Genetic Variability Studies in Early Segregating Generation of Cowpea (*Vigna unguiculata* (L.) Walp subsp *unguiculata*)

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ABSTRACT

Aims: In a self-pollinated crop like cowpea, most breeding approaches predominantly use different techniques of handling the segregating generations. It is important to select and increase the frequency of the desirable genotypes for efficient management of segregating generations and gradual improvement of important characters in the material. For the selection to be efficient, a complete knowledge of the features of the segregating material in terms of genetic variability with regard to important characters is crucial. So the objective of the study was to comprehend the genetic variability in segregating generations and to estimate the percentage of transressive segregants.

Study design: The experiment was laid out in Augmented design II during *kharif*, 2023.

Place and Duration of Study: The current experiment was undergone at the Botany garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka to evaluate 36 F_4 families and six checks during *kharif* 2023

Methodology: Observations were taken for ten yield and yield related traits *viz.,* total yield (kg/ha), single plant yield (g), number of pods per plant, test weight (g), number of seeds per pod, pod length (cm), number of clusters per plant, number of pods per cluster, days to fifty per cent flowering and days to maturity. Analysis of variance (ANOVA) for yield and yield related traits of 36 F_4 families of diverse crosses and pedigree along with checks in grain type cowpea was carried out in augmented design II as proposed by Federer and Raghavarao, 1975. Different genetic parameters were estimated to characterize the material for nature and amount of genetic variability. Percentage of transressive segregants was calculated using the mean±1 SD for all characters.

Results: The variances between genotypes were shown to be highly significant among all the characters under study. All traits exhibited high heritability (>60%) except the trait number of pods per cluster. High heritability coupled with high genetic advance (>20%) was obtained in traits like total yield (kg/ha) (71.00% and 43.59%), single plant yield (g) (76.18% and 35.01%), number of pods per plant (71.98% and 33.49%), pod length (cm) (75.99% and 22.00%) and number of clusters per plant (64.90% and 30.02%), indicating the possibility of effective selection for these characters. Highest percentage of transgressive segregants was revealed for the traits total yield (19.44%) and days to fifty per cent flowering (19.44%).

Conclusion: Sufficient amount of genetic variability present among the F_4 families ensures profound scope of selection which in turn indicates possibility of improvement in the population.

Keywords: Cowpea, Genetic variability, Heritability, Genetic advance

1. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp subsp *unguiculata*] is one of the most ancient legumes majorly cultivated in tropical and sub-tropical regions of the world. It belongs to the group of dicotyledons, the order Fabales, family Fabaceae, subfamily Faboideae, tribe Phaseoleae, subtribe Phaseolinae and genus *Vigna* (Timko *et al.,* 2007[1]). Maxted *et al.* (2004) [2] divided the genus *Vigna* into six sections, *viz*., *Vigna, Comosae, Macrodontae, Reticulatae, Liebrechtsia*, and *Catiang*. The section *Catiang* contains species *unguiculata*. Cowpea, *Vigna unguiculata* subspecies *unguiculata* is used as a grain type as well as fodder type. Owing to this early introduction in Neolithic period, India possesses exceptional diversity in the forms of both wild cowpea and cultivated cowpea. Therefore, India is regarded as the secondary centre of diversity for the crop (Deshpande *et al.,* 2018[3]).

On a global scale, cowpea is cultivated in around 15.20 mha of area along with a production of 9.78 mt and a productivity of 643.00 kg ha^{-1} (Anon., 2022-23[4]). In India cowpea is cultivated in total of 4.00 mha area producing 2.70 mt leading to a productivity of 567.00 kg ha^{-1}(Anon., 2019-20[5]). The productivity in the country relatively low which is due to several reasons. Among the cowpea growers of the state, there is a tendency of cultivating local landraces and lack of adoption of high yielding improved varieties. This necessitates development of early maturing and high yielding cowpea varieties with farmers' interest in mind.

Careful handling of segregating generations generated from well-planned crosses is the most common method of improving a self-pollinating crop like cowpea. Understanding the genetic variability available in the early segregating generations helps a breeder to select the desirable genotypes. Also, based on the mean performance of the population, it is possible to estimate the percentage of transgressive segregants to understand the frequency of the superior desirable families with respect to various characters. Considering this hypothesis, numerous studies on genetic variability in different segregating generations of cowpea has been undertaken by many breeders [Mary and Gopalan, 2006[6]; Bhadru and Navale, 2012[7]; Khan *et al.*, 2013[8]; Kumar *et al.*, 2017[9]; Lokesh and Murthy, 2017[10]; Meenatchi *et al.*, 2019[11] and Gaiwal *et al.*, 2022[12]]. With this background, the current study was undertaken with the objective to estimate the genetic variability in the F_4 generation of diverse crosses in grain cowpea.

2. MATERIAL AND METHODS

The experiment was carried out using augmented design-II during *kharif* 2023 for evaluation of F_4 families of various crosses. Each of the families along with checks and promising stabilised lines were raised in three rows of three-meter length with row spacing of 45 cm and plant to plant spacing of 15 cm. All the recommended agronomic and plant protection practices were followed during cropping period to ensure optimal plant growth. Observations were taken for ten yield and yield related traits *viz.,* total yield (kg/ha), single plant yield (g), number of pods per plant, test weight (g), number of seeds per pod, pod length (cm), number of clusters per plant, number of pods per cluster, days to fifty per cent flowering and days to maturity.

2.1 Genetic variability study: Analysis of variance (ANOVA) for yield and yield related traits of early segregating generations of diverse crosses and pedigree along with checks in grain type cowpea was carried out in augmented design II as proposed by Federer and Raghavarao, 1975[13]. Different genetic variability parameter *viz*., mean, variance suggested by Cochran (1957) [14], phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) as suggested by Burton and De Vane (1953) [15], heritability (h^2_{bs}) as suggested by Hanson *et al*., 1956[16] and Lush, 1949[17], and genetic advance as suggested by Johnson *et al.*, 1955[18] for all the characters were calculated by following standard procedures.

2.2 Transgressive segregants: Based on the mean *per se* performance of F_4 families of various crosses and checks, percentage of transgressive segregants were calculated for yield and yield attributing traits. The F_4 means and standard deviations for all traits were calculated. Then the numbers of genotypes exceeding or subceeding (for maturity traits only) the value of F_4 mean + 1SD or F_4 mean -1SD (for maturity traits only) were worked out for each trait. This helped to find out the percentage of transgressive segregants for all yield and yield attributing traits among F_4 families and checks.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance for yield and yield attributing traits in F_4 families of various crosses and checks

From the ANOVA, the variances between genotypes were shown to be highly significant among all the characters under study. Also the variances between F_4 families were highly significant suggesting ample scope of selection in all the characters. This observation indicated the presence of ample amount of genetic variability among the entries (Table 1). These findings align with the results obtained by multiple works [Araméndiz-Tatis *et al.*, 2018[19] and Owusu *et al.*, 2021[20]].

Table 1. Analysis of Variance for yield and yield attributing traits among F_4 families of diverse crosses and checks for yield and yield attributing traits in grain cowpea during *kharif*-2023

Sources of Variation	Degrees of freedom	Total Yield (kg/ha)	Single Plant Yield (g)	Number of pods per plant	Test weight (g)	Number of seeds per pod	Pod Length (cm)	Number of clusters per plant	Days to fifty per cent flowering	Days to maturity	Number of pods per cluster
Block (ignoring Genotypes)	3	121479.17	21.08*	10.29**	5.25**	1.05	1.62**	1.33*	29.08**	15.03*	0.21*
Genotypes (F_4 Families + Checks)	41	305542.37**	18.05**	17.27**	4.80**	3.46**	6.17**	7.87**	17.94**	35.16**	0.21**
Checks (Released varieties + Advanced breeding lines)	5	946661.58**	64.35**	49.18**	26.18**	13.18**	29.12**	21.23**	20.57**	107.70**	0.27*
Genotypes vs F_4 Families	36	216498.03**	11.62*	12.84**	1.83*	2.11**	2.98**	6.01**	17.58**	25.09**	0.20*
Blocks (eliminating Genotypes)	3	53375.16	3.66	5.07	0.90	0.38	0.17	0.76	3.39	1.94	0.01
Genotypes (ignoring blocks)	41	310525.59**	19.33**	17.65**	5.12**	3.51**	6.27**	7.91**	19.82**	36.12**	0.22**
F_4 Families	35	222235.58**	13.43*	11.72**	1.84*	2.00**	2.92**	5.22**	13.79**	23.56**	0.18*
Checks vs F_4 Families	1	219995.94*	0.62*	67.60**	14.68**	7.98**	9.33**	35.35**	227.21**	117.88**	1.32**
Error	15	64519.26	4.83	2.18	0.58	0.21	0.27	0.35	2.32	3.61	0.06

***Significant at 5% level of probability **Significant at 1% level of probability**

3.2 Estimation of genetic variability parameters for yield and yield attributing traits in F_4 families of various crosses and checks

The parameters like mean, range, PCV, GCV, Heritability, GA and GAM for each yield and yield related traits has been presented in Table 2. The PCV and GCV were high (>20%) for total yield (kg/ha). This indicated that the F_4 families are significantly differs from one another with respect to their total yield providing a chance to identify high yielding families. Similar results were obtained by many scientists [Ugale *et al.*, 2020[21] and Abha *et al.*, 2024[22]] in various materials of grain cowpea. High PCV along with moderate GCV was evident in characters like single plant yield (g), number of pods per plant, number of clusters per plant and number of pods per cluster. Moderate PCV and GCV was obtained in traits like test weight (g), number of seeds per pod and pod length (cm). Therefore, these characters also provide ample amount of variability to practice selection. Similar estimates were obtained by Chaudhary *et al.,* 2020[23] and Phyu *et al.*, 2023[24] for single plant yield (g) and number of pods per plant, by Kumar *et al.*, 2015[25] and Sharma *et al.*, 2017[26] for number of clusters per plant, by Kavyashree *et al.*, 2023[27] for test weight (g) and by Bamji Rukhsar *et al.*, 2020[28] and Parmar *et al.*, 2024[29] for number of seeds per pod and pod length (cm). The characters days to fifty per cent flowering and days to maturity exhibited low estimates of both PCV and GCV (<10%) which was parallel with the findings of Bamji Rukhsar *et al.*, 2020[28]. This suggested that compared to other yield related characters, maturity traits exhibited less amount of variability.

All traits exhibited high heritability (>60%) except the trait number of pods per cluster. High heritability coupled with high genetic advance was obtained in traits like total yield (kg/ha), single plant yield (g), number of pods per plant, pod length (cm) and number of clusters per plant, indicating the possibility of effective selection. A similar report was obtained from the studies of Bamji Rukhsar *et al.*, 2020[28] for total yield (kg/ha) and pod length (cm), Phyu *et al.*, 2023[24] for single plant yield (g), number of pods per plant and number of clusters per plant. High broad sense heritability coupled with moderate GAM was evident in the characters test weight (g), number of seeds per pod, days to fifty per cent flowering and days to maturity. For test weight (g), Singh *et al.*, 2022[30] and Gaiwal *et al.*, 2022[12] reported a similar estimate. Khanpara *et al.*, 2015[31] and Khandait *et al.,* 2016[32] reported parallel findings for number of seeds per pod. For maturity traits the study of Bamji Rukhsar *et al.*, 2020[28] provided a similar conclusion.

Therefore, characters like total yield (kg/ha), single plant yield (g), number of pods per plant, number of clusters per plant, test weight (g), number of seeds per pod and pod length (cm) exhibited high heritability broad sense along with high to moderate estimates of PCV, GCV and GAM. So these characters can be confidently targeted for improvement through selection in the material under study.

3.3 Estimation of percentage of transgressive segregants for yield and yield attributing traits

The percentage of transgressive segregants was highest for the traits total yield (19.44%) and days to fifty per cent flowering (19.44%) followed by single plant yield (16.67%) and number of pods per plant (16.67%). For all other characters, test weight, number of seeds per pod, pod length, number of clusters per plant and days to maturity, 13.89% of transgressive segregants was reported (Table 3).

A high frequency of transgressive segregants with respect to total yield indicates presence of high yielding families which can be selected and advanced in the further generations for stabilization. Even though the population was shown to be less variable with respect to maturity traits, the high frequency of transgressive segregants with respect to days to fifty per cent flowering suggests the number of earlier flowering genotypes is higher and therefore can be selected for.

Table 2. *Per se* mean, range and parameters of genetic variability for yield and yield attributing traits among F_4 families of diverse crosses and checks in grain cowpea during *kharif*-2023

Parameters	**Range**		**Mean**	***Vp***	***Vg***	***Ve***	***h^2_{bs}(%)***	***GA***	***GAM (%)***	***PCV (%)***	***GCV (%)***
	Minimum	**Maximum**									
Total Yield (kg/ha)	850.57	2480.94	1585.99	222235.55	157715.91	64519.65	71.00	690.19	43.59	29.77	25.08
Single Plant Yield (g)	11.38	26.44	17.07	14.60	11.12	3.48	76.18	6.00	35.01	22.31	19.47
Number of pods per plant	10.60	24.20	17.67	14.94	10.76	4.19	71.98	5.73	33.49	22.58	19.16
Test weight (g)	9.90	16.90	13.54	2.44	1.96	0.48	80.40	2.59	19.47	11.76	10.54
Number of seeds per pod	9.98	16.84	13.41	3.13	2.28	0.85	72.80	2.65	20.08	13.39	11.42
Pod Length (cm)	12.34	20.04	16.58	5.30	4.03	1.27	75.99	3.60	22.00	14.06	12.25
Number of clusters per plant	7.80	16.65	12.12	7.91	5.13	2.78	64.90	3.76	30.02	22.45	18.09
Days to fifty per cent flowering	44.00	59.00	53.18	14.29	12.42	1.88	86.88	6.77	12.48	6.98	6.50
Days to maturity	69.00	90.00	81.80	25.68	23.18	2.50	90.27	9.42	11.42	6.14	5.83
Number of pods per cluster	1.00	3.00	1.73	0.46	0.08	0.38	16.00	0.23	12.74	37.49	15.23

Table 3: Estimates of percentage of transgressive segregants for yield and yield attributing traits among the F_4 families of diverse crosses in grain cowpea

Sl No	F_4 families	Total Yield (kg/ha)	Single Plant Yield (g)	Number of pods per plant	Test weight (g)	Number of seeds per pod	Pod Length (cm)	Number of clusters per plant	Days to fifty per cent flowering	Days to maturity
1	EC 724160 × EC 724157	2041.53	21.20	24.20	15.80	13.00	17.58	11.40	47.00	78.00
2	EC 724160× EC 738126	968.77	11.89	17.20	15.80	13.20	16.16	7.80	44.00	71.00
3	EC 724160 × DC 15	1543.65	20.17	20.40	12.80	14.80	18.06	11.60	50.00	81.00
4	EC 724160 × DC 16	1367.28	19.78	20.60	12.40	14.60	16.22	15.60	49.00	79.00
5	EC-724160 × DC 17	2465.78	24.36	23.20	15.60	13.80	17.76	13.60	55.00	81.00
6	EC 724160 × GC 3	1233.90	15.14	19.00	14.00	12.80	16.68	11.20	49.00	79.00
7	EC 724157 × EC 738126	1407.04	15.40	13.80	13.78	13.00	16.04	10.40	52.00	79.00
8	EC 724157× GC 3	2412.99	24.43	19.80	14.00	14.60	18.50	12.20	54.00	88.00
9	EC 724157× DCS 47-1	1433.83	17.60	23.20	15.40	13.20	19.80	13.80	53.00	84.00
10	EC 724157× DC 16	2367.93	19.57	20.40	14.60	13.00	18.36	14.40	54.00	82.00
11	EC 724157× DC 17	1262.96	15.98	17.80	14.40	14.60	17.12	13.60	50.00	81.00
12	EC 724157× RC 101	1611.78	17.64	22.20	14.60	12.60	19.14	11.80	51.00	82.00
13	EC 724157× EC 724153	2059.83	17.75	20.20	14.80	13.30	16.10	8.80	46.00	69.00
14	EC 724153 × DC 16	1894.77	17.05	17.40	12.60	13.70	15.60	15.40	53.00	76.00
15	EC 724153× DC 17	2480.94	26.44	19.20	16.60	16.84	20.04	13.00	58.00	88.00
16	EC 3180 × GC 3	850.57	12.76	10.60	12.80	11.54	14.42	10.00	56.00	87.00
17	EC 724153× DCS 47-1	1690.49	18.50	21.00	13.40	12.62	15.98	14.40	52.00	86.00
18	EC 724153× DC 15	1785.63	17.64	16.00	13.60	13.16	16.86	12.80	51.00	77.00
19	EC 724153× GC 3	1657.33	20.98	16.20	14.00	12.84	15.36	11.60	51.00	82.00
20	EC 724153× RC 101	1163.31	17.45	17.60	13.40	10.88	13.16	11.00	55.00	80.00
21	EC 738126 × DC 15	1486.07	17.20	17.60	14.20	13.52	16.70	8.40	50.00	75.00
22	EC 738126× DC 16	1165.80	16.86	13.40	14.80	13.40	15.76	11.20	51.00	73.00
23	EC 738126 × DC 17	1464.69	16.03	22.40	14.20	15.30	18.10	10.40	53.00	87.00
24	EC 738126× GC 3	871.09	11.38	14.80	13.00	11.08	14.24	8.20	59.00	90.00
25	EC 738126× DCS 47-1	1845.36	16.99	22.60	13.40	14.56	17.66	10.40	46.00	78.00
26	EC 738126× RC 101	1310.00	13.96	15.80	12.80	13.76	16.10	7.80	49.00	81.00
27	DC 15 × DCS 47-1	2193.58	17.08	20.00	14.20	14.60	19.20	15.80	57.00	87.00

28	DC 15 × RC 101	1138.67	11.53	12.80	10.00	10.56	13.72	10.40	59.00	81.00
29	DC 16 × RC 101	2476.05	21.80	18.60	10.80	14.20	18.30	12.40	57.00	83.00
30	DC 16 × Phule CP05040	1516.27	14.62	12.60	12.40	10.80	13.14	15.00	56.00	86.00
31	DC 16 × DC 17	1883.90	14.13	18.80	14.20	15.20	16.36	15.40	53.00	84.00
32	DC 16× GC 3	1412.84	13.00	15.80	12.80	15.14	17.56	10.00	56.00	86.00
33	DC 15 × DCS 47-1× Phule CP05040× RC 101	1342.77	12.95	12.60	12.00	13.96	17.12	10.60	54.00	84.00
34	DCS 47-1× RC 101	1525.38	14.71	15.20	12.90	12.76	16.28	11.00	53.00	80.00
35	EC 724160 × DCS 47-1	883.95	13.77	17.00	13.00	14.00	16.06	13.80	56.00	85.00
36	DCS 47-1× DC 17	1514.44	15.73	17.40	13.60	15.60	15.80	13.20	55.00	80.00
	Checks									
37	DC 15	1330.95	17.85	16.15	13.00	15.18	16.58	12.60	54.00	78.25
38	DCS 47-1	1441.84	18.08	16.60	13.51	13.58	15.23	15.60	58.50	87.25
39	RC 101	1030.88	13.16	12.75	10.16	13.49	12.34	10.50	53.50	77.00
40	GC 3	952.04	12.09	10.85	9.90	13.51	13.59	11.95	57.00	86.75
41	DC 17	2038.21	22.82	20.45	16.90	12.91	19.32	13.50	58.50	87.50
42	DC 16	2086.30	19.49	18.10	12.60	12.85	18.31	16.65	58.00	88.75
Mean		1585.99	17.07	17.67	13.54	13.52	16.58	12.12	53.18	81.80
Standard Deviation		463.94	3.62	3.44	1.56	1.32	1.84	2.30	3.75	4.88
Mean±1SD		2049.93	20.69	21.11	15.10	14.85	18.42	14.42	49.43	76.91
Number of families exceeding/subseeding Mean±1SD		7	6	6	5	5	5	5	7	5
Percentage of transgressive segregants (%)		19.44	16.67	16.67	13.89	13.89	13.89	13.89	19.44	13.89

4. CONCLUSION

From the current experiment, it can be concluded that a wide range of variability exists among the families of various crosses in F_4 generation. This variability can be effectively utilized for selecting desirable genotypes regarding several important economic traits like total yield (kg/ha), single plant yield (g), number of pods per plant, number of clusters per plant, test weight (g), number of seeds per pod and pod length (cm). The estimates of transgressive segregants further characterises the material for the frequency of genotypes exhibiting excellent performance for each yield and yield attributing traits. It is evident from the study that the material is highly variable for most of the characters under consideration and it contains ample amount of superior genotypes that can be selected to advance in the next generations and also can be used as excellent source of different yield and yield attributing traits.

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