



ASSESSMENT OF GENETIC VARIATIONS USING PRINCIPAL COMPONENT ANALYSIS IN COWPEA (*Vigna unguiculata* (L.) Walp) GERMPLASMS.

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Abstract

A field experiment was carried out during the 2020 cropping season at the Federal University of Agriculture Makurdi Teaching and Research Farm, in the Southern Guinea Savannah of Nigeria to evaluate the genetic variability among different agronomic traits and the yield of 11 cowpea genotypes. These diversity parameters were taken; days to first flowering, days to fifty percent flowering, numbers of branches per plant, days to ninety-five percent maturity, number of pods per plant, hundred seed weight, total pod weight and total seed weight were subjected to analysis of variance, PCA and cluster analysis. The mean value for days to first flowering ranged from 33.67- 41.67 days with an overall mean of 37.79 days, the following flower between 34 - 37 days after planting (IT07K-230-2-9, UAM09-1056-2, UAM09-1055-6, IT99K-573-1-1 and IT07-243-1-10). Number of branches per plant varied between 2.667 - 5.667 with genotype IT10K-817-7 having the highest number of branches per plant. Total seed weight per plant ranged from 636.8-1046.5 with genotype IT07K-573-1-10 having the highest number of seeds. Cluster analysis grouped the 11 genotypes into four (4), clusters. Three (3) Principal components (PC) identified by PCA (with eigen values >1.0) out of eight (8) components accounting for 82.40% of the total variation. The first three (3) PCs accounted for 43.3%, 24.7% and 14.5% respectively. Traits of highest loading were mainly (flowering, days to maturity, pod weight and seed weight) and were therefore associated with PC1. Genotypes IT07K-234-1-10 and IT99K-573-1-1 are recommended for adoption by farmers for high grain yield.

Keywords: Cowpea, Genetic variation, Principal component analysis, Cluster Analysis.

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) $2n=22$ is one of the principal food and cash crop legume grown in the semi-arid tropics covering Africa, Asia and Central America with great socio-economic, cultural, nutritional importance and a valuable component of the traditional cropping systems (FAO/WFP/IFAD 2022). Cowpea belongs to the family *Fabaceae* and sub-family *Faboideae* (Agbogidi, 2010). Other commonly used names of cowpea include southern pea, black eye pea, crowder pea, labia, niece, coupe, or frijole (Horn and Shimelis, 2020). Cowpea is a major food crop that is grown in over 100 countries and provides a source of income for over 40 million farmers. It is also a good source of protein, oil, vitamins, and minerals for millions of people, especially in developing countries (FAO 2022, NRIN, 2022). About 6.5 million metric tons of cowpea were reported produced annually on about 14.5 million hectares worldwide (Boukar *et al.*, 2018). In Sub-Saharan Africa (SSA), West Africa is regarded as the major cowpea producing region with 80% of the total regional production reported for Nigeria and Niger at first and second positions respectively for 14 years in a row (Aboki, and Yuguda, 2013; Huynh *et al.*, 2016; FAO 2022). In addition, Nigeria has been the leading producer and consumer of cowpea globally with an approximately 3.3 million tonnes (FAO 2022).

Genetic variability is the pre-requisite for any plant breeding program and the basis for adaptability, stability and evolution of agronomic species. The success of most crop improvement programs largely depends upon the genetic variability and the heritability of desired traits (Mullar Stark *et al.*, 1992; Falconer and Mackay 1996). The magnitude and type of variability helps the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. In this regards estimations of genotypic variance for various quantitative characters preceded by

selection for yield and its components are useful in designing an effective breeding programme (Serath and Reshma, 2017). Direct selection for yield is not much effective as quantitative characters are controlled by polygene. Hence, knowledge about association of character which will directly or indirectly contribute to yield is crucial. Correlation coefficients explain the degree of association among the characters. However, it is difficult to explain a system of correlation when the indirect association between the characters' increases. The method of principal component analysis developed by Harold Hotelling in the 1930s is helpful in partitioning correlation into direct and indirect effects and in the assessment of relative contributions of each component to the yield (Hotelling 1993). The PCA and cluster analysis is a multivariate statistical technique that attempt to simplify and analyze the inter relationship among a large set of variables in term of a relatively small set of variable or component without losing any essential information of the original data set (Jain *et al.*, 1999; Abdi and Williams, 2010). This research aimed at evaluating the genetic variations in selected varieties of cowpea for yield characters

Materials and Methods

The study was conducted during the 2020 cropping season at the College of Agronomy Teaching and Research Farm, Joseph Sarwuan Tarka University, Makurdi located at Latitude $7^{\circ}14'$ North and longitude $8^{\circ}24'$ East, elevation 98m, which falls within the Southern Guinea Savannah agro-ecological zone of Nigeria. Seeds of cowpea germplasms were obtained from the International Institute of Tropical Agriculture (IITA) through the Molecular Biology Laboratory, Joseph Sarwuan Tarka University, Makurdi. Lists of accessions are presented in Table 1. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three (3) replications. The experimental area was ploughed and

harrowed. Field was marked and demarcated into three replications spaced 1m apart. Each replication consists of eleven plots and each plot contains four rows at 4m in length,

spaced at 0.75m apart. Harvesting was done manually, when the pods have turned straw brown. That is 95% of the pods had matured for each variety.

Table.1: List of genotypes evaluated to estimate the genetic variations in cowpea

S/N	Germplasms	Source
1	IT07K-243-1-10	IITA
2	IT07K-230-2-9	IITA
3	IT07K-291-69	IITA
4	IT10K-837-1	IITA
5	IT10K-817-7	IITA
6	IT10K-817-3	IITA
7	IT99K-573-1-1	IITA
8	UAM14-143-4-1	UAM
9	UAM14-175-31-1	UAM
10	UAM09-1055-6	UAM
11	UAM09-1056-2	UAM

Data was collected and recorded for analysis from each individual plot on the following parameters:

days to first flowering, days to 50 % flowering, number of branches per plant, 95% pod maturity, numbers of pods per plant, 100 seed weight, total pod weight, total seed weight. All data collected were subjected to analysis of variance (ANOVA) using the Genstat Statistical Software 17th edition. Means were separated using the turkey pairwise comparison at 95% level of significance, where significant means exist. Principal component analysis and Cluster analysis procedure was carried out using MiniTab-17.

Results

Mean squares from analysis of variance for yield and yield components in cowpea germplasms is presented in Table.2. The result showed that significant variations were observed among the eleven (11)

cowpea germplasms for days to first flowering, days to fifty percent flowering, days to ninety-five percent maturity, hundred seed weight, total pod weight, and total seed weight. There was however no significant variation observed for numbers of branches per plant and numbers of pods per plant.

The Mean performance of eleven cowpea germplasms for yield and yield component is presented in Table 3. Days to first flowering ranged from 33.67-41.67 with an overall mean of 37.97 days (Table 3). Cowpea accession IT07K-243-1-10, IT99K-573-1-1, UAM09-1055-6, UAM09-1056-2 and IT07K-230-2-9 are among the earliest flowering germplasms within the range of 34-37 days after planting, while cowpea accession IT10K-817-3, IT10K-817-7 and UAM14-143-4-1 took longer days to flower (≥ 40 days) as shown in Table.3. The number of branches per plant (Table.3) ranged from 2.667-4.667 with an

overall mean of 4.15. Although no significant variations were observed for number of branches among the eleven accessions evaluated, cowpea accession UAM09-1055-6 had the least average number of branches per plant (2.67 branches) while IT07K-243-1-10 had the highest average number of branches per plant (5.67 branches). Significant variation in the number days to ninety-five percent (95%) maturity is presented in table 3. The number of days to maturity ranged from the 60.67 days to 71.00 days, with the grand mean as 67.24 days. Accession IT07K-243-1-10 took more days to reach ninety-five percent maturity (71.00 days) while accession UAM09-1056-2 took lesser number of days to reach ninety-five percent maturity (60.67 days). The number of pods per plant among the eleven cowpea accessions is also presented in table 3. The average number of pods ranged from 53.33 pods per plant to 91.67 with an overall mean of 73.94. Although no significant variation was observed, accession IT10K-837-1 produced the least number of pods per plant

(55.33 pods), while accession IT99K-573-1-1 recorded the highest average number of pods per plant (91.67 pods). Hundred seed weight of cowpea showed significant variation. Weight of hundred seeds ranged from 12.67 grams to 18.73 grams with a grand mean of 16.39. Both accession IT10K-837-1 and IT99K-573-1-1 recording significant higher weights of 18.70 grams and 18.73 grams respectively, differed statistically from the reduced weight of hundred seeds (12.67 grams) recorded in accession UAM09-1056-2. The result also shows that pod weight varied significantly among the cowpea germplasms studied. Total pod weight ranged from 917 kg ha⁻¹ for accession UAM14-143-4-1 to 1556 kg ha⁻¹ for genotype IT07K-243-1-10, with a mean of 1183.55 kg ha⁻¹. Similarly, significant variation in accessions for total seed weight was also observed from the result of the study. Weights of total seed ranged from 636.8 kg ha⁻¹ for accession UAM14-143-4-1 to 1046.5 kg ha⁻¹ for accession IT07K-243-1-10 with a mean of 820.31 kg ha⁻¹.

Table 2: Analysis of Variance Showing Mean Squares for Yield and Yield Components in Cowpea Germplasms.

Sources of variations	Degree of freedom	Days to first flowering	Days to 50% Flowering	Numbers of branches per plant	Days to 95% Maturity	Numbers. of pod per plant	100 seed weight	Total pod weight	Total seed weight
Replication	2	1.49	0.36	0.94	1.49	142.80	4.06	6204.00	3309.00
Variety	10	21.02**	39.09**	1.96 ^{ns}	49.67**	447.70 ^{ns}	11.70**	91313.00**	39446.00**
Error	20	2.02	2.66	1.04	2.22	683.80	1.67	11555.00	5817.00
Total	32								
CV%		3.8	3.8	24.6	2.2	35.4	7.9	9.1	9.3

KEY: ** = Highly significant at $P \leq 0.01$, ns = not significant, CV = Coefficient of variation,

Table.3: Mean Performance for Yield and Yield Component of Eleven Cowpea Germplasms

Germplasms	Days to first flowering	Days to 50% Flowering	Numbers of branches per plant	Days to 95% Maturity	Numbers. of pod per plant	100 seed weight	Total pod weight	Total seed weight
IT07K-243-1-10	37.00 ^{cd}	42.33 ^{de}	4.67 ^{ab}	71.00 ^a	82.33 ^a	16.73 ^{abc}	1556.00 ^a	1046.50 ^a
IT07K-230-2-9	33.67 ^f	37.33 ^f	3.33 ^{bcd}	63.33 ^{bc}	74.00 ^a	15.90 ^{bcd}	1316.00 ^{bc}	943.30 ^{ab}
IT07K-291-69	38.67 ^{bcd}	45.67 ^{abc}	4.33 ^{abcd}	70.33 ^a	84.67 ^a	14.47 ^{cde}	1148.00 ^{cd}	809.00 ^{bc}
IT10K-837-1	39.00 ^{bc}	44.33 ^{bcd}	4.00 ^{abcd}	64.33 ^b	53.33 ^a	18.70 ^a	1007.00 ^{de}	754.50 ^{cd}
IT10K-817-7	41.00 ^{ab}	47.33 ^{ab}	5.67 ^a	70.00 ^a	55.00 ^a	17.67 ^{ab}	1113.00 ^{cde}	719.40 ^{cd}
IT10K-817-3	40.00 ^{ab}	46.33 ^{abc}	4.33 ^{abcd}	68.33 ^a	85.00 ^a	15.67 ^{bcd}	1192.00 ^{bcd}	804.70 ^{bc}
IT99K-537-1-1	36.33 ^{cde}	42.00 ^{de}	4.33 ^{abcd}	69.67 ^a	91.67 ^a	18.73 ^a	1353.00 ^b	930.00 ^{ab}
UAM14-143-4-1	41.67 ^a	48.00 ^a	4.33 ^{abcd}	70.33 ^a	76.33 ^a	17.90 ^{ab}	917.00 ^c	636.80 ^d
UAM14-175-31-1	38.33 ^{bcd}	43.67 ^{cd}	4.67 ^{abc}	70.67 ^a	69.33 ^a	17.60 ^{ab}	1098.00 ^{de}	785.80 ^c
UAM09-1055-6	36.00 ^{def}	39.67 ^{ef}	2.67 ^{bd}	61.00 ^{cd}	66.33 ^a	14.30 ^{de}	1124.00 ^{cd}	762.70 ^{cd}
UAM09-1056-2	34.00 ^{ef}	38.33 ^f	3.33 ^{bcd}	60.67 ^d	75.33 ^a	12.67 ^e	1195.00 ^{bcd}	830.70 ^{bc}
MEAN	37.97	43.18	4.15	67.24	73.94	16.39	1183.55	820.31

Note: Mean with same or similar alphabets are not statistically different from each other

To access the overall diversity pattern among the germplasms, the PC analysis were conducted (Table.4), using eight variables evaluated in this study. The result of the PCA showed that three of the eight principal component axes had eigen values greater than one (1) and altogether accounted for 82.4% of the total variation. The first three accounted for 82.40% with PC 1 accounting for 43.27%, PC 2 accounting for 24.68% and PC3 accounting for 14.5%. PC1 variation was loaded in days to fifty percent flowering, days to first flowering, ninety-five percent maturity, Number of Branches per plant and hundred seed weight. The remaining variables had weak or no discriminating power. Thus the most important descriptors of variability are those associated with PCA 1.

The cluster analysis procedure grouped the cowpea germplasms into four (4) clusters, with cluster I having two (2) accessions, cluster II having seven (7) accessions, cluster III and IV having one (1) accession each (Figure 1). Cluster I contain accession IT07K-243-1-10, and IT07K-230-2-9 at a distance of 130.783. Cluster II contains accession IT07K-291-69, IT10K-817-3, UAM09-1056-2, IT10K-837-1, IT10K-817-7, UAM14-175-31-1 and UAM09-1056-6 with an average distance of 61.926. Also, Cluster III contains accession UAM14-143-4-1, while Cluster IV contains accession IT99K-573-1-1. This grouping suggests that cowpea crop improvement programs can select germplasms from the different clusters to maximize the greatest genetic diversity among the germplasms.

Table.4: Principal Component Analysis (PCA) of Cowpea Germplasms Showing the Principal Component Cores, Eigen Values and Percentage Total Variance Account for by the Eight Principal Component Axes.

VARIABLES	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Days to first flowering	0.485	-0.040	0.084	0.382	-0.027	0.490	-0.600	0.098
Days to 50% Flowering	0.498	-0.081	0.031	0.322	-0.092	0.190	0.772	-0.027
Numbers of branches per plant	0.313	-0.322	-0.318	-0.428	0.709	0.106	0.014	0.013
Days to 95% Maturity	0.341	-0.475	0.009	0.185	-0.136	-0.756	-0.176	0.054
Numbers. of pod per plant	-0.098	-0.372	-0.683	-0.132	-0.547	0.247	-0.022	-0.091
100 seed weight	0.283	-0.142	0.527	-0.677	-0.378	0.123	-0.015	-0.081
Total pod weight	-0.307	-0.507	0.294	0.227	0.164	0.163	-0.006	-0.676
Total seed weight	-0.345	-0.497	0.246	0.077	0.039	0.197	0.109	0.718
EIGEN VALUE	3.4616	1.9740	1.1583	0.6495	0.4319	0.2061	0.0837	0.0349
PROPORTION %	0.433	0.247	0.145	0.081	0.054	0.026	0.010	0.004
CUMULATIVE %	0.433	0.679	0.824	0.905	0.959	0.985	0.996	1.000

Cluster Analysis

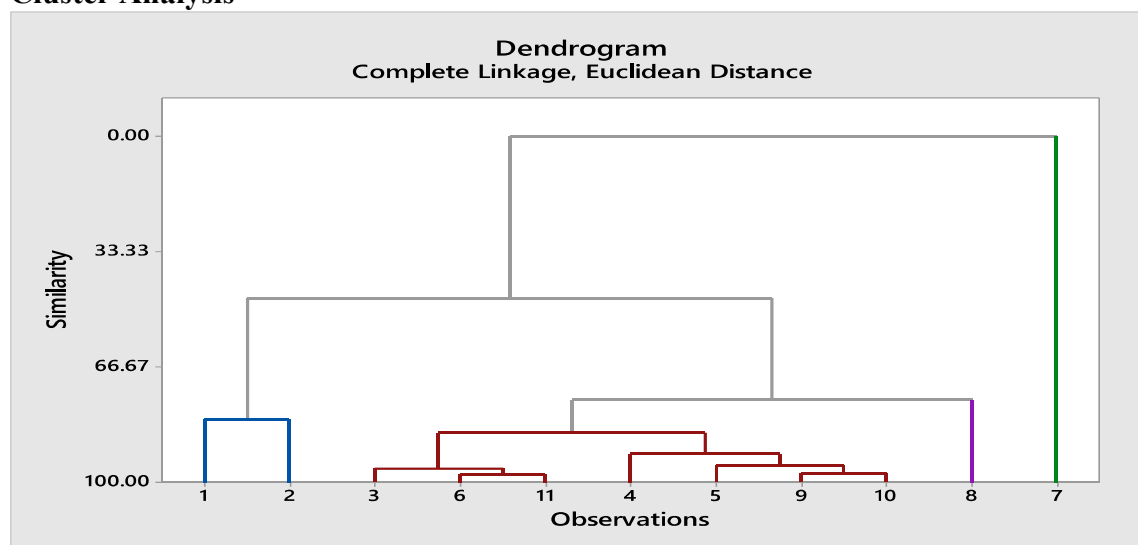


Figure 1: Dendrogram Showing the Clusters of Eleven (11) Cowpea Germplasms.

Discussion

The variation observed among the eleven cowpea germplasms evaluated may be attributed to the different genetic makeup of the genotypes under study, which gives an ample scope for improvement in population through various breeding approaches. Cowpea genotype IT07K-230-2-9 was the first to flower, first to attain fifty percent flowering and one of the varieties with the highest seed yield. This early flowering might be attributed to inherent genetic composition as well as prevailing environmental factors e.g. temperature, photoperiod, altitude and soil conditions. Oladejo *et al.*, (2021) reported that days to first flowering varies significantly among cowpea genotypes and are influenced by environmental factors, particularly temperature, and photoperiod. Different numbers of days to flowering have been reported for several cowpea germplasms. Nagalaskshmi *et al.*, (2010) reported a value of 27 to 50 days after planting in India while in Ghana; Cabbina *et al.*, (2011) reported 31 to 38 days to 50% flowering in some genotypes. Seed yield and yield component traits revealed high significant variations among all germplasms studied, cowpea accession IT07K-243-1-10 weighed more for pod weight and seed weight than all other

genotypes evaluated, while cowpea accession UAM14-143-4-1 weighed the least for pod weight and seed weight. This result is slightly in tandem with the value reported by Lartey and Oferi (2000) and Egbe *et al.*, (2010) in Ghana and Nigeria respectively for different cowpea genotypes, they also reported that the variation may be due to genotypic and environmental interactions. In general, high level of genetic variability was observed in all traits among the cowpea germplasms. According to Memo *et al.*, (2005), the expression of the traits depends on the genetic characteristics of the planting materials under consideration as well as the environment in which they are grown. The Principal component analysis reveal that there are eight (8) principal component axes for the parameters observed. The first three accounted for 82.40% with PC 1 accounting for 43.27%, PC 2 accounting for 24.68% and PC3 accounting for 14.5%. This result corroborates that of Oladejo *et al.* (2011), who reported that Seven PCs identified by PCA (with eigen values >1.0) out of 22 components accounted for 79% of total variation. The first three (3) PCs accounted for 32%, 16%, and 8% respectively of the total variation. They further explained that traits of highest loading were mainly

phenological traits (days to maturity, days to 50% flowering, and days to seed fill) and were therefore associated to PC1 and they concluded by saying days to fifty-percent maturity, days to fifty percent flowering and days to seed fill were among the principal determinants of yield.

Conclusions

This study shows that the germplasms evaluated are highly diverse. Based on principal component analysis, this diversity is attributed to traits like days to first flowering, days to fifty percent flowering, days to ninety-five percent maturity, hundred seed weight and numbers of branches per plant. For future cowpea genetic crop improvement, cowpea breeding lines can be selected from the different clusters to maximize diversity in traits improvements. The findings of the study also identified three high yielding accessions (IT07K-234-1-10, IT07K-230-2-9 and IT99K-537-1-1). For earliness, cowpea accession UAM14-143-4-1 and IT10K-817-7 are suggested in drought prone areas however, Further studies are recommended to consolidate this work, to enhance adoption by farmers.

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References

- Abdi, H., and Williams, L. J. (2010). Principal component analysis. Wiley Interdisciplinary Reviews: *Computational Statistics*, 2:437-455.
- Aboki, E. and Yuguda, R. (2013). Determinant of Profitability in Cowpea Production in Takum Local Government Area of Taraba State, Nigeria. *Journal of Agricultural Sciences*, 4:33-37.
- Agbogidi, O. (2010) Screening Six Cultivars of Cowpea (*Vigna unguiculata* L. Walp) for Adaptation to Soil Contaminated with Spent Engine Oil. *Journal of Environmental and Chemical Ecotoxicology*, 2:103-109
- Boukar, O., Belko, N., Chamarthi, S., Togola, A., Batieno, J., Owusu, E., Haruna, M., Diallo, S., Umar, M.L., Olufajo, O. and Fatokun, C. (2018) Cowpea (*Vigna unguiculata* L. Walp): *Genetics, Genomics and Breeding Plant Breeding*, 138:415-424.
- Cabbina, A. O., Ologunde, O. O., Adebola, A. T., and Adewale, A. A. (2010). Evaluation of cowpea (*Vigna unguiculata* (L.) Walp.) genotypes for yield and quality in the humid tropics of Nigeria. *African Journal of Agricultural Research*, 6:5278-5286.
- Egbe, E. A., Iheka, S. C., and Ijeoma, N. C. (2010). Evaluation of cowpea (*Vigna unguiculata* (L.) Walp.) genotypes for resistance to anthracnose (*Colletotrichum gloeosporioides*) in Nigeria. *African Journal of Agricultural Research*, 5:2614-2621.
- Falconer, D.S. and Mackay, T.F.C. (1996) Introduction to Quantitative Genetics. 4th Edition, Addison Wesley Longman, Harlow.
- FAO/WFP/IFAD (2022). The State of Food Security and Nutrition in the World 2022. Turning food systems into engines for inclusive human development and sustainable peace. Rome, Italy: FAO.
- Food and Agriculture Organization of the United Nations (FAO). (2022). FAOSTAT statistical database.
- Horn, L.N. and Shimelis, H. (2020) Production Constraints and Breeding Approaches for Cowpea Improvement for Drought Prone Agro-Ecologies in Sub-Saharan Africa. *Annals of Agricultural Sciences*, 65:83-91.

- Hotelling, H. (1933) Analysis of a complex of statistical variables into principal Components. *Journal of Educational Psychology*, 24:417-441.
- Huynh, B.L., Matthews, W.C., Ehlers, J.D., Lucas, M.R., Santos, J.R., Ndeve, A., Close, T.J. and
- Jain, A. K., Murty, M. N., and Flynn, P. J. (1999). Data clustering: A review. *ACM Computing Surveys (CSUR)*, 31:264-323.
- Lartey, S. A., and Oferi, O. A. (2000). Identification of cowpea genotypes with resistance to bacterial blight (*Xanthomonas campestris* pv. *Vignae*) in Ghana. *African Journal of Biotechnology*, 9:1365-1369.
- Memo, A. I., Afolayan, A. J. and Ogunsanwo, O. O. (2005). Evaluation of cowpea (*Vigna unguiculata* (L.) Walp.) genotypes for resistance to termite attack in Nigeria. *African Journal of Agricultural Research*, 1:1-5.
- Mullar S., Coyne, M., and Kluepfel. D. M., (1992). Genetic variability for yield and yield components in cowpea (*Vigna unguiculata* (L.) Walp.). *Crop Science*, 32(6):1249-1254.
- Nagalakshmi, V., Venkatachalam, P., and Siddiq, E. A. (2010). Genetic variability and heritability studies in cowpea (*Vigna unguiculata* (L.) Walp.). *Journal of Agricultural Sciences*, 22:114-119.
- National Research Institute for Nuts (NRIN). (2022). Groundnut production in Nigeria: Challenges and prospects. Ibadan, Nigeria: NRIN.
- Oladejo, A. O., Ologunde, O. O., Adebola, A. T., and Adewale, A. A. (2021). Genetic variability and heritability of agronomic traits in cowpea (*Vigna unguiculata* (L.) Walp.) genotypes. *Journal of Agricultural Science and Technology*, 23:1091-1104.
- Oladejo, A. O., Ologunde, O. O., Adebola, A. T., and Adewale, A. A. (2011). Genetic variability and heritability of agronomic traits in cowpea (*Vigna unguiculata* (L.) Walp.) genotypes. *Journal of Agricultural Sciences*, 23:1091-1104.
- Serath, T. U., and Reshma. M. A. (2017). Genetic variability and heritability studies for yield and other traits in cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Science, Environment and Technology*, 6(3):2039-2045.