International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(1): 984-987
www.biochemjournal.com
Received: 17-11-2025
Accepted: 21-12-2025

Jyoti Kumari
Department of Plant Breeding and Genetics, Nalanda College of Horticulture, BAU, Sabour, Bihar, India

DA Chauhan
Department of Plant Breeding and Genetics, Navsari Agricultural University, Navsari, Gujarat, India

Corresponding Author:
Jyoti Kumari
Department of Plant Breeding and Genetics, Nalanda College of Horticulture, BAU, Sabour, Bihar, India

Estimation of combining ability and phenotypic stability for green pod yield and its contributing characters in cowpea [*Vigna unguiculata* (L.) Walp.]

Jyoti Kumari and DA Chauhan

DOI: https://www.doi.org/10.33545/26174693.2026.v10.i1Sl.7141

Abstract

Background: Cowpea is a warm-season vegetable crop cultivated extensively throughout the world. Besides nutritional quality, it also boosts soil through the fixation of atmospheric nitrogen. The main goal of cowpea breeding is to develop consistent high-yielding varieties which show resistance to biotic and abiotic stresses. Identifying the best-performing lines and lines that can be used as parents in future crosses are two principal objectives considered in most crop breeding programs. So, to fulfil these objectives, the best-performing lines for the required characteristics are selected based on combining ability and stability by conducting multi-environment trials.

Methods: The present investigations were conducted to determine the extent of combining ability and G X E interaction in cowpeas (*Vigna unguiculata*). Thirty hybrids were developed by adopting a full diallel mating design. A set of thirty-eight cowpea entries, including six parents, thirty crosses, and two check varieties, GC-3 and GDVC-2, were evaluated at three locations, *viz.* Navsari, Mangrol and Achhalia used a randomised block design with three replications during Kharif-2017-2018. The mean values of pod yield and the contributing traits of parental lines and their offspring for each replication were used for statistical analysis, including GCA, SCA, and Stability.

Result: The GCA and SCA revealed significant findings, highlighting the intricate interplay of both additive and non-additive gene actions at work. Parents, NCK-15-10, NC-15-41 and NC-15-45 were found to be most promising due to their high-yielding potential and significant general combining ability effects for Pod yield and attributes. The cross-combination NC-15-45 x NCK-15-10, NC-15-45 x NC-15-41 and NCK-15-10 x NC-15-45 recorded high per se performance for green pod yield per plant, resulting from good x good general combiners. Cross NC-15-45 x NCK-15-10 advocated a negative SCA effect for green pod yield per plant. The pooled analysis of variance for different characters revealed significant differences among the genotypes, environments and genotype × environment interaction for all the characters, indicating the existence of considerable variability in the materials studied and between the environments. Parent NCK-15-10 was found average stable for green pod yield per plant, it is remarkable that parent NC-15-45 was found average stable for most of the characters under study. Out of the best five crosses for stability for green pod yield per plant, NC-15-45 x NC-15-41 was found to be average stable and best suited for all the environments for green pod yield per plant. In contrast, based on per se performance, heterosis, combining ability estimates and stability for yield and its components, parent NCK-15-10, NC-15-41, and NC-15-45 were identified as good for green pod yield per plant in cowpea and involvement of these parents will be worthful in future breeding programme. For the development of a high green pod-yielding variety, the pedigree breeding method may be advocated in hybrid NC-15-45 x NCK-15-10 as it exhibited negative and non-significant SCA for green pod yield.

Keywords: Cowpea, GCA, SCA, stability, pod yield

Introduction

Cowpea, or black-eyed pea, belongs to section Catjang (DC) of the genus Vigna, in the tribe Phaseoleae, Family Fabaceae (Marechal *et al*., 1978) [13]. It is a self-pollinating diploid with a chromosome number of 2n = 22 and a genome size of 640.6 Mb (Lonardi *et al*., 2019) [12]. It is cultivated from very ancient times in the tropics of the Old World. The Cowpea weather utilized for green pods as vegetables or dry seed as pulse forms an important component of farming systems from the arid to the humid tropics. It has the greatest potential among all food legumes in the semiarid to subtropical areas. Cowpea is a vital legume grown for food and feed on several continents, including Africa, Asia, Europe, the United States, and Central and South America. Cowpea originated in Southern Africa and was later introduced to East and West Africa and Asia. Wild relatives are found throughout Africa. This crop, with 25% protein and vital minerals and vitamins, is essential for addressing global food security challenges. It is grown widely throughout the year in all forms-tender pod, dry seed, fodder, green manure and cover crops both as sole and mixed crops. It is the key dietary staple for the poorest sector of many underdeveloped and developing countries of Africa, Latin America and Asia.

In the crop improvement programme, the nature of gene action depends on the genetic structure and divergence between populations involved in hybridization. It may happen that high-yielding genotypes may not be able to transmit their superiority in cross combinations and vice-versa. Therefore, a breeder should know the genetic potential of the parents by estimating their combining ability. The general combining ability (GCA) indicates additive gene effects for selecting parental lines based on average performance in hybrids, while the specific combining ability (SCA) shows non-additive effects to identify superior hybrids through hybrid vigour. Diallel analysis is a common method to assess parental combining ability It also provides, in quantitative characters, estimates of variability in a population. The study of such genetic parameters attempted in this investigation would not only help the breeders in selecting suitable parents for hybridization but could also contribute towards the evaluation. The study aimed to improve the nutritional quality and productivity of an important pulse through effective breeding methods by assessing combining abilities for pod yield and related traits.

Materials and Methods

The statistical procedure given by Singh (1973, 1979) was used for the analysis of diallel cross data over different environments for combining ability analysis using method I, model I (fixed effect model) of Griffings (1956) [7]. The mathematical model underlying the experimental method I, model I (parents, F_1s and reciprocals) are as under.

$$Y_{ijkl} = u+g_i+g_i+s_{ij}+r_{ij}+l_k+(gl)_{ik}+(gl)_{jk}+(sl)_{ijk}+(rl)_{ijk}+ \frac{\frac{1}{bc}\sum_{m}.\frac{1}{bc}}{\sum_{m}\sum_{n}.} e_{ijkmr}$$

Where,

Notations like μ, g_i, g_j, s_{ij}, r_{ij} are the same as given earlier and

l_k = the effect of kth environment

$(gl)_{ik}$ = the interaction corresponding to g_i and l_k

$(gl)_{jk}$ = the interaction corresponding to g_j and l_k

$(sl)_{ijk}$ = the interaction corresponding to s_{ij} and l_k and

$(rl)_{ijk}$ = the interaction corresponding to r_{ij} and l_k and

e_{ijkmr} = environmental effect peculiar to the individual

b = the number of blocks

c = the number of plants in each block

Analysis of variance for phenotypic stability

The statistical analysis for genotype x environment interaction and stability parameters was carried out according to the method of Eberhart and Russell (1966) [9] to calculate the analysis of variance.

Stability parameters

The stability parameters for the various characters were computed following the methodology of Eberhart and Russell (1966) [9]. For each genotype, stability is described by three parameters, mean performance, the regression of mean performance on an environmental index and the function of squared deviation from this regression. Eberhart and Russell (1966) [9] suggested that the ideal variety has a high mean, unit regression coefficient ($b_i = 1.0$) and the least deviation from regression ($S^2d_i = 0$).

These parameters are defined in a linear model as follows:

$Y_{ij} = \mu_i + b_iI_j + \delta_{ij}$

Where,

Y_{ij} = Mean of ith genotype in jth environment,

μ_i = ith genotype means over all the environment,

b_i = Regression coefficient that measures the response of the ith genotype to changing environments,

δ_{ij} = Deviation from regression of the ith genotype in the jth environment,

I_j = Environmental index, obtained as a mean of all the genotypes at the jth environment minus grand mean

i_j = $(\Sigma\ Y_{ij}/g)-(\Sigma\ \Sigma\ Y_{ij}/ge)$
i i j

Where,

e = Number of environments

Results and Discussion

Variance analysis revealed significant differences among all the parents and their hybrid combinations for the all-quantitative traits studied.

A study of combining ability revealed that all the parents exhibited significant GCA effect, for pod yield per plant but only three parents *viz.* NC-15-45 (10.34), NCK-15-10 (7.14), and NC-15-41 (3.55) attained their value in a desirable direction. Parents NC-15-45 and NCK-15-10 also showed significant GCA effect at all three locations, Navsari, Mangrol and Achhalia while parent NC-15-41 manifested a significant GCA effect for pod yield per plant in a desirable direction at Navsari (4.60) and Achhalia (7.20) location.

The SCA effect for pod yield per plant in pooled analysis for direct crosses and reciprocals varied from-7.05 (NCK-15-9 x NC-15-41) to 8.37 (NCK-15-10 x NC-15-45) and from-8.74 (NC-15-42 x NC-15-41) to 17.53 (NC-15-44 x NC-15-41) respectively. Eight direct crosses and five reciprocals exhibited a positive significant SCA effect in pooled study. On the basis of pooled analysis top three direct crosses for pod yield per plant were NCK-15-10 x NC-15-45 (8.37) followed by NCK-15-9 x NC-15-44 (8.05) and NCK-15-10 x NC-15-41(7.16) and top three reciprocals were NC-15-44 x NC-15-41 (17.53) followed by NC-15-45 x NC-15-41 (11.62) and NC-15-44 x NCK-15-10 (7.52). Top two reciprocals *viz.* NC-15-44 x NC-15-41 and NC-15-45 x NC-15-41 also exhibited significant and positive SCA effect for pod yield per plant at all the three locations of study.

Among parents, the highest mean value for green pod yield per plant accompanied by non-significant deviation from regression was found for NC-15-45 (mean, 98.84; b_i <1), followed by NCK-15-10 (mean, 94.63; $b_i \cong 1$) and NC-15-41 (mean, 91.71; b_i >1). Six crosses revealed a high mean as compared to the direct crosses mean (96.59), of which high per se performance was exhibited by cross NCK-15-10X.NC-15-45 (123.79) along with non-significant deviation from regression and significant regression coefficient ($b_i > 1$), while crosses, NCK-15-9 x NC-15-45 (99.06), NCK-15-10 x NC-15-41(109.02), NC-15-41 x NC-15-42 (107.83) and NC-15-44 x NC-15-45 (100.28) have attained all the three criteria of stability (Higher mean, $b_i \cong 1$, and S^2d_i value near to zero). Among reciprocals, seven crosses have showed higher mean value than reciprocal mean (101.68), out of which cross NC-15-45 x NC-15-41(126.30) showed highest mean with non-significant deviation from regression and non-significant value of regression coefficient followed by NC-15-45 x NCK-15-10 (mean, 121.28, $b_i < 1$, S^2d_i value near to zero), NC-15-41 x NCK-15-10 (mean, 120.06, $b_i \cong 1$, S^2d_i value near to zero) and NC-15-44 x NCK-15-10 (mean, 107.78, $b_i \cong 1$, S^2d_i value near to zero). The identification of parents having high mean, good GCA effects and high stability across the environments is of great value to the plant breeder, while formulating a breeding programme. In the light of the present investigation, parents *viz.* NCK-15-10, NC-15-41 and NC-15-45 were found to be promising due to their high yield potential, and significant general combining ability for green pod yield per plant and grain yield per plant. This indicated that parents with high GCA effects are desirable for crosses having high SCA effects for rationalization of maximum heterosis. High SCA effect with good x good combiner reflects additive x additive type of gene interaction and superiority of favourable genes contributed by their parents, while those involving good x poor or poor x poor indicated the interaction of additive x dominance and dominance x dominance respectively. Biparental progeny selection suggested by Andrus (1963) [1] might be useful to get some useful transgressive segregants from crosses involving good x good and good x poor combination. These findings are in agreement with the earlier findings of Singh *et al.* (2006) [22], Valarmathi *et al.* (2007) [24], Kwaye *et al.* (2008) [11], Patel *et al.* (2008) [16], Bhawna Pandey and Singh (2010) [2], Meena *et al.* (2010) [14], Uma and Kalibowilla (2010) [6] and Chaugule *et al.* (2023) [5].

Top ranking three hybrids *viz.* NC-15-45 x NC-15-41 (G x G) and NCK-15-10 x NC-15-45 (G x G) were found to possess high mean performance and desirable SCA effect for green pod yield per plant. Therefore hybrid *viz.* NC-15-45 x NC-15-41 (G x G) and NCK-15-10 x NC-15-45 (G x G) having high SCA effect which indicated additive x additive type gene interaction may produce desirable transgressive segregates in subsequent generations or could be considered as valuable for future breeding programme. In such case, repeated backcross methods should be allocated to have good recombinants from selected segregants.

Based on the overall experimental result, we concluded that low SCA effects with the high heterotic expression of the topmost hybrids are the indication of additive gene effects that could be exploited by the pedigree method, looking towards the dual-purpose varietal improvement programme cross NC-15-45 x NCK-15-10, had shown negative SCA effect for green pod yield per plant with parents having good x good combiner indicating the importance of additive gene action. The presence of additive gene action would enhance the chance for improving the simple selection of transgressive segregates in later generations. Similar findings for stability were also observed by Singh and Singh (1991) [21], Chauhan *et al.* (2004) [4], Henry (2004) [10], Cholin *et al.* (2010) [6], Patel and Jain (2012) [17], Olayiwola *et al.* (2015) [15] and Shaieny *et al.* (2015) [18].

Conclusion

Parents NCK-15-10, NC-15-41, and NC-15-45 were identified as promising parents due to significant GCA effects on pod yield per plant and other traits. So involvement of these parents will be worthwhile in future breeding programmes. Top ranking three hybrids *viz.* NC-15-45 x NC-15-41 (GXG) and NCK-15-10 x NC-15-45 (G X G) were found to possess high mean performance, high heterosis over better parent and standard check GC-3 and GDVC-2 and desirable SCA effect for green pod yield per plant. Therefore hybrid *viz.* NC-15-45 x NC-15-41 (GXG) and NCK-15-10 x NC-15-45 (G X G) having high SCA effect which indicated additive x additive type gene interaction may produce desirable transgressive segregants in subsequent generations or could be considered as valuable for a future breeding programme, in such case as such repeated backcross method may be allocated to have good recombinant. For the development of a high green pod-yielding variety, the pedigree method of breeding may be advocated in hybrid NC-15-45 x NCK-15-10 as it exhibited negative and non-significant SCA for green pod yield.

Acknowledgement

The work on cowpea of this research has been supported financially by DST-INSPIRE, Dept. of Science and Technology, Ministry of Science and Technology, Govt. of India.

References

1. Andrus CF. Plant breeding systems. Euphytica. 1963;12:205-228.
2. Bhawna, Pandey, Singh YV. Combining ability for yield over the environment in cowpea (*Vigna unguiculata* (L.) Walp). Legume Res. 2010;33(3):190-195.
3. Chaudhary SB, Naik MR, Patil SS, Patel JD. Heterosis in cowpea for seed yield and its attributes over different environments. Trends Biosci. 2013;6(4):464-466.
4. Chauhan RM, Solanki SD, Shah DS, Patel JB, Tikka SBS. Stability analysis in cowpea (*Vigna unguiculata* (L.) Walp). GAU Res J. 2004;29(1-2):19-21.
5. Chaugule OK, Pethe UB, Palshetkar MG, More SS, Kale SN, Misal SS. Combining ability analysis for yield and quality traits in cowpea (*Vigna unguiculata* (L.) Walp). Pharma Innovation J. 2023;12(11):2380-2383.
6. Cholin S, Uma MS, Suma B, Salimath PM. Stability analysis for yield and yield components over seasons in cowpea (*Vigna unguiculata* (L.) Walp). Electron J Plant Breed. 2010;1(6):1392-1395.
7. Griffing B. Concept of general and specific combining ability in relation to diallel crossing systems. Aust J Biol Sci. 1956;9:463-493.
8. Griffing B. A general treatment of the use of the diallel cross in quantitative inheritance. Heredity. 1956;10:31-50.

9. Eberhart SA, Russell WL. Stability parameters for comparing varieties. Crop Sci. 1966;6:36-40.
10. Henry A, Kumar D, Singh NB. Heterosis and inbreeding depression for grain characters in cowpea. Adv Arid Legume Res. 2003;38-41.
11. Kwaye GR, Hussein S, Mashela WP. Combining ability analysis and association of yield and yield components among selected cowpea lines. Euphytica. 2008;162:205-210.
12. Lonardi S, Muñoz-Amatriaín M, Liang Q, Shu S, Wanamaker SI, *et al*. The genome of cowpea (*Vigna unguiculata* (L.) Walp). Plant J. 2019;98(5):767-782.
13. Maréchal R, Masherpa JM, Stainier F. Étude taxonomique d'un groupe complexe d'espèces des genres *Phaseolus* et *Vigna* (Papilionaceae) sur la base de données morphologiques et polliniques. Boissiera. 1978;28:1-273.
14. Meena R, Pithia MS, Savaliya J, Pansuriya AG. Heterosis in vegetable cowpea (*Vigna unguiculata* (L.) Walp). Crop Impro. 2009;36(1):1-5.
15. Olayiwola MO, Soremi PAS, Okeleye KA. Evaluation of some cowpea (*Vigna unguiculata* (L.) Walp) genotypes for stability of performance over four years. Curr Res Agric Sci. 2015;2(1):22-30.
16. Patel SP, Dhedhi KK, Bharodia PS, Joshi AK. Genetic analysis of pod yield and its attributes in vegetable cowpea. J Food Legumes. 2008;21(2):89-92.
17. Patel PR, Jain SK. Stability analysis for yield and yield component traits in new breeding lines of cowpea. Legume Res. 2012;35(1):23-30.
18. Shaieny AAH, Abdel-Ati YY, El-Damarany AM, Rashwan AM. Stability analysis of component characters in cowpea (*Vigna unguiculata* (L.) Walp). J Hortic For. 2015;7(2):24-35.
19. Singh D. Diallel analysis for combining ability over several environments II. Indian J Genet. 1973;33(3):469-481.
20. Singh D. Diallel analysis for combining ability over several environments. Indian J Genet. 1979;39(3):383-386.
21. Singh VP, Singh RD. Stability analysis in cowpea (*Vigna unguiculata* (L.) Walp). Veg Sci. 1991;18(2):161-166.
22. Singh I, Badaya SN, Tikka SBS. Combining ability for yield over environments in cowpea (*Vigna unguiculata* (L.) Walp). Indian J Crop Sci. 2006;1(1-2):205-206.
23. Uma MS, Kalubowila I. Line × tester analysis for yield and rust resistance in cowpea (*Vigna unguiculata* (L.) Walp). Electron J Plant Breed. 2010;1(3):254-267.
24. Valarmathi G, Surendran C, Muthiah AR. Combining ability for yield and yield traits in inter-subspecies of cowpea (*Vigna unguiculata* ssp. *unguiculata* × ssp. *sesquipedalis*). Legume Res. 2007;30(3):173-179.