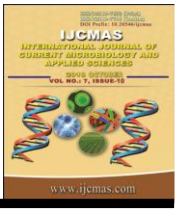
Int.J.Curr.Microbiol.App.Sci **(2018) *7*(10): 887-894**

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 7 Number 10 (2018)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2018.710.098

Stability Analysis for Yield and Yield Attributing Characters among Advanced Stabilized Promising Lines in Cowpea [*Vigna unguiculata* (L.) Walp.]

Sanjeev K. Deshpande* and A.R. Vishwas

Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka - 580005, India

**Corresponding author*

A B S T R A C T

Keywords

Genotype × environment interaction, Legume, Promising lines, Stable

Article Info

Accepted:
06 September 2018
Available Online:
10 October 2018

Cowpea is an important legume in many developing countries and it is a major vegetable source of protein for human consumption especially in Africa and Asia countries including India. Cowpea is grown in almost all the agro ecological zones in India, the performance of genotypes exhibits a wide range of variation within and between environments because of genotype × environment interaction, so in the present study the seventeen promising advanced lines of cowpea and three checks were evaluated for yield and yield attributing traits across three environments E_1, E_2, and E_3. Stability analysis was carried out using Eberhart and Russell (1966) model. Based on stability parameters, the F_6 stabilized lines of DC 15 × CPD 118 and DC15 × DCS 47-1-1 were identified as most stable genotypes for seed yield. Likewise F_6 Promising lines C 152 × IC 202860, DC 15 × CPD 118 and GC 3 × CPD 115 for pod length, C 152 × GL3, DC16 and C 152 × IC 202860 for pod number, C 152 × P 206, C 152 × DCS 5-3-20, DC 15 × Job 129 and DCS 47-1 × DC 15 for number of number of seeds per pod were found to be stable. All the superior stabilized families can be further tested in different locality to ascertain their superiority in different agro climatic regions.

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important legume in many developing countries including india (Adam and Baidoo, 2008). It is a major vegetable source of protein for human consumption especially in Africa and India. Cowpea seeds contain about 25% protein, making it extremely valuable in areas where many people cannot afford protein foods from animal sources namely meat and fish (Deshpande *et al.,* 2011). It can be a unique dietary protein source for poor people and is one of the cheapest source (Rangel *et al.,* 2003). Cowpea is a drought tolerant crop and thrives in warm weather and well adapted to the drier regions of the tropics like India (Singh, 2005). Cowpea can be grown in almost all the agro ecological zones in India. The performance of genotypes exhibits a wide range of variation within and between environments because of genotype × environment interaction (Uttam *et al.,* 2014). When interaction between genotype and environment exists, it may cause a difference in relative ranking of varieties when they are compared over a series of environments. This makes the efforts in cowpea varietal development more challenging and skillful. Phenotypically stable genotypes are of great importance because the environmental conditions vary from season to season and year to year (Silva *et al.*, 2016). The adaptability and stability of genotypes deserve attention in breeding program. So in this context the present investigation was carried to identify the stable cowpea genotypes across the varied environments.

Materials and Methods

The experiment was conducted at 3 locations such as Agriculture Research Station Malagi (E_1) with Red soil, and protective irrigation during *Rabi* 2017, Agriculture Research Station, Mugad (E_2) with Sandy loamy soil in paddy fallows in *Rabi* 2017 and Main Agriculture Research Station, University of Agricultural Sciences, Dharwad (E_3) with deep black soil and assured rainfall (transitional zone) during *Summer* 2018.

Materials used in the study were 17 promising advanced stabilized F_6 lines of different crosses combinations generated at the Department of Genetics and Plant Breeding, UAS Dharwad, along with three checks such as DC 15, DC 16 and DCS 47-1. Stabilized lines and checks were grown in all three locations by following RCBD design with two replications along with normal agronomic practices.

Results were analyzed according to stability model given by Eberhart and Russell model (1966). The model involves the estimation of three stability parameters *viz.,* mean, regression coefficient and deviation from regression, and which are defined by the mathematical formula as given below.

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

Where,

Y_{ij} = Mean of the i^{th} genotype at the j^{th} environment

μ_i = Mean of i^{th} genotype over all environments

b_i = Regression coefficient that measures the response of i^{th} genotype to varying environments

I_j = Environmental index obtained by subtracting the grand mean from the mean of all genotypes at the j^{th} environment

S_{ij} = Deviation from regression of the i^{th} genotype at the j^{th} environment

Where,

Environment index = I_j = environment mean – grand mean

In this model the variance due to environments and genotype × environment are partitioned into environment (linear), genotype × environment (linear) and deviation from the regression coefficient. Observations were recorded on five competitive plants in respect of three important traits *viz.*, pod length, number of number of pods per plantand number of number of seeds per pod, seed yield (kg ha^{-1}) was recorded on plot basis. The stability parameter mean provides a measure of the performance of a genotype as compared to other entries. The b_i and S^2d_i values are the measure of the G × E interactions. In general if G × E interaction is non-significant or predominantly linear as compared to its non-linear component, the prediction of stability of a genotype over environments becomes more precise and accurate. As per the Eberhart and Russell (1966) model of stability, components S^2d_i measure the predictability whereas b_i

measures the stability. Stability of a genotype can be predicted more precisely if G × E interaction and S^2d_i values are non-significant. They defined an ideal genotype as the one having highest mean value with a regression coefficient (b_i) equal to unity and deviation from regression (S^2d_i) close to zero. They further suggested that genotypes could be classified as below average stable performing only in favorable environments ($b_i>1$), above average stable that are adapted specifically to poor environment ($b_i<1$) and average stable performing in most of the environment.

Results and Discussion

The analysis of variance showed highly significant mean sum of squares (MSS) for genotypes and environments for all the characters *viz*., pod length, number of pods per plant, number of seeds per pod and seed yield (kg ha^{-1}) which inferred the presence of variation among genotypes and environments. The genotypes × environment interactions were significant for all traits which revealed that genotypes under study are having significant differential response to the changing environments. Further analysis of environment + (genotype × environment) component showed that it was significant for all the traits studied. Partitioning of this variation into linear and non-linear components revealed that the mean sum of square due to environment (linear) was significant for all the characters. The significant mean sum of squares confirms that the environments were random and different and they exercised influence on the expression of the traits. This variation could have arisen due to the linear response of the regression of the cultivar to the environment. The mean sums of squares due to the G × E (linear) were significant for the all characters. This revealed that the behavior of the genotypes could be predicted over the environments 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 the heterogeneity measured as mean square due to the pooled deviation was significant for pod number and seed yield (kg ha^{-1}) revealed the presence of non-linear response of the genotypes to the changing environment for these traits. The significance of pooled deviation for the pod number and seed yield (kg ha^{-1}) confirms contribution of the non-linear component to the total G × E interaction for them. The genotypes differed with respect to the 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 times higher than the non-linear component (pooled deviation) for most of the characters. This trend revealed that the prediction of stability could be reliable though it may get affected to some extent. The results obtained in the present study are in agreement with the finding of (Ali *et al.*, 2004), (Akande, 2007) and (Adewale *et al.*, 2010). The mean of the characters, namely, pod length, number of pods per plant, number of seeds per pod and seed yield (kg ha^{-1}), along with the two stability parameters, viz., regression coefficients (b_i) and deviation from regression (S^2d_i) are presented in Table 2.

It was clear from environmental indices (-225 to 426) that locations were highly distinct from one another in affecting seed yield (kg ha^{-1}). So the extent of influence of environment was significant (Table 1). The average seed yield recorded over all three environments was 1821.74 kg ha^{-1} (Table 2). Due to the highest environmental indices and site mean in E_1 (ARS, Malagi), it found to be suitable environment for *per se* seed yield compared to other two environments. The F_6 genotype C 152 × GL 3 was highest yielder

(2297.26 kg ha^{-1}) while, the F_6 line (GC 3 × CPD 115) was lowest (1392.61 kg ha^{-1}) among all the 20 genotypes studied (Table 2).

The genotypes which gave higher mean seed yield over three environments were C 152 × GL3 (2297.3 kgha^{-1}), DC 15 x CPD 118 (2125.14 kgha^{-1}), DC15 × SHUBRA (2108.847 kg ha^{-1}), C 152 × IC 202860 (2064.23 kg ha^{-1}), DC15 × DCS 47-1-1 (2029.5 kg ha^{-1}), V 118 × IC257437 (1927.398 kg ha^{-1}), DC15 × DCS 47-1-2 (1913.845 kg ha^{-1}), C 152 × P 206 (1889.83 kg ha^{-1}) and DC 15 × C 152 (1888.925 kg ha^{-1}). However the results indicated that the genotypes DC 15 × CPD 118 and DC 15 × DCS 47-1-2 were found to be most stable since these showed regression coefficient values near to unity, least non-significant deviation from regression and higher seed yield (Table 2).

The highly unstable genotypes were DC 15 × DCS 47-1-1, GC 3 × CPD 115 and DCS 47-1 × DC 15, since they indicated significant deviation from regression. The genotypes DC 15 × SHUBRA, C 152 × IC 202860 and V 118 × GL3 showed b_i values greater than unity and non-significant deviation from regression. It means these genotypes could perform better under favorable environments only. The genotypes which could perform better under poor environments were C 152 × GL 3 and V 118 × IC257437, since these have b_i values significantly deviating from unity. The genotypes DC 15 × DCS 47-1-1, DC 15 × SHUBRA found to be specifically adapted to the favorable environment E_1 (ARS Malagi); likewise genotypes DC15 × CPD 115 specifically suitable for paddy fallows (ARS, Mugad) whereas the genotypes such as V118 × IC257437 and C 152 × GL 3 were found to be adopted particularly to E_3 (MARS, Dharwad).

Locations varied with regard to pod length as seen from the environmental indices -1.10 to 1.52 (Table 1), so the character was much affected by environment. The average pod length over three environments is 16 cm (Table 2) and on the basis of site mean and environment indices E_1 (Malagi) was most favorable for this trait compare to E_2 and E_3. The F_6 line C 152 × IC 202860 exhibited the longest pods (17.79 cm) while, the check DC 16 was having the shortest pods (14.34 cm) among all genotypes studied in all environments (Table 2).

While considering the genotypes suitable for breeding of pod length, the genotypes namely, C152 × IC 202860, DC15 × DCS 47-1-3, DC15(Check), C 152 × GL 3, DC15 × DCS 47-1-2, DC 15 × C 152, V 118 × IC257437, DC 15 × CPD 118 and GC 3 × CPD 115 showed higher mean. However from stability point of view, the genotypes C 152 × IC 202860, DC 15 × CPD 118 and GC 3 × CPD 115 were found most stable since they showed regression coefficient value (1.54, 1.11, 1.49) near to unity, least non-significant deviation from regression (Table 2). The genotypes which showed b_i value greater than unity and non-significant deviation from regression were DC15 and DC 15 × C 152. This means that genotypes could perform better under favorable environments only and whereas genotype V 118 × IC257437 perform better under poor environments since it has significant b_i value lower than unity (0.215).

With respect to number of pods per plants, locations have much effect as it was evident by having environmental indices ranging from -1.93 to 3.29 (Table 1). The average number of pods considering all environments is 28.66 (Table 2) and on the basis of location mean and environmental indices E_1 (Malagi) was most suitable for this trait. The F_6 progeny C 152 × GL3 borne maximum number of pods per plant (35.62) whereas DC 15 × GL 3 having minimum number of pods per plant (23.34) as shown in Table 2.

Table.1 Mean values and environmental indices of yield and yield attributing characters across three environments of cowpea

Sl. No.	Genotype (F_6 Generation	Seed yield (kg ha^{-1})			Pod length(cm)			Number pods per plant			Number of seeds per pod		
	of different crosses)	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
1	**DC15 × DCS 47-1 -1**	2839.5	1623.4	1625.7	16.46	14.865	14.385	33.205	22.665	21.165	12.625	13.33	14.33
2	**C 152 × P 206**	2579.5	1606.4	1483.6	17.54	14.75	15.47	28.315	28.17	24.835	14.62	14.835	15.5
3	**DC15 × SHUBRA**	3139.8	1565.9	1620.8	16.68	15.83	14.38	26.66	27.835	27.835	11.95	15.665	16.335
4	**DC15 × DCS 47-1-2**	2344.6	1739.3	1657.7	18.01	16.335	16.665	24.835	26.335	24.5	14.45	15.335	15.83
5	**DC15 × DCS 47-1-3**	1448.6	1697.8	1348.1	20.49	17.58	14.78	26.535	23	22.835	14.62	17.665	16
6	**C 152 × DCS 5-3-20**	2222.2	1566.3	1555.3	14.78	16.215	14.885	31.38	26.67	27.5	13.615	14.665	15.5
7	**V 118 × GL3**	3018.8	1242.7	1074.1	16.975	16.67	12.7	22.18	26.335	24.67	14.945	13.17	13.835
8	**DC15 × Job 129**	1427.7	1609.2	1233.2	15.79	12.7	14.785	22.925	25	24	14.68	13.165	14.835
9	**DCS 47-1 × DC 15**	2400.8	1374.8	1246.3	16.79	15.335	15.015	27.88	20.835	23.335	12.29	15.17	15.17
10	**DC 15 × GL3**	2514.7	1434	1200.5	17.125	14.835	14.565	24.835	19.5	25.67	13.46	15.165	13.335
11	**V 118 × IC 257425**	2270.1	1419.9	1213	14.515	14.42	15.92	27.48	19.5	25.83	13.115	13.835	14.67
12	**V 118 × IC257437**	2259.4	1694.7	1828.1	17.01	15.63	16.815	31.525	29.835	28.335	11.595	15.5	14.165
13	**DC 15 × C 152**	2484.1	1511.7	1671	19.29	17.085	13.25	32.425	28.83	31.165	13.345	16.83	14.5
14	**C 152 × IC 202860**	2979.8	1645.8	1567.1	19.96	17.885	15.53	41.915	29.33	29.83	13.79	16.335	14.5
15	**GC 3 × CPD 115**	1160.1	1544.5	1473.2	18.68	14.22	15.35	34.425	37.5	31.835	12.015	13.835	13.835
16	**DC 15 × CPD 118**	1843.4	2186.3	2345.7	18.125	15.335	15.415	39.08	31.33	26	11.79	15.335	13.83
17	**C 152 × GL3**	2096.6	2469.3	2325.9	19.96	17.085	14.65	41.525	33.67	31.67	15.015	14.17	15.165
18	**DC15 (Check)**	2231	1412.3	1485.9	21.77	15.15	15.15	39.915	29.665	27.835	15.345	14.835	15
19	**DC16 (Check)**	1896.7	1525.6	2000.2	16.01	13.58	13.43	41.425	32.335	31.67	13.945	12.165	12.33
20	**DCS 47-1 (Check)**	1798.3	1545.8	1978.3	14.665	16	14.88	40.615	27.67	24	14.27	14.5	14.165
	E. Indices	**426.04**	**-200.97**	**-225.06**	**1.529**	**-0.427**	**-1.102**	**3.294**	**-1.36**	**-1.934**	**-0.756**	**0.445**	**0.311**
	Site Mean	**2247.8**	**1620.8**	**1596.7**	**17.531**	**15.575**	**14.901**	**31.954**	**27.301**	**26.726**	**13.574**	**14.775**	**14.642**

E_1: Agriculture Research Station, Malagi (Red soil with protective irrigation).
E_2: Agriculture Research Station, Mugad (Sandy loamy soil and in paddy fallows field).
E_3: Main Research Station, UAS, Dharwad (Deep black soil and assured rainfal).

Table.2 Stability parameters for different characters in cowpea genotypes

Sl. No.	Genotype (F_6 Generation	Seed yield (kg ha^{-1})			Pod length (cm)			Number of pods per plant			Number of seeds per pod		
	of different crosses)	Mean	b_i	S^2di	Mean	b_i	S^2di	Mean	b_i	S^2di	Mean	b_i	S^2di
1	**DC15 × DCS 47-1-1**	2029.55	1.89*	106826*	15.24	0.8	1.39	25.68	2.28*	5.8	13.428	2.059*	0.37
2	**C 152 × P 206**	1889.83	1.62	-104471	15.92	0.93	-0.4	27.11	0.42	0.99	14.985	0.95	0.15
3	**DC15 × SHUBRA**	2108.85	2.41*	86327	15.63	0.78	0.93	27.44	0.23*	5.81	14.65	0.38*	1.34
4	**DC15 × DCS 47-1-2**	1913.85	1.01	8063	17	0.59	-1.1	25.22	-0.09	-4.03	15.205	0.42	1.09
5	**DC15 × DCS 47-1-3**	1498.17	-0.1	45931	17.62	2.01*	0.29	24.12	0.73	5.79	16.095	2.20*	0.74
6	**C 152 × DCS 5-3-20**	1781.25	1.03	107881	15.29	-0.2	0.25	28.52	0.85	-4.94	14.593	1.56	-0.01
7	**V 118 × GL3**	1778.5	2.91*	103138	15.45	1.3	3.71	24.4	-0.64	3.73	13.983	-0.38	-0.9
8	**DC15 × Job129**	1423.39	0.03	37460	14.43	0.65	2.02	23.98	-0.3	-5.12	14.227	1.48	0.7
9	**DCS 47-1 × DC 15**	1673.96	1.71	104161*	15.71	0.69	1.38	24.02	1.12	0.83	14.21	1.22	-0.85
10	**DC 15 × GL3**	1716.4	1.88	90273	15.51	1.02	-1.3	23.34	0.34	14.66	13.987	0.08	1.3
11	**V 118 × IC 257425**	1634.32	1.5	93385	14.95	-0.4	0.59	24.27	0.85	17.68*	13.873	-0.72	-0.1
12	**V 118 × IC257437**	1927.4	0.77*	-96412	16.49	0.21*	-0.5	29.9	0.52	-5.09	13.753	2.51	1.29
13	**DC 15 × C 152**	1888.93	1.39	89390	16.54	2.03*	0.84	30.81	0.44*	2.43	14.892	0.83	0.14
14	**C 152 × IC 202860**	2064.23	2.15*	96325	17.79	1.55	0.47	33.69	1.46	-3.96	14.875	-1.31	1.23
15	**GC 3 × CPD 115**	1392.61	0.542*	104424*	16.08	1.49	1.04	34.59	0.05	10.23*	13.228	0.93	-0.88
16	**Dc 15 × CPD 118**	2125.14	0.67	9770	16.29	1.12	1.02	32.14	2.18*	2.58	13.652	2.93	-0.9
17	**C 152 × GL3**	2297.26	0.46*	9602	17.23	1.89*	-0.7	35.62	1.13	5.35	14.783	2.55	0.67
18	**DC15 (Check)**	1709.71	1.22	-102677	17.36	2.71*	0.39	32.47	2.26*	-5.68	15.06	1.59	-1.33
19	**DC16 (Check)**	1807.53	0.19	6957	14.34	1.04	1.23	35.14	1.23	5.73	12.813	0.97	0.7
20	**DCS 47-1 (Check)**	1774.11	0.04	-13944	15.18	-0.22	0.54	30.76	3.03	-3.93	14.312	-1.49	1.35
P. mean		**1821.75**			**16**			**28.66**			**14.33**		
SE for mean		**106.9**			**0.78**			**1.52**			**0.54**		
SE for b_i			**0.3**			**0.57**			**0.53**			**0.82**	

The genotypes which showed higher mean values for number of pods per plant over three environments were C 152 × GL3, DC16 (check), GC 3 × CPD 115, C 152 × IC 202860, DC15(check), DC 15 × CPD 118, DC 15 × C 152, DCS 47-1 (check) and V 118 x IC257437. Out of them, the genotypes namely C 152 × GL3, DC16 and C 152 × IC 202860 were found stable since they showed regression values (1.13, 1.23, and 1.46 respectively) near to unity, non-significant deviation from regression and higher mean (Table 2). The highly unstable genotypes were GC 3 × CPD 115 and V 118 × IC257425, since they indicated significant deviation from regression. The genotypes which showed b_i value more than unity and non-significant deviation from regression were DC15 (check) and DC 15 × CPD 118, so these genotypes could perform better under favorable environments only and performance these genotypes could be predicted. The genotype which could perform better under poor environments was DC 15 × C 152 since it has b_i less than unity and least non-significant deviation.

With respect to number of seeds per pod, the environmental indices ranged from -0.75 to 0.44 (Table 1) indicated significant variation across the three locations, whereas the average number of seeds per pod across all environments is 14.33. Since E_2 (Mugad) was having higher site mean and environmental indices among three locations, so this environment is most favorable for number of number of seeds per pod. The highest number of number of seeds per pod (16.05) was observed in F_6 line DC15 × DCS 47-1-3 while DC 16 (Check) had the lowest number of seeds per pod (12.81) as shown in Table 2.

While considering the genotypes suitable for breeding of number of seeds per pod, the genotypes namely, DC15 × DCS 47-1-3, DC15 × DCS 47-1-2, DC15(check), C 152 × P 206, DC 15 × C 152, C 152 × IC 202860, C 152 × GL3, DC15 × SHUBRA and C 152 × DCS 5-3-20 showed good performance by having higher mean. However from stability point of view the genotypes C 152 × P 206, C 152 × DCS 5-3-20, DC 15 × Job 129 and DCS 47-1 × DC 15 were found most stable for number of seeds per pod since these showed regression coefficient values (0.95, 1.56, 1.48, 1.22 respectively) near to unity, least non-significant deviation from regression and higher mean (Table 2).

The genotypes which showed b_i values greater than unity and non-significant deviation from regression were DC15 × DCS 47-1-1 and DC15 × DCS 47-1-3. It means these genotypes perform better under favorable environments only and performance of these genotypes could be predicted. The genotype which performs better under poor environments was DC15 × SHUBRA since it has significant b_i value less than unity (0.38).

Thus it can be concluded that the E_1 (Malagi) environment is most favorable for characters such as seed yield, pod length and number of number of pods per plant whereas E_2 (Mugad) is suitable for number of number of seeds per pods trait. On the basis of seed yield (kg ha^{-1}) over environments, the F_6 lines of DC 15 × CPD118 and DC 15× DCS47-1-2 were found to be most stable. Based on stability parameters, stable genotypes that can be used directly for breeding program are C 152 × IC 202860, DC 15 × CPD 118 and GC 3 × CPD 115 for pod length, C 152 × GL3, DC16 and C 152 × IC 202860 for pod number, C 152 × P 206, C 152 × DCS 5-3-20, DC 15 × Job 129 and DCS 47-1 × DC 15 for number of seeds per pod respectively.

References

Adam, J. I., Baidoo P. K., 2008, Susceptibility of five cowpea varieties to attack by

Callasobruchus maculatus. *J. Ghana Sce. Ass*., 10 (2): 85-92.

Adewale B. D., Okonji C., Oyekanmi A. A., Akintobi D.A. C. and Aremu C. O., 2010, Genotypic variability and stability of some grain yield components of Cowpea. *African J. Agric. Res*., 5: 874-880.

Akande S. R., 2007, Genotype by environment interaction for cowpea seed yield and disease reaction in the forest and derived savanna agro-ecologies of south west Nigeria. *American-Eurasian J. Agric. Environ. Sci*., 2: 163-168.

Ali Y., Aslam Z., Hussain F. and Shakur A., 2004, Genotype and environmental interactions in cowpea for yield and disease resistance. *Inter. J. Environ. Sci. Tech.*, 1: 119-123.

Deshpande, V.K., Makanur, B., Deshpande, S.K., Adiger, S., and Salimath, P.M., 2011, "Quantitative and Qualitative losses caused by *Callosobruchus maculates* in Cowpea during Seed Storage". *Plant Archi.*, 11(2): 723-731.

Eberhart S. and Russel W.A., 1966, Stability parameters for comparing varieties. *Crop Sc*i., 6: 36-40.

Rangel, A., Domont, G. B., Pedrosa, C., and Ferreira, S. T., 2003, Functional properties of purified vicilins from cowpea (*Vigna unguiculata*) and pea (*Pisum sativum*) and cowpea protein isolate. *J. of Agric. Food Chem*., 51: 5792- 5797.

Silva, D. O. M., Santos, C. A. F. and Boiteux, L. S., 2016, Adaptability and stability parameters of total seed yield and protein content in cowpea (*Vigna unguiculata*) genotypes subjected to semi-arid conditions. *Australian J. Crop Sci*., 10 (8): 1164-1169.

Singh, B.B., 2005, "Cowpea (*Vigna unguiculata* (L.) Walp.)", In: Singh, R.J. & Jauhar, P.P. (Eds), Genetic resources, chromosome engineering and crop improvement. Vol. 1. CRC Press, Boca Raton, FL, USA, 117-162.

Uttam, C., Ashok, N. T., Niraj, K., Kul, B. S. and Sunil, C., 2014, Yield stability in pigeon pea hybrids (*Cajanus cajan* (L.) Mill) under varying agro-climatic regions. *Ratar. Povrt*, 51(1): 7-17.

How to cite this article:

Sanjeev K. Deshpande and Vishwas, A.R. 2018. Stability Analysis for Yield and Yield Attributing Characters among Advanced Stabilized Promising Lines in Cowpea [*Vigna unguiculata* (L.) Walp.]. *Int.J.Curr.Microbiol.App.Sci.* 7(10): 887-894.
doi: https://doi.org/10.20546/ijcmas.2018.710.098