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Estimation of Genetic Parameters for Selected Quantitative Traits in Introduced African Yam Bean (*Sphenosylis stenocarpa* Hochst. ex. A. Rich Harms) Genotypes

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Abstract

A solid understanding of the genetic control of traits within breeding populations is essential for selecting superior genotypes and parent plants for African yam bean (AYB) cultivation. In this study, we explored the phenotypic breeding values and genetic parameter estimates for various traits in 10 introduced AYB varieties. These traits included seed emergence speed (SES), seedling vigor index (SVI), final germination percentage (FGP), seed yield, days to first flower bud initiation (DAYSFBI), days to first flowering (DAYSF), and days to first pod initiation (DAYSPI). We conducted the trial using a randomized complete block (RCB) design with the following varieties: TSs2, TSs60, TSs11, TSs33, TSs282, TSs450, TSs10, TSs432, TSs424, and TSs151B. Traits showing high and medium genotypic coefficient of variation (GCV) were seed yield (20.7), SVI (12.1), and seed emergence speed (10.8), respectively. Traits with high phenotypic coefficient of variation (PCV) included seed yield (36.8), SVI (22.8), and SES (37.5). The presence of variability in all studied traits was evident from both GCV and PCV values. However, PCV values were slightly higher than GCV, suggesting the influence of environmental factors on these traits. Seed yield exhibited high genetic advance (23.9) and intermediate heritability (31.5%), while SES showed low heritability (8.4%) and low genetic advance (6.5), and FGP displayed low heritability (8.3%) and low genetic advance (2.1). High heritability and genetic advance in certain traits indicate the presence of additive gene action, suggesting that these traits can be improved through direct selection. These findings suggest the presence of valuable variations that can be harnessed for AYB genetic enhancement and selection purposes. Our study results offer valuable insights for the genetic improvement, conservation, management, multi-location evaluations, short-term recommendations, and potential release of new AYB genotypes

Keywords: quantitative traits, breeding values, genetic parameter estimates, genetic variability, African yam bean

Introduction

African yam bean (Sphenostylis stenocarpa Hochst ex. a Rich) belongs to the Leguminosae family and the Papilionacaea sub-family. This crop is highly regarded as one of the most valuable legumes within the Fabaceae family. African yam bean is part of the larger genus Sphenostylis E. Meyer (Leguminosae: Papilionoideae: Phaseoleae), which comprises seven species found in dry forests, open areas, and forested savannas across tropical and southern Africa (Adegboyega et al., 2020). African yam bean stands out for its significant nutritional value, boasting health-protective nutrients such as phenolics. It offers an affordable source of dietary protein, minerals, carbohydrates, and vitamins, containing approximately twice as much protein as cereals (Kamboj and Nanda, 2017; Adegboyega et al., 2020). This species is not only widely distributed but also exhibits considerable morphological diversity within the genus. Economically, it holds paramount importance (Shitta et al., 2022). Despite its potential, African yam bean remains an underutilized legume in Africa. Nevertheless, it holds immense promise as a crucial crop for enhancing food and nutrition security in the region.

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Despite its importance, little is known about variations in the breeding values and genetic parameter estimates of growth, yield and reproductive traits of African yam bean that could be exploited for breeding. A good understanding of genetic parameter estimates is necessary for better exploitation of heterosis existing in the genotypes for growth and reproductive traits including seed yield. Knowledge of genetic variability and genetic parameter estimates including genotypic coefficient of variation, heritability and genetic advance is imperative for plant breeders to start a judicious crop improvement programme. Heritability is referred to as the relative amount of the heritable portion of variation, while genetic advance measures the amount of progress that could be expected with selection in a character. High heritability combined with high genetic advance are more valid for selection than heritability estimates alone (Johnson et al., 1955). Determination of genetic variability, heritability and genetic advance unravels the possible improvement of the character through selection. A good understanding of genetic structure of different traits helps breeders to employ suitable breeding strategy for their improvement (Nduwumuremyi et al., 2013). The genotypic evaluation of plants will facilitate identification of elite genotypes based on their inherent breeding values and genetic parameter estimates. This will subsequently guide the selection process of the breeder for further multi-location testing and subsequent recommendation for short term release.

Reproductive biology is a useful phenomenon in genetic improvement, conservation and utilization of crop biodiversity, that involves flowering phenology, floral biology, pollen-pollinator interaction, mating systems and gene flow via pollen and seeds (Aslay et al., 2023; Norman, 2019). A good understanding of flowering time and duration, fruit and seed set are vital to guide and complement the development of improved yam genotypes. However, little is known about reproductive traits in AYB.

The objectives of this study were to: (i) determine the phenotypic breeding values of selected growth, yield and reproductive traits of introduced African yam bean genotypes; and (ii) determine the genetic variability and genetic parameter estimates among 10 introduced African yam bean genotypes.

Material and Methods

Experimental Location

This experiment was carried out at the Njala Agricultural Research Centre (NARC), Njala, southern Sierra Leone, during early June of 2021/2022 and 2022/2023 cropping seasons. Njala is situated at an elevation of 50 m above sea level on longitude 12° 05 ' W and latitude 8° 07' N. The annual rainfall of Njala ranges from 2000 mm - 2900 mm per annum. The mean monthly air temperature ranges between 21°C and 28°C for the greater part of the day and night especially during the rainy season. Light intensity varies substantially with the photoperiod of 6-8 h per day during the rainy period. Relative humidity is generally very high (95-100%), especially during the rainy season.

Experimental Materials, Layout, Design and Management

The experimental African yam bean materials utilized in this study were introductions from International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. These materials comprised African yam bean seeds from 10 different genotypes (TSs2, TSs60, TSs11, TSs33, TSs282, TSs450, TSs10, TSs432, TSs424, and TSs151B).

The trial was laid out in a randomized complete block design with two replications due to limited planting materials. A total of 40 seeds per genotype per plot was planted at planting distance of 1 m × 0.5 m. No chemical fertilizers and pesticides were applied during the field experiment.

Data Collection

Data collected included seed emergence, seedling vigor index, final germination percentage, seed yield, and reproductive traits (days to first flower bud initiation (DAYSFBI), days to first flowering (DAYSF) and days to first pod initiation (DAYSPI).

The seed emergence speed (SES) was estimated as described by Islam et al. (2009) and Norman et al. (2020).

$$\mathrm{SES} = \frac{(\text{No. of germinated seeds at 9 days after sowing})}{(\text{No. of germinated seeds at 13 days after sowing})} \times 100$$

Seedling vigor index (SVI) was estimated as described by Hossain et al. (2006) as germination percent × seedling height. The SVI was measured at 21 days after sowing (DAS).

The plant height was measured using a meter rule. Seed yield was calculated after harvesting and drying to 15% moisture content.

Phenotypic and statistical data analysis

The data collected were firstly subjected to the

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linear mixed model by residual maximum likelihood (REML) procedure (Patterson and Thompson, 1971) for determination of the variance component analysis using the GenStat Statistical package version (12th edition, VSN international, Hemel Hempstead). This was followed by determination of different genetic parameters including broad sense (H^2), genotypic coefficients of variation (GCV), phenotypic coefficient of variation (PCV), and expected genetic advance (GA). estimation of both GCV and PCV were done in accordance to the formula described in Burton and Devane (1953) as: $\frac{\sqrt{\sigma^2 v}}{\bar{x}} \times 100$ where $\sigma^2 v$ represents the respective variance for genetic and phenotypic components for the trait from the final model in REML analysis and $\bar{x}$ is the trait mean value. The GCV and PCV values were independently categorized based on proposition by Deshmukh et al. (1986): values <10% = low, values that are 10–20% = medium and values >20% = high.

Broad sense heritability values were calculated according to the formula given by Robinson et al. (1949):

$$H^2 = \frac{\sigma^2 \mathrm{g}}{\sigma^2 \mathrm{p}} \times 100$$

Where $\sigma^2\mathrm{g}$, and $\sigma^2\mathrm{p}$ represent the total genetic variance and phenotypic variance, respectively.

The H^2 values were considered as low for values that range from 0–30%, moderate for values that range from 30–60% and high for those >60% as described by Robinson et al. (1949).

The expected genetic advance (GA) and genetic advance as percentage of mean (GAM) were determined following the formula given by Shukla et al. (2006) as:

$$GA = \mathrm{K} \times \mathrm{H}^2 \times \sigma p$$

where, K represents the selection differential which is 2.06 at 5% intensity, H^2 is the heritability due to total genetic effect (broad sense) and σp is the phenotypic standard deviation. The GA and GAM values were classified as low for values <10%, moderate for values ranging from 10–20% and high for values >20% as described by Shukla et al. (2006).

The phenotypic breeding values were determined using a one-step linear mixed model involving G-matrix for computation of the best linear unbiased predictor (BLUP) values of an individual genotype for each trait from the best fit model using the average information criterion (AIC) in restricted maximum likelihood (REML) algorithm (Gilmour et al., 1995; Piepho et al., 2008; Agre et al., 2021). The model used was:

$$\boldsymbol{y_{ij}} = \mu + \boldsymbol{\beta_i} + \boldsymbol{\tau_j} + \mathbf{y}_{\boldsymbol{k}} + \mathcal{E}_{\boldsymbol{ij}} + \mathbf{Z}_{\boldsymbol{u}}\mathbf{u}$$

where $\boldsymbol{y_{ij}}$ is the phenotypic value, μ is the overall mean, $\beta_{\boldsymbol{i}}$ is the effect of block i, $\tau_{\boldsymbol{j}}$ is the specific effect to genotype j, $\mathrm{y}_{\boldsymbol{k}}$ is the specific effect to trial k and $\mathcal{E}_{\boldsymbol{ij}}$ is an effect specific to each experimental unit (combined effects of block and genotype) and $\mathbf{Z}_{\boldsymbol{u}}\mathbf{u}$ is the the vectors of random additive and non-additive genetic effects, respectively, with corresponding design matrix Zu.

Result and Discussion

Success of any hybrid development program largely depends on the selection of elite parental genotypes. Selection of superior genotypes is contingent upon the existence of adequate useful variability in the gene pool. The higher the amount of variation present for desired traits in the breeding material, the greater is the scope for its improvement through selection.

The phenotypic breeding values of seedling growth and yield traits significantly ($p<0.05$) varied among genotypes (Tables 1 and 2). Genotypes TSs11 (72.2 %) had the highest phenotypic breeding values for seed emergence speed followed by TSs2 (65.0 %), TSs424 (58.3 %), TSs282 (58.1 %), TSs433 (57.0 %) and TSs60 (51.1 %), while TSs450 had the lowest value of 41.0 %. For seedling vigor index, genotypes TSs432 (1464), TSs424 (1405), TSs11 (1384), TSs151B (1371) and TSs2 (1348) had highest values for the trait, while TSs60 had the lowest of 954. For final percent germination, genotypes TSs282 (95.8%), TSs2 (95.0%), TSs432 (94.2%), TSs151B (92.5%) and TSs10A (92.5%) exhibited highest values for the trait, while TSs60 had the lowest of 80.0%. TSs10A (998.6 kg.ha^{-1}) had the highest seed yield, whereas TSs11 (388.3 kg ha^{-1}) had the lowest. The breeding values of reproductive traits significantly ($p<0.001$) varied among genotypes (Tables 1 and 2). Genotype TSs11 significantly took the longest period to initiate flower bud (110.3 days after planting), flower (121.8 days after planting) and initiate pod (124.8 days after planting) whereas TSs151B took the shortest periods of 103.3, 109.5 and 113.2 days after planting, respectively.

Generally, phenotypic coefficient of variation (PCV) values was slightly higher than the genotypic coefficient of variation (GCV) values for the measured traits (Tables 3 and 4). The slightly higher PCV values compared to the GCV values indicate their less sensitivity to environmental effects. Seed emergence speed (37.5%), seedling vigor index (22.8%) and

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Table 1. Seed emergence, seedling vigor index and final germination percentage of African yam bean genotypes.

Variety	Seed emergence (%)	Seedling vigor index	Final germination percentage (%)	Seed yield (kg.ha^{-1})
TSs10A	42.9	1074	92.5	998.6
TSs11	72.2	1384	86.7	388.3
TSs151B	48.9	1371	92.5	804.0
TSs2	65.0	1348	95.0	529.2
TSs282	58.1	1226	95.8	703.0
TSs424	58.3	1405	86.7	817.6
TSs432	47.0	1464	94.2	687.3
TSs433	57.0	1004	84.2	754.4
TSs450	41.0	1316	91.7	608.6
TSs60	51.1	954	80.0	660.9
SE	6.3	140.2	6.0	162.3

Note: SE=standard error; TSs=Tropical *Sphenostylis stenocarpa*

Table 2. Days to flower bud initiation, days to flowering, and days to pod initiation of African yam bean genotypes.

Variety	Days to flower bud initiation (days)	Days to flowering (days)	Days to pod initiation (days)
TSs10A	105.8	111.3	115.5
TSs11	110.3	121.8	124.8
TSs151B	103.3	109.5	113.2
TSs2	107.5	112.7	116.3
TSs282	107.2	114.0	117.7
TSs424	106.3	116.7	119.8
TSs432	107.7	116.8	119.2
TSs433	107.2	112.8	115.3
TSs450	106.8	114.3	117.3
TSs60	102.5	111.0	117.7
SE	0.9	1.2	1.4

Note: SE=standard error; TSs=Tropical *Sphenostylis stenocarpa*

seed yield (36.8%) had high PCV, whereas final germination percent (12.0%) had intermediate PCV and the remaining traits low PCV values. Seed yield (20.7%) had high GCV, whereas seed emergence speed (10.8%) and seedling vigor index (12.1%) had intermediate, and the remaining traits exhibited low GCV values ranging from 2.0-3.5. Findings indicate that traits with high PCV and GCV depict high possibility of selecting clones possessing superior values for those traits in the next clonal generation.

Knowledge of heritability contributes to the plant breeder's efficiency in deciding on the course of selection procedure to utilize under a given situation. Broad sense heritability measures the relative amount of heritable portion of total variability and provides information on the extent to which a particular morphogenetic trait can be transmitted to successive generation. Heritability, genetic advance and genetic advance of mean estimates are presented in Tables 3 and 4.

In this study, high broad sense heritability was recorded for days to flower bud initiation (62.4%), whereas seed yield (31.5%), days to flowering (56.8%) and days to pod initiation (59.1%) had medium heritability, and the remaining including seedling vigor index (28.1%), seed emergence speed (8.4%), and final germination percent (8.3%) had low heritability. The trait with high heritability indicates that it was less influenced by environment and that selection would be effective for its improvement.

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Table 3. Statistical and genetic parameter estimates of growth and yields of African yam bean.

Parameter	Seed emergence speed (%)	Seedling vigor index	Germination percent (%)	Seed yield (kg.ha^{-1})
Statistical parameter				
Mean	54.1	1255.0	89.9	695.2
Minimum	8.3	554.4	55.0	249.8
Maximum	100.0	1984.0	100.0	1810.0
Standard error	47.6	15616.0	13.5	13333.0
Genetic parameter				
Phenotypic coefficient of variation (%)	37.5	22.8	12.0	36.8
Genotypic coefficient of variation (%)	10.8	12.1	3.5	20.7
Broad sense heritability (%)	8.4	28.1	8.3	31.5
Genetic advance (%)	6.5	13.2	2.1	23.9
Genetic advance of mean (%)	12.0	1.1	2.3	3.4

Table 4. Statistical and genetic parameter estimates of reproductive traits of African yam bean.

Parameter	Days to flower bud initiation (days)	Days to flowering (days)	Days to pod initiation (days)
Statistical parameter			
Mean	106.5	114.3	117.7
Minimum	98.0	102.0	106.0
Maximum	112.0	130.0	135.0
Standard error	2.3	6.1	4.7
Genetic parameter			
Phenotypic coefficient of variation (%)	2.5	3.9	3.3
Genotypic coefficient of variation (%)	2.0	3.0	2.6
Broad sense heritability (%)	62.4	56.8	59.1
Genetic advance (%)	3.2	4.6	4.0
Genetic advance of mean (%)	3.0	4.0	3.4

Seed yield (23.9%) and seedling vigor index (13.2%) exhibited high and medium genetic advance, respectively, while the remaining traits had low genetic advance. All the traits had low genetic advance as per cent of mean (1.1-4.0%) except seed emergence speed (12.0%), which exhibited medium value. Traits with high genetic advance indicate favorable attributes for genetic improvement through selection.

Seed yield combined high genetic advance (23.9%) and intermediate heritability (31.5%), while seedling vigor index combined medium genetic advance (13.2%) and low heritability (28.1%). Days to flower bud initiation combined high heritability (62.4%) and low genetic advance (3.2%), days to flowering combined intermediate heritability (56.8%) and low genetic advance (4.6%), days to pod initiation combined intermediate heritability (59.1%) and low genetic advance (4.0%), seed emergence speed combined low heritability (8.4%) and low genetic advance (6.5%) and final germination percent combined low heritability (8.3%) and low genetic advance (2.1%). Our findings imply that traits with high heritability and high genetic advance are indicative that they were under the control of additive genes. This implies that direct selection would be an effective method for further improvement of these traits. Traits with high heritability and low genetic advance are under the control of non-additive genes. These findings agree with the view that both heritability and genetic advance should be considered for efficient predictability of response to selection (Johnson et al., 1955).

Each of the AYB genotypes utilized in this study exhibited some superior growth and reproductive features that make them potential putative parents in hybridization for the genetic improvement of the crop

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as well as recommendation for short term release after multi-environment testing. Genotypes with the highest breeding values for seed emergence speed indicate increased chance of their seeds to establish in the field. Genotypes with high seedling vigor index indicate consistent growth of germinated seedlings and optimum germination, whereas those with low seedling vigor index lacked optimal emergence and uniform growth of emergent seedlings. The seed germination and seedling emergence are the most important and vulnerable phases of a crop growth cycle. The duration to seed emergence and percent viability may influence crop yield by altering the crop population density, spatial arrangement and effective growth duration (Norman et al., 2020). A good understanding of the existing variability among genotypes for seed viability and dormancy serves as a good guide for selection of crop genotypes possessing dormant or non-dormant seeds (Burson et al., 2009). Improvement of germination, seedling vigor and related growth traits would probably contribute to robust identification of superior genotypes at the early-stage African yam bean breeding trials. Improvement of seed vigor would contribute to enhancement of the crop establishment and higher yield in the agricultural industry and the seed/breeding companies (Finch-Savage and Bassel, 2016).

Seed-related traits are very important in determining the genetic and taxonomic relationships in food crops (Wang et al., 2014; Aina et al., 2020; Ley-López et al., 2023) including legumes (Adegboyega et al., 2020). The variation in days to flower bud initiation, days to flowering and days to pod initiation could be attributable to genetic factors as the mean numbers of the studied traits were consistent in both years. The flowering duration in the studied African yam bean genotypes ranged from short (50 days) to long period, which is indicative of the significance of effective and efficient plan for crossing of ready flowers with viable pollens in a congenial pollination environment. Production of higher number of flowers per plant is imperative so that even where fruit set is slightly hindered by agents of flower abortion and pollen feeders, sufficient amounts of fruit and seed sets would be achieved (Norman et al., 2018).

Genetic advance as percent of mean is considered as a more reliable index to explore the effectiveness of selection in improving traits since its estimation involves heritability, phenotypic standard deviation and intensity of selection. Thus, heritability coupled genetic advance as per cent of mean provide clear picture regarding the effectiveness of selection for improving the traits of interest (Singh et al., 2018; Norman et al., 2021).

When we encounter traits with both high genetic advance and high heritability, it indicates that these traits primarily operate through additive gene actions. In simpler terms, this means that the favourable attributes related to these traits can be effectively enhanced through selective breeding methods. On the other hand, traits with high heritability but low genetic advance are influenced by non-additive genes. In such cases, direct selection for these traits may not yield significant improvements. In summary, traits with high heritability and high genetic advance are likely controlled by additive genes, making them suitable for targeted breeding efforts. Conversely, traits with high heritability but low genetic advance are influenced by non-additive genes, making them less amenable to direct selection, especially in crops that undergo outcrossing. These findings align with the idea that traits displaying high heritability estimates hold promise for genetic improvement (Piaskowski et al., 2018) and are more predictable in terms of their response to selective breeding, as proposed by Johnson et al. (1955).

Conclusion

This study demonstrated the presence of variations in the phenotypic breeding values and genetic parameter estimates of selected growth, yield and reproductive traits of introduced African yam bean genotypes that could be exploited for breeding. The high estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for seed yield and therefore, selection would be effective for this character. Seed yield combined high genetic advance and intermediate heritability indicating the predominance of additive gene action. Hence, direct selection would be effective for further improvement of this character.

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References

Agre, P. A., Norman, P. E., Asiedu, R., and Asfaw, A. (2021). Identification of quantitative trait nucleotides and candidate gene for tuber yield and mosaic virus tolerance in an elite

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population of white Guinea yam (*Dioscorea rotundata*) using genome-wide association scan. *BMC Plant Biology* **21**, 552. https://doi.org/10.1186/s12870-021-03314-w.

Aina, A. I., Ilori, C. O., Ekanem, U. O., Oyatomi, O., Potter, D., and Abberton, M. T. (2020). Morphological characterization and variability analysis of African Yam Bean (*Sphenostylis stenocarpa* Hochst. ex. A. Rich) Harms. *International Journal of Plant Research* **10**, 45–52. DOI: 10.5923/j.plant.20201003.01

Burson, B. L., Tischler, C. R., and Ocumpaugh, W. R. (2009). Breeding for reduced post-harvest seed dormancy in switchgrass: Registration of TEM-LoDorm switchgrass germplasm. *Journal of Plant Registration* **3**, 99–103. https://doi.org/10.3198/jpr2008.07.0433crg

Burton, W. G., and Devane, E. H. (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* **45**, 478–481. https://doi.org/10.2134/agronj1953.00021962004500100005x

Deshmukh, S. N. N., Basu, M. S., and Reddy, P. S. (1986). Genetic variability, character association and path coefficients of quantitative traits in virginia bunch varieties of groundnut. *Indian Journal of Agricultural Science* **56**, 816–821.

Gilmour, A. R., Thompson, R., and Cullis, B. R. (1995). Average information REML: An efficient algorithm for variance parameter estimation. *Biometrics* **51**, 1440–1450. https://doi.org/10.2307/2533274.

Gonzalez-Andres, F., and Ortiz, J. M. (1995). Seed morphology of *Cytisopyllum*, *Cytisus*, *Chamaecytisus* and *Genista* (Fabaceae: Genisteae) species for characterization. *Seed Science Technology* **23**, 289–300.

Gopalakrishnan, K. K., and Thomas, T. D. (2014). Reproductive biology of *Pittosporum dasycaulon* Miq., (Family Pittosporaceae) a rare medicinal tree endemic to Western Ghats. *Botanical Studies* **55**, 15. doi:10.1186/1999-3110-55-15

Hossain, M. A., Arefin, M. K., Khan, B. M., and Rahman, M. A. (2006). Effects of Seed treatments on germination and seedling growth attributes of horitaki (*Terminalia chebula* Retz.) in the nursery. *Research Journal of Agriculture and Biological Sciences* **1**, 135–141.

Islam, A. K. M. A., Anuar, N., and Yaakob, Z. (2009). Effects of genotypes and pre-sowing treatments on seed germination behavior of Jatropha. Asian Journal of Plant Sciences 8, 433–439. https://doi.org/10.3923/ajps.2009.433.439

Johnson, H. W., Robinson, H. F., and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soyabean. *Agronomy Journal* **47**, 477–483. https://doi.org/10.2134/agronj1955.00021962004700070009x

Kamboj, R., and Nanda, V. (2017). Proximate composition, nutritional profile and health benefits of legumes—a review. *Legume Research International Journal* **41**, 325–332.

Kroma, S., Norman, P. E., Barrie, A. U., and Norman, S. Y. (2016). Efficacy of chicken manure on the growth, yield and profitability of maize in the upland and inland valley swamp of Sierra Leone. *International Journal of Sciences* **5**, 7–13. https://doi.org/10.18483/ijSci.1116

Maiti, R. K., Hernandez-Pineiro, J. L., and Valdez-Marroquin, M. (1994). Seed ultra-structure and germination of some species of Cactaceae. *Fiton* **55**, 97–105.

Nduwumuremyi, A., Tongoona, P., and Habimana, S. (2013). Mating designs: helpful tool for quantitative plant breeding analysis. *Journal of Plant Breeding and Genetics* **1**, 117–129.

Norman, P. E., Tongoona, P. B., Danquah, A., Danquah, E. Y., Agbona, A., Asiedu, R., and Asfaw, A. (2021). Genetic parameter estimation and selection in advanced breeding population of white Guinea yam. *Journal of Crop Improvement* **35**, 790–815. https:// doi.org/10.1080/15427528.2021.1881012

Norman, P. E., Danquah, A., Asfaw, A., Tongoona, P. B., Danquah, E. Y., and Asiedu, R. (2020). Seed Viability, Seedling Growth and Yield in White Guinea Yam. *Agronomy Journal* **11**, 1–10. https:// dx.doi.org/10.3390/agronomy11010002

Norman, P. E., Asfaw, A., Tongoona, P. B., Danquah, A., Danquah, E. Y., De Koeyer, D., and Asiedu, R. (2018). Pollination success in some white yam genotypes under polycross and nested mating designs. *International Journal of Biological Sciences and Applications* **5**, 19-28.

Obiagwu, C. J. (1997). Screening process for ideal food legume cover crops in the tropical

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https://doi.org/10.29244/jtcs.10.03.205-212

ecosystem: (II) Application of the selection method for grain legume crops of the Benue River Basins of Nigeria (BRBN). *Journal of Sustainable Agriculture* (USA) **10**, 15–31. https://doi.org/10.1300/J064v10n01_04

Patterson, H. D., and Thompson, R. (1971). Recovery of inter-block information when block sizes are unequal. *Biometrika* **58**, 545–554. https://doi.org/10.2307/2334389

Piaskowski, J., Hardner, C., Cai, L., Zhao, Y., Iezzoni, A., and Peace, C. (2018). Genomic heritability estimates in sweet cherry reveal non-additive genetic variance is relevant for industry-prioritized traits. *BMC Genetics* **19**, 23. doi:10.1186/s12863-018-0609-8.

Piepho, H.P., Möhring, J., Melchinger, A.E., and Büchse, A. (2008). BLUP for phenotypic selection in plant breeding and variety testing. *Euphytica* **161**, 209–228. https://doi.org/10.1007/s10681-007-9449-8

Potter, D. (1992). Economic botany of Sphenostylis (Leguminosae). *Economic Botany* **46**, 262–275. https://www.jstor.org/stable/4255442

Robinson, H. F., Comstock, R. E., and Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal* **41**, 353–359. https://doi.org/10.2134/agronj1949.00021962004100080005x

Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, J., Singh, N., and Singh, S. P. (2006). Mineral profile and variability in vegetable amaranth (*Amaranthus tricolour*). *Plant Foods for Human Nutrition* **61**, 23–28. doi:10.1007/s11130-006-0004-x.

Singh, A. K., Mishra, S. P., and Parihar, R. (2018). Studies on genetic variability parameters on grain yield and its yield attributing traits in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences* **7**, 1261–1266. https://doi.org/10.20546/ijcmas.2018.709.150