials to identify uniform, high-performing lines for incorporation into future breeding and selection programs.

Keywords: Genetic diversity, Agro-morphological traits, Breeding programs.

ISFSSE014

Genetics of Nitrogen Use Efficiency in Cassava

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Abstract

Cassava is an important food security crop; it is a reliable food source and highly resistant to drought, ensuring a stable food supply even when other crops fail due to climate variability. Low nitrogen (N) stress remains a significant constraint to cassava production. Enhancing nitrogen use efficiency (NUE) in cassava is essential for improving system resilience, promoting sustainable intensification, and mitigating the economic and environmental costs associated with N fertilisation in cassava-based production systems. This study aimed to develop cassava varieties with enhanced nitrogen use efficiency (NUE) by identifying genomic regions and candidate genes associated with NUE. A genome-wide association study (GWAS) was conducted using the Genome Association and Prediction Integrated Tool (GAPIT) on a panel of 265 diverse cassava genotypes. These genotypes were phenotyped for 10 physiological and agronomic traits under both optimum and low-nitrogen conditions. Whole-genome genotyping was performed using the Diversity Arrays Technology sequencing platform (DArTseq), yielding 68,814 single-nucleotide polymorphisms (SNPs) distributed across the 18 cassava chromosomes. Fifty-two SNPs were significantly associated with NUE and yield-related traits. The putative genes identified through GWAS, particularly those with significantly associated SNP markers, represent valuable targets for marker-assisted selection to develop cassava varieties with enhanced nitrogen use efficiency (NUE). Such improvements can potentially reduce reliance on exogenous nitrogen inputs, thereby mitigating their adverse environmental impacts and promoting sustainability.

Keywords: *Cassava, GWAS, SNPs, Nitrogen use efficiency (NUE).*

ISFSSE015

PBR Cowpea in Food Systems Development in Africa: Delivery for Impact and the Next Stream of Products.

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Abstract

Over 200 million people in Africa depend on cowpea as a major source of protein and nutrition, yet the crop faces devastating losses from insect pests, with *Maruca vitrata* alone causing over 80% yield reduction. The absence of natural resistance in cowpea germplasm made biotechnology the most effective solution, leading to the development of pod borer resistant (PBR) cowpea through a public-private partnership involving institutions in Africa, Australia, and the United States. Using the Cry1Ab gene, the first PBR cowpea varieties were released as SAMPEA 20-T in Nigeria in 2019 and Songotra in Ghana in 2023. On farmers' fields, yields increased from about 200 kg/ha under traditional practices to 0.8–1.0 t/ha, with potential to reach 2.0 t/ha under improved agronomic management. Farmers now spray insecticides only twice per season instead of 8–10 times, reducing production costs while lowering risks to health and the environment. To expand adoption, the Bt trait has been introgressed into farmer-preferred varieties, with two candidate lines in Nigeria and four in Ghana close to release. Stewardship plans, including insect resistance management and seed quality monitoring, confirm over 99% trait stability under field conditions. Seed system capacities have been strengthened to deliver 500 tons of certified seed annually, with output expected to double by 2026. In addition, a molecular stack combining Cry1Ab and Cry2Ab has been developed, with a lead event identified for deregulation. PBR cowpea is therefore a breakthrough innovation that enhances food security, supports sustainable farming, and improves livelihoods across Africa.

Keywords: *Cowpea, Biotechnology, Food security, Pod borer resistance, Seed systems.*

Sub-Theme 4

**Climate Adaptation Strategies for Sustainable Food
Security**

(CASSFS)

CASSFS 001

Morphological, Physiological, and Biochemical Evaluation of Drought Tolerance in Selected Accessions of African Yam Bea (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich Harms)

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Abstract

Drought stress poses a major constraint to agricultural productivity, adversely affecting plant growth, physiology, and yield. This study evaluated the drought tolerance of nine accessions of African Yam Bean (AYB) (*Sphenostylis stenocarpa*), a nutrient-rich legume with potential to enhance food security in drought-prone regions. The experiment was conducted using standard methods in a screenhouse under a completely randomized design (CRD), with plants subjected to three drought treatments: control, mild drought, and severe drought. Morphological, physiological, biochemical, and growth traits were assessed. Significant reductions ($p \leq 0.05$) were observed in morphological traits under drought stress. Plant height decreased in Ohong (33.3 cm) and Ediba (28.7 cm) relative to control values of 41.3 cm and 29.7 cm, respectively. Leaf area declined in Gakem (32.4 cm²) and Wula (21.3 cm²). Shoot fresh weight dropped in Okpoma (1.4 g) and Adadama (1.6 g) from 4.2 g and 3.8 g, respectively. While most accessions recorded negative relative growth rates (RGR), Ediba maintained a positive RGR (0.002). Ediba and Ohong also exhibited higher peroxidase and catalase activities, while Ukwel and Gakem showed the lowest. Root-to-shoot ratio increased under severe drought, with Ohong (0.36) and Okpoma (0.27) showing the highest adjustments. Drought stress response indices (DSRIs) identified Ediba (10.42) and Ohong (10.54) as the most drought-tolerant accessions. These findings suggest that Ediba and Ohong possess superior drought-resilience traits and should be prioritized in breeding programs aimed at improving drought tolerance in AYB for sustainable agriculture.

Keywords: African Yam Bean, drought stress, morpho-physiological traits, Antioxidant enzymes, Biomass

CASSFS 002

Assessing The Yield Potential Of Drought-Tolerant Three-Way Cross And Top-Cross Maize Hybrids For Climate Adaptation In Nigeria

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Abstract

Maize (*Zea mays* L.) is a staple crop in Nigeria, vital for human consumption and animal feed. However, its productivity is increasingly constrained by climate change, particularly the frequent occurrence of drought and heat stress. These stresses, which often simultaneously occur in farmers' fields, can reduce maize yield by up to 40%. This study evaluated the effects of heat stress and combined drought–heat stress on the yield performance of drought-tolerant three-way cross and top-cross maize hybrids. Thirty three-way crosses and twenty top-cross hybrids, together with four checks in each trial, were tested across two experiments conducted at Kadawa, Kano State, a hotspot for heat stress, over two consecutive dry seasons. The findings showed that three-way cross and top-cross hybrids performed similarly under heat stress alone. However, under combined drought and heat stress, three-way crosses consistently outperformed top-cross hybrids. Grain yield reductions under combined stress were 30.4% for three-way crosses and 40.7% for top-cross hybrids. The best-performing three-way cross hybrid yielded 2,306 kg ha⁻¹, while the lowest produced 211 kg ha⁻¹. For top-cross hybrids, yields ranged from 1,767 to 75 kg ha⁻¹ under the same conditions. Notably, the top five three-way crosses under heat stress also ranked among the best under combined stress, with yields between 1,573 and 1,778 kg ha⁻¹. In contrast, only two top-cross hybrids maintained top rankings under combined stress, with maximum yields of 1,767 and 1,214 kg ha⁻¹. The results indicate that three-way cross hybrids offer superior resilience and yield stability under simultaneous drought and heat stress, making them a valuable option for smallholder farmers in climate-vulnerable regions.

Keywords: *Drought stress, Heat stress, Climate adaptation, Maize hybrids, Top-cross hybrid, Three-way cross hybrid.*

CASSFS 003

Effect Of Land Use Types And Mineral Fertilizer On The Performance Of Celosia (*Celosia Argentea*)

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Abstract

This study examined the impact of land use types and nitrogen-based mineral fertilisers on the growth performance of *Celosia argentea* in Ogbomosho, Nigeria. Soils were sourced from three locations: arable land (S1), abandoned soap production site (S2), and cocoa plantation (S3). Urea fertiliser was applied at 0, 30, and 60 kgN/ha in a completely randomised design with three replicates. Data were collected on plant height, number of leaves, stem girth, and fresh leaves weight at weekly intervals up to 5 weeks after planting. Results showed that soil from the abandoned soap site (S2) significantly enhanced growth parameters, particularly in combination with 60 kgN/ha of urea. Fertiliser application significantly increased the number of leaves, plant height, and fresh weight compared to the control. The best growth performance was observed in plants grown on S2 soil with 60 kgN/ha, suggesting this site has residual fertility conducive to *Celosia* cultivation. However, fertiliser application had limited effects on stem girth, indicating that girth development may be less responsive to nitrogen inputs over the short term. The study highlights the potential of utilising underused or degraded soils, such as former industrial sites, for vegetable production when properly managed. Furthermore, moderate urea application (60 kgN/ha) can significantly improve yield without excessive input costs.

Keywords: *Celosia argentea*, land use, urea fertiliser, soil fertility, leafy vegetable yield

CASSFS 004

Evaluation of Groundnut Elite Breeding Lines for Drought Tolerance and Productivity Traits

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Sub-Theme: Climate Adaptation Strategies for Sustainable Food Security

Abstract

Groundnut (*Arachis hypogaea* L.) productivity is low in the semiarid tropics mainly because of drought caused by low and erratic rainfall. Identification of genotypes that have the ability to withstand the periods and conserve water for proper development and yield productivity is necessary for breeding of groundnut. In order to study the effect of drought on yield components and yield of groundnut in semi-arid region. 90 genotypes collected from International Crops Research Institute for Semi-Arid Tropics evaluated for their responses to drought at seedling stages using the pipe and the screen house. The genotypes were also evaluated in the field using randomized complete block design with three replications under well watered and water stressed condition. The results of the analysis of variance across the three mode of study (screen house, pipe and field) showed that there is a significant difference among the genotypes for most of the traits observed. Based on the performance of yield and yield related traits under field conditions, nine genotypes were drought tolerant. The genotypes including CS 060, CS 032, ICGV IS 07999, CS009, ICGV IS 13980, ICGV IS 07965, ICGV IS 13980, ICGV 07999, ICGV IS 94379 also showed the ability to withstand early seedling drought under screen house tests. Principal component analysis showed that traits such as SPAD and NDVI contributed to the drought tolerance using pipe screen house whereas other traits like the LAI,POD,FODDER FIELD,NPLE contributed to the variability observed among the genotypes in the field drought study.

Keywords: *Drought, Tolerance, Yield, Productivity and Variability.*

CASSFS 005

Seedling-Stage Drought Tolerance in Common Bean (*Phaseolus vulgaris* L.) and its Relationship with Chlorophyll Content

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Presentation Type: Physical Poster

Abstract

Common bean (*Phaseolus vulgaris* L.) is a widely cultivated legume in Nigeria. Despite its importance as a staple crop, the productivity is constrained by drought. Different sets of genes are known to confer resistance at different stages of growth. This study aimed to screen some common bean accessions for seedling-stage drought tolerance and determine the relationship between drought tolerance and chlorophyll content. Twenty accessions from Burundi were used for the study which was carried out in a glasshouse. The medium, air-dried sieved sand and top soil mixed in the ratio 3:1, was used to fill wooden boxes and watered to field capacity. The experimental design was completely randomized design with three replications. The seeds were watered every other day till 11 days after planting, followed by water withdrawal. Stem greenness, wilting score, unifoliate leaf senescence and trifoliate leaf abscission were scored on a scale of 0-4 at different intervals after water withdrawal. Data was also collected on chlorophyll content. Differences in wilting, stem greenness, unifoliate leaf senescence and trifoliate leaf abscission among the intervals were significant. The accessions differed significantly for chlorophyll content. Key indicators of drought tolerance at the seedling stage included low wilting (< 1.50), high stem greenness (> 3.10), reduced unifoliate leaf senescence (< 2.0), and minimal trifoliate leaf abscission (< 1.5). Accessions TPv-853, TPv-948, TPv-930, TPv-905, and TPv-799 were identified as drought-tolerant. The relationship between chlorophyll content and drought stress indicators (wilting score: $r = -0.30$, trifoliate abscission: $r = -0.29$) were low.

Keywords: Common bean, seedling-stage drought tolerance, chlorophyll content, wilting

CASSFS 006

GGE and AMMI biplot analyses of Early Maize Hybrids for yield and its Associated Traits

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Physical Oral Presentation

Abstract

Early maize hybrids are essential for addressing hunger gap most especial when food reserve is depleted in Sub-Saharan Africa. Their rapid maturity and adaptability make them strategic for enhancing food security, improving yield resilience, and sustaining maize production under changing climatic conditions. Understanding the interaction between genotypes and environments is critical for the development of maize cultivars with high yielding and stability across diverse agro-ecological zones. This study evaluated 22 early maize hybrids and three checks across four locations: Bagauda, Kafin Soli, Minjibir, and Zaria during the 2024 growing season. A randomized complete block design was used with three replications. Data collected on grain yield and associated agronomic traits were analyzed using appropriate software. Combined ANOVA showed significant ($p < 0.05$) effects of environment and genotype $\times$ environment interaction on grain yield, indicating deferential ranking of hybrids in different environment. Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype $\times$ Environment interaction (GGE) biplot models revealed distinct patterns of adaptability and stability among the hybrids. Hybrid EYH-149, EYH-107, EYH-148, EYH-150 and EYH-127 were identified as both high-yielding and widely adapted, while EYH-158, CHCK1, EYH-144 and EYH-153 showed specific adaptation to Minjibir, Bagauda, Kafinsoli and Zaria, respectively. This study provides valuable insights for maize breeding programs and supports the identification of stable and productive hybrids for release and commercialization in Nigeria.

Keywords: Early maize hybrids, genotype $\times$ environment interaction, AMMI, GGE biplot, yield stability.

CASSFS 007

Enhancing Bambara Groundnut Productivity through Arbuscular Mycorrhizal Fungi and Phosphorus Application

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Abstract

Bambara groundnut (BG) is a nutrient-dense legume, rich in high-quality proteins, essential amino acids, carbohydrates, and nutrients such as iron, potassium, and magnesium. Bambara groundnut is a promising crop for improving food and nutritional security because of its dietary values. However, its growth and yield are often constrained by nutrient imbalance particularly under phosphorus-deficient conditions. Arbuscular mycorrhizal fungi (AMF) enhance nutrient uptake by forming symbiotic associations with plant roots. This study investigates the combined effects of AMF inoculation and Triple Super Phosphate (TSP) application on the growth and yield of BG. The experiment was conducted during the 2022 cropping season at the International Institute of Tropical Agriculture (IITA), Ibadan, using a 5 × 4 factorial arrangements in a Randomized Complete Block Design (RCBD) with three replications. Five accessions of BG were evaluated under four treatment combinations: control, TSP, AMF, and TSP+AMF. Treatments were applied five weeks after planting. Data were collected on plant height, pod length, and seed weight. The results were analysed using ANOVA in SAS 9.2. Results revealed that the combined application of AMF and TSP significantly enhanced growth and yield compared to sole treatments. Accession TVSu-2269 produced the highest seed weight (89.4 g/plant) at 0.005 kg/ha TSP and 5.6 g AMF. The combination of AMF and inorganic phosphorus fertilizer is therefore recommended to improve Bambara groundnut productivity, with TVSu-2269 showing the best response.

Keywords: *Inorganic fertilizer, arbuscular mycorrhizal fungi, Bambara groundnut, nutrient enhancement, seed yield*

CASSFS 008

Evaluation of Stem Borer-Resistant Sorghum Genotypes for Resistance to Fall Armyworm (*Spodoptera frugiperda* J.E. SMITH)

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Abstract

Fall armyworm (FAW) is an economic pest affecting sorghum when susceptible cultivars are grown and environmental conditions are supportive. Resistance breeding to FAW is, therefore, of crucial importance to offer effective, sustainable, and environmentally friendly management options. Having varieties combining resistance to stem borer and FAW would enhance and stabilize sorghum productivity in SSA. This study was performed to assess some stem borer resistant sorghum genotypes for FAW resistance under artificial infestations. The study was carried out in the screen house and open field of ABU/IAR Zaria. 19 sorghum stem borer resistant lines were sourced and arranged in a randomized block design in two replications and were assessed based on the fall armyworm leaf damage score on a scale of 1 to 9. Each treatment stands were infested twice using camel hair brush at days 14 and 21 after seedling emergence with 5 FAW first instar larvae. Observations of foliar leave damage started 4th days after the first infestation and subsequently six days interval for 5 weeks after the second infestations. The results revealed significant differences (0.01 and 0.5%) among the genotypes for all the agronomic traits evaluated and foliar leaf damage scores. About 73.7% of genotypes recorded leaf damage scores of 4–5 and were classified as moderately resistant. These genotypes could be exploited as a resistance source in breeding for resistance to FAW.

Keywords: *Sorghum genotypes, fall armyworm, artificial infestation, leaf damage*

presentation Type: physical Oral

CASSFS 009

Screening for Salinity-Tolerance in Mungbean Genotypes using a Multi-Trait Index

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Abstract

Salinity stress, exacerbated by the effects of climate change, poses a significant threat to agricultural productivity by impairing plant growth and reducing crop yields. Ten Mungbean genotypes were evaluated based on morphological traits to assess their responses to varying salinity levels (0 mM, 100 mM, and 150 mM) at the seedling stage. The experiment was performed using a Randomized complete block design in a split plot arrangement with three replications. Significant genotype $\times$ salinity levels interactions were observed for shoot length (SL), root length (RL), fresh shoot weight (FSW), dry shoot weight (DSW), fresh root weight (FRW) and dry root weight (DRW). Significant differences in salinity levels effect were observed for shoot length (SL), dry shoot weight (DSW), dry root weight (DRW), root length to shoot length ratio (RLSLR) and root to shoot dry weight ratio (RSDWR). Using a selection intensity of 15%, the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) identified genotypes Tvr-14 and Tvr-102 as the most promising performers under control conditions. At a salinity level of 100 mM, genotypes Tvr-14 and Tvr-1 exhibited superior performance, while genotypes Tvr-1 and Tvr-6 were identified as the top-performing genotypes under a salinity level of 150 Mm. The highest broad sense heritability observed was in the RSDWR under 150 mM salinity level with a selection gain of 71.30 % indicating genetic variability exploitable for selection. These findings underpin the utility of multi-trait selection in developing salinity resilient Mungbean genotypes at the early seedling stage and identified genotypes with potential salinity tolerance for development of genotypes in salinity stressed areas.

Keywords: *Mungbean, Salinity stress, MGIDI index, Selection gain, Multi-trait selection*

CASSFS 010

Growth of Transgenic Cassava (*Manihot esculenta* Crantz) as Influenced by Cutting Type and Planting Orientation

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Abstract

Cassava (*Manihot esculenta* Crantz) is a perennial tropical root crop and a vital source of dietary calories, particularly in Africa. Conventional breeding has achieved limited improvement in cassava, thereby necessitating the use of biotechnology to generate transgenic varieties with desirable traits. Optimising propagation techniques is essential for the establishment and performance of such lines. This study evaluated the influence of cutting type and planting orientation on the regeneration and early growth of transgenic cassava TME 12-2010 under screen house conditions. A factorial experiment involving three cutting types (hardwood region, middle region, and softwood region) and three planting orientations (vertical, horizontal, and slantwise) was laid out in a completely randomised design. Analysis of variance revealed that at the 1% probability level, cutting type had highly significant effects on stem height (369.51) and leaf area (334.60), while planting orientation significantly influenced number of leaves (51.47), leaf area (201.04), stem diameter (0.43), and canopy spread (152.60). At the 5% probability level, cutting type significantly influenced stem circumference (0.12) and stem height, while planting orientation also affected stem height (293.80). The interaction between cutting type and planting orientation was significant only for stem height (46.30; $p > 0.05$). The study showed that both cutting type and planting orientation play important roles in the early establishment of transgenic cassava. Among the treatments tested, slantwise planting of hardwood cuttings consistently supported stronger growth and better plant establishment. The finding provides an effective strategy that can be adopted to improve the propagation and performance of transgenic cassava lines.

Keywords: cassava, transgenic plants, cutting type, planting orientation, early growth, regeneration.

CASSFS011

Assessment of *Dioscorea rotundata* Accessions Using Morphological and Genomic Characterization for Duplicate Identification and Management

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Abstract

Dioscorea rotundata (white yam) is a vital staple crop in West Africa, requiring effective conservation strategies to ensure sustainable food security. However, germplasm collections often contain duplicate accessions within and between genebanks, resulting in an increase in the cost and complexity of maintenance. Accurate identification and elimination of such duplicates are critical for efficient genetic resource management. Morphological traits, although relevant, are influenced by environmental factors and developmental stages. In contrast, genomic fingerprinting provides a reliable, environment-independent method of identifying duplicates. Therefore, the integration of both approaches will enhance the accuracy of accession differentiation. This study employed both morphological and molecular characterization to identify duplicates of *D. rotundata* accessions conserved at the genebank of the International Institute of Tropical Agriculture (IITA). A total of 38 *D. rotundata* accessions were evaluated using 30 qualitative and quantitative morphological traits and genotyped using Diversity Arrays Technology sequencing (DArTseq) which yielded 7,026 Single Nucleotide Polymorphism (SNP) markers. Morphological analysis identified only 5 unique accessions, while 33 were suspected duplicates. Similarly, SNP-based cluster analysis confirmed 34 accessions as true duplicates. These findings demonstrate a high level of redundancy within the *D. rotundata* collections. Identifying and removing such duplicates will allow genebanks to focus on the characterization, evaluation, and conservation of unique genetic materials, thereby contributing to the efficient management of genetic resources.

Keywords: DArTseq, *Dioscorea rotundata*, Duplicate accessions, Genomic fingerprinting, Morphological Characterization

CASSFS 012

Breeding beyond yield: sensory evaluation of advanced sweetpotato (*ipomoea batatas* (l). Lam) genotypes for fresh root market segment

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Abstract

Despite the release of improved varieties and subsequent promotion to aid adoption, the level of adoption of released sweetpotato varieties remain low due to mismatch between end-users' preference traits and those of the varieties. As such, sensory evaluation of genotypes to be released has been identified as a means to improving adoption. Therefore, this work was aimed at evaluating seven sweetpotato genotypes at advanced breeding stage for sensory attributes of the boiled and fried roots, the predominant utilization ends, using 12 trained panellists to aid final selection for nomination for release. For the boiled roots, all the genotypes (except Apomuden) exhibited acceptable sensory attributes that ranged from being liked slightly (5.53) to being liked very much (7.96) across all the attributes with four genotypes (Okumkom, NAN, PGA17265 and PGA14011-43) showing General Acceptability rating higher than the two checks. For the fried roots, all the advanced genotypes were rated from liked slightly (PGA17265) to liked very much (NAN) with others rated as liked moderately for General Acceptability. The PCA biplot clustering showed the poor sensory attributes of both Mother's Delight and Apomuden, the two orange-fleshed genotypes (OFSP), for boiled and fried roots, indicating the need for more focus on breeding acceptable OFSP varieties. This work has therefore showed the adoption potential of most of the advanced genotypes for both boiled and fries market segments.

Keywords: *sensory evaluation, sweetpotato, advanced genotypes, general acceptability, market segment*

CASSFS013

Seventeen years of Cassava Breeding in Nigeria: Genetic Gains for Disease Resistance

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Abstract

Cassava (*Manihot esculenta* Crantz) plays a vital role in food security across Sub-Saharan Africa. Over the years, concerted breeding efforts have been made towards developing improved cassava varieties with enhanced root yield, increased dry matter content, and resistance to key biotic and abiotic stresses. Biotic stresses such as Cassava Mosaic disease (CMD), Cassava Bacterial Blight (CBB), and Cassava Anthracnose Disease (CAD) cause significant yield losses in cassava production in Nigeria. These challenges have necessitated continuous evaluation of breeding progress to ensure that released varieties meet resistance targets and remain relevant under evolving disease pressures. Monitoring genetic gains over time provides insight into the effectiveness of selection strategies and helps guide future breeding priorities. The study herein therefore assessed genetic gains for disease resistance among cassava varieties released by the National Root Crops Research Institute (NRCRI), Umudike, between 2005 and 2022. 31 varieties, including those developed under NextGen and HarvestPlus breeding initiatives, were evaluated using standard field protocols in Umudike, Nigeria, a known hotspot for cassava disease screening. Performance was measured for key disease traits: cassava mosaic disease (CMD), cassava anthracnose disease (CAD), and cassava bacterial blight (CBB), using best linear unbiased predictors (BLUPs) to estimate genetic merit across unbalanced data. Analysis showed a clear improvement in resistance among recently released varieties, particularly those from 2022. Regression models revealed annual genetic gains of 5% for CMD resistance and 4% for CAD, highlighting the impact of breeding efforts over 17 years. Correlation analysis confirmed a significant negative relationship between year of release and disease severity, reinforcing the observed trends. These results suggest that NRCRI's cassava breeding programme is effectively selecting for disease resistance and delivering genetic progress. The findings provide essential insights for refining selection strategies and setting breeding targets aimed at developing improved cassava varieties for smallholder farmers in Nigeria and beyond.

Keywords: *Genetic Gain, Cassava, Sub-Sahara, Regression Model and Resistance.*

CASSFS014**Genetic Diversity of Maize Landraces Using Phenotypic and Molecular Analysis**Idowu O.G¹², Abberton M.T¹, Ogunkanmi L.A², Oyatomi O.A¹¹ Genetic Resources Center, International Institute of Tropical Agriculture (IITA), Ibadan, Oyo state, Nigeria.²Department of Cell Biology and Genetics, Faculty of Science, University of Lagos, NigeriaCorresponding author: m.abberton@cgiar.org, o.oyatomi@cgiar.org; og.idowu@cgiar.org; l.ogunkanmi@unilag.edu.ng

Abstract

Maize is a major staple crop and source of food and feed across sub-Saharan Africa. The increasing impact of climate changes poses major threats to maize production, income and livelihood of smallholder farmers in SSA. Germplasm are valuable source for identifying novel sources of resilient genotypes for future and emerging climatic conditions. This study assessed the genetic diversity and agronomic performance of 96 maize landraces accessions sourced from IITA Genebank across three locations in Nigeria using an 8 x 12 Alpha lattice design replicated thrice. The accessions were genotyped using 34,725 high quality DArT-Seq SNPs. Data were subjected to combined analysis of variance, broad sense heritability, phenotypic and genotypic correlation while yield stability was assessed through Genotype and Genotype x Environment (GGE) Biplot techniques. Results revealed significant phenotypic variations for key traits such as plant height, ear length, kernel weight, and grain yield. Genotypic correlations were consistently higher than phenotypic correlations in all environments. GGE biplot analysis identified six elite accessions with superior yield stability, with TZm-2402 identified as the most stable and highest grain across test environments. DArT-Seq SNPs revealed significant genetic diversity among the accessions grouping with five distinct clusters identified. Clustering patterns for both morphological and molecular analysis revealed 90% similarity. Findings from this study offers potentials for the identified maize high yielding and stable maize accessions to be deployed into maize breeding programs for the development of improved and climate resilient maize varieties across sub-Saharan Africa. In addition, this study also showed the importance of germplasm as valuable resources for climate adaption and breeding for sustainable food security.

Keywords: Phenotypic variations, DArT-seq SNPs, Germplasm, Climate change, Genotypic variations

CASSFS015

Key Metabolites implicated in *Dioscorea rotundata* (white yam) Tuber Dormancy Regulation

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Abstract

Yams are economic and medicinal crops with a long growth cycle, spanning between 9–11 months due to their prolonged tuber dormancy. Tuber dormancy has constituted a major constraint in yam production and genetic improvement. In this study, we performed non-targeted comparative metabolomic profiling of tubers of two white yam genotypes, (*Obiaoturugo* and *TDr1100873*), to identify metabolites that regulate yam tuber dormancy using gas chromatography–mass spectrometry (GC–MS). Yam tubers were sampled from 42 days after physiological maturity (DAPM) till tuber sprouting. The sampling points include 42-DAPM, 56-DAPM, 87DAPM, 101-DAPM, 115-DAPM, and 143-DAPM. A total of 949 metabolites were annotated, 559 in *TDr1100873* and 390 in *Obiaoturugo*. A total of 39 differentially accumulated metabolites (DAMs) were identified across the studied tuber dormancy stages in the two genotypes. A total of 27 DAMs were conserved between the two genotypes, whereas 5 DAMs were unique in the tubers of *TDr1100873* and 7 DAMs were in the tubers of *Obiaoturugo*. The differentially accumulated metabolites (DAMs) spread across 14 major functional chemical groups. Amines and biogenic polyamines, amino acids and derivatives, alcohols, flavonoids, alkaloids, phenols, esters, coumarins, and phytohormone positively regulated yam tuber dormancy induction and maintenance, whereas fatty acids, lipids, nucleotides, carboxylic acids, sugars, terpenoids, benzoquinones, and benzene derivatives positively regulated dormancy breaking and sprouting in tubers of both yam genotypes. Metabolite set enrichment analysis (MSEA) revealed that 12 metabolisms were significantly enriched during yam tuber dormancy stages. Metabolic pathway topology analysis further revealed that six metabolic pathways (linoleic acid metabolic pathway, phenylalanine metabolic pathway, galactose metabolic pathway, starch and sucrose metabolic pathway, alanine-aspartate-glutamine metabolic pathways, and purine metabolic pathway) exerted significant impact on yam tuber dormancy regulation. This result provides vital insights into molecular mechanisms regulating yam tuber dormancy.

Keywords: metabolites; differential–accumulation; energy; antioxidant; metabolism; molecular–mechanism; dormancy; regulation

CASSFS016

Assessment of Experimental Sorghum Hybrids for Yield, Agronomic Traits, and Stability Across Environments in Nigeria

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Abstract

The development of high-yielding and stable sorghum hybrids is essential for improving grain productivity in Nigeria's diverse agro-ecologies. Four experimental hybrids (EXP. HT1, HT2, HT3, HT7) and a commercial check (CSR-01) were evaluated through on-station, multi-location, and on-farm trials during 2022 and 2023. On-station evaluations were conducted at Chiromawa (Kano) and Likoro (Zaria) under two fertilizer blends (NPK 27:13:13 and NPK 20:10:10+), while multi-location trials spanned up to 15 environments across the Sudan and Northern Guinea savannas. On-farm testing involved farmers' fields across five states (Kano, Kaduna, Katsina, Jigawa, and Nasarawa). Trials were laid out in randomized complete block designs with standard agronomic management, and data on phenology, plant architecture, yield components, and grain yield were analyzed using ANOVA and genotype plus genotype $\times$ environment (GGE) biplot analysis. On-station trials revealed significant variation among genotypes, with hybrid EXP. HT3 producing the highest mean yield (4.43 t ha⁻¹), followed by HT1 (4.24 t ha⁻¹), compared with 4.06 t ha⁻¹ for CSR-01. Experimental hybrids flowered earlier (72.5–80.9 days) and were shorter in stature than the check, with favorable plant aspect. Across locations, yields were higher in 2022 than 2023, but EXP. HT1 consistently out-performed CSR-01 by an average of 0.5 t ha⁻¹. At Chiromawa and Lafia, HT1 recorded 6.2 and 5.7 t ha⁻¹, respectively. GGE biplot analysis identified EXP. HT1 as the highest-yielding and most stable hybrid across environments. On-farm trials confirmed this advantage, with HT1 yielding 4.4 t ha⁻¹ compared with 3.9 t ha⁻¹ for CSR-01 and 1.7 t ha⁻¹ for farmers' varieties, translating to a 12.1% yield gain over the commercial check. Overall, EXP. HT1 combined superior yield potential, wide adaptation, stability, and desirable agronomic traits, highlighting its promise for enhancing sorghum productivity and farmer adoption in Nigeria.

Keywords: grain sorghum, on-farm evaluation, GGE biplot, hybrids, Yield stability

CASSFS017**Microbial Metabolites in Agriculture: Current Trends and Future Prospects – A Review**

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Abstract

Metabolites are chemical compounds produced by microorganisms during metabolic processes and are useful in human, plant, and veterinary life. In traditional agricultural practice, there is a heavy dependence on synthetic chemicals (such as fertilizers and pesticides), which have undoubtedly improved agricultural production but also have deleterious outcomes on both life and the environment. Microbial metabolites are of great importance to present-day agriculture as they are green alternatives to synthetic fertilizers. These naturally occurring compounds, produced by microorganisms such as fungi and bacteria, engage in many functions in agricultural ecosystems. Microorganisms such as *Rhizobium* sp., *Bacillus* sp., *Pseudomonas* sp., *Trichoderma* sp., and Arbuscular Mycorrhizal Fungi (AMF) synthesize these useful metabolites. These metabolites are divided into primary and secondary metabolites. Primary metabolites such as amino acids, organic acids; secondary metabolites such as antibiotics and hormones. They function as plant growth promoters, soil fertility enhancers, biological control of pests and diseases, and improve stress tolerance in plants. Currently, these metabolites are used as biofertilizers, biopesticides, and biostimulators in the agricultural sector. Advanced biotechnologies such as genetic engineering and omics tools offer a greater and better understanding of the microbes and their metabolites and real-time monitoring of microbial-plant interaction. Despite their importance, applications are faced with challenges ranging from efficacy, quality, cost of production, regulation, and public awareness. With further investment in biotechnology, policy support, and farmer education, microbial solutions could be integral to the future of food security.

Keywords: *Metabolites, bacteria, fungi, agriculture and biotechnology.*

CASSFS018**Time Series Planting Of Two Variants Of Zobo Plants (*Hibiscus Sabdariffa*) For Photoperiodic Evaluation In Ibadan, South West Nigeria****Okpara S.C., Akinpelu O.A., *AdeOluwa O.O., Lawal, I.T. and Opatola O.G.**

National Horticultural Research Institute, Ibadan, Oyo State, Nigeria.

*Correspondence Author: olusolaodutayo@yahoo.co.uk**Abstract**

Zobo beverages, saffron and other *Hibiscus* drinks top the list of beverages with health benefits especially for non-communicable health issues like heat stroke, paralysis, high sugar levels and cancerous cell growth. Two distinct *Hibiscus sabdariffa* variants namely; the purple to red Zobo plant called Yakuwa in Hausa and the green type called Isapa in Yoruba were evaluated using multiple planting series for photoperiodic evaluation to assess days to flowerings and fruiting. Planting was done in four series: March, May, July and September. Three plants spacing used; 0.75m x 0.75m; 0.75m x 1.0m; 1.0m x 1.0m, laid out in RCBD with three replications. Data taken on growth parameters (plant heights, canopy spread diameters, stem girths, number of leaves and branches) on monthly basis until September were subjected to ANOVA and means were separated using Fisher's LSD at 5% probability level. Sampled plants of same time series, irrespective of their varying spacing were not significant ($p > 0.05$). However, significant differences ($p < 0.01$) were observed among the planting series for all parameters evaluated. The March series had the statistically highest mean values of 199.0cm; 105cm; 2.5cm; 181 and 23 for plant heights, canopy spread diameters, stem girths, number of leaves and branches, while July series recorded means of 24.5cm; 27.1cm; 0.4cm; 17 and 2.0, respectively, for the tested parameters. From the above result, previous series significantly ($p < 0.05$) out grew twice or near twice their successive series records. Thus, the more stay on the field the more vegetative growth. September series is on-going. At the end, if all the series flower and fruit through November to January 2026, we may affirm Zobo plant as photosensitive in Ibadan South west Nigeria. This result will serve as a planting guide especially in these recent times that NIHORT has intensified institutional strength by organically producing Zobo tea bags and beverages within and around Ibadan vicinity and may need to expand their Zobo plant germplasm.

Keywords: *Variability, Hibiscus sabdariffa, photoperiodic, time series, variants and Zobo.*

CASSFS019**Relationship between Drought Adaptive and Agronomic Traits of Cowpea (*Vigna unguiculata* (L.) Walp.)**

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Abstract

Cowpea (*Vigna unguiculata*) is a vital legume food crop in tropical and sub-tropical regions, especially in Nigeria, where it serves as a major source of nutrition, income, and soil fertility enhancement. However, drought stress poses a significant threat to its productivity under rain-fed conditions. This study was conducted to assess the performance of 306 cowpea genotypes for drought adaptive and agronomic traits; identify genotype combining drought tolerance with high yield potential; and investigate the relationship between drought adaptive and agronomic traits in cowpea. Field trials that evaluated three hundred and six (306) cowpea genotypes were conducted under both optimal and drought-stress conditions using an 18 × 17 alpha lattice design in two replicates at the Teaching and Research Farm, Obafemi Awolowo University, Ile-Ife. Data were collected on emergence, flowering, pod development, and yield-related traits and subjected to ANOVA, Rank Summation Index, and Pearson's correlation. Results revealed substantial genetic variability among genotypes. Notably, genotypes such as TVu-13485, TVu-1016, and TVu-201 demonstrated superior drought resilience and yield performance. Correlation analyses indicated limited relationships between traits under optimal conditions and drought tolerance scores, underscoring the complexity of trait integration under stress, while suggesting the need for targeted selection strategies. These findings provide valuable insights for breeding programs aimed at enhancing drought resilience and yield in cowpea, contributing to food security and sustainable agriculture in drought-prone regions.

Keywords: Agronomic traits, drought resilience, optimal condition, and traits association

CASSFS020

Agronomic Trait and Genetic Diversity of some Selected Accessions of Soybean (*Glycine max* (L.) Merrill) Germplasm.

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Abstract

Soybean (*Glycine max* (L.) Merrill) is a vital crop providing high-quality protein and vegetable oil. Despite its importance, soybean grain yield in Nigeria has remained stagnant for nearly a decade, with limited data on genetic diversity using Diversity Array Technology (DArT) sequencing. This study evaluated 54 soybean accessions, including four checks, for yield and genetic diversity using DArT-derived Single Nucleotide Polymorphism (SNP) markers during the 2022 late cropping season at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The experiment utilized an augmented design with spacing of 75 cm × 5 cm. Agronomic traits were analyzed using SAS (9.0), while principal component analysis (PCA) identified key contributors to phenotypic variation. Molecular diversity was assessed through 33,598 SNPs analyzed with R, Plink, and TASSEL software. Significant differences ($P < 0.05$) were observed for plant height, leaf area, days to flowering, and nodulation, whereas branches and stems per plant showed no significant variation. Accessions TGM-4723, TGM-4694, TGM-4446, TGM-1835, TGM-4683, and TGM-4153 exhibited the highest grain yields, which were statistically similar but superior to others. Phenotypic variation was also noted in pod length, pod width, seed length, seed width, and pod weight. Genetic analysis identified 20,373 high-quality DArT markers grouping accessions into four subpopulations, indicating substantial genetic diversity. DArT markers effectively characterized the soybean germplasm, supporting future breeding efforts. Accessions TGx 2024-7E, TGM-4723, TGM-4694, and others are recommended for use in breeding programs targeting yield improvement.

Keywords: *Genetic diversity, DArT sequencing, Single Nucleotide Polymorphisms (SNP), Grain yield.*

CASSFS021

Assessment of Experimental Sorghum Hybrids for Yield, Agronomic Traits, and Stability Across Environments in Nigeria

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Abstract

The development of high-yielding and stable sorghum hybrids is essential for improving grain productivity in Nigeria's diverse agro-ecologies. Four experimental hybrids (EXP. HT1, HT2, HT3, HT7) and a commercial check (CSR-01) were evaluated through on-station, multi-location, and on-farm trials during 2022 and 2023. On-station evaluations were conducted at Chiromawa (Kano) and Likoro (Zaria) under two fertilizer blends (NPK 27:13:13 and NPK 20:10:10+), while multi-location trials spanned up to 15 environments across the Sudan and Northern Guinea savannas. On-farm testing involved farmers' fields across five states (Kano, Kaduna, Katsina, Jigawa, and Nasarawa). Trials were laid out in randomized complete block designs with standard agronomic management, and data on phenology, plant architecture, yield components, and grain yield were analyzed using ANOVA and genotype plus genotype $\times$ environment (GGE) biplot analysis. On-station trials revealed significant variation among genotypes, with hybrid EXP. HT3 producing the highest mean yield (4.43 t ha⁻¹), followed by HT1 (4.24 t ha⁻¹), compared with 4.06 t ha⁻¹ for CSR-01. Experimental hybrids flowered earlier (72.5–80.9 days) and were shorter in stature than the check, with favorable plant aspect. Across locations, yields were higher in 2022 than 2023, but EXP. HT1 consistently out-performed CSR-01 by an average of 0.5 t ha⁻¹. At Chiromawa and Lafia, HT1 recorded 6.2 and 5.7 t ha⁻¹, respectively. GGE biplot analysis identified EXP. HT1 as the highest-yielding and most stable hybrid across environments. On-farm trials confirmed this advantage, with HT1 yielding 4.4 t ha⁻¹ compared with 3.9 t ha⁻¹ for CSR-01 and 1.7 t ha⁻¹ for farmers' varieties, translating to a 12.1% yield gain over the commercial check. Overall, EXP. HT1 combined superior yield potential, wide adaptation, stability, and desirable agronomic traits, highlighting its promise for enhancing sorghum productivity and farmer adoption in Nigeria.

Keywords: grain sorghum, on-farm evaluation, GGE biplot, hybrids, Yield stability

Sub-Theme 5

Plant Genetic Diversity and Resilience

(RPBCISA)

RPBCISA 001

Molecular Characterization of Some Wild Accessions of Cowpea (*Vigna spp*) Using Single Nucleotide Polymorphism (SNP) Marker.

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Abstract

Molecular characterization of five wild accessions (TVnu-561, TVuu-563, TVnu-1148, TVnu-1395, and TVnu-59) of cowpea (*Vigna spp*) was carried out at African Bioscience Molecular Laboratory, Ibadan, Oyo State, Nigeria. The samples of the wild accessions were collected using molecular kits. A single-nucleotide polymorphism (SNP) marker was used to analyze the five wild accessions. The number of single-nucleotide alleles ranged from 48-86, showing the variation of positions of the nucleotide in the DNA sequence of each accession. All accessions exhibited a singleton allele, indicating rare variation in their genetic structure. SNP generated a moderate level of polymorphism and revealed the existence of similar genetic diversity among the transcribed four accessions (TVnu-561, TVnu-563, TVnu-1148, and TVnu-1395) out of the five wild accessions. TVnu-59 showed no transcription. All the accessions had a high Minor Allele Frequency (MAF) of 0.8 and moderate heterozygosity of 0.32, indicating polymorphic and similar genetic diversity. SNP with Polymorphic Information Content (PIC) of 0.26 showed information with many alleles of similar frequencies ($PIC \geq 0.25$). The forward and backward alignment of the allele sequences showed multiple alleles co-existed at a specific locus. The three sequences revealed polymorphism between the four wild accessions of cowpea, two (TVnu-561 and TVnu-1395) (haplotypes 1 and 3), of which were 40% monomorphic, and three (TVnu-563, TVnu-1148, and TVnu-1395) (haplotype 2), which exhibited 60% Polymorphism. However, TVnu-1395 demonstrated both monomorphism and polymorphism, a distinct character that showed its slightly similar genetic diversity from others. The variation in the haplotype sequence is influenced by the number of annealing sites in the genome. Thus, information on intra-specific variation from this study might be useful in deciding on the improvement of cowpea.

Keywords: *SNP, Polymorphic, Monomorphic, Singleton, Haplotype, Wild Cowpea*

RPBCISA 002

Application of SCoT and ISSR Molecular Markers in Assessing Genetic Diversity of Lima Bean (*Phaseolus Lunatus*) Germplasm.

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Abstract

This study evaluated the genetic diversity of 30 *Phaseolus lunatus* (Lima bean) accessions using two molecular marker systems—Start Codon Targeted (SCoT) and Inter-Simple Sequence Repeat (ISSR), alongside agro-morphological assessments. A total of 25 primers (10 SCoT and 15 ISSR) were used to amplify DNA, producing 199 scorable bands. Genetic diversity indices revealed significant polymorphism across the accessions. Major allele frequency ranged from 0.13 to 0.93, with a mean of 0.48. The number of alleles per marker varied from 2 to 23, averaging 7.96 alleles. Gene diversity values ranged from 0.12 to 0.94, with a mean of 0.64, while the polymorphic information content (PIC) ranged from 0.12 to 0.94, with a mean of 0.61. ISSR markers, particularly UBC 840 (PIC = 0.94), UBC 880 (PIC = 0.86), and UBC 825 (PIC = 0.84), showed higher polymorphism than SCoT markers, indicating greater discriminatory power. Phylogenetic analyses based on Jaccard's similarity coefficient grouped the accessions into four main clusters, with pairwise similarity values ranging from 0.38 to 0.92. Notably, accessions TPI-2438, TPI-1600, and TPI-1590 were identified as genetically distinct, suggesting potential use in breeding programs. Morphological analysis also showed significant variability in traits such as leaf color (range: 2.67–7.00), branching orientation (1.00–6.33), and plant height (up to 74.93 cm by week 8). The integration of molecular and morphological data revealed a broad genetic base among accessions, underscoring the potential of these resources for crop improvement. These findings provide critical insights into the effective utilization and conservation of *P. lunatus* germplasm, supporting future breeding efforts aimed at enhancing stress tolerance and yield.

Keywords: *Molecular markers, ISSR, SCOT, Polymorphism, Phaseolus lunatus*

RPBCISA 003

Developing a robust CRISPR-Cas9 system targeting the Salicylic Acid 5-Hydroxylase (*OsS5H*) Gene for Mutation in Rice

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Presentation type: Physical, Oral

Abstract

Salicylic acid (SA) is an essential plant hormone that plays critical roles in basal defence and amplification of local immune responses and establishes resistance against various pathogens. Salicylic acid 5-hydroxylase (S5H) converts Salicylic acid into 2,5-dihydroxybenzoic acid (2,5-DHBA) and has been implicated in the regulation of broad-spectrum disease resistance in rice. Here we amplified and sequenced the *OsS5H* gene from rice with the aim of targeting the coding sequences (CDS) for mutation. The *OsS5H* gene was amplified from four farmer-preferred rice varieties in Nigeria and sequenced. Guide RNAs (gRNAs) were designed from the first exon and inserted into gRNA expression vectors pYPQ131C (gRNA1) and pYPQ132C (gRNA2). The gRNAs were then multiplexed into a gRNA recipient pYPQ142C by Golden Gate assembly. Finally, the gRNA recipient plasmid (pYPQ142) and the Cas9 plasmid (pYPQ167) were integrated into the destination vector (pMDC32) by Gateway recombination reaction. At each cloning stage, *E. coli* DH5 α was transformed and plated on LB media containing appropriate antibiotics. Positive colonies were analysed by restriction enzyme digestion or PCR followed by sequencing. Sequence analysis of the pMDC32 plasmid from positive bacteria colonies indicates successful cloning of the gRNAs and the Cas9 plasmid into the destination vector. The success recorded here opens up the opportunity to edit the *OsS5H* gene in rice, thereby conferring a broad-spectrum disease resistance in rice.

Keywords: *Cas9*; *CRISPR*; *gRNA*; *Rice*; *Salicylic Acid*

RPBCISA 004

**Utilizing Crispr-Cas9 Technology To Unlock The Potentials Of Underutilized Legumes For
Enhance Food Security In Nigeria: A Scoping Review**Onimisi, A. O.¹, Ogbeche, C.¹ and Ojua, E. O.^{2*}¹Department of Biology, Federal College of Education, Okene, Kogi State²Department of Plant Science and Biotechnology, Faculty of Biological Sciences,
University of Nigeria, Nsukka*Corresponding author: eugene.ojua.pg78127@unn.edu.ng**Abstract**

Food insecurity remains a major challenge in Nigeria because the population is growing, the environment is getting worse, and people depend on a small number of staple crops. Legumes like Bambara groundnut, African yam bean, and pigeon pea are not used enough, but they have a lot of potential to help with food and nutrition security. However, researchers and agricultural developers have not extensively investigated or developed these crops, leading to low yields, restricted genetic advancement, and inadequate market integration. CRISPR-Cas9 is an innovative method for genome modification that significantly accelerates the enhancement of these legumes genetically. This scoping study concentrates on Nigeria and examines the current knowledge on the application of CRISPR-Cas9 on underutilised legumes. This analysis examines existing studies, identifies gaps for further research, and evaluates the efficacy of CRISPR-Cas9 in enhancing traits such as drought tolerance, pest and disease resistance, early maturity, and nutritional quality. The review discusses the ethical, social, economic, and legal implications of utilising gene editing in Nigerian agriculture. The findings indicate a growing global interest among researchers in employing CRISPR-Cas9 for crop enhancement. Nevertheless, they indicate that Nigeria requires far more research and infrastructure. To get the most out of this technology, we need to make smart investments in building capacity, making rules, and getting everyone involved. The review emphasizes the need for a coordinated research agenda to maximize CRISPR-Cas9's potential in improving food security.

Keywords: Food insecurity; Genome editing; Nigeria; Sustainable Agriculture; Underutilized Legumes.

RPBCISA 005**Impact Of Silver Nanoparticles On Growth, Bioactive Peptides, Antioxidant And Functional Properties On Germination Of African Yam Bean (*Sphenostylis Stenocarpa*)**¹Ussuh, M.W. and ²Kwon-Ndung, E. H.

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Abstract

The study investigated the impact of silver nanoparticles concentrations (20, 40, 60, 80, and 100 ppm) on the germination of African yam beans. Using standard procedures, silver nanoparticles was applied to African yam bean for 2 hours followed by germination process for 5-days in culture plates. The results showed that, the concentration of 60 ppm exhibited the longest root length and highest percentage of germination as compared to other concentrations. Percentage moisture content of germinated African yam bean treated with 100 ppm silver nanoparticles exhibited 16.49% whereas both non-germinated African yam bean (NAYB) and germinated African yam bean (GAYB) showed a reduction in total ash content and fat contents as compared to other samples. The fiber content of African yam bean increased up to 78 ppm but decreased to 95 ppm. However, addition effect of 60 ppm silver nanoparticles resulted in the highest total phenolic content (145.51 mg GAE/100 g), flavonoids (445.52 mg catechin/100 g) and ferric reducing antioxidant power (FRAP) (8.97 mmol Fe(II) Eq/g). The antioxidant profile was the highest in germinated African yam bean treated with 78 ppm (85%). Functional properties of germinated samples treated with 60 ppm of silver nanoparticles resulted in improved fat absorption capacity (FAC), Carr's index and Hausner ratio. In conclusion, the study showed that, the incorporation of silver nanoparticles into African yam bean at a concentration of 60 ppm significantly enhanced germination, antioxidant activity, total phenolic content (TPC), germination percentage as compared to other samples.

Keywords: African yam bean, growth, silver nanoparticles, bioactive peptides, functional properties.

RPBCISA006

Identification of the Gene SRWD2 Involved in Salt Tolerance in Selected Rice (*Oryza sativa* .L.) Landraces and Varieties in Nigeria

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Abstract

Salinization of soil is one of the major factors limiting crop production particularly in saline prone coastal regions. It reduces the growth of glycophytes and occupies a prominent place amongst soil problems that threaten the sustainability of Agriculture. Among PCR based markers, -SSR markers are more popular in rice because they can detect high level of allelic diversity and have been extensively used for selection of salinity tolerant genotypes of rice. This study is based on identifying salinity tolerant genotypes using Simple Sequences Repeat marker(SRWD2) was used to identify salinity tolerance in two conventional varieties (faro 44 and faro 67) in addition to three landraces; (C-price, CHI and Iron). The marker- SRWD2 was designed and used to identify the candidate gene SRWD2 at 150 bp in the local landrace; iron. Others did not reveal any amplification for the allele carrying the resistant gene (SRWD2). The landrace is then recommended for use as a potential donor for rice breeding programmes. The genotypes could be further tested in saline areas to observe yield potential for developing high yielding genotypes suitable for saline areas. The markers used in this study is capable of detecting major gene locus for plants breeders to develop new salt tolerant genotypes.

Keywords *Salinization, QTL, makers, candidate gene, landraces.*

RPBCISA007

Public Perception and Acceptance of Genetically Modified (GM) Crops in Plateau State

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Abstract

Amid global efforts to enhance food security and agricultural resilience, genetically modified (GM) crops have gained prominence as a potential solution. However, their acceptance remains subject to public perception, influenced by a complex interplay of sociocultural, religion believes, educational, and informational factors. This study assessed public perception and acceptance of GM crops in Plateau State, Nigeria, through a well-structured, anonymous online survey distributed via Google Forms. Findings revealed that 73.2% of respondents had prior awareness of GM crops, yet knowledge levels varied, with only 28.8% self-identifying as very knowledgeable. While 44.8% perceived GM crops as safe, a substantial proportion expressed ambivalence or concern, largely driven by perceived health and environmental risks. Factors such as scientific evidence, government regulation, and endorsement by trusted organizations were identified as critical influences on acceptance. Media was regarded as a significant driver of public opinion (59.6% rated it as influential), while nearly half of the respondents (48.8%) indicated that educational resources on GM crops were insufficient. Although a cross-tabulation between education level and acceptance did not yield statistically significant differences. The findings stress the critical need for targeted public education, transparent regulatory communication, inclusive policy development, and sustained stakeholder engagement to bridge the gap between scientific innovation and public trust in the adoption of genetically modified crops in Nigeria.

Keywords: *Genetically modified, Resilience, Plateau State and Perception*

RPBCISA008

Biotechnological Approaches for Enhancing Seed-Borne Disease Resistance in Groundnut: Bridging Molecular Innovation with Applied Breeding

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Abstract

Seed-borne diseases remain a major constraint to the productivity, quality, and economic value of groundnut (*Arachis hypogaea*), a key oilseed crop in Nigeria and globally. Fungal pathogens such as *Aspergillus flavus*, *Cercospora* spp., and *Rhizoctonia solani*, significantly impair seed germination, reduce yield, and pose serious health risks through aflatoxin contamination. Traditional management practices, including chemical seed treatments and cultural methods, have shown limited effectiveness under escalating pathogen pressure and shifting climatic conditions. This review article critically examines the limitations of conventional approaches while highlighting recent biotechnological innovations such as the use of molecular markers, genome-wide association studies (GWAS), RNA interference (RNAi), and CRISPR/Cas9 for the development of seed-borne disease-resistant cultivars. It also highlights the importance of integrating omics technologies, strengthening institutional and technical capacity to facilitate the effective application of these innovations. However, widespread implementation remains hindered by infrastructural challenges, weak policy support, limited stakeholder engagement, and socio-political resistance to certain technologies. The review calls for robust interdisciplinary collaboration to transform cutting-edge molecular research into field-ready solutions capable of strengthening crop resilience and securing Nigeria's agricultural future.

Keyword: *Seed-Borne, Disease Resistance, Conventional, Groundnut and Cultivars.*



Nigerian
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Sub-Theme 6

**Advancing Plant Genetics and Genomics: Decoding
Nature for Next-Generation Crop**

(APGDNGC)

APGDNGC 001

Congruence Between Morphological and Molecular Characterization of Nigerian Coconut Cultivars.

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Abstract

This study evaluated the congruence of grouping patterns from morphological and molecular data to assess their effectiveness in revealing genetic relationships among Nigerian coconut cultivars. Accurate grouping is crucial for plant breeders to make informed decisions on parent selection and breeding strategies. We conducted a morphological analysis on 12 cultivars using 30 fruit traits, and a molecular analysis on a subset of 8 cultivars using SSR markers. Morphological data were analyzed using hierarchical cluster analysis (SPSS), while molecular data were analyzed with UPGMA (MEGA software); the results from both were visualized in dendrograms. The analyses revealed a strong congruence between the two methods' clustering patterns. For example, both methods consistently grouped the 'MYD' and 'Edo Tall' cultivars, as well as the 'MYD' and 'CGD' cultivars. These findings suggest that integrating both morphological and molecular techniques can provide higher precision for parent selection, thus improving the efficiency of breeding programmes.

Keywords: *Coconut cultivars, Genetic relationships, Morphological characterization, Molecular markers, SSR markers, Cluster analysis.*

APGDNGC 002

Gene Expression Studies to Identify Key Genes Influencing the Mechanism of Striga Resistance in Maize (*Zea mays*)

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Abstract

Striga (*Striga hermonthica*) poses a significant threat to maize production, causing up to 100% yield loss under stress conditions. This study investigates the gene expression profiles of key genes influencing *Striga* resistance in maize to enhance crop improvement strategies for food security. Two maize lines, TZSTRI101 (resistant, L12) and 5012 (susceptible, L25), were subjected to RNA-Seq analysis under *Striga*-infested and control conditions across three time points (1, 3, and 7 days after infestation). Differential gene expression (DGE) analysis revealed distinct transcriptional responses, with L25 exhibiting stronger upregulation of defense-related genes, particularly on Day 7 (2,813 unique DEGs), indicating a sustained resistance mechanism. Notably, *Zm00001eb404750* (Clp R domain-containing protein), upregulated in L25 (log2FC 0.90), was identified as a key candidate gene involved in strigolactone signaling suppression, potentially limiting *Striga* germination. Conversely, *Zm00001eb114700* (Beta-carotene isomerase D27), downregulated in L25 (log2FC -1.46), reduces strigolactone biosynthesis, further supporting resistance by decreasing host-derived signals. Pathway analysis confirmed the roles of these genes in strigolactone metabolism, critical for *Striga* parasitism. These findings highlight the molecular mechanisms underlying *Striga* resistance and provide valuable insights for developing *Striga*-resistant maize varieties through marker-assisted selection, contributing to sustainable agricultural systems in *Striga*-endemic regions.

Keywords: *Striga* resistance, Maize, Gene expression, Strigolactone, RNA-Seq

APGDNGC 003

Genetic Underpinnings of Morphological, β -carotene, Tryptophan, and Agronomic Traits in Extra-early Bio-fortified Maize under Southern Leaf Blight Pressure

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Abstract

Developing extra-early maturing, nutrient-dense, and disease-resistant maize is essential for enhancing food and nutrition security in sub-Saharan Africa, where erratic rainfall and Southern Leaf Blight (SLB) limit productivity. This study evaluated 20 extra-early biofortified SAMMAZ quality protein maize inbred lines, including two checks, under natural SLB infestation across two rainfed seasons. There was significant phenotypic variation among genotypes for major agronomic, nutritional, and disease resistance traits. Grain yield ranged from 4.7 to 8.8 t ha⁻¹, with SAMMAZ 58, 63, and 62 emerging as top performers, also exhibiting favourable plant architecture and synchrony in flowering. Nutritional quality varied markedly, with β -carotene ranging from 4.7 to 9.0 μ g/g and tryptophan from 0.070% to 0.090%, exceeding biofortification thresholds in several genotypes. Disease severity scores ranged from 1.6 to 3.5, and area under the disease progress curve from 110.7 to 178.9, with genotypes SAMMAZ 59, 62, 55, and 34 showing strong SLB tolerance. High heritability estimates and genetic advance for most traits indicate the predominance of additive genetic effects and strong potential for genetic gains. These findings highlight promising inbred lines combining early maturity, high yield, nutritional quality, and SLB resistance for integration into climate-resilient maize improvement programmes.

Keywords: *Agronomic traits, Heritability, Genetic advance, Nutritional quality, Disease severity.*

APGDNGC 004

Performance of Temperate Maize-Derived Aflatoxin Resistance QTLs in Tropical Maize Inbred Lines

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Abstract

Aflatoxin, a toxic secondary metabolite produced by fungal species, is a major global public health constraint affecting the quality and economic value of maize, leading to huge losses by farmers. Developing host-plant resistant varieties is the most economical, environmentally friendly and sustainable approach to effectively control aflatoxin contamination in maize grains. With the aim of developing resistant maize hybrids, tropical-adapted lines from IITA, Ibadan were enriched with five aflatoxin-resistant QTLs from temperate maize germplasm using marker-assisted backcrossing followed by repeated selfing. In this study, the presence and number of aflatoxin-resistant QTLs in 83 inbred lines, and their association with resistance to aflatoxin accumulation were assessed. The 83 lines were genotyped using 12 aflatoxin-specific KASP SNP markers. The lines, along with two complementary checks, were field-grown, and harvested grains screened for aflatoxin contamination using a kernel-based screening assay inoculated with *Aspergillus flavus*. Aflatoxin levels in the grains were quantified via thin-layer chromatography. Aflatoxin-resistant QTLs were detected, with each line harbouring one to five QTLs. The lines differed significantly for aflatoxin levels, with lines L6, L27, and L59 with four, three, and three QTLs, respectively, exhibiting significantly lower aflatoxin accumulation than the resistant check. Association between aflatoxin content and spore production ($r=0.64$) was significant. Although many lines showed highly reduced aflatoxin accumulation, this was not significantly correlated with the number or effect of aflatoxin-resistant QTLs. These findings highlight the complexity of transferring QTLs across genomic backgrounds and emphasize the need for validating QTL functionality across diverse environments and genetic contexts.

Keywords: Tropical maize, Aflatoxin-resistant QTLs, Aflatoxin contamination, KASP genotyping, Plant-host resistance

APGDNGC 005

Phenotypic Variation and Non-Mendelian Segregation of Tuber Shape in Biparental Populations of White Yam (*Dioscorea rotundata*)

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Physical Oral

Abstract

Yam (*Dioscorea rotundata*) tuber shape is an important morphological trait influencing market preference, postharvest handling, and breeding selection. This study aimed to assess phenotypic variation and segregation patterns of tuber shape in a biparental *D. rotundata* population. A total of 890 progenies were generated from crosses between an oval-shaped female parent (TDr1669010) and two cylindrical-shaped male parents (TDr1689029AB, male 1; TDr1680013AB, male 2), producing families TDr23001 (n = 609) and TDr23003 (n = 281). Yield and morphometric traits including tuber length, diameter, area, perimeter, aspect ratio, roundness, compactness, and elongation index were measured. ANOVA revealed significant family differences ($p < 0.05$) in three shape-related traits - aspect ratio, roundness, and elongation index - while yield and other size traits were conserved across families. Tuber shape distribution showed a predominance of long tubers in both families, particularly TDr23003 (72.2%), with oval and irregular shapes less common. Chi-square tests demonstrated significant deviations ($p < 0.001$) from both Mendelian 1:2:1 expectation and the equal proportion hypothesis, indicating non-Mendelian inheritance. The overrepresentation of long shapes and underrepresentation of irregular shapes suggest potential dominance effects, epistasis, or selection against irregular forms. These findings highlight the complexity of tuber shape inheritance in *D. rotundata* and underscore the importance of integrating morphometric and genetic analysis to inform breeding strategies targeting desirable market-preferred shapes.

Keywords: *Dioscorea rotundata*, tuber shape, morphometric traits, ANOVA, segregation analysis

APGDNGC 006

Genotypic and Phenotypic Correlation for Iron, Zinc and some Agronomic Traits in Sorghum (*Sorghum Bicolor* L. Moench)

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Presentation type: Oral

Abstract

Improvement of Sorghum mineral content is important in Nigeria. The poor and majority of the population depends on sorghum for their calorie and micronutrient requirement since they have less access to nutrient-rich foods like vegetables, fruits and animal products. To address this, an alternative solution is to increase mineral concentrations in edible crops using conventional plant breeding. This research was conducted to estimate correlation for Iron, Zinc and some agronomic traits. Six generations: (P₁), (P₂), (F₁), (F₂), (BCP₁) and (BCP₂) populations were developed and evaluated during 2021-2023 raining season at IAR farm, Samaru Zaria, Kaduna state, and IAR farm, Minjibir, Kano state, using randomized complete block design with two replications at each location for one year. Data were recorded for days to 50% flowering, days to maturity, panicle weight, number of leaves, grains weight per panicle, grain size, grain weight per plant, grain yield and Iron, Zinc concentrations. The data collected were analyzed. Significant differences were observed for Iron, Zinc and some agronomic traits. The result of genotypic and phenotypic correlation revealed significant positive genotypic and phenotypic correlations $G=(r=0.83^*)$ $P=(r=0.81^*)$ in cross 1 and $G=(r=0.79^*)$ and $P=(r=0.73^*)$ in cross 2 between Iron, Zinc concentration which may likely result from common and overlapping Quantitative Trait Loci (QTL), and existence of non-significant positive genotypic correlation between yield and the two minerals which implies improvement of Iron and Zinc may not result in yield reduction. This study revealed that the two minerals (Fe and Zn) may simultaneously be improved.

Keywords: Iron, Zinc, correlation, genotypic, phenotypic.

APGDNGC 007

Biotechnological Approaches for Enhancing Seed-Borne Disease Resistance in Groundnut: Bridging Molecular Innovation with Applied Breeding

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Abstract

Seed-borne diseases remain a major constraint to the productivity, quality, and economic value of groundnut (*Arachis hypogaea*), a key oilseed crop in Nigeria and globally. Fungal pathogens such as *Aspergillus flavus*, *Cercospora* spp., and *Rhizoctonia solani*, significantly impair seed germination, reduce yield, and pose serious health risks through aflatoxin contamination. Traditional management practices, including chemical seed treatments and cultural methods, have shown limited effectiveness under escalating pathogen pressure and shifting climatic conditions. This review article critically examines the limitations of conventional approaches while highlighting recent biotechnological innovations such as the use of molecular markers, genome-wide association studies (GWAS), RNA interference (RNAi), and CRISPR/Cas9 for the development of seed-borne disease-resistant cultivars. It also highlights the importance of integrating omics technologies, strengthening institutional and technical capacity to facilitate the effective application of these innovations. However, widespread implementation remains hindered by infrastructural challenges, weak policy support, limited stakeholder engagement, and socio-political resistance to certain technologies. The review calls for robust interdisciplinary collaboration to transform cutting-edge molecular research into field-ready solutions capable of strengthening crop resilience and securing Nigeria's agricultural future.

APGDNGC 008

Identifying genetic loci associated with early maturity in cowpea (*vigna unguiculata* L.) Through genome -wide association analysis

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Abstract

Early-maturing cowpea varieties are a real game-changer in areas prone to drought and with shorter growing seasons. When maturity is delayed, it can lead to yield losses from moisture stress, pests, and diseases. In our study, we set out to conduct genome-wide association studies (GWAS) focusing on achieving 95% pod maturity in cowpea (*Vigna unguiculata* L. Walp.). We worked with a diverse set of cowpea genotypes known as the DArT Panel Population, which included four distinct groups with varying genetic backgrounds. This collection comprised elite breeding lines, germplasm accessions from the IITA Genetic Resources Centre, and both multi- and bi-parental recombinant inbred, totalling 300 genotypes. Our research involved a comprehensive genome-wide scan of these 300 cowpea genotypes to pinpoint markers linked to early maturity. We phenotypically screened the population at two locations: Wudil and Minjibir in Kano state. Interestingly, we found significant variations in the days to reach 95% pod maturity among the different populations. For the GWAS, we utilized TASSEL v.5.2.79, applying a mixed linear model (MLM) with (Q + K) models, which included principal components and kinship matrices to account for population structure. The statistical models from TASSEL enabled us to create Manhattan and quantile-quantile (QQ) plots. Our genome-wide scan uncovered two major regions on chromosomes Vu09 and Vu07, along with three minor regions on chromosomes Vu01, Vu03, and Vu05, all significantly associated with early maturity. Among these regions, the gene Vigun09g056300 was identified as being closest to the peak SNP positions, acting as a developmental speed governor: increased activities promotes early maturity by facilitating precocious ethylene signalling. We suggest that future research should focus on creating a marker-assisted breeding platform and developing extra-early cowpea cultivars. Additionally, the SNP markers linked to early maturity should be evaluated for consistent associations across various genetic backgrounds.

Keywords: *Cowpea, SNP, DArTag, mid-density panel, Markers, Early Maturity*

APGDNGC 009

From Lab to Field: Challenges and Prospects of Deploying Transgenic Drought-Tolerant Rice in Nigeria

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Abstract

Rice is an important staple food for much of the world population especially the developing regions like Nigeria. It provides as high as 80% of daily food energy intake and a major livelihood source. However, its production is threatened by climate-related stress conditions like drought which adversely impacts on agricultural production particularly rice, a semi-aquatic crop. Addressing food insecurity under climate stress requires translational research in agricultural biotechnology. One of such research strategies is the development of a transgenic lines for nitrogen efficient use, water efficient and salt tolerance (*NEWEST*) rice varieties. A significant progress has been made on this project up to field trials stage in Nigeria. Nevertheless, translating the laboratory success of transgenic drought tolerant rice variety to practical field-scale reality faces multiple challenges. We highlight the vital link between scientific discoveries and real-world applications in the Nigerian context. Despite satisfactory field trials and commercial release readiness, there still exist obstacles. These include: long bureaucratic approval procedures, inconsistent biosafety frameworks and policies, limited institutional capacity, public skepticism, that prevent timely implementation and commercialization. Additional concerns of biosafety issues relating to, ecological and food safety, are yet controversial viewpoints that need clearer elucidations and proper communication. Farmer-adoption also needs to be addressed because even with possible agronomic advantages, uptake depends on access to seed systems, cultural views and trust in biotechnology. This review underscores the need for an inclusive stakeholder involvement in transgenic drought-tolerant rice development in Nigeria to mitigate food insecurity due to climate-change induced drought.

Keywords: *Transgenic, Drought-tolerant rice, Translational research, Climate change, Food security*

APGDNGC 010**Assessment of genotypic divergence for hybrid development in tomato (*Solanum lycopersicum* L.)**Olayinka, A.O.^{1*}, Ibitoye, D.O.² and Fatoki, O.O.¹¹Department of Crop Production and Soil Science, Faculty of Agricultural Sciences, Ladoké Akintola University of Technology, Department of Crop Production and Soil Science, Ogbomoso, Nigeria² Genetic Resources Unit, National Horticultural Research Institute, Ibadan, Nigeria

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Abstract

Tomato (*Solanum lycopersicum* L.) is a globally important fruit vegetable exhibiting considerable genetic diversity, particularly with respect to fruit yield, quality, and resistance to diseases and pests. The application of molecular markers has facilitated the assessment of this diversity, thereby supporting breeding programs in the characterization, selection, and development of hybrids with improved yield and specific horticultural traits. The objective of this study was to evaluate the genetic diversity among 43 tomato genotypes sourced from the Tomato Genetic Resource Center (USA), the World Vegetable Center (Taiwan), and the National Horticultural Research Institute (Nigeria) using 13 simple sequence repeat (SSR) markers. Additionally, a half-diallel crossing scheme was implemented to develop commercial F₁ hybrids. Genetic data were analyzed in R. The SSR analysis revealed an average of 3.15 alleles per locus, an average gene diversity of 0.34, and an average polymorphism information content (PIC) of 0.34. Hierarchical clustering analysis grouped the genotypes into four distinct clusters, corroborating the results of population structure analysis. Based on the observed genetic divergence, ten genotypes - LA 1714, NHTO 0400, NHTO 0249, LA 4345, NHTO 0239, NHTO 0568, NHTO 0752, NHTO 0358, NHTO 0404, and NHTO 0201 were selected as parents for the development of 45 F₁ hybrids. These hybrids will be further evaluated for combining ability and heterosis. This study provides valuable insights for advancing tomato breeding programmes. The findings will offer opportunities to identify superior hybrids that can meet the yield and nutritional demands of both farmers and consumers.

Keywords: *Genetic diversity, Population structure, Simple sequence repeats, Tomato*

APGDNGC 011

Unraveling the Genomic Architecture of boiled Cassava root Texture using Multi-model Genomic Prediction Approaches

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Abstract

Cassava (*Manihot esculenta* Crantz) is a major staple in sub-Saharan Africa, where root texture attributes - such as mealiness, fibre content, softness, taste, colour, aroma, and firmness – play a critical role in consumer preference and marketability. However, improving these traits through conventional breeding has been constrained by their complex genetic architecture and the challenges associated with accurate phenotyping. In this study, we assessed the predictive performance of eleven genomic prediction (GP) models — including GBLUP, EGBLUP, ridge regression (RR), LASSO, Bayesian ridge regression (BRR), Bayes Lasso (BL), BayesA (BA), BayesB (BB), BayesC (BC), reproducing kernel Hilbert space (RKHS), and random forest (RF) — for seven texture-related traits in boiled cassava roots using high-density SNP markers. Phenotypic data were obtained from genetically diverse cassava clones evaluated under standardized boiling conditions using a portable near-infrared spectrometer. Prediction accuracies varied across traits and models. EGBLUP consistently outperformed GBLUP, particularly for fibre content ($r = 0.32$), highlighting the potential role of epistatic interactions. RF yielded competitive accuracies for traits such as mealiness ($r = 0.32$) and colour ($r = 0.36$). Among the Bayesian methods, BayesB and BayesC showed strong performance across multiple traits, supporting their ability to capture both major and minor effect loci. To our knowledge, this represents the first comprehensive application of genomic prediction to boiled root texture traits in cassava. These findings demonstrate the promise of genomic selection for accelerating the development of cassava varieties aligned with consumer preferences and provide new insights into the genetic architecture of complex sensory traits.

Keywords: *Cassava, Genomic selection, Textural attributes, Sensory evaluation, GBLUP*

APGDNGC 012**NIR-Based Prediction and Genome-Wide Association Study for Protein, Oil and Fatty Acids in Soybean [*Glycine max* (L.) Merrill] Seeds**

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Abstract

To identify fast and non-destructive ways in determining the nutritional traits, mathematical models to predicting the nutritional contents (using Near Infrared Reflectance Spectroscopy (NIRS)) and identify genomic regions linked to the nutritional contents in soybean seeds. Fifty samples of soybean accessions were scanned over a wavelength of 400 – 2500 nm at 0.5 nm interval at the Center for Dryland Agriculture (CDA) instrumentation laboratory and further analysed for oil, protein and fatty acid contents at the proximate laboratory of CDA. Thirty samples were used for calibration and twenty were used for validation. The spectral data was analyzed using multivariate data analysis software (Unscrambler v9.7). Partial least square regression was conducted using the spectral data from the calibration dataset to develop an empirical equation to estimate the soybean nutritional contents. Genotyping of soybean accessions was performed using the DArT-based genotype by sequencing platform of SEQART-AFRICA. The result showed an excellent correlation ($r^2 > 0.97$) between the predicted and references. The SEC, SEP and RPD was between 0.16 – 2.09, 0.21 – 0.38 and 3.88 – 7.61 respectively. A total of 13 marker-trait associations (MTA) for the oil and protein contents and 29 MTAs for fatty acid were identified across different chromosomes of soybean. The study demonstrates that NIRS may be utilized for estimation of nutrients in soybeans.

Keywords: *NIRS, Nutritional contents, Soybean, MTAs, Quantitative traits loci*

APGDNGC013

Genetic Diversity of Gamma-irradiated White Guinea Yam revealed by Flow-Cytometer and SNP markers

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ABSTRACT

White Guinea yam (*Dioscorea spp.*) is a highly valued staple crop, yet its genetic improvement is hindered by inconsistent flowering, polyploidy, and both self- and cross-incompatibility. To overcome these limitations, mutation breeding has been explored as a strategy to broaden genetic diversity. In this study, two improved yam varieties, *Asiedu* and *Kpamyo*, were subjected to gamma irradiation at doses of 20, 40, and 60 Gy, alongside a non-irradiated control (0 Gy). Leaf samples from the M2 population were analyzed 12 weeks after planting using flow cytometry for ploidy assessment while SNP markers were used for DNA fingerprinting. Three ploidy groups (2x, 3x, and 4x) were identified, with proportions of 50% diploids, 12.5% triploids, and 37.5% tetraploids, indicating dose-dependent variation in chromosome sets. Genotyping with 619 SNP markers revealed moderate genetic diversity among the mutants, with an average heterozygosity of 0.281, minor allele frequency of 0.182, and polymorphic information content of 0.237. Cluster analysis grouped the genotypes into three major clusters: Cluster 1 contained *Kpamyo* and *Asiedu* at 40 Gy; Cluster 2 included only the *Asiedu* control; and Cluster 3 comprised *Asiedu* (20 and 60 Gy) and *Kpamyo* (0, 20, and 60 Gy), which further subdivided into three subgroups based on treatment-specific genetic similarities. This study provide a valuable insight for generating novel diversity in yam, thereby supporting breeding strategies for crop improvement in this genetically constrained species.

Keywords: *Flow cytometry, Gamma radiation, SNP markers, Yam*

APGDNGC014

Genome-Wide Characterization of Stress-Responsive Aquaporin Gene Family in *Dioscorea* speciesChukwurah, P. N.^{1,2}, Chineke, D. O.¹, Uyoh, E. A.¹, Ntui, V. O.^{1,2*}¹Department of Genetics and Biotechnology, Faculty of Biological Sciences, University of Calabar, Calabar, Cross River State, Nigeria²African Genome Center, University Mohammed VI Polytechnic, Ben Guerir, Moroccopnchukwurah@unical.edu.ng, ochineke@unical.edu.ng, uyoh_gen@yahoo.com,
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Abstract

Abiotic stress significantly limit agricultural productivity globally, with major impacts on key crops in sub-Saharan Africa, including yam (*Dioscorea* spp.). Aquaporins (AQPs), a family of membrane channel proteins, facilitate the transport of water and small solutes across biological membranes and play critical roles in plant nutrient uptake and stress responses. In this study, we conducted a comprehensive genome-wide analysis of AQP genes across several yam species within the *Dioscorea* genus. Using domain and motif characterization alongside phylogenetic clustering with AQP families from both model (e.g., *Arabidopsis*) and non-model (e.g., cassava, sweet potato) species, we identified over 90 AQP genes in yam. These genes were classified into four sub-families - plasma membrane intrinsic proteins (PIPs), nodulin-like intrinsic proteins (NIPs), tonoplast intrinsic proteins (TIPs), and small intrinsic proteins (SIPs), and formed distinct phylogenetic clades consistent with established plant AQP classification. Motif analysis revealed 12 conserved motifs characteristic of the aquaporin superfamily distributed across the four major subfamilies. Furthermore, promoter analysis of 30 *Dioscorea* accessions uncovered *cis*-acting regulatory elements (CAREs) associated with responses to both abiotic and biotic stresses, indicating a strong regulatory potential for stress adaptation within the *Dioscorea* species. The AQP genes identified in this study could serve as valuable molecular targets for enhancing abiotic stress resilience in yam breeding programs.

Keywords: *Dioscorea* species; Genome-Wide; Aquaporins; Stress; AQPs

APGDNGC015

Assessment of genetic diversity among Pro-vitamin A maize (*Zea mays L.*) inbred lines using single nucleotide polymorphism (SNP) markers

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Abstract

Background: maize is one of the most important cereals in the world. To maximize hybrid potential, knowledge and understanding of genetic diversity is crucial. The objectives of this study were to examine the population structure, genetic diversity and identify the best putative hybrid combinations of newly developed 110 maize inbred lines using single nucleotide polymorphism (SNP) markers. Leaf samples of the 110 inbred lines were genotyped using mid-density 3305 DArTAG -based SNP markers. Following quality checks, 2135 SNP markers were retained for further analysis. Polymorphic SNP markers averaged 0.37 and were well distributed across the genome. On average, 213 SNP markers were mapped per chromosome, with chromosome 6 having the highest number of markers (283). The principal component analysis (PCA) results demonstrated that PC1 explained 41% of the total variation observed among the studied inbred lines while PC2 account for 14% of the total variation. The minor allele frequency and observed heterozygosity ranged from 0.05 to 0.50 and 0.1 to 0.5, respectively. Analysis of molecular variance indicated genetic differentiation among and within groups and the pairwise genetic distance had a mean of 0.37, indicating the existence of substantial genetic variation in the germplasm panel. Wide genetic variability existed among the inbred lines, making all possible cross combinations of putative parents difficult. Therefore, planned crosses involving representative lines from opposing heterotic groups would be required. The results of this study would help breeders in developing breeding strategies for sustainable genetic improvement in maize.

Keywords: genetic variation, heterotic groups, maize hybrid, molecular markers

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