GENETIC VARIABILITY AND STABILITY ANALYSIS OF YIELD AND YIELD-ASSOCIATED TRAITS OF RICE (*Oryza sativa* L.)

Abubakar Danlami GARBA
PAU-UI-0733
PLANT BREEDING

Genotypes evaluation for variability and stability of yield in rice is an important factor for sustainable rice production and food security. These evaluations are especially important when the core objective of the breeding program is to select lines with high adaptability and stability. This study was conducted to investigate genetic variability and stability of rice genotypes over three environments across the Northwestern Nigeria for yield stability in sixty-four rice genotypes obtained from the Africa Rice - International Institute for Tropical Agriculture (IITA), Nigeria, and AGRA germplasm, Uniport.

The experiment was laid out in a square lattice design (simple lattice design), with two replications. Agronomic and yield component traits were evaluated and measured as leaf area index, number of grains per panicle, weight of 1000 grains, total grain yield, days to 50% flowering, and weight of grains per panicle. Data analyses were through analyses of variance and stability analyses were conducted for univariate and multivariate stability parameters. The pooled data were subjected to analyses of variance, stability analyses were conducted using GGE biplot and Shukla stability variances.

The pooled analysis of variance showed highly significant differences among genotypes, environments, and genotypes by environment (G $\times$ E interaction) for all the traits. The rice genotypes were divided into three distinct groups based on univariate (σi^2) and multivariate (GGE biplot) stability parameters. First, genotypes having high stability along with high yield. These genotypes are widely adapted to the different environmental conditions. The second group are genotypes that showed high yield but low stability, these genotypes are suitable for specific environments. Lastly, are genotypes with low yield and high stability. Genotypes in this class are more suitable for breeding specific traits or yield component compensation such as the capacity to recover rapidly from stresses. Leading grain yield produced by UPN 811 possess intermediate stability was given 23 ranks for Shukla's stability variance. According to Sh-σi^2, despite being moderately unstable, UPN 811 has the highest yield mean value.

This study has shown that yield traits and genotype stability are not complementary in action therefore selection for high and stable yield in the region should be environment-specific, with genotypes exhibiting high yield traits in one environment but less stable in the other environments. The winning genotypes of each trait can be used as parents to develop regional specialty cultivars by fine-tuning favorable traits, and recommended genotypes can be utilised as parents that can aid breeders in improving yield potential and stability across the planting seasons and regions.

Keywords: Stability, genetic variation, genotype x environment, variance components

VARIATION AMONG CASSAVA GENOTYPES FOR HYDROGEN CYANIDE CONTENT AT DIFFERENT AGE AND STORAGE ROOT YIELD

Abdoul-Razak OUMAROU MAHAMANE
PAU-UI-0668
PLANT BREEDING

Cassava is a significant starchy root crop widely cultivated in tropical and subtropical regions around the world. Efforts have been made to improve its desirable characteristics in order to increase food and nutritional quality. The cyanide found in cassava roots poses a health challenge as it can be a potent poison when poorly processed. This study was therefore conducted to evaluate the performance of selected cassava genotypes at advanced breeding stage across two years and determine the trend of accumulation of hydrogen cyanide in cassava roots at different developmental stage. Using a randomized complete block design with two replications, 16 genotypes; a yellow root variety (TMS07/0593) and a white root variety (TMS30572) as checks were evaluated for yield, yield-related traits and hydrogen cyanide content in cassava root.

There were highly significant ($P < 0.001$) variations among the cassava genotypes for yield-related traits but no genetic variation was reported for fresh root yield and dry root yield. Effect of season and interaction between genotypes and season were found to be significant only for harvest index and the percentage of survival plants, respectively. Genotype UIC-17-2428 and the two national check varieties (TMS07/0593 and TMS30572) did not exhibit complete resistance to cassava mosaic disease. At harvest, genotype UIC-17-2031 had the highest fresh root yield (39.0 t/ha), dry root yield (10.5 t/ha), and harvest index (0.63). Genotype UIC-17-58 had the highest dry matter content (37.2%) at harvesting followed by UIC-17-46 (36.4%) while genotype UIC-17-583 had the lowest value (22.8%).

There was no significant variation in HCN content among the genotypes due to age except for genotype UIC-17-2031 for which it decreased with age. Genotypes TMS07/0593 (469.8 mg/kg), TMS30572 (377.8 mg/kg), UIC-17-2081 (370.6 mg/kg), and UIC-17-2040 (335.6 mg/kg) had the highest HCN content at 6 MAP, 8 MAP, 10 MAP and 12 MAP respectively, while genotypes UIC-17-2081 (175.5 mg/kg), UIC-17-2009 (299.7 mg/kg), UIC-17-583 (250.5 mg/kg), and TMS30572 (204.2 mg/kg) had the lowest HCN content at 6MAP, 8MAP, 10MAP and 12MAP respectively. The genotypes evaluated have promising premium agronomic traits. Genotypes with outstanding dry root yield need to be evaluated across multiple environments to assess their stability.

Keywords: Cassava improvement, Genotype × season interaction, Storage root yield, Dry matter content, Hydrogen cyanide content, Harvest index.

GENETIC DIVERSITY AND VARIANCE COMPONENTS OF MORPHOLOGICAL AND YIELD TRAITS OF SOYABEAN [*Glycine max* (L.) MERRILL] GENOTYPES

Abebawork Tilahun ASSFAW

PAU-UI-0663

PLANT BREEDING

Soyabean is one of the most important oil seed crops in the world with adaptation to a wide range of environmental conditions. However, yield of soyabean is relatively low in Nigeria due to many biophysical constraints, hence, the need for improvement of soyabean grown in the country. A fundamental step in establishing any breeding programme is identification of existing genetic variability for the crop of interest. The objectives of this study were therefore to evaluate genetic diversity and variance components, heritability and genetic advance and associations among the traits of the International Institute of Tropical Agriculture (IITA) soyabean genotypes for yield and yield related traits. Forty-five soyabean genotypes were evaluated during the 2022 cropping season at three stations i,e., Ibadan, Zaria and Ikenne of the International Institute of Tropical Agriculture in Nigeria. In each site the experiment was conducted using an alpha-lattice design, with three replications. Data were collected on days to 50% flowering, days to 95% maturity, plant height, hundred seed weight, root nodule score, shattering score, lodging score and grain yield. The data were subjected to analysis of variance, estimation of variance component, correlation coefficient, path analysis, principal component analysis and cluster analysis using R software. The genotypes were further assessed for genetic diversity using 10,630 single nucleotide polymorphisms (SNPs) marker. The combined analysis of variance revealed significant genotype x location interaction for grain yield, and highly significant difference in days to 50% flowering and days to 95% maturity. This implies that the genotypes exhibited differential response or relative performance across the study locations for these traits. High broad sense heritability was found for plant height, hundred seed weight, shattering and lodging. The highest genetic advance estimate was found for grain yield. High heritability along with high genetic advance as percent mean was found for plant height, shattering and lodging, implies that these traits are controlled by additive gene action and can be improved through the use of simple selection approach. The correlation coefficient revealed a significant and positive association between grain yield and hundred seed weight at the genotypic level. On the other hand, grain yield showed a positive but non-significant association with hundred seed weight at the phenotypic level. Path analysis showed that hundred seed weight, plant height, days to 50% flowering, shattering and lodging had positive direct effect on grain yield. Principal component analysis showed that the first three principal components accounted for 64.8% of the total variation. Hierarchical cluster analysis based on phenotypic data distinguished five groups whereas, the corresponding analysis with SNP markers indicated three genetic groups. This indicates the existence of a considerable amount of genetic variation among the soyabean genotypes evaluated in this study. Average observed heterozygosity, expected heterozygosity, minor allele frequency and polymorphic information content were 0.08, 0.27, 0.20 and 0,22, respectively. These values were generally moderate considering the bi-allelic nature of SNPs. To explore further the diversity of soyabean, utilizing of more SNP markers that cover genome/chromosomes of soyabean would be desirable.

Keywords: Soyabean grain yield, Genetic advance, Pod shattering, Principal component analysis, Root nodule.

GENETIC RELATEDNESS OF *IN VITRO* CASSAVA (*Manihot esculenta* Crantz) ACCESSIONS BASED ON MORPHOLOGICAL CHARACTERIZATION AND DarTseq SNP MARKERS

Moise Hubert BYIRINGIRO

PAU-UI-0667

PLANT BREEDING

Deep knowledge of the structure and potential of genetic variability in breeding programs and gene-bank management is critical for achieving genetic gain and managing gene-banks to maintain genetic diversity. This study assessed the genetic relatedness and pinpoint duplicates using quantitative morphological characters (plant height, root length, number of roots, number of leaves, leaf length, leaf width, and number of leaf lobes) and SNP markers of 101 *in vitro* cassava (*Manihot esculenta* Crantz) accessions from the International Institute of Tropical Agriculture (IITA), Genetic Resources Centre, in 2023.

Analysis of Variance (ANOVA) of morphological traits revealed significant differences (P<0.01) of all traits across accessions and weeks. Root length and number of leaf lobes had significant differences (P<0.01) across interaction between accessions and weeks, with mean squares of 6.19*** and 0.871***, respectively. Cluster analysis identified four distinct clusters. The accessions TMe-3373 and TMe-4132 had the closest similar phenotypes (≤1.0 of heigh dissimilarity Euclidian distance) followed by TMe-178 and TMe-892. According to Principal Component Analysis (PCA), Three principal components (30.72% of PC1, 20.47% of PC2, and 16.06% of PC3) significantly captured 67.26% of the total variation among the accessions. The leaf length (LL), Leaf width (LW), Number of roots (NR), Plant height (PH), and Root Length (RL) had the highest eigenvalues of -0.551, -0.531, -0.398, -0.383, and -0.298 respectively in principal component 1 (PC1). The relationship between leaf width and leaf length was highly significant and positive (r=0.81***).

Genome-wide SNP markers were developed using the DArTseq genotype-by-sequencing approach. In polygenetic analysis, the cassava population was grouped into four clusters using the neighbor-joining method and 19,467 high-quality SNP markers. Phylogenetic analysis results were coherent with PCA analysis. The first three principal components (PC) contributed 15%, 4.74%, and 3.7% of the variance in the cassava population. In duplicate analysis, 17 duplicates were identified out of 89 accessions using cutoff of 0.15IBS (identity-by-state) genetic distance as a threshold.

The SNP markers discovered in this study offer a robust tool to explore the genetic diversity of cassava collection and identify duplicates of cassava accession from cassava collection. These results have important implications for cassava genebank management, quality control, conservation strategy, germplasm exchange, and future cassava breeding.

Keywords: ANOVA; cluster analysis; correlation coefficient; genetic relatedness; *in vitro*; *Manihot esculenta* Crantz; morphological descriptors; PCA; SNP markers

GENETIC DIVERSITY AND POPULATION STRUCTURE OF EARLY-MATURING WHITE MAIZE *(Zea mays* L.) INBRED LINES ADAPTED TO SUB-SAHARAN AFRICA

Hellen Mawia MUKITI
PAU-UI-0666
PLANT BREEDING

Maize is a means of sustenance for millions of people in sub-Saharan Africa, but its productivity is still low due to a myriad of constraints. Improvement of the yield potential of maize requires adequate knowledge of available genetic diversity and heterotic patterns, particularly of newly developed inbred lines for outstanding hybrid production. Hybrid maize is a product of heterosis resulting from crossing of inbreds from two distinct heterotic groups.

Defining appropriate heterotic groups requires an efficient clustering method. The objectives of this study were to assess the level of genetic diversity, and population structure, and identify appropriate clustering methods for assigning early white inbreds into distinct heterotic groups. Three hundred and seventy-six elite inbred lines extracted from three different populations were genotyped using DArTtag mid-density genotyping. Results revealed 3305 SNP markers out of which 1904 were retained after quality control.

The average marker PIC was 0.39, observed heterozygosity was 0.02, gene diversity was 0.37, whereas the minor allele frequency was 0.29. The optimum sub-population had K=3. The average genetic distance was 0.303 and ranged from 0.03 (between the inbred pair, TZEI 2772 and TZEI 2761) to 0.372 (between TZEI 2273 and TZEI 2832). Principal component analysis revealed greater similarity between subpopulations 1 and 2. Hierarchical clustering assigned the 376 inbreds into three distinct heterotic groups using the average linkage as the best clustering method.

The pedigree-based phylogenetic tree revealed the possibility of shared alleles among inbreds from the subpopulations. The F-statistics based on the underlying population structure revealed 10% variation among sub-populations and 90% variation within sub-populations with a moderate level of population differentiation (0.10). A high level of genetic variability was present among the elite inbreds, which could be exploited for the development of superior early maturing white hybrids.

Keywords; Early-maturing maize, genetic variability, heterotic groups, single nucleotide polymorphic markers

SCREENING OF ACCESSIONS OF COWPEA FROM TOGO FOR DROUGHT TOLERANCE

Nyimasata MANNEH
PAU-UI-0664
PLANT BREEDING

Cowpea is among the most leguminous crops globally especially in the tropics serving as a source of food for both humans and animals. It is an excellent and easily affordable protein source for millions of people. Several studies has shown cowpea to be drought tolerant to some extent but many cultivars have been shown to be affected by drought stress at the flowering and seedling stage. This study was conducted to assess how cowpea accessions responded to moisture-stress. A total of 255 cowpea accessions from Togo and four checks from IITA were assessed. The trials were conducted in the open field (which was divided into moisture-stressed and non-moisture stressed) and in the screen house. Experimental design in the field was alpha lattice with three replications while completely randomized design (CRD) with two replications was used in the screen house.

Data on the field were collected on days to first flower (DFF), days to 50% flowering (D50FL), days to 90% pod maturity (D90MAT), plant stand at harvest (PL_STAND_H), biomass weight (BW), pod weight (POD_WT), 100 seed weight (SEED100WT) and seed weight (SEED_WT). Data in the screen house were collected on days to 50% emergence (D50E), days to 90% emergence (D90E), days to permanent wilting (DPW), number of plants (NOP), number of recovered plants (NORP), percentage of recovered plants (PPR), stem greenness at 21 days after planting (SG21D.A.P), stem greenness at 30 days after planting (SG30D.A.P), wilting at 15, 21, 30 & 34 days after planting.

R statistical program (version 4.3.1, 2023) was used to perform analyses of variance, correlation analysis, best linear unbiased prediction (BLUPs), and heritability analysis on the data. Strong positive correlations between biomass and seed weight, pod weight and seed weight, and biomass and pod weight were found in both moisture-stressed and non-stressed field conditions, suggesting that one can be used to determine the outcome of the other. Wilting and stem greenness were negatively correlated showing that, stem greenness diminishes as plants continue to wilt.

In the non-stressed environment compared to the moisture-stressed environment, there was a greater heritability for agronomic traits like biomass, seed weight, and pod weight. The accessions with the highest seed weights (yield related traits), surpassing the checks under both moisture-stressed and non-stressed conditions in the field were six viz. RK173, RP225, RP232, RM357, RK148 and Vu081_2_2. The most promising accession was RK173; this was ranked first under moisture-stressed condition and ranked second under non-stressed condition with a loss in weight of 44.9% due to drought conditions. In the screen house, out of the 35 accessions that recovered after watering resumed, following moisture-stress, only five had a recovery percentage higher than 10% viz; RS029, RK121, RS007, RS037 and RK123. These should be exploited further for improvement in drought tolerance breeding programs.

Key Words: Drought tolerant, Heritability, Cowpea accessions, Experimental design, Best linear unbiased prediction (BLUPs)

GENETIC DIVERSITY ANALYSIS OF SOME SOYA BEAN [*Glycine max* (L). Merrill] GENOTYPES FOR YIELD AND YIELD RELATED COMPONENTS.

Felicity Kido CHIEMEKE
PAU-UI-0661
PLANT BREEDING

Soyabean is the world's most important leguminous oilseed crop, generating roughly half of all major oilseeds due to its adaptability to diverse latitudes, climates, and soil conditions. However, its yield in Nigeria is very low compared to what is obtainable in other countries, hence, the need to improve soyabean for yield. The knowledge of genetic parameters are very crucial in improvement of a crop. Therefore, the objectives of this study was to evaluate morphological and yield traits of some soyabean genotypes for assessment of variance components and genetic diversity for enhanced genetic recombination and improvement of soyabean based on phenotypic and SNP markers.

The study was carried at three locations in Nigeria (Ibadan, Zaria and Ikenne). Thirty-five soyabean genotypes obtained from international institute of tropical agriculture (IITA) soyabean breeding unit, Ibadan Oyo state evaluated morphological and yield traits which include plant height, days to fifty percent flowering, days to ninety-five percent maturity, lodging and shattering score, hundred seed weight and grain yield, Thirty-three of the genotypes were further analysed using Single nucleotide polymorphism (SNP) markers to study their genetic diversity. Data collected were subjected to correlation, coefficient of variation, heritability, genetic mean percent, cluster, principal component (PCs), and path coefficient analyses as well as analysis of variance at $\alpha_{0.05}$.

The genotypes were grouped into four clusters of 4, 9, 10 and 12 members. The first two principal components accounted for 62.8% of the total variation with PC1 and PC2 contributing 34.6% and 28.2% respectively. Grain yield had a significant correlation with days to fifty percent flowering (-0.633***), days to ninety-five percent maturity (-0.972***), and hundred seed weight (0.350*). Phenotypic variance and phenotypic coefficient of variation were generally higher than their corresponding genotypic variance and genotypic coefficient of variation, respectively. High broad sense heritability was observed for almost all the traits except grain yield (35%), days to 95% maturity (56%) and shattering score (46%) which were moderate. Genetic gain as percent of mean was low for days to 95% maturity (2.99), grain yield (8.14) and days to 50% flowering (7.67) and high for all other traits. Hundred seed weight (0.231), shattering score (0.411) and plant height (0.044) had direct positive effect while days to 50% flowering (-0.214), days to 95% maturity (-0.101) and lodging score (-0.049) showed negative direct effect on grain yield. There was highly significant differences (P < 0.001) among the genotypes for all the traits.

There was highly significant genotype × environment interaction for all the traits and across the locations except for plant height. Mean values for minor allele frequency (MAF), polymorphic information content (PIC), observed heterozygosity (Ho) and expected heterozygosity (He) were 0.16, 0.19, 0.067 and 0.227, respectively. Using 10,630 filtered SNPs across 20 soyabean chromosomes, the 33 genotypes were grouped into four major clusters. Genetic diversity exists among the genotypes for morphological and yield related traits, hence, the traits can be improved through selection among the evaluated genotypes.

Key Words: Soyabean diversity, Yield components, Multilocational trial, Lodging and shattering scores

EFFECTS OF SILVER NITRATE ON *IN VITRO* DEVELOPMENT OF YAM (*Dioscorea rotundata* L.) PLANTS

Yetunde Ruth OLUWASEGUN
PAU-UI-0662
PLANT BREEDING

Yam production is constrained by many factors including insufficient planting materials, diseases, and climate change. Plant tissue culture (PTC) techniques offer practical solutions for rapid propagation of planting materials. However, ethylene build-up during PTC is a major challenge to plant growth and development. This study evaluated the performance of four *in vitro* grown accessions of *D. rotundata* (TDr 3134, TDr 2745, TDr 3291 and TDr 2859) on each treatment.

Different concentrations of silver nitrate ($AgNO_3$) were added as part of the yam tissue culture media composition to test its effects on the plant growth and development, due to its known properties to regulate ethylene production.

A $7 \times 6 \times 4$ factorial layout in a completely randomized design (CRD) consisting of 7 treatments, 6 weeks and 4 accessions, was used. There were five (5) replicates per treatment, each replicate consisting of five (5) explants per accessions, making 140 per replication (35 explants per accession) and a total number of 700 explants. Nodal segments from three weeks old *in vitro* yam shoots were transferred to Murashige and Skoog (MS) culture media containing $AgNO_3$ (0, 1, 2, 3, 4, 5 and 6 mg/L) for 6 weeks while following standard tissue culture techniques or procedures. The number of leaves, number of shoots, plant heights, number of roots, and length of roots per explant were recorded weekly for each treatment up to six weeks. The *in vitro* plantlets with well-established roots were selected for acclimatization in the screen house (5 replicates per treatment, each replicate consists of 3 plants per accession). The survival percentage of the plantlets were recorded twice (14th and 24th day) of the 8 weeks post-flask (acclimatization) period. The number of each new leaf, length & breadth of leaves, number of new shoots and plants height per plant at the 8th week of acclimatization.

The results revealed that the effects of $AgNO_3$ on *in vitro* yam plants was genotype dependent: TDr 2745 and TDr 2849 had the highest (3.92) and lowest (3.47) numbers of shoots, respectively; TDr 3291 had the tallest plant (7.22 cm), while TDr 2859 had the shortest plant height (5.69cm); TDr 3134 and TDr 3291 had the highest (2.78) and lowest (2.30) numbers of leaves, respectively; TDr 3134 had the most roots (2.34) and the longest roots (9.20 cm), whereas TDr 2745 had the fewest roots (1.36) and the shortest roots (4.87 cm). Inclusion of 1 mg/L $AgNO_3$ in the culture medium significantly aided *in vitro* growth and development of the shoots while, 2 mg/L $AgNO_3$ significantly influenced root induction. Irrespective of the accessions, all $AgNO_3$ pre-treated plants responded well to growth during the post-flask management with over 85% survival rates.

Keywords: planting materials, culture media, acclimatization, *in vitro plantlets*

GENETIC DIVERSITY AND POPULATION STRUCTURE OF EARLY MATURING YELLOW AND PROVITAMIN-A MAIZE INBRED LINES ADAPTED TO SUB-SAHARAN AFRICA

Neo Jeremiah MAHULA

PAU-UI-0727

PLANT BREEDING

Maize is a staple crop in Sub-Saharan Africa (SSA), and early maturing cultivars have played a key role in its rapid expansion into diverse agro-ecologies over the past two decades. Genetic diversity and population structure data are essential for breeding programs to enhance desirable qualities and develop exceptional products for commercialization. This study investigated the population structure and genetic variability of 376 early yellow and provitamin-A maize inbred lines developed by the International Institute of Tropical Agriculture Maize Improvement Program (IITA-MIP). Using 1954 evenly spaced single nucleotide polymorphisms (SNPs) across the maize genome, the inbred lines were genotyped.

The minor allele frequency (MAF) ranged from 0.05 to 0.50, while the polymorphic information content (PIC) ranged from 0.00 to 0.50. Principal component analysis, neighbor-joining phylogenetic tree, and STRUCTURE analysis classified the inbred lines into two major groups based on their pedigree and selection history. However, strict reliance on molecular markers to identify heterotic groups may be challenging. Therefore, planned crosses with representative testers from opposing heterotic groups are needed to improve the current heterotic groups.

The current inbred population is a valuable resource for new advantageous alleles for population growth, hybridization, and line development, which could support future breeding initiatives. This study's findings will support nutrition and food security in SSA by assisting breeders in developing breeding strategies for genetic enhancement and sustainable maize production.

Keywords: Genetic diversity, Population structure, Early maturing maize inbred lines, Sub-Saharan Africa, Nutrition, Food security, Breeding