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Inheritance and Stability of some Agronomic Traits of African Yam Bean (*Sphenostylis stenocarpa* (Hochst ex. A. Rich) Harms)

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ABSTRACT

African yam bean (AYB), *Sphenostylis stenocarpa*, an indigenous African pulse has immense nutritional significance. The understanding of inheritance pattern and stability status of agronomic trait is primary to their genetic improvement. Thirty AYB genotypes were evaluated for 100 seed weight (100SW), seed weight per pod (SWP), days to 50% flowering (D50F) and days to seedling emergence (DSE) in a randomized complete block design of three replications. This study was conducted at Ibadan, Ikenne, Mokwa and Ubiaja in Nigeria. Genotypic variation was significant ($p \leq 0.05$) for all characters except DSE. Location and Genotype x Location interactions were significant ($p \leq 0.05$) for the four characters. D50F had the least genotypic and phenotypic coefficient of variation (GCV and PCV) of 10.26% and 11.05% , respectively. The highest GCV, PCV and genetic advance occurred in SWP at 34.55%, 37.88% and 64.94% , respectively. Broad sense heritability ranged between 77.61% (DSE) to 89.07% (100SW). Repeatability was highest (13.83%) in 100SW. The performance of TSs87, TSs91 and TSs125 was highly significant for DSE and 100SW. The joint regression analysis identified TSs24 and TSs82 as the most stable genotypes for DSE and SWP with regression coefficient (b_i) of 0.94 and 0.97 and deviation from linearity (S_{di}^2) of 0.028 and -0.028 respectively. The most stable genotypes for D50F and 100SW were TSs61 and TSs84 with b = 1.015 and 1.017 respectively. The study revealed potential breeding values of four agronomic traits in AYB.

Keywords: African yam bean, accessions, underutilized species, agronomic traits, joint regression analysis.

Introduction

Global survey of useful crops identified 7,000 plant species; however, only about 150 are traded on the significant global scale (Padulosi *et al.* 2006). For example, over 50 percent of the global requirement for proteins and calories are met by just three: maize, wheat and rice. The policy which limits research and utilization on the few crops has greatly promoted the neglect of other crops. Benefits from the neglected and underutilized species includes, enhancement and support of food security, income generation, environmental health, food culture etc. Among the notable attending problems to their neglect are unquantifiable loss of their genetic resources, valuable cultures, etc. through genetic erosion, disappearance from cultural meals and under or none utilization of their potentials. The later would have not been a problem if awareness of these species is improved.

Sphenostylis stenocarpa (African yam bean) is one of such species; the record of the extent of its loss and rescue of its genetic resources in Africa is unknown (Adewale *et al.*, 2012). The seeds and tubers are the two organs of economic importance providing food for human and livestock. For the humans in Africa, there is cultural and regional preference for each of the two economic products (Potter, 1992; Nwokolo, 1996).

Yield had been on focus in most stability assessment; however, other quantitative traits are likewise influenced by the environment (Aremu *et al.*, 2007; Adewale *et al.*, 2010; Sameh *et al.*, 2011). Crop yield improvements have been achieved through directional selections for yield components (Akbar and Kamran, 2006). Therefore, an assessment of some genetic parameters and stability of some quantitative traits whose contribution to grain yield had been remarked positive (Adewale, 2011) is primary for African yam bean (AYB) improvement.

The inconsistency in the performance of the same genotype in many environments for specific trait makes prediction of its phenotypic performance across a wide environment impossible (Perkins and Jinks, 1968). The same has grossly affected crop breeding programme formulation (Kang *et al*., 1987), such that phenotypic performance assessment of genotypes for various targeted environments has become a necessary component any breeding programme. If there were no genotype by environment (G x E) interaction associated with the genotype-environment system relevant to a breeding objective, selection would be greatly simplified because the 'best' genotype in one environment would also be the 'best' genotype for all target environments. If such scenario had been real, crop varieties trial would be conducted in a single replication at only one location to provide universal results (Gauch and Zobel, 1996).

The impossibility of such phenomenon therefore underscores the importance of G x E in varieties evaluations. Reliable recommendation and release of genotypes for specific environment with higher confidence can only be achieved through the understanding of the adaptability or stability of each genotype to respective environment. One of the most popular univariate and extensively used method (Ariyo, 1990; Makinde and Ariyo 2011; Sameh *et al*., 2011; Yonas, 2014) for determining stability across environments has been the joint regression analysis approach. It was proposed by Yates and Cochran (1938) and further developed by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). The popularity among other methods may be due to its simplicity of calculation and application (Becker and Leon, 1988), moreover, it provides a conceptual model for genotypic stability.

The proportion of the phenotypic expression of a genotype that is genetic is key to the determinant of how much of the variation in the trait is linked to genetic factors and how much of the genetic advance is passed to the offspring. Simply, if heritability is greater than zero, then the inherent genetic component of the genotype has a measure of contribution to the phenotype in the respective environment. For every quantitative trait, the genetic component is a function of the heritability, but the phenotypic performance of individual genotype is dependent on the measure of flexibility or elasticity with respect to specific environment. Therefore, the breeding value of a quantitative trait is partly dependent on heritability and stability of the genotype.

Study on inheritance and stability of agronomic traits of African yam bean has not been attempted. The present study identified four quantitative traits: days to seedling emergence, days to 50% flowering, 100 seed weight and seed weight per pod to be under G x E interaction. Understanding their heritability and stability would be good information for subsequent breeding programme plans, especially for grain yield. Initial test for relationship of these traits with grain yield (Adewale, 2011) revealed high and positive correlation.

Materials and Methods

Thirty accessions of AYB were selected across some generated clusters obtained from an initial characterization of eighty AYB accessions. The 30 AYB accessions were presented for a multi-locational evaluation to understand the stability and heritability of four agronomic traits. This experiment was laid out in Randomized Complete block Design of three replications in four agro-ecologies within Nigeria: namely Ibadan, Ikenne, Mokwa and Ubiaja. The ecological properties of the four locations are presented in Table 1. Three seeds were planted per hill at 1metre apart. Thinning was done two weeks after planting to reduce plants/hill to two and the seedlings were staked three weeks after planting. Nuvacron (2.5ml L^{-1}) was applied at interval of two weeks from flowering inception to control the floral and pod pests. Manual weeding was done regularly to keep the field free of weeds. Data was collected on days to seedling emergence, days to 50% flowering, 100 seed weight and seed weight per pod.

Data were subjected to Analysis of Variance (ANOVA) using PROC GLM in SAS for each of the locations and then for the combined locations. The means of genotypes were compared using critical difference (CD), using the formula of Singh and Chaudhary (1985):

$$CD = (2\ MS_e/r)^{1/2} \text{ x } t$$

where; MS_e is the error mean square, r is the number of replicates and t is the tabulated value at 5% or 1% level of significance for the degree of freedom of error mean square.

The phenotypic variance (σ^2_P) was estimated following the method of Toker (2004) as:

$$\sigma^2_P = \sigma^2_G + \sigma^2_{GL}/L + \sigma^2 e/rL$$

where;

G, L and r are genotypes, locations and replication respectively. σ^2_G, $\sigma^2 e$ and σ^2_{GL} are components of variance for genotype, error and the interaction between genotypes and location respectively.

Broad sense heritability (Hb) was estimated following Tenkouano *et al*. (2002) and Toker (2004) as:

$$Hb = \sigma^2_G / (\sigma^2_G + \sigma^2_{GL}/L + \sigma^2 e/rL)$$

Phenotypic and genotypic coefficients of variation were estimated by the formula suggested by Gopal (2001) as:

Phenotypic Coefficient of Variation (PCV) = $100\sqrt{\sigma_p^2}/x$

Genotypic Coefficient of Variation (GCV) = $100\sqrt{\sigma_g^2}/x$

where; x is the population mean, σ^2_p is the addition of the genotypic mean square and the error mean square and σ^2_g is the genotypic mean square – error mean square/number of replications.

Repeatability (r_c) was estimated according to the formula presented by Ortiz and Ng (2000), as follows:

$r_c = \sigma^2_G/(\sigma^2_L + \sigma^2_{GL})$

where; σ^2_G is the variance of the genotypes, σ^2_L is the variance of the environment (Location)

σ^2_{GL} is the variance of the genotype (Genotype) and the environment (Location).

Joint Regression Analysis (See equation below) was performed following the approach of Eberhart and Russell (1966)

$Y_{ij} = m_i + \beta_i I_j + \delta_{ij}$

Where, Yij = Mean of the ith genotype at the jth environment (i = 1, 2, 3, 4, 5…………30, j = 1, 2, 3, 4)

m_i = The mean of ith genotype over all the environments

βi = The regression coefficient that measures the response of ith genotype to varying environment

δ_{ij} = The deviation from regression of the ith genotype of jth environment

Ij = The environmental index obtained by subtracting the regression of the ith genotype the grand mean from the mean of all genotype at jth environment.

Based on the recommendation of Eberhart and Russell (1966), the significant Genotype x Location interaction component from the initial ANOVA was further partitioned into linear/predictable (Locations and Genotypes x Locations) and non-linear/unpredictable (Pooled Deviations) components. Mean squares for both components and each of the accessions were tested against the pooled error mean square of the four traits. Moreover, all sources of variation in the linear component were further ascertained for significance by testing with the pooled deviation, following the Gonçalves *et al.* (2003), Akcura *et al.* (2006) and Islam *et al.* (2006). Following the procedure of Kenga *et al.* (2003), standard errors of regression (b_i) values were generated to test the significant deviation of b from 1.0. Moreover, the test for significant deviation from regression (S^2d_i) from zero was done using F-test involving the comparison of the mean squares due to deviations from regression with pooled error mean squares for each of the four traits.

Results and Discussion

In Table 2, the 30 accessions differed significantly ($P \le 0.05$) from each other for most of the traits in each of the locations. Under the combined analysis of variance, days to seedling emergence (DSE) did not differ among the thirty genotypes. However, highly significant ($P \le 0.001$) variation existed among the 30 accessions for the other traits (Table 2). The four locations differed significantly ($P \le 0.001$) and Genotype by Location (G x L) interaction equally differed significantly ($P \le 0.05$) for the four traits. The proportions of the G x L for each of the traits were less than 10%; the least (1.78%) and the highest (5.17%) occurred in days to 50% flowering (D50F) and one hundred seed weight (100SW), respectively. The very low G x L and very high heritability observed for D50F in this study re-emphasize earlier remarks (Upadhyaya *et al.*, 2002; Aazami and Jalili, 2011, Adewale *et al.*, 2012) that flowering trait are less influenced by the environmental factor. This may have informed the common prominence of flowering traits as effective discriminatory descriptor component for intra-specific morpho-genetic characterization.

Mean number of days to seedling emergence and attainment of 50% flowering among the 30 AYB accessions were approximately 6 and 95, respectively. Moreover, mean weight of seeds per pod (SWP) and that of 100SW were 3.35g and 23.62g, respectively (Table 3). Broad sense heritability of the four traits was high, ranging from 77.61% (DSE) and 89.07% (100SW); the highest repeatability (13.83%) in the study occurred in 100 seed weight. Generally from Table 3, the phenotypic coefficients of variation (PCV) were higher than the genotypic coefficients of variation (GCV). Proportionately, the contributions of the genetic component to the phenotypic variation in the four traits were high, ranging between 86.38 and 94.38. Relevance of the ratio of GCV to PCV as a reliable guide to selection of genotypes has been largely reported (Ortiz and Ng, 2000; Kaushik *et al.*, 2007; Adewale *et al.*, 2010). Repeatability is a useful tool for quantifying the extent to which individual performances remain consistent over time and space (Arnold, 1994). Therefore, a reliable breeding selection programme for AYB can be based on the following criteria: high GCV: PCV ratio, high broad sense heritability, high genetic advance and high repeatability.

Partitioning of the G x L interaction was done by Eberhart and Russell (1966) regeneration method. The identified significant difference among the thirty accessions for the four traits in Table 4 simply indicates that the genotypes differed in their performances for the four traits. It is therefore possible to improve them through selection breeding programme (Yonas, 2014). The mean square due to environment (linear) was significant, indicating that differences existed between environments. However, the significant interaction effect of the accessions across the four locations (observed from Table 4) would complicate any selection programme based on the differential performances of the accessions because accessions at one environment did not have correlated at the other environments.

The G x L interaction component was further partitioned into linear (Location and Genotype x

Locations = predictable) and non-linear (pooled deviations = unpredictable) components. Mean squares for both components were tested by the pooled error mean square. The linear component was highly significant, indicating that the predictable components had a vast share in the G x L interactions. The high contribution of the linear component to G x L interaction is of great practical importance, implying that there are differences among linear regression coefficients for each accession with respect to each of the four traits.

The G × L (linear) was found to be non significant (Table 4) when tested against pooled deviation. This ought to indicate the preponderance of non-linear component; however, the test for significance of the non-linear (pooled deviation) component using the pooled error was also not significant for the four traits studied. According to Islam *et al.*(2006) and Akcura *et al.*(2006), non significance of the G x L (linear) component seem to reveal that the source of the G x L interaction is not well defined, hence, prediction for responses of the genotypes to the environments for DSE, D50F and 100SW would be difficult. However, mean square due to G × L (linear) and Location (linear) for SWP were found to be significant ($P<0.01$) when tested against pooled deviation (Table 4). According to Da and Saleh (2003), the significance of the two sources of variation is an indication that there is heterogeneity in the regression coefficients of the genotypes. In Table 4, the accessions with significant ($P<0.01$) performances for DSE include TSs23, TSs81, TSs86, TSs87, TSs96, TSs118 and TSs125. Other significant ($P<0.01$) accessions are TSs91 (D50F) and TSs96 (100SW).

The stability analysis showed a wide variation among accessions; some exhibited wide adaptation while other showed specific adaptation either to favorable or un-favorable environments. Days to seedling emergence and 50% flowering would be meaningful and desirable when their mean values are low. Therefore from Table 5, days to reaching seedling emergence ranged between 5.67(TSs9) and 7.00(TSs61). Among the thirty accessions, the least number of days to attaining flowering was 90.75(TSs48) and the highest (103.83) was observed in TSs91. Based on the recommendation depicting stability by Eberhart and Russell (1966), genotype(s) with $b_i = 1.0$ and $S^2d_i = 0$ are approved to be stable. For DSE in Table 5, seven accessions had significant b_i values >1.0 (1.487 – 1.954), six other accessions had b_i values that were significantly <1.0 (0.016 – 0.548). For D50F, only three and one accessions respectively had b_i values >1.0 and <1.0 respectively. Coupled with lower mean value (desirable for DSE and D50F), some of the accessions with stable characteristics for DSE were: TSs 24 and TSs89. TSs48 and TSs61 was stable accessions for D50F. TSs86 and TSs96 (DSE) and TSs91 (D50F) had $b_i > 1.0$ and $S^2d_i > 0$ (Table 5); their adaptability with respect to earlier days of seedling emergence and 50% flowering was to favorable or high yielding environment. TSs9, TSs10, TSs33 and TSs67 had $b_i > 1.0$ and $S^2d_i < 0$ for DSE, this is an indication that their response to earlier germination is enhanced under a harsh or unfavourable environment.

Desirability of a hundred seed weight and seed weight per pod is in the higher mean value.TSs10, TSs67, TSs81, TSs91, TSs101 and TSs125 had greater than the mean value for 100SW, $b_i = 1.0$ and $S^2d_i = 0$ (Table 6). Other accessions with stable characteristic for 100SW but with lower than the grand mean of 23.62g were: TSs9, TSs23, TSs48 and TSs48. Moreover, TSs86, TSs91, TSs93, TSs94, TSs96, TSs104B and TSs125 were stable with respect to SWP; because they had higher mean value and their b_i and S^2d_i were significantly equals to 1.0 and 0.0 respectively. TSs89 produced the highest seed weight per pod, however, the b_i was significantly <1.0. Moreover, TSs96 whose 100 seed weight of 26.15g was much higher than the mean (23.62g) had significantly $b_i > 1.0$ and $S^2d_i > 0.0$(Table 6). For these traits, TSs89 and TSs96 were unstable and their performances over the four environments cannot be predicted. Moreover, the adaptive response of TSs58 and TSs86 (100SW) and TSs10 (SWP) for better performances would be enhanced in favourable environment. TSs33 was also identified to be favoured for higher seed weight per pod in poorly enhanced environment.

As remarked by Makinde and Ariyo (2011) and Yonas (2014), stable genotypes with desirable characteristics (such as earliness in DSE and D50F and high yield in 100SW and SWP) could be selected as parent for further improvement of the trait of concern. Although the 30 AYB accessions differed in stability for the four studied characters across the different environments, the potential performances and stability for the four traits were not mutually exclusive. The significantly higher than zero S^2d_i value obtained for TSs125 (DSE), TSs91 (D50F) and TSs96 (100SW), according to Kenga *et al.* (2003) suggests that their response were not adequately described by the linear regression and that most of the rest accessions exhibited general adaptability in the environments. The heterogeneity in response of the accessions to the environments earlier remarked was further confirmed by the differential and significant b_i values (< 1.0, 1.0 and >1.0) observed for the accessions for the four traits.

The concept of repeatability is expressed as the correlation between measures of a given trait in an individual genotype repeated in time or space (Benin *et al.,* 2005). This coefficient expresses the proportion of total variation that is explained by the variation of the genotype and those attributable to the environment (i.e. the environment plus G x E). High values of this coefficient according to Falconer and Mackay (1996) indicate that the genotype or the trait is expressed with high stability. In this study therefore, the sequence of stability of the four traits by comparison is: 100SW>SWP>DSE>D50F.

Table1. Description of the test location in terms of the coordinates, agro-ecology and total monthly rainfall in 2007 cropping season.

Locations	**Ibadan**	**Ikenne**	**Mokwa**	**Ubiaja**
Coordinates	**7.5^{0}N, 3.9^{0}E**	**6.9^{0}N, 3.7^{0}E**	**9.3^{0}N, 5.05^{0}E**	**6.65^{0}N, 6.38^{0}E**
Agro-ecology	**Forest-savanna transition zone**	**Lowland Humid forest**	**Southern Guinea Savanna**	**Humid Rainforest**
Months	**Total monthly rainfall (mm)**			
January	-	-	-	-
February	0.05	-	-	42.0
March	15.9	38.4	10.0	71.8
April	70.7	16.0	116.0	111.3
May	201.27	141.0	202.5	215.2
June	308.25	409.7	127.5	205.4
July	145.5	286.8	106.0	298.2
August	121.55	144.4	414.0	150.1
September	264.75	313.6	363.0	416.8
October	203.95	170.2	39.5	185.2
November	9.85	70.1	-	0.7
December	0.05	4.5	-	21.5
Total	1341.82	1594.7	1378.5	1718.2
Mean	111.82	132.89	114.88	143.18

[*] Source: Geo-Spatial Laboratory at IITA, Ibadan,

Table 2. Summary of the analysis of variance of four agronomic traits of African yam bean

Sources of variation	**Mean Square**				
	Df	**DSE**	**D50F**	**100SW**	**SWP**
			Ibadan		
Genotypes	29	1.32ns	76.04***	22.81***	1.13**
Error	58	1.68	13.84	5.07	0.44
			Ikenne		
Genotypes	29	1.002***	39.48ns	17.06***	1.06*
Error	58	0.24	51.25	6.16	0.63
			Mokwa		
Genotypes	29	1.06ns	95.63ns	42.87**	1.09*
Error	58	1.3	63.61	15.73	0.62
			Ubiaja		
Genotypes	29	1.6***	32.75***	18.35**	0.78*
Error	58	0.4	6.45	7.6	0.45
			Combined Location		
Locations	3	27.36***	2626.08***	302.16***	19.69***
Genotypes	29	1.32ns	95.77***	44.39***	1.34***
Genotypes x Location	87	1.22*	49.38*	18.9***	0.91**
Error	232	0.91	33.79	8.64	0.54
GEI Proportion (%)		4.08	1.78	5.17	4.15

DSE – Days to seedling emergence, D50F – Days to 50% flowering, 100SW – 100-seed weight, SWP – Seed weight per pod
GEI Proportion (%) – Proportion of the total variance due to Genotypes x Location interaction
*, **, *** - Significance at $P \leq 0.05$, 0.01 and 0.001

Table 3. Estimates of some genetic parameters of four agronomic traits of 30 African yam bean genotypes

Agronomic traits	**Mean**	**GCV**	**PCV**	**GCV:PCV**	**Hbs**	**r_c**
Days to seedling emergence (days)	6.17	18.26	21.14	86.38	77.61	4.62
Days to 50% flowering (days)	95.35	10.26	11.05	92.85	86.33	3.58
100-seed weight (g)	23.62	28.20	29.88	94.38	89.07	13.83
Seed weight per pod (g)	3.35	34.55	37.88	91.21	83.10	6.25

NB: Hbs – Broad sense heritability (%), GCV – Genotypic coefficient of variation (%),
PCV – Phenotypic coefficient of variation (%), r_c – Repeatability (%)

Table 4. Actual sources of the variation due to G x L interaction derived through partitioning for the estimation of stability parameters of the four traits

Source of Variation	DF	DSE	D50F	100SW	SWP
Genotypes	29	1.76^{**}	62.01^{**}	29.30^{**}	1.12^{**}
GxL	87	1.00^{**}	46.32^{**}	19.55^{***}	0.71^{**}
Location + (GxL)	90	1.53^{**}	64.76^{**}	28.33^{**}	1.05^{**}
Location(Linear)	1	27.36^{***}	3161.84^{***}	270.44^{***}	20.56^{***}
Genotype x Location (Linear)	29	0.22	10.64	8.24	0.43^{**}
Pooled Deviation	60	0.49	16.06	7.33	0.11
TSs9	2	0.17	5.19	4.62	0.16
TSs10	2	0.03	6.75	2.76	0.63
TSs23	2	1.21^{**}	0.49	3.25	0.04
TSs24	2	0.61	16.37	1.32	0.40
TSs33	2	0.38	23.60	15.60	0.13
TSs48	2	0.95	11.33	8.05	0.21
TSs49	2	0.38	20.60	14.14	0.16
TSs57	2	0.04	2.25	2.06	0.19
TSs58	2	0.29	10.47	6.20	0.12
TSs61	2	0.71	3.79	1.21	0.13
TSs67	2	0.19	12.31	5.17	0.03
TSs69	2	0.02	3.00	2.44	0.24
TSs81	2	1.21^{**}	26.57	2.62	0.06
TSs82	2	0.57	24.01	7.53	0.18
TSs84	2	0.37	26.34	5.71	0.35
TSs86	2	1.49^{**}	20.00	2.82	0.55
TSs87	2	4.29^{**}	1.40	13.69	0.27
TSs89	2	0.61	1.82	16.63	0.34
TSs91	2	0.95	104.66^{**}	10.52	0.50
TSs93	2	0.43	3.05	7.41	0.31
TSs94	2	0.33	5.03	4.37	0.19
TSs95	2	0.89	38.05	3.83	0.33
TSs96	2	1.88^{**}	4.05	37.01^{**}	0.02
TSs101	2	0.97	26.52	2.90	0.25
TSs104B	2	0.90	7.59	3.15	0.05
TSs109	2	0.13	17.27	2.97	0.10
TSs111	2	0.67	1.48	4.42	0.05
TSs116	2	0.28	56.53	7.36	0.22
TSs118	2	3.64^{**}	1.31	2.37	0.12
TSs125	2	4.59^{**}	0.01	17.79	0.50
Pooled Error	240	0.65	29.82	8.42	0.47

NB: Hbs – Broad sense heritability (%), GCV – Genotypic coefficient of variation (%),
PCV – Phenotypic coefficient of variation (%), r_c – Repeatability (%)

Table 5. Mean and Parametric stability estimates of Joint Regression Analysis for Days to Seedling Emergence and Days to 50% flowering of African yam bean

Genotypes	**DSE**				**D50F**			
	Mean (days)	**b**	**SE(bi)**	**S^2d_i**	**Mean (days)**	**b**	**SE(bi)**	**S^2d_i**
TSs9	5.67	0.739	0.092	-0.195	91.83	1.085	0.041	-7.849
TSs10	5.83	1.247	0.015	-0.266	94.83	1.090	0.046	-6.284
TSs23	6.42	1.633	0.662	0.325	93.00	0.791	0.012	-12.547
TSs24	5.75	0.938	0.337	0.028	96.00	1.648	0.072	3.339
TSs33	6.08	1.954	0.209	-0.089	93.50	1.017	0.086	10.561
TSs48	6.00	0.816	0.520	0.195	90.75	1.048	0.060	-1.703
TSs49	6.33	1.024	0.207	-0.090	94.33	0.985	0.081	7.560
TSs57	5.50	0.755	0.019	-0.262	93.75	0.628	0.027	-10.786
TSs58	6.25	1.487	0.159	-0.134	93.83	1.207	0.058	-2.562
TSs61	7.00	1.548	0.387	0.073	91.67	1.015	0.035	-9.247
TSs67	6.08	1.259	0.106	-0.183	97.25	1.225	0.062	-0.725
TSs69	6.25	1.239	0.009	-0.271	97.33	0.740	0.031	-10.035
TSs81	6.42	1.300	0.663	0.325	96.42	1.196	0.092	13.532
TSs82	6.33	0.321	0.314	0.007	95.50	0.702	0.087	10.971
TSs84	5.83	0.967	0.203	-0.094	96.00	0.919	0.091	13.301
TSs86	6.08	1.535	0.817	0.465	97.25	1.318	0.080	6.962
TSs87	6.83	1.125	2.352	1.866	101.83	1.012	0.021	-11.633
TSs89	6.08	0.938	0.337	0.028	95.83	0.753	0.024	-11.212
TSs91	6.33	0.418	0.522	0.196	103.83	1.804	0.182	91.624*
TSs93	6.50	0.792	0.235	-0.065	93.58	1.172	0.031	-9.983
TSs94	5.83	0.016	0.183	-0.113	99.25	0.718	0.040	-8.011
TSs95	6.08	0.309	0.485	0.163	94.42	1.423	0.110	25.009
TSs96	6.00	1.604	1.028	0.658	92.92	0.942	0.036	-8.983
TSs101	6.33	1.271	0.532	0.206	93.83	0.902	0.092	13.488
TSs104B	5.92	0.751	0.494	0.172	93.25	1.025	0.049	-5.445
TSs109	6.17	0.471	0.072	-0.214	96.50	0.980	0.074	4.238
TSs111	6.25	1.803	0.369	0.057	96.17	1.008	0.022	-11.561
TSs116	5.83	0.548	0.154	-0.139	94.00	0.749	0.134	43.495
TSs118	6.50	0.520	1.997	1.542	98.58	0.108	0.020	-11.722
TSs125	6.50	0.670	2.517	2.016*	93.50	0.791	0.002	-13.023
Grand Mean	6.17				95.36			
CD (5%)	1.52				9.30			

*, **, *** - Significance at $P \leq 0.05$, 0.01 and 0.001

Table 6. Mean and parametric stability estimates of Joint Regression Analysis for 100 Seed weight and Seed weight per pod of African yam bean

Genotypes	100SW				SWP			
	Mean (g.)	b	SE(bi)	S^2d_i	Mean (g.)	b	SE(bi)	S^2d_i
TSs9	19.64	1.123	0.131	0.934	3.25	0.269	0.487	-0.042
TSs10	24.00	0.705	0.101	-0.922	3.56	1.909	0.956	0.420
TSs23	23.48	0.634	0.110	-0.431	3.01	1.364	0.249	-0.163
TSs24	23.99	1.917	0.070	-2.359	3.38	2.177	0.761	0.192
TSs33	23.35	2.254	0.240	11.921	3.97	3.499	0.441	-0.072
TSs48	22.94	0.966	0.173	4.372	2.88	1.480	0.554	0.005
TSs49	18.51	1.281	0.229	10.454	3.23	1.109	0.478	-0.049
TSs57	23.64	1.495	0.087	-1.623	3.28	1.019	0.528	-0.014
TSs58	24.19	2.417	0.151	2.521	3.12	1.703	0.425	-0.081
TSs61	22.28	0.281	0.067	-2.476	3.17	0.762	0.440	-0.073
TSs67	26.83	0.776	0.138	1.486	3.18	0.245	0.217	-0.173
TSs69	23.60	1.513	0.095	-1.242	2.89	1.032	0.595	0.037
TSs81	24.40	1.205	0.098	-1.062	3.56	1.436	0.304	-0.142
TSs82	23.76	2.092	0.167	3.844	3.43	0.970	0.508	-0.028
TSs84	23.33	1.017	0.145	2.025	3.33	1.124	0.712	0.142
TSs86	25.18	2.077	0.102	-0.864	3.65	1.212	0.900	0.350
TSs87	23.19	1.851	0.225	10.005	2.94	1.503	0.623	0.061
TSs89	25.57	-1.066	0.248	12.952	4.22	-0.296	0.703	0.134
TSs91	23.95	1.173	0.197	6.836	3.47	1.009	0.856	0.297
TSs93	23.80	1.609	0.166	3.728	3.53	0.769	0.672	0.105
TSs94	21.78	-0.495	0.127	0.689	3.54	-0.895	0.524	-0.017
TSs95	25.98	0.335	0.119	0.147	3.57	0.001	0.697	0.128
TSs96	26.15	-1.759	0.370	33.323*	3.82	1.014	0.163	-0.187
TSs101	23.81	0.732	0.104	-0.785	3.15	0.662	0.606	0.046
TSs104B	22.96	0.309	0.108	-0.534	3.48	0.830	0.261	-0.159
TSs109	23.03	1.417	0.105	-0.711	2.96	1.181	0.373	-0.110
TSs111	21.64	1.550	0.128	0.741	2.75	1.117	0.274	-0.154
TSs116	22.43	1.812	0.165	3.675	3.28	0.490	0.563	0.012
TSs118	23.02	0.074	0.094	-1.311	3.17	0.406	0.425	-0.081
TSs125	28.29	0.705	0.256	14.109	3.69	0.901	0.854	0.295
Grand Mean	23.62	-	-	-	3.35	-	-	-
CD (5%)	4.70	-	-	-	1.17	-	-	-

*, **, *** - Significance at $P \leq 0.05$, 0.01 and 0.001

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