Received: 20 May 2024 | Revised: 08 Aug 2024 | Accepted: 19 Aug 2024

Electronic Journal of Plant Breeding

Research Note

Selection parameters for the improvement of seed yield and attributes in cowpea (*Vigna unguiculata* L. Walp.)

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Abstract

The present investigation was carried out with 53 genotypes of cowpea to study association among yield contributing traits. The genotypes were sown in a randomized block design replicated with three replications at the National Pulse Research Centre, TNAU , Vamban, Pudukkottai, during *Kharif,*2022. Observations on ten traits were recorded and subjected to statistical analysis. The coefficient of phenotypic differences was substantially greater than the genotypic variation for all the characters under study, showing that the prevailing variation is mainly governed by the genotypic factor and substantial environmental factors. High heritability and genetic advance as percentage of mean were observed for the traits seed yield and 100 seed weight. This showed the role of additive gene action in the inheritance of these traits which gives the best chance of their improvement through simple selection. Association analysis revealed that number of cluster/plant and number of pods/plant had a significant and positive correlation on seed yield. Yield component traits *viz.,* plant height, number of branches/plant, number of pods/cluster, number of pods/plant, 100 seed weight and seed yield were high inter-correlated among themselves. Furthermore, it was observed that the number of pods/plant, pod length, and 100 seed weight had the maximum positive direct effects on seed yield. So direct selection for these three traits could help to improve the seed yield potential of cowpea.

Keywords: Cowpea, heritability, genetic advance, association analysis.

Cowpea (*Vigna unguiculata* (L.) Walp.,) is an important annual legume crop. It is native of Central Africa and a member of the *Fabaceae* family. It is cultivated for its seeds, vegetables, and animal feed in various tropical and subtropical regions, particularly in African, Asian, Central America, and South America (Singh *et al.* (1997). According to Kumar *et al.* (2020), cowpea is grown in arid and semi-arid parts of Rajasthan, Gujarat, Maharashtra, Karnataka, and Tamil Nadu. According to FAOSTAT (2020), the global production of Cowpea in 2019-2020 reached 89.16 tons per hectare. In 2022, India produced approximately 3.14 million metric tons of cowpea (Source: NHB, Ministry of Agriculture & Farmers Welfare, 2021- 22). Cowpea seeds comprises of 23.4% protein, 1.8% fat, 60.3% carbohydrate , calcium and Iron (Ano and Ubochi 2008). In the recent past, cow pea cultivars have registered less productivity, non-synchronous maturity and low response to high doses of fertilizers. Additionally, the crop shows signs of being unsuitable for various eco system, lodging and breaking of pods, a protracted maturation period, and a breakdown in its genetic resistance to insect pests, all of which seriously impair harvest indices and result in severe financial loss. The yield and cultivable area have been greatly enhanced by the development of elite lines having early and synchronized maturity, adequate grain features, resistant to pests and diseases (Ehlers and Hall 1997). One of the best approaches for improving production in this crop is to exploit the diversity available in the germplasm of this crop. To improve yield potential of any crop, it is essential to determine the level of genetic diversity in the population prior to beginning the breeding program (Singh *et al*., 2016). An efficient breeding program also requires knowledge on the inheritance of quantitative and qualitative traits through the estimation of phenotypic and genotypic coefficients of variability, heritability, and genetic advancement in order to formulate selection criteria. For selecting the best genotypes, the information on the relationship between yield and other yield contributing characteristics would be helpful. According to Hemalatha *et al.* (2017), association analysis evaluates the relationships between different plant traits and identifies contributing characters that can be used as a basis for selection to improve economically important traits. In light of these considerations, the current study aims to evaluate genetic advance, heritability, and variability in order to identify superior cowpea genotypes that can be used in breeding programs in future.

The experiment was conducted with 53 cowpea genotypes at the research farm of National Pulses Research Centre, TNAU, Vamban, Pudukkottai District, Tamil Nadu during *Kharif,* 2022. The genotypes were evaluated for yield and its attributing traits *viz.,* plant height (cm), days to 50% flowering, no. of branches/plant, no. of cluster/plant, no. of pods/cluster, no. of pods/plant, pod length (cm), no. of seeds/pod, 100 seed weight (g) and seed yield (kg/ha). The trial was raised in RBD with three replications and the plot size was 10.8 m^2. The spacing adopted between rows was 45 cm and the plant to plant spacing was 15 cm. Observation on the above traits were recorded on five randomly chosen plants in each plot and in each replication and the mean data were subjected to statistical analysis.

Statistical Analysis: Analyses of variance (ANOVA) for all traits were worked out for all traits as per Panse and Sukhatme (1967). Variability present in the genotypes for seed yield and yield contributing traits were analyzed as per the method proposed by Burton (1952). As recommended by authors Burton and Devane (1953), the estimates of GCV and PCV were divided into three categories namely, low (< 10%), moderate (10-20%), and high (> 20%). Broad sense heritability was estimated and expressed in term of percentage as suggested by Allard (1960). The traits were categorized as low (less than 50%), moderate (50-70%), high (more than 70%) as per Robinson (1949). The genetic advance was estimated by method suggested by Lush (1949). Genetic advance as percentage of mean (GAM) was classified as suggested by Johnson *et al.* (1955). GAM ranging from 0-10% were grouped as low, 10-20% were grouped as moderate and more than 20% as high. The methodology described by Al-Jibouri *et al*. (1958) was followed to calculate correlation coefficients at the genotypic and phenotypic levels. Path analysis was carried out as per the method of Dewey and Lu (1959). All the above statistical analyses were carried out using TNAUSTAT software (Manivannan, 2014).

The ANOVA presented in the **Table 1** showed that there was a significant difference among the cultivars for all the traits studied except pod length. It pointed out the presence of sufficient variation among the genetic material under investigation and hence presenting sufficient scope for breeding efforts. *Per se* performance and variability parameters of cowpea genotypes for 10 quantitative parameters are presented in **Table 2**. More accuracy in the estimate is indicated by a lower coefficient of variation value, which varied from 1.6 to 13.7 for all the traits in the study.

Genotypic and Phenotypic Coefficient of Variation (GCV and PCV): For every trait under examination, the PCV was slightly greater than the GCV, suggesting that environmental influences have less impact on the expression of traits. Greater variability among genotypes is defined by the wide range of GCV and PCV, which makes better improvement through selection. The traits namely plant height (cm), no. of clusters/plant, no. of pods/plant, pod length, and seed yield (kg/ha) showed a broad range of genotypic and phenotypic variance. The result was similar to the report by Chetukuri *et al.* (2013) and Gupta *et al*. (2019).

Higher GCV was observed for seed yield (23.9%), moderate GCV for no. of pods/plant (10.7%), 100 seed weight (14.2%), and low GCV for the remaining characteristics under study. The seed yield recorded the highest magnitude of PCV (26.6%), while the no. of pods/plant (16.0%), plant height (15.9%), 100 seed weight (14.6%), no. of branches/plant (13.4%), and plant height (11.1%) showed moderate PCV. Days to 50% flowering (8.1%), no. of cluster/plant (8.7%), pod length (9.5%), and no. of seeds/pod (5.8%) showed the lowest magnitude

Table 1. Analysis of variance

Particulars	Degrees of freedom	Days to 50% flowering	Plant height (cm)	No. of branches/ plant	No. of cluster/ plant	No. of Pod/ cluster	No. of pods/ plant	Pod length (cm)	No. of seeds/ pod	100 seed weight (g)	Seed yield (kg/ha)
Replication	2	0.12	10.90	0.37	0.77	0.06	3.38	2.71	0.55	0.21	1389.13
Treatments	53	33.61*	145.07*	0.32*	2.85*	0.05*	12.58*	3.31	0.91*	7.31*	156769.73*
Error	104	0.42	23.94	0.15	1.43	0.02	3.70	1.44	0.58	0.13	11547.49

https://doi.org/10.37992/2024.1503.087

Table 2. Genetic components of variance for various quantitative traits

Particulars	Days to 50% flowering	Plant height (cm)	No. of branches/ plant	No. of cluster/ plant	No. of Pod/ cluster	No. of pods/ plant	Pod length (cm)	No. of seeds/ pod	100 seed weight (g)	Seed yield (kg/ha)
Grand Mean	41.8	72.5	3.4	8.7	1.9	16.1	15.1	14.2	10.9	919.9
Range	37.3-50.0	44.8-82.4	2.7-4.1	6.9-11.0	1.5-2.2	11.7-20.7	13.3-18.0	13.2-15.4	6.8-18.1	502.7-1300.0
S.E	0.4	2.8	0.2	0.7	0.1	1.1	0.7	0.4	0.2	62.0
CD (0.05%	1.0	7.8	0.6	1.9	0.2	3.1	1.9	1.2	0.6	172.0
CV (%)	1.6	6.8	11.5	13.7	7.0	11.9	7.9	5.4	3.3	11.7
PV	11.5	64.3	0.2	1.9	0.0	6.7	2.1	0.7	2.5	59955.1
GV	11.1	40.4	0.1	0.5	0.0	3.0	0.6	0.1	2.4	48407.1
EV	0.4	23.9	0.2	1.4	0.0	3.7	1.4	0.6	0.1	11548.1
PCV(%)	8.1	11.1	13.4	15.9	8.7	16.0	9.5	5.8	14.6	26.6
GCV(%)	8.0	8.8	6.9	7.9	5.2	10.7	5.2	2.3	14.2	23.9
h^2(%)	96.3	62.8	26.4	25.0	35.5	44.6	30.2	16.0	94.7	80.7
GAM(%)	16.1	14.3	7.3	8.2	6.4	14.7	5.9	1.9	28.4	44.3

of variability. Aishwarya and Deepanshu (2023) and Khandait *et al*. (2016) reported similar results for seed yield . Khandait *et al*. (2016) reported similar results for 100 seed weight. Low GCV and PCV were observed for days to 50% flowering (8.0%, 8.1%), no. of pods/ cluster (5.2%, 8.7%), pod length (5.2%, 9.5%) and no. of seeds/pod (2.3%, 5.8%). These results indicate minimum variability in these traits. Similar findings for the no. of seeds/pod and days to 50% flowering were reported by Aishwarya and Deepanshu (2023).

Heritability and Genetic Advance: The degree of similarity between parents and their offspring is determined by heritability, which articulates the percentage of total variability that is attributable to the average effect of allelic pairs. It is a reliable indicator of how parents transmit their traits to their offsprings (Falconer, 1981). A high value of broad-sense heritability aids in selecting the right traits for selection and empowers the breeder to choose elite genotypes based on the phenotypic expression of the trait. Numerous additive factors are indicated by high heritability values (Panse, 1957).

High value of heritability for days to 50% flowering (96.3%), 100 seed weight (94.7%), and seed yield (80.7%) was recorded in the current study. Gupta *et al.* (2019) and Owusu *et al.* (2021) reported similar findings. For plant height, moderate estimate of heritability (62.8%) was observed. No. of branches/plant (24.5%), cluster/ plant (25.0%), pods/cluster (35.5%), pods/plant (44.6%), length of pod (30.2%), and seeds/plant (16.0%) showed low estimates of heritability. Similar results were also reported by Diriba Shanko *et al.* (2014) for no. of pods/ plant and no, of branches/plant, and by Sabale *et al.* (2018) for the no. of clusters/plant.

There is limited choice to estimate the heritable variation with the coefficient of variation. Genetic progress expressed as a percentage of mean and heritability estimates are used to determine the relative amount of variation.

For traits such as seed yield (80.7%, 44.3%) and 100 seed weight (94.7%, 28.4%), high heritability coupled with high genetic advance as a percentage of mean was observed in the current investigation. This suggests that additive gene action predominates in the inheritance of these traits and provides the best opportunity for improving these traits by direct selection. Similar observations were reported by Hasan Khan *et al.* (2015) in cowpea for 100 seed weight; Khanpara *et al.* (2015) and Diwaker *et al.* (2017) for seed yield (kg/ha) .

High heritability with moderate genetic advance as percentage of mean was observed days to 50% flowering (96.3%, 16.1%). This is in line with the findings of Owusu *et al.* (2021). Moderate heritability and genetic advance as percentage of mean was observed for plant height (62.8%, 14.3%). In case of no. of pod/plant (44.6%, 14.7%), low heritability and moderate genetic advance as a percentage of mean was observed.

Characteristics such as no. of branches/plant (24.5%, 7.3%), no. of clusters/plant (25.0%, 8.2%), no. of pods/ cluster (35.5%, 6.4%), pod length (30.2%, 5.9%), and no. of seeds/plant (16.0%, 1.9%) registered low level heritability combined with low genetic advance as percentage of mean. This suggests that for these traits, selection method of breeding would be futile. Sabale *et al.* (2018) reported a similar outcome for the trait number of pods per cluster.

Correlation Studies: Correlation coefficients, which were calculated to evaluate the strength of the relationship between seed yield and its related traits, are furnished in **Table 3**. No. of clusters/plant and no. of pods/plant showed

Table 3. Genotypic (Above diagonal) and phenotypic (Below diagonal) correlations of various quantitative traits

Character	Days to 50% flowering	Plant height (cm)	No. of branches/ plant	No. of cluster/ plant	No. of Pod/ cluster	No. of pods/ plant	Pod length (cm)	No. of seeds/ pod	100 seed weight (g)	Seed yield (kg/ha)
Days to 50% flowering	**1.000**	0.261*	-0.321*	-0.100	-0.183	-0.044	0.210*	0.075	-0.109	-0.250*
Plant height (cm)	0.202*	**1.000**	0.130	0.047	0.171	0.082	0.046	-0.126	0.299*	-0.074
Number of branches/plant	-0.176	0.160	**1.000**	0.065	0.301*	0.300*	-0.111	0.075	-0.263*	0.125
Number of cluster/plant	-0.038	0.145	0.254*	**1.000**	0.196*	0.759*	-0.073	-0.061	0.025	0.399*
Number of pod/cluster	-0.075	0.050	0.043	0.122	**1.000**	0.524*	-0.525*	-0.251*	-0.373*	0.189
Number of pods/plant	0.003	0.099	0.256*	0.651*	0.405*	**1.000**	-0.163	0.212*	-0.239*	0.738*
Pod length (cm)	0.074	0.070	0.065	0.237*	-0.177	0.081	**1.000**	0.662*	0.185	-0.103
Number of seeds/ pod	-0.006	0.057	0.129	0.321*	0.043	0.207*	0.671*	**1.000**	0.111	0.114
100 seed weight (g)	-0.101	0.259*	-0.141	0.024	-0.228*	-0.147	0.098	0.053	**1.000**	-0.186
Seed yield (kg/ha)	-0.214*	-0.047	0.028	0.179	0.186	0.444*	-0.048	0.059	-0.154	**1.000**

a strong and favourable correlation with seed yield. Similar findings were previously published for both traits by Aishwarya and Deepanshu (2023) and no. of pods/ plant by Owusu *et al.,* 2021. Hence improvement of the above characters could result in concurrent improvement in yield. Significant negative genotypic correlation was observed between days to 50% flowering (-0.250) and seed yield (Aishwarya and Deepanshu, 2023).The traits no. of branches/plant (0.125), no. of pods/plant (0.189) and no. of seeds/pod (0.114) exhibited weak but positive correlation with yield, indicating that they were not highly associated with seed yield. On the other hand, there was a negative and insignificant correlation between seed yield and plant height (-0.074), pod length (-0.013), and 100 seed weight (-0.186).

With respect to inter-correlation between the characters under study at genotypic level, the trait days to 50% flowering was observed to have a strong positive relation with plant height, pod length and strong negative bond with no. of branches/plant. The trait plant height had a strong positive correlation with plant height. No. of branches/plant registered positive and significant association with no. of pods/cluster. No. of pods/plant was observed to have significant negative association with 100 seed weight. The trait no. of clusters/plant recorded positive and significant association with no. of pods/ cluster and no. of pods/plant. No. of pods/cluster had a strong positive correlation with and no. of pods/plant and had a strong negative association with pod length, no. of seeds/pod and 100 seed weight. The trait pod length had significant positive association with no. of seeds/pod. The aforementioned data made it evident that there was a strong correlation between the yield component traits namely plant height, no. of branches/plant, no. of pods/ cluster, no. of pods/plant, 100 seed weight, and seed yield. Therefore, it could be more beneficial to select for the aforementioned traits simultaneously in order to improve cowpea.

Direct and indirect effect studies: The direct and indirect effects of various attributes on seed yield were not depicted by the correlation coefficient estimates; instead, they only demonstrated the relationship between the yield components. This is due to the fact that the characteristics that are associated are connected to other elements rather than existing independently. Lenka and Misra (1973) stated that the path co-efficient procedure is useful in understanding the direct influence of one character on another because it splits the correlation coefficient into its components for direct and indirect effects. Important component traits that are helpful in indirect selection of complex traits like yield are identified as a result of this analysis. Path coefficient analysis of nine traits on yield revealed high favourable direct effects on seed yield were recorded by no. of pods/plant (3.772), pod length (0.914), and 100 seed weight (0.240) (**Table 4**). This suggests that direct selection for these three traits is necessary to increase cowpea seed yield. This observation was accordance with earlier findings of Meena, *et al.* (2015); and Patel *et al.* (2016) for pod length and no. of pods/ plant. Aishwarya and Deepanshu (2023), Jogdhande *et al.*

Table 4. Direct and indirect effects of various traits on seed yield at the genotypic level

Character	Days to 50% flowering	Plant height (cm)	No. of branches/ plant	No. of cluster/ plant	No. of pod/ cluster	No. of pods/ plant	Pod length (cm)	No. of seeds/ pod	100 seed weight (g)	Seed yield (kg/ha)
Days to 50% flowering	**-0.648***	-0.047	0.129	0.230*	0.212*	-0.166	0.192	-0.126	-0.026	-0.250*
Plant height (cm)	-0.169	**-0.181**	-0.052	-0.108	-0.198*	0.307*	0.042	0.213*	0.072	-0.074
Number of branches/plant	0.208*	-0.024	**-0.401***	-0.151	-0.349*	1.133*	-0.101	-0.127	-0.063	0.125
Number of cluster/plant	0.065	-0.009	-0.026	**-2.309***	-0.227*	2.863*	-0.067	0.103	0.006	0.399*
Number of pod/cluster	0.118	-0.031	-0.121	-0.453*	**-1.160***	1.978*	-0.480*	0.426*	-0.089	0.189
Number of pods/plant	0.029	-0.015	-0.120	-1.753*	-0.608*	**3.772***	-0.149	-0.360*	-0.057	0.738*
Pod length (cm)	-0.136	-0.008	0.045	0.169	0.609*	-0.617*	**0.914***	-1.123*	0.044	-0.103
Number of seeds/ pod	-0.048	0.023	-0.030	0.140	0.292*	0.800*	0.605*	**-1.695***	0.027	0.114
100 seed weight (g)	0.071	-0.054	0.105	-0.057	0.432*	-0.903*	0.169	-0.189	**0.240***	-0.186

Residual Effect: - 0.6620

(2017) and Singh *et al*. 2003 for 100 seed weight. On the contrary, Walle *et al.* (2018) reported that 100 seed weight have high direct adverse influence on seed yield at the genotypic level. Days for 50% flowering, no. of branches/ plant, no. of cluster/plant, no. of pods/cluster and no. of seeds/pod recorded significant negative direct effect on seed yield. Remaining traits had negligible effect on seed yield per plant. Similar finding were reported earlier by Meena, *et al.,* (2015) and Aishwarya and Deepanshu (2023) for days to 50% flowering and no. of seeds/pod and Patel *et al.* (2016) for no. of branches/plant, no. of cluster/plant and no. of seeds/pod.

Through plant height, no. of branches/plant, no. of clusters/plant, no. of pods/cluster, and no. of seed/pod the pods/plant had a positive and indirect significant effect on seed yield. The remaining traits under study had very little impact on seed yield. Therefore, increasing the no. of pods/plant and no. of cluster/plant will aid in improving the cowpea seed yield. This is in line with the findings of Jogdhande *et al.* (2017).

The results of the current study showed that traits like seed yield per plant and 100 seed weight have a high level of heritability and a high amount of genetic advance as a percentage of the mean. This suggests that additive gene action predominates in the inheritance of these characters and provides the best opportunity for improving through simple selection processes. Association analysis revealed that no. of cluster/plant and no. of pods/plant had significant and positive correlation seed yield. Yield contributing traits *viz.,* plant height, no. of branches/ plant, no. of pods/cluster, no. of pods/plant, 100 seed weight and seed yield were highly inter correlated among themselves. Moreover, it was observed that the no. of pod/ plant, pod length, and 100 seed weight had the greatest positive direct effects on the amount of seed produced per hectare. This suggests that direct selection for these three characteristics is necessary to increase cowpea seed yield and also no. of pods/plant had a positive and significant indirect effect on seed yield through height of plant, branches/plant, clusters/plant, pods/cluster and seeds/pods. Hence selection of plants based on cluster/ plant and pods/plant will help the genetic improvement of seed yield in cowpea.

REFERENCES

Aishwarya, G. and Deepanshu. 2023. Investigation on genetic variability, heritability, correlation studies in cowpea (*Vigna unguiculata* L.). *International Journal of Environment and Climate Change,* **13**(10): 173-182. [Cross Ref]

Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. 1958. Genotypic and environmental variances and covariances in upland cotton crosses of inter-specific origin. *Agron. J.,* **50**: 633-637. [Cross Ref]

Allard, R.W. 1960. Principles of plant breeding. John Wiley and Sons Inc. London. **83**-108.

Ano, A.O. and Ubochi. 2008. Nutrient composition of climbing and prostrate vegetable cowpea accessions. *African Journal of Biotechnology,* **7**(20):3795-3798.

Burton, G.W. 1952. Quantitative inheritance in grasses. Proc. 6th Int. Grzassland Congr. **19**:277-283.

Burton, G.W. and Devane, E.H. 1953. Estimating the heritability in tall fescue (*Festuca arundinancea*) from replicated clonal material. *Agronomy J.,* **45**: 478-481. [Cross Ref]

Chetukuri, A., Vijayalakshmi, P., Bhargavi, V., Pavan, K. and Siddiq, E.A. 2013. Correlation, variability and heritability in pigeon pea, *Adv. Biores,* **4**(2): 129-139.

Dewey, D.R. and Lu, K.H. 1959. A correlation and path co-efficient analysis of components of crested wheat grass seed Production. *Agron. J.*, **51**: 515-518. [Cross Ref]

Diriba Shanko, Mebeaselassie Andargie and Habtamu Zelleke.2014. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.). *Research in Plant Biology*, **4**(2): 21-26.

Diwaker, P., Sharma, M.K., Diwakar. A, Singh, P., Bhadala, K. and Meena S. 2017. Genetic variability assessment in vegetable cowpea (*Vigna unguiculata* (L.) Walp.) genotypes. *International Journal of Chemical Studies*, **5**(5):150-155.

Ehlers, J.D. and Hall. A.E. 1997. Cowpea (*Vigna unguiculata* (L.) Walp.). *Field Crops Research*. **53**:187-204. [Cross Ref]

Falconer, D.S. 1981. An introduction to quantitative genetics. Longman, NEW YORK, U.S.A.

FAOSTAT. 2020. Food and Agriculture Organization of the United Nations, Rome, Italy.

Gupta, R.K., Parmila, Maduri, A., Kumar, A. and Kumari, P. 2019. Study on genetic variability in cowpea [*Vigna unguiculata* (L.) Walp]. *Current Journal Applied Science and Technology,* **33**(2): 1-8. [Cross Ref]

Hasan Khan, K.P. and Viswanatha, Sowmya H.C. 2015. Study of genetic variability parameters in cowpea (*vigna unguiculata* (L.) walp.) germplsam lines. *An International Quarterly Journal of Life Sciences*, **10**(2):747-750.

Hemalatha, K., Sapna, L.S. and Gabril, M.L. 2017. Study on genetic variability and correlation in black-gram (*Vigna mungo* (L.). Hepper). *Journal of Pharmacognosy and Phytochemistry,* **6**(4): 674-676.

Jogdhande, S., Vijay, S.K. and Nagre, K. 2017. Correlation and path analysis study in cowpea [*Vigna unguiculata* (L.) Walp.] Genotypes. *International Journal Current Microbiology Application Sciences,* **6**(6):3305-3313. [Cross Ref]

Johnson, H.W., Robinson, H. F and Comstock, R.F. 1955. Estimation of genetic environmental variability in soyabean. *Agronomy Journal*, **47**:314-318. [Cross Ref]

Khandait, R., Jain, P.K, Singh, Y, Prajapati, S. and Solanki, S. 2016. Genetic variability in diverse genotypes of cowpea (*Vigna unguiculata* L.). *Technofame- A J. Multidisciplinary Advance Res.,* **5**(2):120-126. [Cross Ref]

Khanpara, S.V., Jivani. L.L, Vachhani. J.H. and Kachhadia. V.H. 2015. Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding*, **7**(2):408-413. [Cross Ref]

Kumar, R., Rai, A,K. and Lata, K. 2020. Assessment of cowpea (*Vigna unguiculata*) varieties under semi-arid conditions of central Gujarat. *Curr Horticult*, **8**(1):47-51. [Cross Ref]

Lenka, D. and Misra, B. 1973. Path coefficient analysis of yield in rice varieties. *Indian Journal of Agricultural Science,* **43:** 376-379.

Lush, J.L. 1949. Heritability of quantitative characters in farm animals. *Proceedings of 8th Congress of Genetics and Heredities,* **35**:356-375. [Cross Ref]

Manivannan,N.2014.TNAUSTAT-Statistical package. Retrieved from https://sites.google.com/site/tnaustat.

Meena, H.K., Krishna, R.K. and Bhuri, S. 2015. Character associations between seed yield and its components traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian Journal of Agricultural Research*, **49:** 567-570. [Cross Ref]

NHB. 2021. nhb.gov.in/statistics/2020-21. Area and production of horticulture crops- All India.

Owusu, E.Y., Karikari, B., Kusi, F., Haruna, M., Amoah, R.A., Attamah, P., Adazebra, G., Sie, E.K. and Issahaku, M. 2021. Genetic variability, heritability and correlation analysis among maturity and yield traits in cowpea (*Vigna unguiculata* (L) Walp) in Northern Ghana. **7** (9):1-9. [Cross Ref]

Panse, V.G. and Sukhatme, P.V. 1967. Statistical methods for agricultural research works. III edition, ICAR, New Delhi.

Panse, VG. 1957. Genetics of quantitative traits in relation to plant breeding. Indian J. Genet. & Plt. Breed.

Patel, UV., Parmar, V.K, Patel, P.B. and Malviya, A.V. 2016. Correlation and path analysis Study in cowpea (*Vigna Unguiculata* (L.) Walp.). *International Journal of Science, Environment and Technology*, **5**(6): 3897-3904

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. [Cross Ref]

Sabale, G.R., Bhave, S.G, Desai, S.S, Dalvi, M.B. and Pawar, P.R. 2018. Variability, heritability and genetic advance studies in F2 generation of cowpea (*Vigna unguiculata sub sp. unguiculata*).*Int.J.Curr. Microbiol.App.Sci*.,**7**(09):33143320.doi:https://doi.org/10.20546/ijcmas.2018.709.411 [Cross Ref]

Singh, B.B. Ajeigbe, H.A, Tarawali, S.A, Fernandez-Rivera, S. and Abubakar, M. 2003. Improving the production and utilization of cowpea as food and fodder. *Field Crops Research*, **84**: 169-177. [Cross Ref]

Singh, B.B., Chambliss, O.L. and Shamar, B. 1997. Recent advances in cowpea breeding. In:Singh BB, Mohan Raj DR, Dashiell KE, Jackai Len (ed.). *Advances in Cowpea Research*. IITAJIRCAS, Ibadan, Nigeria.

Singh, M., Swamp, I., Gaikwad, P.D. and Singh, J. 2016. Variability and heritability analysis in blackgram. *Advances of Life Sciences.,* **5**:2619-2621.

Walle, T., Mekbib, F., Amsalu, B. and Gedil, M. 2018. Correlation and path coefficient analyses of cowpea (*Vigna unguiculata* L.) Landraces in Ethiopia. *American Journal of Plant Sciences*, **9**: 2794-2812. [Cross Ref]