

MASTER OF SCIENCE
PLANT BREEDING

RESPONSE OF SOYBEAN (*Glycine max* (L.) Merr.) ACCESSIONS TO CRYOPRESERVATION BY DROPLET VITRIFICATION

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PLANT BREEDING

Soybean (*Glycine max* (L.) Merr.) is one of the major crops of global economic importance because it has high levels of protein and oil. Various *in situ* and *ex situ* methods of germplasm conservation are available for soybean but not for indefinite periods. The seeds have short lifespan because of the problems of its short-lived viability. Cryopreservation (storage in liquid nitrogen at -196°C) is an appropriate indefinite storage method for seeds with short lifespan and different protocols of it are available even for similar crop types, although the protocols require modification before they can be adapted to soybean. This experiment was carried out with the objective of evaluating the response of four soybean accessions to cryopreservation. The experiment was carried out via completely randomized design with two factors which include the accession and the exposure duration to cryoprotectant solution having four and three levels, respectively. The seeds of soybean accessions were surface disinfected or sterilized and soaked in sterile distilled water for a period of 2 hours, followed by embryo excision. The embryos were cultured on MS agar medium in a Petri dish within an hour of excision and until they were used for experimentation to compare two cryopreservation protocols. The embryos were exposed to loading solution (MS with 0.4M sucrose and glycerol) and also treated with the plant vitrification solution #2 (PVS2) before cryopreservation by droplet vitrification, whereas for the V-cryoplate protocol, the embryos were encapsulated with calcium alginate matrix on the cryoplate before exposure to PVS2. Pretreated embryos were rapidly immersed into liquid Nitrogen for a period of 1 hour, and then thawed in a 1.2 M sucrose recovery solution. The parameters evaluated for this experiment included survival rate (%), browning rate (%), number of leaves and number of roots per plant at 14- and 21-days post cryopreservation, as well as root length on the 28th day after cryopreservation. The highest average survival rate of soybean accessions was 79.37% with the droplet vitrification protocol compared to 40.56% with the V-cryoplate protocol. The most average survival rate occurred following 30 minutes of exposure to PVS2 with either of the two protocols. Accession TGM861 had the most survival (84.16%) with droplet vitrification followed by accession TGM976 (77.50%). The least survival occurred with accession TGM1401 (32.50 %). For the V-cryoplate, accession TGM1418 had significantly higher survival rate (44.58%) compared to the other accessions. The genotype response to stress varied significantly with TGM 1418 having a significantly higher browning rate (26.66%) than TGM861 (15.00%) following the droplet vitrification protocol. Accession TGM861 had significantly more browning rate (15%) than accession TGM1401 (0.91%) following the droplet vitrification protocol. All recovered embryos appeared physiologically normal. This study demonstrates that the viability of soybean accessions can be maintained indefinitely through cryopreservation. Future studies to screen several accessions of soybean with the droplet vitrification protocol for validation of this protocol prior to routine use is recommended.

Key Words: Cryopreservation, embryos, Cryoprotectant, Survival, Recovery

ASSESSMENT OF VARIABILITY AMONG SWEET POTATO (*Ipomoea batatas* (L.) Lam) GENOTYPES USING TRAITS PROFILING AND SINGLE-NUCLEOTIDE POLYMORPHISM (SNP) MARKERS

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PLANT BREEDING

Sweet potato is a globally significant crop and serves as a major source of food and income generation for many farmers in Africa including Nigeria. Apart from its adaptability to different agroecological conditions, the value of the crop does not arise only from its nutritional benefits, which include high levels of vitamins and antioxidants. Its genetic diversity is important for breeding programs working to increase disease resistance, yield, and nutritional content. Despite their importance, the genetic and phenotypic diversity of sweet potato has not been well explored, there are limiting efforts to improve the genetics of sweet potato. New advanced methods for characterizing genetic diversity, such as the use of SNP markers, have been introduced. This study aimed at evaluating genetic diversity among sweet potato genotypes via single-nucleotide polymorphism (SNP) markers and phenotypic profiling. Phenotypic data were analysed and genotypic data were analysed using 9,647 informative SNP markers for 71 sweet potato genotypes. The number of flowers, non-commercial storage roots, vine internode length and the root yield components showed significant variation ($P \leq 0.001$) among genotypes. Strong positive correlations ($r > 0.80$) were found between storage root weight and commercial root yield. Principal component analysis (PCA) of the observed traits revealed seven components that explained 75.68% of the total variability. Hierarchical clustering using Ward's method grouped the genotypes into four major clusters, with Cluster I exhibiting the highest genetic diversity. The Multi-Trait Genotype Ideotype Distance Index identified the top 15 sweet potato genotypes, of which the highest was SP3, followed by SP22, and SP59. Sweet potato genotype genetic diversity based on SNPs presented an expected heterozygosity of 0.10 to 0.82 and an observed heterozygosity of 0.00 to 0.85. Four distinct clusters were identified through the Bayesian Information Criterion (BIC). Principal component analysis (PCA) based on SNP markers explained 37.2% of the total variation across the first two components, effectively separating genetically distinct clusters. Subpopulation analysis revealed admixture in some genotypes, with subpopulation 1 being the most diverse. This study revealed that most of the genotypes showed genetic diversity on the basis of phenotypic and genotypic analysis. Therefore, these findings reveal the ability of these genotypes to be used in breeding programs. This study revealed substantial genetic and phenotypic diversity in sweet potato genotypes, which include traits important for breeding programs and classified genotypes on the basis of high-yield, disease resistance, and nutritional value.

Key Words: Breeding programs, Genetic diversity, Phenotypic traits, SNP markers, sweet potato

**VALIDATION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNP) MARKERS
LINKED TO KEY YIELD RELATED TRAITS IN WHITE GUINEA YAM
(*Dioscorea rotundata* POIR)**

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PLANT BREEDING

In Sub-Saharan Africa, white Guinea yam (*Dioscorea rotundata* Poir) is a crucial staple crop contributing to livelihoods and food security. Nonetheless, the long breeding cycle associated with conventional methods constrains the development of new yam varieties. This study aimed to validate single-nucleotide polymorphism (SNP) markers associated with essential yield-related traits to improve breeding efficiency via marker-assisted selection (MAS). The main objectives were to assess SNP marker precision and efficacy and identify desirable alleles within breeding populations for essential traits. The study was conducted at the International Institute of Tropical Agriculture (IITA) in Ibadan, Nigeria, utilizing 3008 progenies selected from seedling nursery trials. Data on phenotypes and genotypes, including plant sex, tuber characteristics, disease resistance, flower intensity, and yield, were collected. The validation of SNP markers utilized logit regression models, 5-fold cross-validation analysis, network visualization analyses, and correlations to assess their predictive ability. Considering the favorable alleles, the findings showed that the markers snpDR00152 and snpDR00153 obtained accuracy rates of 96.5% and 93.1%, respectively, for early plant sex determination. The marker snpDR00168 associated with tuber appearance, achieved an accuracy of 89% while snpDR00160 and snpDR00162 demonstrated impressive accuracy rates of 98% and 98.8%, respectively, in predicting susceptibility to yam mosaic virus. Additionally, snpDR00159 was a reliable marker for flower intensity, whereas snpDR00164 exhibited moderate accuracy (65.38%) in yield prediction. This was attributed to the inherent complexity of yield as a polygenic trait influenced by numerous genetic and environmental factors, and the unbiased selection of a diverse genotype panel for marker validation, which prioritizes broad applicability over potentially inflated accuracy from pre-selected high-yielding lines. These findings demonstrate the potential for the advancement of SNP markers in improving yam breeding cycles and allowing the accurate selection of high-yield genotypes that are resistant to disease and desired by the market. The study highlights important breeding issues in White Guinea yam by laying the foundation for the integration of validated markers into MAS systems. This study contributes significantly to the development of yam genomics resources and their deployment in breeding programs.

Key Words: Marker assisted selection, Single Nucleotide Polymorphism Markers, White Guinea yam

SCREENING AFRICAN RICE GERMPLASM AND ADVANCED ELITE BREEDING LINE FOR DROUGHT TOLERANCE

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PLANT BREEDING

Rice is one of the most important crops worldwide, particularly in sub-Saharan Africa (SSA); however, drought stress is a major factor adversely affecting its productivity. This study was conducted to screen African rice germplasms and advanced elite breeding lines for their response to drought stress and to select outstanding genotypes. A total of 16 upland and 25 lowland rice genotypes from the Africa Rice Center's rainfed lowland rice breeding unit, which is in IITA, Ibadan, Nigeria, were used for the study. Each set of genotypes was tested under Control (Co) and Stress (DS) conditions under both low and upland ecologies. Compared with DS, Co presented greater heritability for some agronomic traits measured under upland conditions, such as biomass, day to 50 % flowering, and the number of panicles per plant, and for those measured in lowlands, greater heritability was observed for grain yield, day to 50% flowering, and the number of panicles per plant. The most promising genotypes with the highest grain yield above the checks under both well-watered and drought-stress conditions in upland ecology were ART331-22-B-1-B-B (3620 kg/ha Co, 2880 kg/ha DS, with 20.44% yield reduction), ART331-245-B-B-B (3510 kg/ha Co and 2710 kg/ha DS, with 26.96% yield reduction), ART331-39-B-1-B-B-B (3300 kg/ha Co and 2820 kg/ha, with 14.54% yield reduction), and ART331-195-B-1-B-B (3300 kg/ha Co and 2800 kg/ha DS, with 15.15% yield reduction). The most promising genotypes in lowland ecology are ART397-5-2-1-1 (5180 kg/ha Co, 4740 kg/ha DS, 8.49% yield reduction under stress), which surpasses all the checks; ART143-150-B-B-B-B-B (5050 kg/ha Co and 4590 kg/ha DS, with 9.10% yield reduction); ARC 1-341-B-1 (5010 kg/ha in Co and 4510 kg/ha DS, with 9.98% yield reduction); and ARC 121-TGR4-2-3-MB1-1 (4545 kg/ha Co and 4060 kg/ha DS; 9.78% yield reduction). Among all the materials evaluated in the present study, five genotypes were repeated under upland and lowland conditions. Among these, ART1233-B-B-B-B-B performed best in both upland (3380 kg/ha Co, 2060 kg/ha DS) and lowland (2650 kg/ha Co, 2400 kg/ha DS) settings. ART1206-B-B-B-B-B, ART1215-B-B-B-B-B, ART1225-B-B-B-B-B, and ART1239-B-B-B-B-B produced favourable results above 3000 kg/ha under Co in upland environments. Some genotypes had good percentage recovery from drought. In the upland, these were ART1233-B-B-B-B (65.84%), ART331-245-B-1-B-B (64.92%), and AR19U001-F4-57-B (59.89%), and in lowland ecology, ART66-6-1-1-B-B (96.63%), ARC 141-TGR 7-3-ARC2-MB1-2 (96.25%) and ART1474-B-B-B-1-3 (92.13%) were recorded. The best-yielding lines and those with a relatively high recovery percentage under drought stress could be exploited further to improve varieties for drought tolerance in future breeding programs.

Key Words: rice, upland genotypes; lowland genotypes; heritability, drought stress; grain yield

GENETIC DIVERSITY AND POPULATION STRUCTURE OF SOYBEAN [*Glycine max.* (L.) Merrill]

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PLANT BREEDING

Soybeans (*Glycine max*) is an essential crop of global economic importance. It is popular for its quality oil rich in polyunsaturated fats that helps lower cholesterol and has the highest protein content. Soybean improvement is key to ensure the development of varieties with improved oil and protein content. To realize this, assessing genetic diversity is primordial to identify reservoirs of beneficial genes for exploitation in the breeding program. This study aimed to use phenotypic and molecular-based approaches to decipher the level and extent of genetic diversity in a breeding population of soybean. Seventy soybean advanced breeding lines were evaluated using a 7×10 alpha lattice design in three replications across three locations (Ikenne, Ibadan, and Mokwa) during the 2024 growing season. In addition, the 70 advanced lines were also genotyped using the 1000K chips Agriplex markers. The results showed significant ($p \leq 0.05$) genotype, environment, and genotype by environment interaction effect for grain yield and other agronomic parameters studied. The genotype TGx 1904-6F had the highest grain yield (11362 kg/ha) and seed weight (1036 kg). While genotype TGx_24_27NG-0056 had the shortest day to 50% flowering (42 days), genotype TGx_24_42NG-0103 had the earliest days to 95% maturity (105.76). Broad-sense heritability estimates vary from low in grain yield (7%) to being high in days to 50% flowering. Principal component analysis showed grain yield, hundred seed weight, total seed weight, average plant height, days to 95% maturity, early shattering score showed high contribution to the three principal components with eigenvector greater than 1.0. Dendrograms from phylogenetics analysis identified two distinct groups with contrasting characters based on the selected agromorphological traits. From the final genotyping results, 982 quality SNP markers were retained after quality control procedures. The diversity indices for these markers showed an average observed and expected heterozygosity of 0.08 and 0.39, respectively, average minor allele frequency of 0.30, and polymorphic information content of 0.15. The population stratification as defined by Admixture ancestry model, principal component analysis, and discriminant analysis of principal component revealed two subpopulations. The dendrogram resulting from the phylogenetic analysis based on the SNP marker showed two distinct genetic groups with each groups having a minimum of two sub-groups. The first main group comprising 20 soybean genotypes with an average genetic distance of 0.33 while the second group comprised 50 soybean genotypes with an average genetic distance of 0.44. The results obtained demonstrates the importance of assessing genetic diversity in soybean breeding populations to identify beneficial genes for improvement of agronomic traits. Overall, the study contributes to the development process of improved soybean varieties, which is critical for meeting the increasing global demand for soybean products.

Key Words: Cluster analysis, Genetic distance, Genetic diversity, SNP Markers

INVESTIGATING THE GENETIC DIVERSITY OF YAM (*Dioscorea* spp.) IN WEST AND CENTRAL AFRICA: IMPLICATIONS FOR CONSERVATION AND BREEDING

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PLANT BREEDING

Millions of people in tropical and subtropical nations depend on yams (*Dioscorea* spp.), which are vital tuber crops for nutrition, food security, and cultural customs. Despite their importance in agriculture and the economy, little is known about the genetic diversity among many yam species. This work examined genotypic information from 1,247 yam accessions that were recovered from a previously sequenced yam collection from six African countries (Nigeria, Benin, Uganda, Ghana, Côte d'Ivoire, and the Democratic Republic of the Congo). A genetic study was performed using 7,648 single-nucleotide polymorphisms (SNPs). The yam genome has an inconsistent distribution of SNP markers, with minor allele frequency (MAF) = 0.213 and polymorphism information content (PIC) = 0.232 on average, expected heterozygosity (H_e) = 0.288, and observed heterozygosity (H_o) = 0.259. Mutation analysis revealed a transition (T.s.) rate of 61.08% and a transversion (T.v.) rate of 38.91%, indicating a relatively high level of genetic variation. The accessions were divided into six clusters based on population structure analysis using multiple approaches, including parametric (ADMIXTURE, DAPC) and nonparametric (hierarchical clustering) methods. These clusters exhibited moderate admixture and high genetic diversity within population than between them. DAPC identified six distinct clusters, maximizing within-group variation while maintaining strong genetic differentiation. PCA confirmed this structure, aligning with ADMIXTURE and DAPC. Hierarchical clustering, based on genetic distance, further validated other findings. The consistency across all methods suggests that any of them can be reliably used in future research on *Dioscorea* genetic diversity. This study provides significant insights into the genetic diversity and organisation of African yam germplasm, which will be useful for breeding programs, conservation efforts, and yam genetic improvement. The results demonstrate the importance of the use of molecular approaches in breeding strategies to increase yam productivity and resistance under a variety of agroecological conditions.

Key Words: Yam (*Dioscorea* spp.), Genetic diversity, SNP markers Population structure analysis, ADMIXTURE, DAPC, PCA, hierarchical clustering.

GENETIC VARIABILITY, HERITABILITY AND CORRELATIONS BETWEEN PROVITAMIN A AND AGRONOMIC PERFORMANCES IN TROPICAL MAIZE (*Zea mays* L.) HYBRIDS

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PLANT BREEDING

Vitamin A is primarily absent from most traditionally consumed maize thus leading to Vitamin A Deficiency (VAD), a condition prevalent among regions who rely heavily on maize-based diets. Developing maize hybrids with higher Provitamin A (PVA) concentrations could be crucial in addressing VAD. The selection efficiency for mechanisms governing the PVA trait and grain yield can be broadened using estimates of genetic variability and heritability. The primary goal of this study was to determine the genetic variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), correlations and heritability of carotenoids, PVA and agronomic traits in tropically adapted PVA maize hybrids. The parental inbred lines for the crosses were divided into three groups based on descriptions, High β -carotene (HBC), High Lutein and Low β -cryptoxanthin (HLULBCRY) and High Zeaxanthin and β -cryptoxanthin (HZZ&BCRY). The groups were divided into six mating sets using North-Carolina II Design. Fifty-four maize hybrids and two commercial checks were evaluated in Alpha Lattice Design with two replications at the trial fields of Ikenne and Zaria, Nigeria in 2024 to assess the magnitude of genetic variability, narrow sense heritability and correlations for the traits under study. The results indicated that PCV was generally higher than GCV for all carotenoids, PVA and agronomic and grain yield (GY). High heritability estimates were observed for PVA (69.07-88.07%), GY (59.65%) and Ear Aspect (EA) (50.15%). The PVA mean values ranged from 14.20-52.74 $\mu\text{g g}^{-1}$. Almost 100% (98.21%) of all the evaluated hybrids had PVA levels that surpassed the set minimum global target ($\geq 15 \mu\text{g g}^{-1}$). Hybrid 6 (TZi2066/TZi1715) had the highest PVA mean concentration, hence is the prime candidate for breeding for a high PVA variety. Hybrid 19 (TZI2006/TZI2161) exhibited the highest GY mean value (7.99 t^{-1}) in Ikenne. The ANOVA showed significant difference ($p < 0.05$). Among genotypes on all carotenoids and PVA evaluated. PVA correlated negatively with Lutein (LT), Zeaxanthin (ZX), β -cryptoxanthin (BCR), α -carotene (AC) and Total xanthophyll (TXA) and positively with Cis-13 (C13), Trans (TRNS), Cis-9 (C9) and Total β -carotene (TBC). TBC did not correlate with any other carotenoids evaluated in their study. GY correlated positively with Ear height (EH) and Ear per plant (EPP). The identification of a high-yielding hybrids with relatively high provitamin A content, indicated the possibility of selecting hybrids with superior agronomic performance and high concentrations of provitamin A and other carotenoids in maize.

Key Words - Genetic Variability, Heritability, Provitamin A, Tropical Maize, Correlations

COMBINING ABILITY AND HETEROTIC GROUPING OF LINES SELECTED FOR RESISTANCE TO MAIZE LETHAL NECROSIS (MLN) UNDER STRIGA-INFESTED AND STRIGA-FREE ENVIRONMENT

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PLANT BREEDING

Striga hermonthica (Del.) Benth and maize lethal necrosis (MLN) limit maize production in sub-Saharan Africa (SSA), causing yield losses of up to 100% under severe infestation. The Maize Improvement Program (MIP) in International Institute of Tropical Agriculture IITA has developed a significant number of inbred lines resistant to Striga, however, there are currently no commercially available hybrids resistant to both MLN and Striga. The objectives of the study were to examine the combining ability effects of recently developed lines for grain yield and other agronomic traits under Striga field infestation, non-infested and optimal condition, use two tropical Striga-resistant testers to determine the heterotic affinities of the MLN inbred lines, employ DArTag markers to assess the genetic diversity of the MLN lines, and identify inbred lines carrying favourable MLN single nucleotide polymorphism (SNP) alleles. A total of 48 hybrids, derived from a line $\times$ tester mating design using 24 inbred lines and two testers, were evaluated across four locations in Nigeria in one year under both Striga-infested and Striga-free field conditions. Substantial genetic variability was identified among the hybrids that were evaluated primarily under the Striga-free environment. Several lines were identified with favourable GCA effects under each research condition with the line (TZISTR1233/KS23-3/TZISTR1233)-50-2 potentially possessing favourable alleles for grain yield improvement across all the test environments. The genetic inheritance of grain yield along with related traits under Striga-infestation and Striga-free environments was predominantly governed by additive gene action but Striga resistance indicator traits were under the influence of non-additive gene actions. Two heterotic groups were identified through both HGCAMT classification and SNP markers methods, with high concordance between the heterotic patterns using HGCAMT under Striga-infested and SNP markers. Four lines were identified as possessing homozygous condition of the three KASP markers favourable alleles indicating resistance to MLN.

Key Words: Combining ability, Diversity Array Technology (DArT) markers, heterotic grouping, hybrids, Kompetitive allele-specific PCR (KASP), maize lethal necrosis, Striga,

DOCTOR OF PHILOSOPHY
PLANT BREEDING

GENETIC DIVERSITY IN NIGERIAN TARO [*Colocasia esculenta* (L.) Schott] GERMPLASM

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PLANT BREEDING

Taro is a resilient, underexploited tropical corm-producing crop that plays a vital role in the nutritional and economic livelihoods of many households in Nigeria. However, its production and productivity are constrained by the incidence of diseases, low-input farming practices and inadequate genetic improvement efforts. To improve the yield and quality of taro in Nigeria, adequate information is needed on the presence of heritable genetic variation among available collections. However, limited information is available on the level of variability among cultivated taro in Nigeria. This study was carried out to assess the extent of phenotypic and molecular diversity among some taro accessions collected from major taro-growing agroecologies in Nigeria. Four hundred and ninety taro landraces comprising 215 Dasheen and 275 Eddoe gene pools were assembled from farms and markets across seven States (Oyo, Kwara, Ekiti, Ondo, Akwa Ibom, Ebonyi and Anambra) in humid forest and derived savanna agroecologies in Nigeria. The 490 landraces were genotyped using 4,748 Diversity Array Technology sequence-based Single Nucleotide Polymorphism (DARtseq-SNP) markers, 3,047 of which were retained after quality filtering. A subset (114) comprising 65 landraces from the first collection and 49 landraces from the second collection were planted in September 2021 and March 2022 respectively, following their collection times using 27 agromorphological descriptors. Phenotypic data were subjected to descriptive statistics, cluster analysis and analysis of variance, while hierarchical clustering, population structure and analysis of molecular variance were carried out on the molecular data. The phenotypic and molecular characterization of the taro landraces revealed higher genetic diversity among the Eddoes than among the Dasheens. For all the quantitative traits, the estimates of genetic variance were higher than those of environmental variance. The total yield (TY) of the landraces ranged from 100 to 32,200 kg/ha (mean = 10,600 kg/ha) for the phenotyped September 2021 set while the range was from 100 to 23,300 kg/ha (mean = 6,800 kg/ha) for the March 2022 set. The taro landraces in both planting clustered into four groups based on 10 phenotypic traits at a threshold of 1.5. Highest yield was recorded in K-I-O1-S1 and A-I-IE Cormel 1 (32,200 kg/ha) from the September 2021 planting and AKN 1-P5 (23,300 kg/ha) from the March 2022 planting. Estimates of gene flow ($N_m = 0.353$) revealed intermixing of landraces among the States of collection. Gene flow was highest (1458.98) between landraces from Anambra and Ondo States and lowest (0.06) between Anambra and Kwara States. The population structure and hierarchical clustering based on the DARtseq-SNP markers delineated four clusters, one which comprised Dasheens, while three comprised Eddoes. The variation between gene pools (49%) was higher than within gene pools (32%). The variation among the States of collection was high (41%), while the variation among individuals within the gene pools (18%) and States of collection (19%) were relatively low. A wide level of genetic diversity was found between the taro gene pools and among the taro landraces from Nigeria. The findings constitute a valuable resource for the genetic improvement of taro in Nigeria.

Key Words: Dasheen, Eddoe, Taro genetic resources, DARtseq-SNP markers, Nigeria

Word Count: 495

**MULTI-TRAIT SELECTION, GENETIC DIVERSITY, AND GENOME-WIDE
ASSOCIATION STUDY FOR AGRONOMIC AND QUALITY TRAITS IN WATER
YAM (*Dioscorea alata* L)**

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PLANT BREEDING

Water yam, the most widely cultivated yam species, possesses good agronomic attributes. However, its production and use are limited due to biotic and abiotic stresses and lower food quality, including low-quality attributes. Breeding for superior genotypes satisfying farmer and end-user needs has been challenging. In addition, knowledge of the architecture and extent of genetic variability within a developed breeding population is essential for the dissection of the genetic basis of economic traits. This study aimed to (i) assess a panel of *D. alata* genotypes from multiple parents for selection of desirable genotypes/ideotypes based on their agronomic and quality characteristics; (ii) assess the genetic diversity by combining phenotypic and molecular markers; and (iii) identify genomic regions associated with agronomic and quality traits using genome-wide association study. Genetic diversity and Genome-Wide Association studies were carried out on a panel of 404 genotypes, and 285 available genotypes among the panel were evaluated based on multi-trait genotype-ideotype distance index (MGIDI) selection. All the studies were performed on eight phenotypic traits and molecular data of 4,646 single nucleotide polymorphism (SNP) markers were used for genetic diversity and genome-wide association studies. The SNP markers used in this study were developed from the Diversity Array Technology platform. Significant variation was detected ($p < 0.01$) in the performance of the genotypes for all the traits in the MGIDI-based selection study. A moderate to high broad-sense heritability ($30\% < H^2-H2 \geq 60\%$) was observed for all traits except for tuber pound ability ($H^2 < 30\%$). Positive correlations were exhibited among the traits. The genotypes were grouped into three clusters through hierarchical clusters, demonstrating the possibility of selecting diverse genotypes for multiple traits. Plant vigor and number of tubers per plant positively contributed ($p < 0.01$) to the yield per plant in the path analysis. Using MGIDI, a total of 39 most promising genotypes were identified. In the genetic diversity study, significant phenotypic variation ($p < 0.001$) was observed among the genotypes, with heritability estimates ranging from low in PndT (20%) to high in YAD and DMC (75%), demonstrating the usefulness of all the assessed traits in discriminating the yam genotypes. Cluster analysis based on phenotypic data demarcated two significant groups. In contrast, population structure analysis revealed three distinct subpopulations with a minor admixture (26.73%), corroborating the analysis with SNP markers indicating three genetic groups. However, joint analysis of the phenotypic and genotypic data revealed two genetic clusters that could be useful for identifying heterotic groups. Association mapping analysis revealed 23 SNP markers linked to the eight traits under study. The phenotypic variance explained by these markers varied from 0.01% in plant vigor to 11.35% in tuber yield. Gene annotation revealed 75 candidate genes near these markers that are essential for plant innate immune signaling, plant growth and development, enzymatic browning, and carbohydrate biosynthesis pathways. Several favorable alleles were identified as critical determinants of the studied traits. These findings offer valuable insights into the genetic control of these traits, paving the way for accelerated improvement of *D. alata* through marker-assisted selection.

Key Words: Multi-trait genotype-ideotype distance index, Water yam genetic diversity, Genome-wide association studies, Yam agronomic and quality traits, Putative genes.

EVALUATION OF TROPICAL PROVITAMIN A MAIZE (*Zea mays* L.) INBRED LINES FOR RESISTANCE TO EAR ROT INFECTION AND MYCOTOXIN CONTAMINATION

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PLANT BREEDING

Tropical maize production is threatened by pre- and post-harvest aflatoxin and fumonisin contamination causing economic losses and affecting humans and domestic animal health. *In vitro* studies have shown that high concentrations of provitamin A (PVA) carotenoids effectively inhibit fungal growth and mycotoxin biosynthesis. Therefore, development of PVA biofortified maize is crucial in reducing Vitamin A deficiency (VAD) and characterization of resistance to mycotoxin accumulation. The objective of this dissertation was to determine combining ability, gene action and mode of inheritance for aflatoxin resistance, carotenoid content and grain yield, and to investigate the association between carotenoid concentrations in maize and resistance to mycotoxin. A set of 120 PVA hybrids generated by crossing 60 PVA inbreds with two PVA testers (low and high PVA; 14.4 and 25.0 µg/g, respectively), and four checks were evaluated for carotenoid content and grain yield in a 31×4 alpha-lattice design with two replications over two years at two locations in Nigeria. Kernels of the testcrosses were inoculated with a highly toxigenic strain of *Aspergillus flavus* to evaluate fungal growth and aflatoxin accumulation. A second study was conducted on a selection of 21 PVA inbred lines among the 60, identified resistant and susceptible to aflatoxin to investigate and confirm their resistance to ear rots contamination, and both aflatoxin and fumonisin accumulation and foliar diseases in a detached leaf assay. The inbreds and two resistant checks were inoculated with toxigenic isolates of *A. flavus* and *Fusarium verticillioides* and evaluated in field trials at two locations in Nigeria during the dry- and rainy seasons for ear rots and mycotoxin resistance. Highly significant ($P \leq 0.001$) combining ability effects indicated that additive effects were more important than non-addictive gene action in determining these major traits (ratio GCA/SCA > 0.5). Inbreds TZI2071 and TZI1715 were identified best combiners with significant negative GCA for aflatoxin and *A. flavus* infection and significant positive GCA for β-carotene (BC) and PVA. Six best performing testcrosses combined high yield (exceeding three of the checks), high PVA content and were tolerant to aflatoxin with TZI2025×T1 (5205 kg/ha, 15.0 µg/g, 4.5 ppb, Log₁₀ values) and TZI1715×T2 (5230 kg/ha, 15.1 µg/g, 4.4 ppb) meeting the HarvestPlus target (15µg/g). PVA had significant ($P \leq 0.05$) negative correlations with *Aspergillus* ear rot (AER) ($r = -0.28$), *Fusarium* ear rot (FER) ($r = -0.37$), aflatoxin ($r = -0.15$ to -0.23), and fumonisin ($r = -0.27$) indicating that maize with high PVA accumulated less mycotoxin than those with low to medium PVA. The most promising inbreds TZI1715, TZI2005-1, and TZI2071 were resistant to mycotoxin and tolerant to foliar diseases under laboratory and natural field infestation are potentially valuable lines for use in breeding programs. TZI1715, being the most resistant within and across locations combined resistance to AER, FER, aflatoxin, and fumonisin with desirable GCA for BC and PVA. In summary, inbreds with desirable GCA effects for the major traits can be used to develop PVA hybrids to address VAD and reduce aflatoxin and fumonisin exposure, demonstrating the feasibility of enhancing maize carotenoids without negatively impacting grain yield.

Key Words: General combining ability, Specific combining ability, Ear rots, Aflatoxin, Fumonisin, Provitamin A, Tropical maize

IMPROVEMENT OF COWPEA [*Vigna unguiculata* (L.) Walp] USING PHENOTYPIC AND GENOMIC TOOLS

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PAU-UI-0611

PLANT BREEDING

Cowpea is one of the most important legumes produced and consumed in sub-Saharan Africa (SSA), due to its high nutritional value in the human diet. However, its production is primarily carried out by smallholder farmers, who often achieve grain yields below the crop's potential because of various biotic and abiotic stresses. Identifying superior genotypes with multiple desirable traits remains a major challenge for breeders. This study integrated phenotypic and genomic approaches to identify high-performing recombinant inbred lines (RILs) and to dissect the genetic architecture of yield- and seed-related traits in cowpea under rainfed conditions and glasshouse. Two sets of F6:7 RILs were developed using the single-seed descent method: 346 lines from the cross RP270 × CB27 and 248 lines from the cross RP270 × BRSImponente. The RILs and parental lines were evaluated over two years in both field and glasshouse trials using a lattice design with three replications at IITA, Ibadan, Nigeria. The cowpea mid-density genotyping panel, consisting of 2,602 high-quality DArTag single nucleotide polymorphisms (SNPs), was used to genotype the RIL population for QTL analysis. Three multi-trait selection indices—multi-trait genotype–ideotype distance index (MGIDI), factor analysis and ideotype BLUP (FAI-BLUP), and the Smith-Hazel (SH) index were used at 10% selection intensity to identify superior genotypes. QTL analysis for seed size traits (seed length, seed width, seed thickness, hilum length, hilum width, and hilum area) was conducted across four environments to improve mapping accuracy and stability. Data collected were subjected to analysis of variance (ANOVA) at $\alpha = 0.05$. Significant genetic variation was observed among the RILs for all measured traits, and environmental mean squares were significant for all traits except days to first flowering and grain yield. High heritability estimates (ranging from 64% to 97%) were recorded across individual seasons, indicating that the traits were highly heritable. Twenty-three superior RILs were consistently selected across the three indices. A total of 37 QTLs for yield-related traits—including days to first flowering (NDFW), number of branches per plant (NBrch), number of peduncles per plant (Nped), peduncle length (PedLt), pod length (PodLt), number of pods per plant (NPod), number of seeds per pod (NSP), 100-seed weight (100SW), and grain yield (GY)—were identified using the interval composite mapping additive model (ICIM-ADD), explaining up to 26.3% of the phenotypic variance with LOD scores up to 35.6. For seed size traits, in total, 174 QTLs were detected for seed size traits, with 18 stable QTLs common across environments. Colocalization of QTLs occurred in five major clusters on chromosomes 3, 4, 6, 7, and 8. For seed colour patterns, 116 pairs of digenic epistatic QTLs were identified, although they exhibited minimal effects compared to main-effect QTLs. Gene annotation and literature revealed 29 candidate genes associated with yield-related traits, 34 with seed size traits, and 14 involved in the flavonoid biosynthesis pathway for seed coat pigmentation. These findings provide a basis for further research on the genetics of important cowpea traits and support future work on map-based cloning of candidate genes and marker-assisted breeding programme in cowpea.

Key Words: *Vigna unguiculata*, multi-trait selection, High-yielding varieties, DArT technology, QTL mapping, Recombinant inbred lines

GENETIC ANALYSIS AND GENOME-WIDE ASSOCIATION STUDY OF SOME DROUGHT-RELATED TRAITS IN SOYBEAN [*Glycine max* (L.) Merrill]

TENENA SILUE
PAU-UI-0731 PLANT BREEDING

Soybean is an important legume crop valued for their oil and protein contents. However, yields in Africa remain less than half the global average, leading to insufficient output to meet the continent's growing demand. This yield gap is attributed to various constraints, with moisture stress, especially during the critical early establishment, flowering and pod-filling stages, being a major limiting factor. There had been some studies on moisture in other regions of the world using different germplasms from those we have in Africa. Therefore, this study was conducted to evaluate a population of soybean germplasm for genetic diversity, agronomic traits and trait association under drought stress conditions. A total of 150 soybean genotypes were evaluated under two contrasting water regimes across two growing seasons using a 10×15 lattice design with three replications. Drought stress was applied intermittently, starting with a 14-day drought period at 35 days after sowing, followed by a two-week irrigation phase, and a second drought period lasting seven days. These stress periods coincided with the critical flowering and pod-filling stages. Genotype selection was based on the Multi-trait Genotype-Ideotype Distance Index (MGIDI) to identify promising drought-resilient candidates. For genetic diversity analysis and Genome-Wide Association Studies (GWAS), the 150 genotypes were assayed using 59,126 Single-Nucleotide Polymorphism (SNP) markers. To evaluate combining ability, a half-diallel mating design was used to generate crosses among seven parental lines selected out of the 150 genotypes based on their drought tolerance and other agronomic traits. The resulting F₂ populations, along with their parents, were evaluated for agronomic traits during the rainy season at Ibadan and Ikenne using a 4×7 alpha lattice design. The study revealed significant genetic variation among soybean genotypes under both drought-stressed and well-watered conditions, with broad-sense heritability estimates ranging from 21.6% to 86.6%. Drought tolerance indices and a 20% selection intensity led to the identification of high-yielding, drought-tolerant genotypes, supported by a moderate positive correlation ($r = 0.38$) between yields in both water regimes. Fifty-two significant SNP markers were identified as being associated with grain yield and related traits under drought stress conditions. Based on candidate gene annotation and allele substitution effect analysis, twenty-one SNPs were informative for marker-assisted selection. The combining ability study exhibited that environmental factors significantly affected several traits. Likewise, genotypic variation was significant for most traits, though not for grain yield and pod clearance. Significant General Combining Ability (GCA) effects were observed for traits such as days to 50% flowering (41.9), plant height (139.8), number of branches (2.0), number of seeds per pod (0.70), 100-seeds weight (2.1) and grain yield (1854213.1), while Specific Combining Ability (SCA) was mostly non-significant except for a few traits. The GCA/SCA ratios ranging from 0.63 to 0.88 highlighted the predominance of additive genetic effects in the expression of the traits evaluated. Considerable genetic diversity was identified among the soybean genotypes under moisture stress at flowering and pod-filling stages. Drought-tolerant soybean genotypes and informative SNP markers provide valuable tools for marker-assisted selection. The predominance of additive genetic effects indicates strong potential for genetic improvement through conventional and molecular breeding.

Key Words: Drought stress, Multi-trait Genotype-ideotype Distance Index, Flowering, Pod-filling stages, Marker-assisted selection.

GENETIC ANALYSIS AND GENOME-WIDE ASSOCIATION STUDY OF DROUGHT ADAPTIVE TRAITS IN EXTRA-EARLY ORANGE MAIZE INBRED LINES

TEGAWENDE ODETTE BONKOUNGOU

PAU-UI-0593

PLANT BREEDING

Drought is a major constraint to maize production in Sub-Saharan Africa. It significantly reduces productivity, affecting the livelihoods of millions of people. Malnutrition due to a lack of essential nutrients like Vitamin A is another major challenge in many African countries. Breeding bio-fortified drought-tolerant maize varieties is a cheap and sustainable approach to addressing these issues. This study aimed to assess the performance of newly developed extra-early orange testcross hybrids under managed drought and well-watered conditions, examine the inheritance patterns in newly developed extra-early orange maize inbreds, assess the levels of genetic diversity and population structure of newly generated extra-early orange inbreds using phenotypic and SNP markers derived from high-density DArTseq genotyping and identify Quantitative Trait Loci (QTLs) associated with grain yield and associated traits under drought. A total of 36 drought-tolerant inbreds selected from a population of 187 extra-early orange flesh maize inbreds were crossed with five testers, to produce 180 testcrosses, with an additional 10 hybrids produced from a half-diallel crossing among the five testers. The 190 hybrids, along with six commercial checks, were evaluated under managed drought and well-watered conditions between 2021 and 2023. A 14×14 lattice design with two replications was used. The 187 orange inbreds were also evaluated under similar conditions as the testcrosses using 11×17 alpha lattice design with two replications and genotyped using 36697 SNP markers. Genetic variation for drought tolerance was present among the hybrids used in the study and facilitated the identification of stable and high yielding hybrids under managed drought and well-watered conditions. Twenty-nine hybrids were selected for superior drought tolerance based on Multiple Trait Base Index (MTBI) and Multi-trait Genotype Ideotype Distance Index (MGIDI) with 72% similarity. Hybrid TZEEIOR 509 $\times$ TZEEIOR 197 combined the highest number of the drought-tolerant traits. Hybrids TZEEIOR 510 $\times$ TZEEIOR 197 and TZEEIOR 458 $\times$ TZEEIOR 197 were the most stable with high yields (4839.88 kg/ha and 5352.57 kg/ha, respectively) across all test environments. Sixteen of the selected drought tolerant hybrids out-yielded the best drought tolerant check. Mean squares for general combining ability (GCA) and specific combining ability (SCA) for grain yield and most of the other traits were significant under both drought stress and well-watered conditions. Additive gene action was more important than non-additive gene action for yield and other traits of importance under drought. Inbred TZEEIOR 510 had positive GCA effect for grain yield, number of ears per plant and negative GCA effects for plant and ear aspect, anthesis-silking interval and stay green characteristic. It exhibited the greatest potential for use as parent for the development of drought-tolerant varieties. Significant positive correlations were observed between grain yield on one hand and heterosis, and specific combining ability in the testcrosses for both environmental conditions. Two heterotic groups resulted from the phenotypic data of the 187 inbreds for each of the two research environments while four groups were obtained using SNP markers. Combination of phenotypic and SNP data resolved the grouping into three. Forty-five SNP markers were significantly associated with six traits under drought viz. grain yield, ear and plant aspects, anthesis-silking interval, stay-green characteristics, and number of ears per plant. Gene annotation of the markers revealed

associations with functions like transcription factors, antioxidants, gene expression regulators, and nutrient transporters. Twenty markers out of the forty five showed significant haplotype segregations and were also adequate in predicting the traits under drought stress. The twenty significant marker-traits association in this study showed promise for facilitating the development of drought-tolerant maize inbreds and hybrids.

Key Words: Candidate genes, genetic diversity, general combining ability, heterotic groups, specific combining ability, single nucleotide polymorphism markers