International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

Crossref

IJBSM January 2023, 14(1):012-018 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR3312

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2023.3312

Genetic Variability and Character Association Studies on Yield and Yield Attributing Traits in Grain Type Cowpea (*Vigna unguiculata* (L.) Walp.)

Kavyashree N. M.[1], Sanjeev K. Deshpande[2], Bhuvaneshwar R. Patil[3], Mahabaleshwar G. Hegde[4], Shamarao Jahagirdar[5]

[1]Dept. of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka (580 005), India
[2,3]Dept. of Genetics and Plant Breeding, College of Agriculture, Dharwad, University of Agricultural Sciences, Dharwad, Karnataka (580 005), India
[4]Dept. of Agricultural Entomology, [5]Dept. of Plant Pathology, University of Agricultural Sciences, Dharwad, Karnataka (580 005), India

Open Access

Corresponding kavyamnaik@gmail.com

0000-0002-0079-9794

ABSTRACT

The experiment was carried out during July, 2021 to November, 2021 at Botany Garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad, Karnataka, India to estimate genetic variability, correlation and path coefficients for various yield and its component characters using 45 F_1 hybrids of cowpea derived from 10×10 half-diallel crosses and their ten parents. The genetic variability studies revealed the presence of sufficient variability between the studied genotypes for yield traits. High GCV, PCV, heritability and GAM were observed for number of pods plant^{-1} and grain yield plant^{-1}, indicating that operating selection for these traits in the material would be fruitful owing to their additive gene action. Further, the correlation studies revealed that grain yield plant^{-1} was positively and significantly associated with the traits number of pods plant^{-1}, pod length, number of seeds pod^{-1} and 100 seed weight at both genotypic and phenotypic levels depicting the scope of indirect selection for yield through these associated characters. Phenotypic and genotypic path coefficient analysis revealed that number of pods plant^{-1} recorded highest positive direct effect on yield plant^{-1} and also highest indirect effect on yield plant^{-1} via pod length and number of seeds pod^{-1}. These results indicated that, grain yield in cowpea can be improved by improving these significantly associated component traits.

KEYWORDS: Correlation, cowpea, genetic variability, grain yield, path coefficients

Citation* (VANCOUVER)*: Kavyashree et al., Genetic Variability and Character Association Studies on Yield and Yield Attributing Traits in Grain Type Cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Bio-resource and Stress Management,* 2023; 14(1), 012-018. HTTPS://DOI.ORG/10.23910/1.2023.3312.

Copyright: © 2023 Kavyashree et al. This is an open access article that permits unrestricted use, distribution and reproduction in any medium after the author(s) and source are credited.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 08th November 2022 RECEIVED in revised form on 24th December 2022 ACCEPTED in final form on 05th January 2023 PUBLISHED on 17th January 2023

1. INTRODUCTION

Cowpea (*Vigna unguiculata* Walp.) is an important arid legume grown for its pods, leaves and grains (Ehlers and Hall, 1997, Boukar et al., 2011). It is a warm-season pulse crop mainly grown in the tropical and subtropical regions of the world (Timko et al., 2007). It belongs to the family Fabaceae and has the chromosome number of 2n=2x=22 (Chaudhary et al., 2021). Cowpea grains are the important source of protein (22–25%) and other essential nutrients (Boukar et al., 2011). Apart from its nutritional benefits, the crop has multiple advantages. It improves soil fertility by fixing the atmospheric nitrogen, and acts as a good cover crop or much crop and thus helps to check soil erosion. Cowpea can be grown as fodder crop, while its tender pods can be used as vegetables. However, it is predominantly grown for its dried grains (Lioi et al., 2019). It is highly drought tolerant and also thrives well in multiple cropping systems (Aliyu et al., 2022). However, despite its multiple uses and nutritional benefits, the crop is still under explored and the production is low (Goncalves et al., 2016). So, breeding for high yielding cowpea varieties is the prime objective of any cowpea breeding programme.

Knowledge on variation in genetic attributes is the foundation for crop improvement (Falconer and Mackay, 1989). The success of any plant breeding programme is dependent on the presence of sufficient variability in the breeding material (Rauf et al., 2016). Hybridization is a known method of creating variations by recombination of diverse alleles from the contrasting parents (Seehausen, 2004). Knowing the potential magnitude of genetic gain that could be achieved by selection of F1s in future generations is aided by studies on genetic variability. Estimation of genetic variability parameters reveal the information on the amount of variability present in a material, heritable portion of that variable and also the genetic advance that can be achieved by operating selection. Hence, estimation of coefficients of genetic variability, heritability and genetic advance are of much relevance while exercising selection to develop high yielding varieties (Mohammadi and Pourdad, 2009).

Yield being a complex trait, is highly influenced by environment and is often confounded by interaction of many component traits (Shi et al., 2009). Studying the association between the component traits of yield helps to choose the best selection criteria to operate indirect selection for yield. Correlation studies indicate the relative importance of characters on which greater emphasis should be made in selection for yield (Lu et al., 2011). However, correlation alone can only reveal the degree and direction of the association between any two characters. In order to split the correlation coefficients into measures of direct and indirect effects, the path coefficient analysis has to be done (Khan et al., 2022). Several genetic variability and correlation studies have been reported in cowpea by various researchers like Suganthi and Murugan (2008), Nehru et al. (2009), Manggoel et al. (2012), Vir and Singh (2014), Devi and Jayamani (2018), Mofokeng et al. (2020), Panchta et al. (2020), Vamshi et al. (2022) etc. However, continuous efforts on exploiting genetic variation and understanding the association among yield component traits are critical for breeding. So, assessing the genetic variability and understanding the association of different yield component traits is vital for breeding productive cultivars. The present investigation was therefore undertaken to elucidate the information on genetic variability, character associations and path coefficients in the cowpea genotypes to identify effective selection criteria for grain yield.

2. MATERIALS AND METHODS

The experiment was conducted during *kharif* 2021 at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India. A total of 45 F_1 hybrids of cowpea derived from 10×10 half diallel crossing programme were evaluated for different yield and yield attributing traits along with their 10 parents. The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications. Each entry was sown in 2 rows of 4m length and a spacing of 45×15 cm^2 was provided. All the necessary agronomic practices and plant protection measures were followed to ensure optimal growth of the plants.

Observations were recorded on seven traits viz., days to 50% flowering, days to maturity, number of pods $plant^{-1}$, pod length (cm), number of seeds pod^{-1}, 100 seed weight (g) and yield $plant^{-1}$ (g). The statistical analyses were carried out using "variability" package in R studio version 4.2.1.

3. RESULTS AND DISCUSSION

Analysis of Variance for different yield and yield attributing traits studied is presented in Table 1. The results revealed the presence of significant variation between the genotypes for all the studied characters. Thus, there is ample scope for selection of different quantitative characters in the experimental material.

3.1. Genetic variability parameters for yield and yield related traits of 55 Cowpea genotypes

The data on mean, range, variability, heritability and genetic advance as per cent mean (GAM) are presented in Table 2. In the present study, days to 50% flowering ranged from 46.00–71.00 with the mean value of 54.11 days. Whereas, days to maturity varied from 75.00–105.00 with the mean of 105.00. The trait number of pods $plant^{-1}$ had the mean value of 18.50 and range varied from 8.00–34.00 in the

Table 1: Analysis of variance for yield and yield attributing traits

Sources of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	No. of pods plant^{-1}	Pod length	No. of seeds pod^{-1}	100 Seed weight	Yield plant^{-1}
Treatment	54	49.29**	70.21**	53.11**	7.59**	3.57**	7.07**	127.58**
Replication	1	2.33	9.90	9.86	1.33	0.02	1.25	2.02
Error	54	11.98	16.84	10.82	1.18	1.49	1.52	14.34

Table 2: Mean performance and parameters of genetic variation estimated for yield and yield attributing traits

Parameters	Range		Mean	Vp	Vg	PCV (%)	GCV (%)	h^2 bs (%)	GAM (%)
	Min	Max							
Days to 50% flowering	46.00	71.00	54.11	30.63	18.66	10.23	7.98	60.91	12.83
Days to maturity	75.00	105.00	86.99	43.53	26.68	7.58	5.94	61.30	9.58
Number of pods plant^{-1}	8.00	34.00	18.50	31.96	21.14	30.56	24.86	66.14	41.64
Pod length	11.02	22.03	16.75	4.38	3.20	12.50	10.68	73.08	18.82
Number of seeds pod^{-1}	7.75	16.25	13.15	2.53	1.04	12.09	7.76	41.24	10.27
100 Seed weight	8.12	25.30	13.95	4.29	2.78	14.85	11.94	64.70	19.79
Yield plant^{-1}	6.80	42.35	24.53	70.96	56.62	34.34	30.67	79.79	56.44

studied genotypes. Similarly, the range of pod length (cm) and number of seeds pod^{-1} was 11.02–22.03 and 7.75–16.25 respectively while the mean was 16.75 cm and 13.15 respectively. The genotypes also displayed huge variation in 100 seed weight (g), that ranged from 8.12–25.30 g with the mean of 13.95 g. Grain yield plant^{-1} on the other hand varied from 6.80–42.35 g and the mean yield was 24.53 g.

Estimation of components of variability revealed that, the genotypic coefficient of variation (GCV) for all the characters studied were lesser than phenotypic coefficient of variation (PCV) indicating the modifying effect of the environment on their expression. High PCV coupled with high GCV was observed for number of pods plant^{-1} (30.56 and 24.86, respectively) and grain yield plant^{-1} (34.34 and 30.67, respectively) indicating the presence of higher magnitude of variability among the studied genotypes for these traits. However, moderate PCV and GCV were observed for pod length (12.50 and 10.68, respectively) and 100 seed weight (14.85 and 11.94, respectively) indicating the moderate amount of variability for these traits in the studied genotypes. Manggoel et al. (2012), Shanko et al. (2014), Devi and Jayamani (2018), Singh et al. (2020), Vinay et al. (2022) also reported similar results for pod length. The results on 100 seed weight are in accordance with Viswanatha and Yogeesh (2017).

Days to 50% flowering exhibited moderate PCV of 10.23% and low GCV of 7.98%. Similarly, number of seeds pod^{-1} also had moderate PCV (12.09%) with a low GCV value (7.76%). This indicated that, the magnitude of variability present in the studied genotypes for the characters viz., days to 50% flowering and number of seeds pod^{-1} is mainly due to environmental influence and has low genetic base. In contrast, the trait days to maturity showed low PCV and GCV of 7.58% and 5.94% respectively indicating that, the genotypes are not highly differing with respect to days to maturity. Similar findings are in conformity with Pandiyan et al. (2020) for days to 50% flowering. However, Devi and Jayamani (2018) reported low GCV and PCV for days to 50% flowering, while Shanko et al. (2014) reported moderate GCV and PCV for days to 50% flowering.

The heritability estimates were high for all the studied characters viz., days to 50% flowering (60.91%), days to maturity (61.30%), number of pods plant^{-1} (66.14), pod length (73.08%), 100 seed weight (64.70%) and yield plant^{-1} (79.79%) except number of seeds pod-1 (41.24%) which showed moderate heritability. However, the GAM was moderate for majority of the traits viz., days to 50% flowering (12.83%), pod length (18.82%), number of seeds pod^{-1} (10.27%) and 100 seed weight (19.79%). High GAM was observed for number of pods plant^{-1} (41.64%) and grain yield plant^{-1} (56.44%) while, the trait days to maturity exhibited low GAM of 9.58%. High heritability and high GAM were also reported by Devi and Jayamani (2018), Viswanatha and Yogeesh (2017) and Vinay et al. (2022) for number of pods plant^{-1} and grain yield plant^{-1}.

The higher estimates of GCV, PCV, heritability (broad sense) and GAM for the traits number of pods plant^{-1} and grain yield plant^{-1} indicated the preponderance of additive gene actions in controlling these characters. Thus, selection for these characters among the studied genotypes may be rewarding.

3.2. Correlation studies

Correlation analysis provides information on degree and direction of association between yield component traits, which is the key to the selection process in developing high-yielding cultivars. The fundamental information about the direct and indirect effects of various independent factors on the final dependent variable (grain yield), is provided by path coefficient analysis. The genotypic and phenotypic correlation coefficients between yield and yield components namely pods plant^{-1}, pod length, number of seeds pod^{-1}, 100 seed weight, were calculated and the results have been presented in Table 3.

Correlation studies in the present experiment revealed that, day to 50% flowering showed significant and positive correlation with days to maturity both at phenotypic and genotypic levels indicating their strong association with one another. The results were in conformity with Romanus et al. (2008), Bhardu and Navale (2011) and Meena et al. (2015). However, both days to 50% flowering and days to maturity had significant negative association with 100-seed weight genotypically as well as phenotypically. But, at phenotypical level, the correlation of both days to 50% flowering and days to maturity with grain yield plant^{-1} was significantly negative, while it was non-significant at genotypic level. This revealed that, the significant negative correlation at phenotypic level with grain yield is mainly due to the environmental influence and, thus the traits days to 50% flowering and days to maturity have no significant influence on grain yield genotypically.

Table 3: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients for yield and yield attributing traits

Traits	Days to 50% flowering	Days to maturity	No. of pods plant^{-1}	Pod length	No. of seeds pod^{-1}	100 Seed weight	Yield plant^{-1}
Days to 50% flowering	1.000	0.904**	-0.050	0.062	-0.033	-0.307**	-0.194*
Days to maturity	0.984**	1.000	-0.010	0.088	-0.024	-0.285**	-0.199*
Number of pods plant^{-1}	-0.100	-0.096	1.000	0.411**	0.451**	0.012	0.688**
Pod length	-0.038	0.023	0.569**	1.000	0.766**	0.270**	0.447**
Number of seeds pod^{-1}	-0.174	-0.152	0.845**	0.834**	1.000	0.339**	0.490**
100 Seed weight	-0.430**	-0.403**	0.139	0.313*	0.403**	1.000	0.242*
Yield plant^{-1}	-0.249	-0.226	0.874**	0.585**	0.763**	0.338*	1.000

*, **: Significant at (*p*=0.05) and (*p*=0.01) level of significance respectively

There was significant and positive association of pods plant^{-1} with pod length, number of seeds pod^{-1}, and yield plant^{-1} both genotypically and phenotypically. However, the association of pods plant^{-1} with 100 seeds weight was non-significant at both genotypic and phenotypic levels. Similar results were also earlier reported by Aliyu et al. (2022).

The phenotypic and genotypic correlation analysis revealed that, positive and significant correlation was observed in pod length with number of seeds pod^{-1}, 100 seed weight and yield plant^{-1}. Hence, selection for longer pods in the experimental set, leads to simultaneous selection of these associated traits.

Seeds pod^{-1} was positively and significantly associated with 100- seed weight and yield plant^{-1}. Similarly, 100-seed weight also displayed significant positive association with yield plant^{-1} at both genotypic and phenotypic levels.

The significant and positive association of grain yield plant^{-1} was noted with pods plant^{-1}, pod length, number of seeds pod^{-1} and 100-seed weight. The results are in accordance with the findings of Romanus et al. (2008), Tyagi et al. (2000), Manggoel et al. (2012), Ajayi et al. (2014), Meena et al. (2015), and Chaudhary et al. (2020).

3.3. Direct and indirect effects of different traits on grain yield plant^{-1}

The estimates of path coefficients are presented in table 4 and 5. In path analysis, at phenotypic level the direct positive effects were recorded highest for number of pods plant^{-1} followed by 100 seed weight, and pod length. Results are in conformity with Shanko et al. (2014) for number of pods plant^{-1} and Aliyu et al. (2022) for number of pods plant^{-1}, and pod length. The highest direct negative effects at phenotypic level were revealed by days to maturity implying that, increased maturity duration leads to low yield in cowpea. At genotypic level, number of pods plant^{-1} had highest direct effect on yield plant^{-1}, followed by days to maturity and number of seeds pod^{-1}. However, days to 50% flowering recorded highest negative direct effect on yield plant^{-1}, followed by pod length. The results are in conformity with Manggoel et al. (2014) and Lal et al. (2018).

The positive indirect effect *via* number of pods plant^{-1} was the main contributor to the correlation of pod length and number of seeds pod^{-1} with grain yield plant^{-1} at both genotypic and phenotypic levels.

Table 4: Phenotypic path coefficients estimated for yield and yield attributing traits

Traits	Days to 50% flowering	Days to maturity	No. of pods plant^{-1}	Pod length	Number of seeds pod^{-1}	100 seed weight	Correlation coefficients of yield attributing traits with yield plant^{-1}
Days to 50% flowering	0.116	-0.242	-0.030	0.007	-0.003	-0.042	-0.194*
Days to maturity	0.105	-0.268	-0.006	0.010	-0.002	-0.039	-0.199*
Number of pods plant^{-1}	-0.006	0.003	0.606	0.049	0.035	0.002	0.688**
Pod length	0.007	-0.024	0.249	0.119	0.059	0.037	0.447**
No. of seeds pod^{-1}	-0.004	0.006	0.273	0.091	0.077	0.046	0.490**
100 seed weight	-0.036	0.076	0.007	0.032	0.026	0.136	0.242*

(Residual effect=0.429); Note: diagonal values represent the direct effects while all other values represent the indirect effects of component traits on yield plant^{-1}

Table 5: Genotypic path coefficients estimated for yield and yield attributing traits

Traits	Days to 50% flowering	Days to maturity	No. of pods plant^{-1}	Pod length	Number of seeds pod^{-1}	100 seed weight	Correlation coefficients of yield attributing traits with yield plant^{-1}
Days to 50% flowering	-0.755	0.682	-0.073	0.008	-0.050	-0.062	-0.249
Days to maturity	-0.743	0.693	-0.070	-0.005	-0.044	-0.058	-0.226
No. of pods plant^{-1}	0.076	-0.067	0.724	-0.121	0.242	0.020	0.874**
Pod length	0.028	0.016	0.412	-0.212	0.296	0.045	0.585**
No. of seeds pod^{-1}	0.131	-0.106	0.612	-0.219	0.286	0.058	0.763**
100 seed weight	0.324	-0.279	0.100	-0.066	0.115	0.144	0.338*

(Residual effect=0.192); Note: diagonal values represent the direct effects while all other values represent the indirect effects of component traits on yield plant^{-1}

4. CONCLUSION

High PCV, GCV, h$^{2}_{(bs)}$ and GAM in number of pods plant^{-1} and yield plant^{-1} indicated predominance of additive gene actions. Grain yield plant^{-1} showed positive significant association with number of pods plant^{-1}, pod length, number of seeds pod^{-1} and 100-seed weight. Path analysis depicted number of pods plant^{-1} as the best selection index in cowpea. Also pod length, number of seeds pod^{-1} and 100-seed weight had significant contribution towards yield. Thus, selection for yield through these traits might be rewarding.

5. ACKNOWLEDGEMENT

We acknowledge Council of Scientific and Industrial Research, Ministry of Science and Technology, Govt. of India for providing financial assistance through CSIR-JRF fellowship to the Ph.D. Scholar.

7. REFERENCES

Ajayi, A.T., Adekola, M.O., Taiwo, B.H., Azuh, V.O., 2014. Character expression and differences in yield potential of ten genotypes of cowpea (*Vigna unguiculata* L. Walp). International Journal of Plant Research 4(3), 63–71.

Aliyu, O.M., Tiamiyu, A.O., Usman, M., Abdulkareem, Y.F., 2022. Variance components, correlation and path analyses in cowpea (*Vigna unguiculata* L., Walp). Journal of Crop Science and Biotechnology 25(2), 173–182.

Bhardu, D., Navale, P.A., 2012. Genetic variability parameters in F$_2$ and F$_3$ populations of cowpea (*Vigna unguiculata* (L.) Walp.). Legume Research: An International Journal 35(1), 75–77.

Boukar, O., Massawe, F., Muranaka, S., Franco, J., Maziya-Dixon, B., Singh, B., Fatokun, C., 2011. Evaluation of cowpea germplasm lines for protein and mineral concentrations in grains. Plant Genetic Resources 9(4), 515–522.

Chaudhary, A.R., Solanki, S.D., Rahevar, P.M., 2021. Comparative diversity analysis of cowpea genotypes using multivariate approaches. Electronic Journal of Plant Breeding 12(4), 1142–1147.

Devi, S.M., Jayamani, P., 2018. Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata* (L.) Walp.]. Electronic Journal of Plant Breeding 9(2), 476–481.

Ehlers, J.D., Hall, A.E., 1997. Cowpea (*Vigna unguiculata* L. walp.). Field Crops Research 53(1–3), 187–204.

Falconer, D.S., Mackay, T.F.C., 1989. Introduction to Quantitative Genetics. Longman Scientific and Technical. Logman House, Burnt Mill, Harlow, Essex, England, 187–208.

Goncalves, A., Goufo, P., Barros, A., Domínguez-Perles, R., Trindade, H., Rosa, E.A., Ferreira, L., Rodrigues, M., 2016. Cowpea (*Vigna unguiculata* L. Walp), a renewed multipurpose crop for a more sustainable agri-food system: nutritional advantages and constraints. Journal of the Science of Food and Agriculture 96(9), 2941–2951.

Khan, M.M.H., Rafii, M.Y., Ramlee, S.I., Jusoh, M., Al Mamun, M., 2022. Path-coefficient and correlation analysis in Bambara groundnut (*Vigna subterranea* [L.] Verdc.) accessions over environments. Scientific Reports 12(1), 1–12.

Lal, H., Reddy, B.R., Nath, V., 2018. Biometrical studies of yield and related traits in advance breeding lines of bush type vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. Legume Research: An international Journal 41, 867–872.

Lioi, L., Morgese, A., Cifarelli, S., Sonnante, G., 2019. Germplasm collection, genetic diversity and on-farm conservation of cowpea [*Vigna unguiculata* (L.) Walp.] landraces from Apulia region (southern Italy). Genetic Resources and Crop Evolution 66(1), 165–175.

Lu, G.Y., Zhang, F., Zheng, P.Y., Cheng, Y., Feng-Ian, L.I.U., Fu, G.P., Zhang, X.K., 2011. Relationship among yield components and selection criteria for yield improvement in early rapeseed (*Brassica napus* L.). Agricultural Sciences in China 10(7), 997–1003.

Manggoel, W., Uguru, M.I., Ndam, O.N., Dasbak, M.A., 2012. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. Journal of Plant Breeding and Crop Science 4(5), 80–86.

Meena, H.K., Krishna, K.R., Singh, B., 2015. Character associations between seed yield and its components traits in cowpea [*Vigna unguiculata* (L.) Walp.]. Indian Journal of Agricultural Research 49(6), 567–570.

Mofokeng, M.A., Mashilo, J., Rantso, P., Shimelis, H., 2020. Genetic variation and genetic advance in cowpea based on yield and yield-related traits. Acta Agriculturae Scandinavica, Section B-Soil & Plant Science 70(5), 381–391.

Mohammadi, R., Pourdad, S.S., 2009. Estimation, interrelationships and repeatability of genetic variability parameters in spring safflower using multi-environment trial data. Euphytica 165(2), 313–324.

Nehru, S.D., Suvarna, P., Manjunath, A., 2009. Genetic variability and character association studies in cowpea in early and late kharif seasons. Legume Research-An International Journal 32(4), 290–292.

Panchta, R., Arya, S., Dalvinder, P.S., Satpal, P., Kumar, R., 2020. Genetic variability and association studies in cowpea [*Vigna unguiculata* (L.) Walp] for seed yield and related traits. Forage Research 46(3), 232–235.

Rauf, S., Al-Khayri, J.M., Zaharieva, M., Monneveux, P., Khalil, F., 2016. Breeding strategies to enhance drought tolerance in crops. In:Advances in plant breeding strategies: Agronomic, abiotic and biotic stress traits Springer, Cham, 397–445.

Romanus, K.G., Hussein, S., Mashela, W.P., 2008. Combining ability analysis and association of yield and yield components among selected cowpea lines. Euphytica 162(2), 205–210.

Seehausen, O., 2004. Hybridization and adaptive radiation. Trends in Ecology & Evolution 19(4), 198–207.

Shanko, D., Andargie, M., Zelleke, H., 2014. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.). Research in Plant Biology 4(2), 21–26.

Shi, J., Li, R., Qiu, D., Jiang, C., Long, Y., Morgan, C., Bancroft, I., Zhao, J., Meng, J., 2009. Unraveling the complex trait of crop yield with quantitative trait loci mapping in *Brassica napus*. Genetics 182(3), 851–861.

Singh, O.V., Shekhawat, N., Singh, K., Gowthami, R., 2020. Assessment of genetic variability and inter-character association in the germplasm of cowpea (*Vigna unguiculata* L. Walp) in hot arid climate. Legume Research 43(3), 362–366.

Suganthi, S., Murugan, S., 2008. Association analysis in cowpea (*Vigna unguiculata* L. Walp). Legume Research 31(2), 130–132.

Timko, M.P., Ehlers, J.D., Roberts, P.A., 2007. Cowpea. In: Kole, C. (Ed.). Genome Mapping and Molecular Breeding in Plants, Pulses, Sugar and Tuber Crops (Vol. 3). Springer, Berlin, Heidelberg, 49–67.

Tyagi, P.C., Kumar, N., Agarwal, M.C., 2000. Genetic variability and association of component characters for seed yield in cowpea [*Vigna unguiculata* (L.) Walp.]. Legume Research-An International Journal 23(2), 92–96.

Vamshi, S.S., Subramanian, A., Ezhilarasi, T., Gurusamy, K., Ganesan, K.N., 2022. Analysis of genetic parameters, trait association and genetic diversity in fodder cowpea [*Vigna unguiculata* (L.) Walp.]. Electronic Journal of Plant Breeding 13(2), 361–368.

Vinay, K., Rao, P.J.M., Kishore, N.S., Hari, Y., 2022. Genetic variability studies for seed yield and yield component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. Electronic Journal of Plant Breeding 13(2), 544–548.

Vir, O., Singh, A.K., 2014. Genetic variability and inter-characters associations studies in the germplasm of cowpea [*Vigna unguiculata* (L.) Walp] in fragile climate of western Rajasthan, India. Legume Research: An International Journal 37(2), 126–132.

Viswanatha, K.P., Yogeesh, L.N., 2017. Genetic variation and morphological diversity in cowpea (*Vigna unguiculata* L. Walp). Archives of Agriculture and Environmental Science 2(3), 176–180.

© 2023 PP House