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Heritability Studies in Different Cowpea (*Vigna unguiculata* [L.] walp)
Varieties

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ABSTRACT

The heritability studies in the three Selected Cowpea (*Vigna unguiculata* [L.] Walp) Varieties (IT87D941 - I, IT97K 499 - 35 and Dankurmi) were conducted at the green house of the Institute for Agricultural Research (IAR), Ahmadu Bello University, Zaria, Nigeria. Many traits recorded a high estimate of phenotypic coefficient of variation ranging from 42.20% for pod length to 71.06% for number of seeds per pod in parents and F₁. Low estimates were however recorded for genotypic coefficient of variation for all the traits except for pod length (40.07%) in the parents and F₁. Similarly, relatively low Broad sense heritability estimates ranging from 0.04 to 0.02 were obtained in the parents and F₁ and 0.09 to 0.17 in the F₂ population. It is recommended that synchronization of flowering dates for genetic studies to be February, March and October, November plantings in studies involving photo-sensitive and Photo-insensitive varieties during which both photo-sensitive and photo-insensitive varieties flower early that coincide with short day length, 12.5 hrs. Besides these, the plant cowpea should be improved through hybridization and the necessary cross combination through selection using traits with high phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) estimates. Characters with low broad sense heritability may not easily be inherited. Also, selection using these traits with high phenotypic coefficient of variation and high genotypic coefficient of variation is suggested to improve productivity.

Keywords: Broad Sense; Genotypic; Phenotypic; Population; Variance.

1.0 INTRODUCTION

Cowpea (*Vigna unguiculata* [L.]) is a major crop worldwide, providing a source of economic livelihood and nutritional wellbeing for millions of farmers and urban consumers in the developed and developing world. Cowpeas are one of the most important food legume crops in the semi-arid tropics covering Asia, Africa, southern Europe and Central and South America (Singh, 2003). Most taxonomists agreed that cowpea belongs to the species *Vigna unguiculata* (L.) Walp. However, classification and nomenclature of taxa at the intraspecific level are still debated. Fery (2002) subdivided the species into three subspecies, i.e., Cowpea (subspecies *unguiculata*), Catjang, (subspecies *Catjang*), and yardlong bean (subspecies *sesquipedalis*). Fery (2000) reclassified the subspecies *unguiculata*, Catjang, and *sesquipedalis* as cultigroups *Unguiculata*, *Biflora* and *Sesquipedalis*, respectively, and lumped these cultigroups under *V. unguiculata* subspecies

unguiculata. Most cowpea breeders seem to have adopted Tellahet *et al.* (2016) cultigroup scheme for classification of cultivated *V. Unguiculata* taxa. Cowpea (*Vigna unguiculata* [L.] Walp).

Cowpea is grown primarily for its edible seeds in Africa, where it serves as a major source of essential nutrients (Oluwatosin, 2002). Cowpea is an important food crop throughout Sub-Saharan Africa. Its grains and leaves are rich sources of high-quality protein and vitamins which provide an excellent supplement to the lower quality cereal or root and tuber consumed in much of this region (Simion, 2018). Several snacks and main dishes are prepared from the grains (Sharma *et al.*, 2017). The tender green leaves are an important food source in Africa and are prepared as a pot herb, like spinach. Immature snapped pods are used in the same way as snapbeans, often being mixed with other foods. Green cowpea seeds are boiled as a fresh vegetable, or may be canned or frozen. Dry mature seeds are

also suitable for boiling and canning (De Ronde and Spreeth, 2007). In many areas of the world, the cowpea is the only available high quality legume hay for livestock feed. Digestibility and yield of certain cultivars have been shown to be comparable to alfalfa. Cowpea may be used green or as dry fodder. It also is used as a green manure crop, a nitrogen fixing crop, or for erosion control. Similar to other grain legumes, cowpea contains trypsin inhibitors which limit protein utilization.

Although cowpea is a plant of economic and pharmaceutical interest, hybridization barriers between the wild and cultivated varieties as well as cross incompatibility among some existing cultivated genotypes exist. Considerable effort on cowpea improvement is needed to sustain the bright future for the crop. Reddy *et al.* (2006) concluded that the cowpea exhibits sufficient heterosis to justify commercial hybrid production if efficient emasculation and crossing produces can be developed. Early maturity is a reflectively important agronomic characteristic. Typically, the trait is measured by such criteria as days to flowering or days to maturity of such traits that are heritable through hybridization. New Combinations result from crossing varieties which contain new heredity factors. An understanding of the heritability of traits such as early maturity, early flowering, seed setting, pod length, pod setting, plant height is important as crop improvement is related to the magnitude of genetic variability and the extent to which characters are heritable. There is therefore the need for studying the role of hybridization technique in the inheritance of some selected quantitative and qualitative traits of Cowpea so as to improve the source of protein and nutrients in our local environments. Most local Cowpea varieties are late maturing and dwarf in height and are generally affected by photoperiod and production rate is at local subsistence level (Ishiyaku *et al.*, 2005). There is the need for improving these varieties through hybridization of quantitative traits using improved varieties due to the frequent use of the local varieties by farmers. Beside these, the massive increase in price of

2.4 Data Analysis

Data were subjected to Analysis of Variance (ANOVA) at 5% level of significance. The analysis was performed using SAS V. 9.2 (2008). The

fertilizer coupled with economic melt-down of the recent years has made the purchase of Nitrogen fertilizer out of the scope of local farmers (Mohammed *et al.*, 2020). Therefore, the need for growing economic crops that have less demand for Nitrogen deemed necessary. As a legume fixes its own nitrogen, cowpeas do not need nitrogen fertilizer (Sharma *et al.*, 2017). Cowpeas do fix nitrogen without the addition of Rhizobium, as long as these bacteria are present in the soil from previous soyabeans cultivation.

This paper aimed at estimating the variance components and broad sense heritability for F₁ and F₂ populations in the three selected cowpea (*Vigna unguiculata* [L.] walp) varieties.

The objectives of this paper are to estimate the variance components for F₁ and F₂ populations in the three selected cowpea (*Vigna unguiculata* [L.] walp) varieties and to determine the broad sense heritability of the selected quantitative traits in F₁ and F₂ in the three selected cowpea (*Vigna unguiculata* [L.] walp) varieties.

2.0 MATERIALS AND METHODS

2.1 Study Area

The study was conducted at the green house of the Institute for Agricultural Research (IAR), Ahmadu Bello University, Zaria, Nigeria (latitude 11° N, longitude 11° 40' E and on altitude 660m above sea level).

2.2 Sources of the Seeds Genotypes

Seeds of three cowpea varieties: IT87D 941-1, IT97K 499-35 and Dankurmi were collected from the Institute for Agricultural Research, Ahmadu Bello University, Zaria.

2.3 Experimental Design

Seeds of the three cowpea varieties were sown in Plastic pots arranged in a Completely Randomized Design (CRD) with six replications in a factorial arrangement. Each pot was labeled accordingly.

variance components were estimated using the functions suggested by Uguru (1995) and formula modified by Ewa-Ubi (2001):

$$\text{Genotypic Variance } (\delta g) = \frac{MSG - MSe}{r} \quad (1)$$

Where MSG = Mean square of genotype, MSe = Mean square error and r = number of replications.

$$\text{Phenotypic Variance } (\delta p) = \frac{\delta g + MSe}{r} \quad (2)$$

$$\begin{aligned} &\text{Genotypic Coefficient of Variance (GCV)} \\ &= \sqrt{\left(\frac{Vg}{x}\right)} \times 100 \quad (3) \end{aligned}$$

3.0 RESULTS AND DISCUSSION

3.1 Estimates of Variance Components, Phenotypic and Genotypic Coefficients of Variation and Broad Sense Heritability

The result of heritability, genotypic and phenotypic coefficient of Variation as well as the genotypic and phenotypic Variances for parents, F_1 and F_2 populations are presented in tables 1 and 2 respectively. The result showed that broad sense heritability was relatively low for all traits ranging from 0.04(4%) to 0.22 (22%) in the parents and F_1 and 0.09 (9%) to 0.17(17%) in the F_2 populations. This was in line with the findings of Singh (2005) who obtained a similar result in his work on heritability of harvest index on TvX 309 x Prima (38%). Estimates of heritability for several maturity traits were lower and less consistent for several years. This could be due to different expression of traits, because genotypes interact differently with the condition of the environment (Adamu *et al.*, 2001). Characters with low heritability indicated that their genotypic variance were relatively low which may be interpreted to mean that their genetic variation was low and hence such characters may not be easily inherited and may thus be difficult to select. Low broad sense heritability estimates in the populations could be due to low variability in traits studied among the genotypes.

Number of days to first flower recorded the highest estimate 0.22(22%) for broad sense heritability with crossability percentage recording the lowest estimate of 0.04(4%) in the parents, F_1 and F_2 populations. Most traits especially plant heights at first flower, pod length, leaf area, days to maturity, height at maturity, number of pods per plant, number seeds per pods, had a similar estimate of 0.16(16%) for broad sense and heritability. The

$$\begin{aligned} &\text{Phenotypic Coefficient of Variance (PCV)} \\ &= \sqrt{\left(\frac{Vp}{x}\right)} \times 100 \quad (4) \end{aligned}$$

Where x is the grand mean for the Phenotypic and Genotypic traits, Vg = genotypic variance and Vp = phenotypic variance.

$$5. \text{ Broad sense heritability } (h^2 b) = \frac{\delta^2 g}{\delta^2 p}$$

Where $\delta^2 g$ = Genotypic Variance
and $\delta^2 p$ = Phenotypic Variance

broad sense heritability estimates of 0.22 in number of days to first flower of the parents and F_1 is encouraging and indicate that selection for this trait may be possible in the population. Singh (2005) reported broad- sense heritability for foliar resistance to be 93.8% and 84.5% for pod resistance which indicates major gene inheritance. Khan *et al.* (2015) reported high heritability for number of primary branches, but heritability for other character was moderate ranging from 48.2% for number of secondary branches to 57.8% for kernel weight and peg/flower ratio. Singh (2011) reported similar broad sense heritability estimates in F_2 and F_3 generation of crosses between a Virginia and two Spanish lines of *Arachis hypogea* for yield, fruit size and maturity. Their findings indicated that heritability estimates for yield were high ranging from 0.42 to 0.82 for four years location environment. McNamara and Houston (2008) advocated that a large number of observations in an experiment are necessary to obtained precise heritability estimates.

Low estimates were recorded for genotypic of variation (GCV) for all traits studied in parents, F_1 and F_2 with the exception of pod length in the parents and F_1 which has a GCV of 40.07% the lowest estimate for GCV was recorded for number of days to first flower in parents, F_1 (2.69%) and for F_2 populations (2.93%) as well as in height at maturity (2.33%) for parents and F_1 . The very low co-efficient of variation (PCV) and low genotypic coefficient of variation (GCV) obtained for some the traits such as number of days to first flower, height at maturity, and leaf area may be due to differences in the genetic variation. The result obtained support the work Singh (2011) who reported low PCV for 100 seed weight.

Many traits recorded a high estimate of phenotypic coefficient of variation ranging from 4.20% for pods lengths in parents and F₁ to 71.02% for number of seeds per pod in parents and F₁. Moderate estimates were also obtained for PCV in traits such as days to maturity, in parent and F₁ (33.74%) and in plant height at first flower (34.76%), leaf area (32.80%), pod length (33.84%) and (27.48%) in number of pods per plant, all recorded for F₂ population.

The phenotypic coefficients of variations were higher than the genotypic coefficients of variation for all traits studied. The genotypic variances were lower than the phenotypic variances. Higher genotypic variances were recorded for plant height at first flower (62.18%) and number of pod per plant in parents and F₁ population. 48.13% was obtained for days to maturity in parents and F₁ populations. The highest genotypic variance was found to be 44.17 for height at maturity in F₂ populations. High PCV was obtained for traits such as plant height at first flower, crossability %, numbers of seeds per pod, number of pods per plant. This result is in conformity with the work of Singh (2011). Number of seeds per pod had the highest phenotypic coefficient of variation (71.06) and pod length had the highest genotypic coefficients of variation (40.07) compared to all the other traits.

All other traits in parents, F₁ and F₂ populations recorded low genotypic variances with the lowest obtained for number of days to first flower in parents and F₁ population (1.69) and (1.89) for F₂ population. Higher phenotypic variances were recorded for most traits ranging from (109.63) for leaf area in F₂ population to (509.35) for days to maturity in parents and F₁ populations. Lower phenotypic variances were however obtained for traits, in parents and F₁ for leaf area (52.51),

number of seeds per pod (33.13), number of days to first flower (22.3), and height at maturity (19.28) in F₂ population. Lower phenotypic variances were also obtained for traits in days to maturity (21.74), number of seeds per pod (15.10), pod length (12.72) and number of days to first flower (12.30). The magnitude of genetic variance as expressed by heritability varies according to the experimental population (Adamu *et al.*, 2001) estimates of variance components for the traits indicated that genotypic variance (σ_g) of the parent and F₁ and F₂ population were generally lower than their respective phenotypic variance (σ_{ph}) for all traits. Generally, $\sigma^2_g / \sigma^2_{ph}$ were high most for traits such as number of pods/plant height at first flower and low for traits such as number of days to first flower and height at maturity. High values for genotypic variance suggest that selection should be more effective in such characters. Likewise, high phenotypic variance indicates that characters are influenced by changes in the environment (Adamu *et al.*, 2001). John *et al.* (2012) reported high genetic variability coupled with high heritability. The result of this study revealed that variability exists among the parents and F₁ and F₂ populations. There appears to be no important genetic reason why early generation should not provide good estimate of average yield potentialities of segregate from segregating population when genetic shift and interactions with environmental factors are control (Ewa-Ubi, 2001). Heidari *et al.* (2020) reported high genotypic and phenotypic variance for yield components in 20 groundnut genotypes and their F₁ hybrids. A knowledge of such of genetic parameters as hereditability, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) among quantitative traits should help improve efficiency of selection.

Table 1: Estimates of Variance Components for Parent and F₁ in Selected Cowpea Varieties

Components	Crossability %	Leaf Area	Pod Length
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	No of Days Plant to flower	Height first at flower	Height first		Days to maturity	to Height Maturity	at Number of pod per plant	Number of seeds per pod	
δ^2g	1.69	62.18	11.85	48.13	0.73	64.07	19.08	4.67	7.8
δ^2p	22.3	377.23	317.77	509.35	19.28	388.25	121.16	33.13	52.51
PCV	5.77	56.29	54.85	33.74	10.74	63.15	42.2	71.06	19.27
GCV	2.69	22.16	10.6	10.37	2.33	25.66	40.07	26.68	7.43
h^2b	0.22	0.16	0.04	0.1	0.05	0.17	0.16	0.14	0.15

Key:

δ^2g = Genotypic Variance, δ^2p = Phenotypic Variance, PCV = Phenotypic Coefficient of Variation GCV = Genotypic coefficient of variation, h^2b = Broad sense heritability.

Table 2: Estimates of Variance Components For F₂ Population in Some Selected Cowpea Varieties

Components	No of Days Plant to first flower	Days Plant Height at first flower	Crossability %	Leaf Area	Days to Maturity	to Height maturity	at No of pods per plant	Pod length	Number of seeds per pod
δ^2g	1.89	23.1	28.68	17.82	3.45	44.17	11.82	2.01	2.42
δ^2p	12.3	139.64	326.67	109.63	21.74	268.6	72.84	12.72	15.1
PCV	7.47	34.76	58.85	32.8	2.73	44.85	27.48	33.84	53.9
GCV	2.93	14.14	17.44	13.22	11.74	18.19	11.13	13.45	21.61
h^2b	0.15	0.17	0.09	0.16	0.16	0.16	0.16	0.16	0.16

Key:

δ^2g = Genotypic Variance, δ^2p = Phenotypic Variance, PCV = Phenotypic Coefficient of Variation GCV = Genotypic coefficient of variation, h^2b = Broad sense heritability

4.0 CONCLUSIONS

It was concluded that there is relatively low broad sense heritability estimate and low genotypic variance for all traits studied between the parents, F₁ and F₂ generations in the populations of selected cowpea varieties. There was recorded increase in plant height and pod length in hybrids produced from the crosses involving the variety Dankurmi.

Selection is effective in traits with high PCV and GCV.

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REFERENCES

- Adamu, A. K., Chung, S. S. and Abubakar, S. (2001). The effect of ionizing radiation (GammaRays) on tornado (S.N) *Nigerian Journal of Experimental Biology*, 5(2): 185-193.
- De Ronde, J. A. and Spreeth, M. H. (2007). Development and evaluation of drought resistant mutant germ-plasm of *Vigna unguiculata*. *Water SA*, 33(3): 381-386.
- Ewa ubi, B., Mignouna, H. and Obigbesan, G. (2001). Segregation for seedweight, pod length and Days to flowering following a cowpea cross. *African Crop Science Journal*, 9 (3): 463 – 470.
- Fery, R. L. (2000). New opportunities in *Vigna*. *Trends in New Crops and New Ideas*, 424-428.
- Fery, R. L. (2002). New opportunities in *Vigna*. *Trends in new crops and new uses*. ASHS Press, Alexandria, VA, 424-428.
- Heidari, S., Heidari, P., Azizinezhad, R., Etminan, A. and Khosroshahli, M. (2020). assessment of genetic variability, heritability and genetic advance for agro-morphological and some in-vitro related traits in durum wheat. *Bulgarian Journal of Agricultural Science*, 26(1): 120-127.
- Ishiyaku, M. F., Singh, B. B. and Craufurd, P. Q. (2005). Inheritance of time to flowering in cowpea (*Vigna unguiculata* [L.] Walp). *Euphytical*, 142: 291 - 300.
- John, K., Reddy, P. R., Reddy, P. H., Sudhakar, P. and Reddy, N. P. (2012). Genetic parameters for morphological, physiological and yield attributes related to moisture stress tolerance in groundnut- A review. *Agricultural Reviews*, 33(2): 104-113.
- Khan, H., Viswanatha, K. P. and Sowmya, H. C. (2015). Study of genetic variability parameters in cowpea [*Vigna unguiculata* (L.) Walp] germplasm lines. *The Bioscan*, 10(2): 747-750.
- McNamara, J. M. and Houston, A. I. (2008). Optimal annual routines: Behavior in the context of physiology and ecology. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 363(1490): 301-319.
- Mohammed, A. S., Adamu, A. K., Mu'azu, S., Nafiu, M. I. and Nura, S. (2020). Effect of Crossability in Improving Some Selected Cowpea (*Vigna Unguiculata* [L.] Walp) Varieties. *International Journal of Science for Global Sustainability*, 6(2). 50 – 57.
- Oluwatosin, O.B. (2000). Inheritance of instability of genes controlling anthocyanin pigmentation, seed pattern and leaf form in cowpea (*Vigna unguiculata* (L.) Walp). *Journal of the science of food and Agriculture*, 78:1-11.
- Oluwatosin, O. B. (2002). Inheritance of genes for leaflet shape and leaflet shape modifier in cowpea. *African Crop Science Journal*, 1: 133-137.
- Reddy, B. V., Ramesh, S. and Reddy, P. S. (2006). Sorghum genetic resources, cytogenetics and improvement. *Genetic Resources, Chromosome Engineering, and Crop Improvement*, 2: 309-363.
- Sharma, P. P., Baranda, B., Haritwal, S. and Sharma, M. (2017). Character association for seed yield and its components in cowpea (*Vigna unguiculata* (L.) Walp). *International Journal of Current Microbiology Applied Science*, 6(9): 967-975.
- Simion, T. (2018). Breeding cowpea *Vigna unguiculata* [L.] Walp for quality traits. *Annals of Reviews and Research*, 3(2): 555 - 609.
- Singh, B. (2003). Improving the production and utilization of cowpea as food and fodder". *Field Crops Research*, 84: 150-169.
- Singh, B. B. (2005). Cowpea [*Vigna unguiculata* (L.) Walp.]. *Genetic Resources, Chromosome Engineering and Crop Improvement*, 1: 117-162.
- Singh, A. L. (2011). Physiological basis for realizing yield potentials in groundnut. *Advances in Plant Physiology*, 12: 131-242.
- Tellah, S., Latati, M., Lazali, M., Ghalmi, N., Ounane, G., Ounane, S. M., ... and Badiani, M. (2016). Agricultural, socioeconomic, and cultural relevance of crop wild relatives, in particular, food legume landraces, in Northern Africa. *Water Stress and Crop Plants: A Sustainable Approach*, 1: 303-342.
- Uguru, M. I. (1995). Inheritance of color patterns in cowpea (*Vigna unguiculata* (L.) Walp). *Indian Journal of Genetics and Plant Breeding*, 5(4):379-383.