International Journal of Research in Agronomy 2025; SP-8(2): 516-519

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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www.agronomyjournals.com
2025; SP-8(2): 516-519
Received: 06-10-2024
Accepted: 11-11-2024

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Stability analysis for grain yield and component characters in cowpea [*Vigna unguiculata* (L.) Walp.]

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DOI: https://doi.org/10.33545/2618060X.2025.v8.i1Sh.2487

Abstract

The present investigations were carried out with a view to know the genotype by environment interaction and stability in cowpea (*Vigna unguiculata* (L.) Walp.). Thirty hybrids were developed by adopting full diallel mating design. A set of thirty-eight cowpea entries including six parents (NCK-15-9, NCK-15-10, NC-15-41, NC-15-42, NC-15-44, NC-15-45) thirty crosses and two check varieties, GC-3 and GDVC-2 evaluated at three locations *viz.* Navsari, Mangrol and Achhalia using randomized block design with three replications during *Kharif*-2017. The observations were recorded on parents and F_1's quantitative traits and quality traits *viz.* days to 50 per cent flowering, plant height (cm), primary branches per plant, pods per plant, pod length (cm), seeds per pod, green seed weight (g), green pod yield per plant (g), grain yield per plant (g), straw yield per plant (g), shelling percentage (per cent), havest index (per cent) and protein content (per cent). 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 while parents NC-15-41, NC-15-44 and NC-15-45 were average stable for grain yield per plant, it is remarkable that parent NC-15-45 was found average stable for most of the characters under study. Out of best five best crosses for stability for green pod yield as well as grain yield per plant NC-15-45 x NC-15-41 was found average stable for both and best suited for all the environments for dual purpose cowpea, while cross NC-15-45 x NCK-15-10 and NCK-15-10 x NC-15-45 were average stable for grain yield per plant.

Keywords: Cowpea, genotype, environment, stability, yield

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is diploid crop with chromosome number of (2n=22), belongs to family Fabaceae, one of the oldest sources of human food, in form of green pods as well as grains has most likely been used as a crop. It is native of West Africa (Vavilov, 1951) [21] but Steele (1976) [20] suggested Ethiopia as the primary and Africa as the secondary centre of diversity. Among all the pulses, cowpea locally known as lobiya, chowla (Chowli), southern pea or black eye pea, is an annual legume that is adopted to warm condition and cultivated in the tropics and sub-tropics for dry grains, green edible pods for vegetable as well as fodder. Cowpea is an annual herbaceous plant with a large tap root and alternate trifoliate leaves with ovate leaflets. It shows considerable diversity in growth habit, flower and seed coat colour. The standard flowers vary in colour from white, cream and yellow to purple and the seeds, which are smooth or wrinkled, range from white, cream or yellow to red, brown or black and are characterized by a marked hilum surrounded by a dark aril. Cowpea is regenerated by seeds and is largely self-pollinating but up to 2% outcrossing has been reported.

Although it is considered as a multi-season crop, its productivity is comparatively high in *kharif* season compared to other seasons as the crop will suffer from water deficit at the physiological maturity in summer. Phenotypically stable genotypes are of great importance because the environmental conditions vary from season to season and year to year. Wide adaptation to a particular environment and consistent performance of recommended varieties/ hybrids are very important for successful cultivation of cowpea. Although many varieties are recommended for the cultivation, the information on the stability is lacking. In the present study, some important genotypes of cowpea have been evaluated for G x E interactions for identifying the high yielding stable genotypes for cultivation and for their utilization in breeding programme.

Materials and Methods

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) [44] 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) [4]. 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) [4] suggested that ideal variety is one which 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:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where,

Y_{ij}	=	Mean of i^{th} genotype in j^{th} environment,
μ_i	=	i^{th} genotype mean over all the environment,
b_i	=	Regression coefficient that measures the response of the i^{th} genotype to changing environments,
$\square_{ij}$	=	Deviation from regression of the i^{th} genotype in the j^{th} environment,
I_j	=	Environmental index, obtained as a mean of all the genotypes at the j^{th} environment minus grand mean
i_j	=	$(\Sigma\, Y_{ij} / g) - (\Sigma\, \Sigma\, Y_{ij} / ge)$ i i j

If S^2d_i values are significantly deviating from zero, the expected result cannot be predicted satisfactorily. When deviations are not significant, the conclusion may be drawn by considering jointly the mean yield and regression value. Mehra and Ramanujan (1979) [10], Singh and Singh (1980) [18] and Nadarajan and Gunasekaran (2005) [11] suggested the methodology to classify different genotypes in to four different group as shown below.

Group	Mean	b_i	S^2d_i	Behaviour
I	High	Around unity	Around zero	Average stable
II	High	Significantly deviating from unity	-	-
		i) bi > 1	Around zero	Below average stable
		ii) bi < 1	Around zero	Above average stable
III	High	Significantly deviating from unity	Significantly deviating from zero	Unpredictable/ unstable
IV	High	Around unity	Significantly deviating from zero	Unpredictable/ unstable

Result and Discussion

Analysis of variance for phenotypic stability

The analysis of variance in each of the three environments indicated significant differences among the genotypes for all the sixteen characters in three environments. 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. Component analyses of environment + (genotype × environment) were significant for all the traits (Tested against pooled error). Partitioning of this variation into linear and non-linear component revealed that the mean square due to environment (Linear) were significant for all the traits. The significant mean square confirm that the environment were random and different and they exercised influence on expression of traits and this variation could have arisen due to linear response of regression of the cultivar to the environment. The mean square due to the G × E (Linear) were significant for all characters (Tested against pooled error) revealed that the behavior of genotype could be predicted over the environment more precisely and accurately as the G × E interaction was the outcome of the linear function of the environmental components. The non-linear component arising due to heterogeneity measured as mean square due to the pooled deviation was significant for all the traits revealed the presence of non-linear response of the genotypes to the changing environment for these traits. The significant of pooled deviation confirms contribution of non-linear component to the total G × E interaction. The genotype differed with respect to stability of these traits making its prediction more difficult. However, the magnitude of linear component *i.e.* environment (Linear) and genotype × environment (Linear) was many time higher than the non-linear component for most of the characters revealed that the prediction of stability could be reliable though it may get affected to some extent.

Stability parameters

The stability is the consistency in performance of a variety over a wide range of environments (Singh and Chaudhary, 1985) [17]. Genotype may react to variable environments in such a way that its development is buffered against environmental variations and more or less similar phenotype is produced under varying environmental conditions. Thus, stability depends upon the relative insensitivity of a genotype to varied environments. Such conditions have been termed as developmental stability (Mather, 1943) [8], phenotypic stability (Lewis, 1954) [7], developmental homeostasis (Lerner, 1954) [6] and canalization (Waddington, 1942) [22]. The genotype of an individual may create different phenotypes in different environments and such phenotype being better adapted to a particular situation. This type of situation has been regarded as individual adaptability and individual buffering. The adaptive response of a population as a whole is known as population buffering. Levin and Kerster (1970) [23] defined adaptive population as one, which contributes most offsprings to the species gene pool of the following generation in relation to other population. Thus, both individual and population buffering can be measured in terms of genotype x environment interaction.

Eberhart and Russell (1966) [44] defined a stable genotype as one, which produced high mean yield and depicted regression coefficient (b_i) around unity and deviations from regression (S^2d_i) near zero. Later on, Breese (1969) [1], Samuel *et al.* (1970) [15] and Paroda and Hayes (1971) [13] suggested that linear regression (b_i) should be regarded as measure of response of a particular genotype, whereas, the deviation from regression

(S^2d_i) as measure of stability. Mehra and Ramanujan (1979) [10], Singh and Singh (1980) [18] and Nadarajan and Gunasekaran (2005) [11] suggested the methodology to classify

With respect to stability parameters, stability performance of parents for yield and yield attributing characters depicted herein Table 1&2. Parent NCK-15-10 was found average stable for green pod yield per plant while parents NC-15-41, NC-15-44 and NC-15-45 were average stable for grain yield per plant, it is remarkable that parent NC-15-45 was found average stable (Suitable for all the environment) for green pod yield per plant as well as grain yield per plant, this parent was also average stable for days to 50% flowering, primary branches per plant, pods per plant, straw yield per plant, havest index, protein content and below average stable for seeds per pod. Parent NCK-15-10 exhibited lower mean than parental mean for yield attributing characters but was stable (non-significant S^2d_i value**)** for most of the characters. Parent NC-15-41 was average stable for days to 50% flowering, pod length, harvest index and shelling ratio and it was stable for most of yield attributing characters, while parent NC-15-44 was average stable for secondary branches per plant, pod length, seeds per pod, straw yield per plant and harvest index. In the present investigation, none of the parents exhibited average stability for all the characters thus generalization regarding stabilitty for all the character is too difficult.

In case of hybrids (Including directs and reciprocals), most of the hybrid most of the parents showed better performance than their corresponding parents. Among hybrids top ranking hybrids on the basis of stability for green pod yield per plant as well as dry seed yield and their stability for others yield attributing traits depicted

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. Component analyses of environment + (Genotype × environment) were significant for all the traits (Tested against pooled error). Partitioning of this variation into linear and non-linear component revealed that the mean square due to environment (linear) were significant for all the traits. The significant mean square confirm that the environment were random and different and they exercised influence on expression of traits and this variation could have arisen due to linear response of regression of the cultivar to the environment. The mean square due to the G × E (linear) were significant for all characters (tested against pooled error) revealed that the behavior of genotype could be predicted over the environment more precisely and accurately as the G × E interaction was the outcome of the linear function of the environmental components.

Parents NC-15-41, NC-15-44 and NC-15-45 were average stable for grain yield per plant, it is remarkable that parent NC-15-45 was found average stable (suitable for all the environment) for green pod yield per plant as well as grain yield per plant, this parent was also average stable for days to 50% flowering, primary branches per plant, pods per plant, protein content and above average stable for pod length, seeds per pod, green pod yield per plant and harvest index. Parent NCK-15-10 exhibited lower mean than parental mean for yield attributing characters but was stable (Non-significant S^2d_i value**)** for most of the characters. Parent NC-15-41 was above average stable for days to 50% flowering, pod length and average stable for harvest index and shelling ratio and it was stable for most of yield attributing characters, while parent NC-15-44 was average stable for secondary branches per plant, pod length, seeds per pod, straw yield per plant and harvest index. Similar finding for stability were also observed by Singh and Singh (1991) [19], Chauhan *et al.* (2004) [14], Henry (2003) [5], Cholin *et al.* (2010) [3], Patel and Jain (2012) [14], Olayiwola *et al.* (2015) [12], Shaieny *et al.* (2015) [16] and Mbeyagala *et al.* (2021) [9]. In the present investigation, none of the parents exhibited average stability for all the characters thus generalization regarding stability for all the character is too difficult.

Table 1: Stability parameters for grain yield per plant (g).

Sr. No.	**Parents/Crosses**	**Grain yield per plant (g)**		
		Mean	**b_i**	**S^2d_i**
	Parents			
1	NCK-15-9	21.51	-0.07	-1.13
2	NCK-15-10	30.42	1.46**	-4.99
3	NC-15-41	34.76	1.01	-5.05
4	NC-15-42	25.31	2.36**	-4.16
5	NC-15-44	36.37	1.58	0.30
6	NC-15-45	35.56	1.53	-3.22
	Parental mean	30.65		
	Direct Crosses			
7	NCK-15-9 x NCK-15-10	30.44	0.05	16.51*
8	NCK-15-9 x NC-15-41	31.68	1.01	-4.54
9	NCK-15-9 x NC-15-42	29.73	1.27	56.23**
10	NCK-15-9 x NC-15-44	35.35	0.73	-3.95
11	NCK-15-9 x NC-15-45	28.69	-2.25	10.70
12	NCK-15-10 x NC-15-41	41.47	1.22	3.59
13	NCK-15-10 x NC-15-42	38.76	4.76	21.36*
14	NCK-15-10 x NC-15-44	38.12	2.20	6.33
15	NCK-15-10 x NC-15-45	49.32	1.35	8.16
16	NC-15-41 x NC-15-42	47.92	-0.93**	-3.29
17	NC-15-41 x NC-15-44	34.12	0.10	96.52**
18	NC-15-41 x NC-15-45	43.21	2.25	-1.33
19	NC-15-42 x NC-15-44	35.98	0.36	0.12
20	NC-15-42 x NC-15-45	39.65	1.35	38.87**
21	NC-15-44 x NC-15-45	37.29	1.28	42.05**
	Hybrid mean	37.45		
	Reciprocals			
22	NCK-15-10 x NCK-15-9	36.90	-3.07*	12.92
23	NC-15-41 x NCK-15-9	39.56	4.77	22.71*
24	NC-15-41 x NCK-15-10	45.41	1.67	49.68**
25	NC-15-42 x NCK-15-9	31.59	0.30	75.69**
26	NC-15-42 x NCK-15-10	37.39	1.86	114.22**
27	NC-15-42 x NC-15-41	36.26	2.05	10.74
28	NC-15-44 x NCK-15-9	38.55	2.34*	-3.67
29	NC-15-44 x NCK-15-10	42.19	0.83	47.92**
30	NC-15-44 x NC-15-41	49.28	2.25**	-4.69
31	NC-15-44 x NC-15-42	38.44	-0.79	19.31*
32	NC-15-45 x NCK-15-9	38.51	-0.44*	-2.86
33	NC-15-45 x NCK-15-10	52.15	0.29	0.83
34	NC-15-45 x NC-15-41	50.11	0.63	0.17
35	NC-15-45 x NC-15-42	43.48	1.28	-4.82
36	NC-15-45 x NC-15-44	44.69	0.65	47.55**
	Reciprocal mean	41.63		
	Checks			
37	GC-3	39.54	1.11	-5.14
38	GDVC-2	37.76	-0.34**	-3.96
	General mean	38.09		

* Significantly differ from zero at 5 per cent level and ** significantly differ from zero at 1per cent level for S^2d_i

* Significantly differ from unity at 5 per cent level and ** significantly differ from unity at 1per cent level for b_i

Table 2: Stability performance of parents for various characters in cowpea

Parents Characters	NCK-15-9	NCK-15-10	NC-15-41	NC-15-42	NC-15-44	NC-15-45
Days to 50per cent flowering	NR	√	√*	NS	NR	√
Plant height (cm)	NR	√	√+	√	NS	NS
Primary branches per plant	NS	NR	NS	√	NS	√
Secondary branches per plant	NR	NS	NR	NS	√	NS
Days to maturity	√	NR	√	NR	NS	√
Pods per plant	NR	NS	NS	NS	NR	√
Pod length (cm)	NS	NS	√*	NS	√	√*
Seeds per pod	NR	NS	NR	NS	√*	√*
Test weight (g)	NR	NR	NS	NR	NS	NR
Green seed weight (g)	NR	NS	NR	NS	NS	√+
Green pod yield per plant (g)	NR	√	√+	NR	NR	√*
Grain yield per plant (g)	NR	NR	√	NR	√	√
Straw yield per plant (g)	NR	NS	√	NS	√	NR
Harvest index (per cent)	NR	NR	√	NR	√	√*
Shelling ratio (per cent)	NR	NR	√	NR	√	√+
Protein content (per cent)	√	NR	NS	√	NR	√

(√=Average stable, √*= Above Average stable, √+= Below Average stable; Having higher mean (Desirable) and non-significant S^2d_i value)
NR= Not having desirable mean; Non- significant S^2d_i value
NS= Having significant S^2d_i, so not stable and unpredictable (Nadarajan and Gunasekaran, 2005) [11]

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.

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