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(Vigna unguiculata L. Walp)*

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# Genetic Variability Studies in F<sub>2</sub> and F<sub>3</sub> Segregating Populations Derived from Two Crosses of Cowpea (*Vigna unguiculata* L. Walp)

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## ABSTRACT

The success of most crop improvement programs depends upon the genetic variability and heritability of desirable traits. The magnitude and type of genetic variability helps the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. The genetic variability and heritability have been studied in F<sub>2</sub> and F<sub>3</sub> segregating generation derived from two crosses of cowpea. The high GCV and PCV were observed for seed yield per plant, number of pods per plant, plant height, number of clusters per plant and test weight in F<sub>2</sub> and F<sub>3</sub> of both the crosses. Heritability and genetic advance over mean were higher for plant height, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, test weight and seed yield per plant in both generation of both the crosses and these characters could be considered for selection to improve the yield as they had high genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance over mean (GAM). This information showed that there is sufficient genetic variability to justify selection for improvement in the cowpea. This result will be of immense practical uses for plant breeders to choose parent of interest to meet different breeding objectives.

**Key words:** *Vigna unguiculata* L. Walp, Genetic variability, Heritability, GCV, PCV, Genetic advance

Cow pea is also called as southern pea and black-eyed pea. It is an important multipurpose grain legume extensively cultivated in arid, semi-arid and subtropics. With its better amount of protein, it referred as poor man's meat. Cowpea grain contains 23.4 per cent protein, 1.8 per cent fat and 60.3 per cent carbohydrates and also it is a good source of vitamins and phosphorus [1]. In addition to this it has many uses like fodder, green manure, cover crop and as a leguminous crop it can fix atmospheric nitrogen about 150 kg per hectare helps in improving soil fertility [2]. Yield being a complex trait, is influenced by many other important yield contributing characters controlled by polygene and also environmental factors. Its improvement through breeding programme is determined by the magnitude and nature of their genetic variability and heritability [3-4]. The efforts to evolve better yielding genotypes are mainly aimed at exercising selection in segregating generation. The selection within a segregating generation partly may fulfill the objective in improving polygenic character like yield.

## MATERIALS AND METHODS

The present investigation was conducted in College of Agriculture, University of Agriculture and Horticultural Sciences, Shimoga during *kharif* 2015 and *summer* 2016 situated in southern transition agro climatic zone of Karnataka (Zone number 7). The experiment comprises of F<sub>2</sub> and F<sub>3</sub>. The experimental materials like F<sub>2</sub> and F<sub>3</sub> were developed by crossing two genetically diverse parents viz. UAHS 47 crossed with UAHS 34 for brown population and UAHS 58 crossed with North bold for white population. The experiment was laid out in augmented design. F<sub>2</sub> generation was raised in *kharif*-2015, while F<sub>3</sub> generation was raised in *summer*-2016. From F<sub>2</sub> 418 individual plants from white population and 112 plants from brown population were selected and planted in F<sub>3</sub> in plant to row method. The seeds were sowed with the spacing of 45cm between rows and 15 cm between plants with recommended package of practice. Observations on twelve traits viz days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, test weight and seed yield per plant were recorded. The data of individual plants in F<sub>2</sub> and mean values of families were analyzed with INDOSTAT software. PCV and GCV were classified as suggested by [5] that are, up to 10 percent is

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denoted as a low, 11-20 percent indicated as a moderate and more than 20 percent considered as a high. The heritability percentage was classified as low (0-30%), moderate (30-60%) and high (more than 60%) [6]. Genetic advance was computed by using the formula given by [6], the genetic advance as per cent mean was categorized as low up to 10 percent, 10 to 30 percent consider as a moderate and more than 20 percent indicate as a high this is suggested by [7].

## RESULTS AND DISCUSSION

The genetic parameters mean, range, phenotypic and genotypic coefficient of variation, heritability estimates and predicted genetic advance as percent mean for characters studied are presented in (Table 1-4). In the cross UAHS 58 × North bold high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for number of clusters per plant, number of pods per plant and

seed yield in both F<sub>2</sub> and F<sub>3</sub> generation [8]. The traits like number of primary branches, number of secondary branches, pods per cluster and test weight showed high phenotypic coefficient of variation (PCV) in F<sub>2</sub> and F<sub>3</sub> generation of this cross [8]. In the same cross the in F<sub>2</sub> higher GCV and PCV values were observed for test weight results [9]. Plant height showed high GCV and PCV in F<sub>2</sub> and moderate GCV and PCV in F<sub>3</sub> [8-9]. Moderate GCV was reported in F<sub>2</sub> and F<sub>3</sub> of this cross for the traits number of primary branches, number of secondary branches, pods per cluster and test weight these results are on par [8]. Moderate GCV and PCV were observed for the trait pod length and numbers of seeds per pod in both generation of this cross [10]. Low GCV and PCV were observed for the traits days to 50% flowering and days to maturity in both F<sub>2</sub> and F<sub>3</sub> of this cross [11]. Test weight showed high GCV and PCV in F<sub>2</sub> and moderate genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in F<sub>3</sub> of this cross [9].

Table 1 Variability parameters for twelve quantitative characters in F<sub>2</sub> generation derived from the cross UAHS 58 × North bold of cowpea

Characters	Mean	Range		GCV (%)	PCV (%)	h <sup>2</sup> (%)	GA	GAM
		Min	Max					
X <sub>1</sub> : Days to 50% flowering	43.88	40.00	52.00	5.92	6.24	90.01	5.08	11.57
X <sub>2</sub> : Days to maturity	73.85	71.00	84.00	5.32	5.61	89.83	7.67	10.39
X <sub>3</sub> : Plant height (cm)	45.2	20.00	75.00	23.48	23.71	98.04	21.65	47.75
X <sub>4</sub> : No. of Primary branches	5.66	2.00	8.00	18.66	22.09	71.33	1.84	32.75
X <sub>5</sub> : No. of Secondary branches	10.88	2.00	9.00	20.12	21.54	87.27	4.21	38.72
X <sub>6</sub> : No. of Clusters per plant	8.30	3.00	26.00	25.17	29.01	74.44	3.71	44.75
X <sub>7</sub> : No. of Pods per plant	15.31	4.00	42.00	24.85	25.57	94.45	7.62	49.76
X <sub>8</sub> : No. of Pods per cluster	2.18	1.00	5.00	17.54	24.22	42.36	0.51	23.53
X <sub>9</sub> : Pod length (cm)	11.68	7.00	19.00	13.28	15.05	77.79	2.81	24.13
X <sub>10</sub> : No. of Seeds per pod	11.62	6.00	16.00	15.23	16.84	81.76	3.3	28.38
X <sub>11</sub> : Test weight (g)	10.04	7.00	21.00	21.12	23.46	81.07	3.93	39.18
X <sub>12</sub> : Seed yield per plant (g)	21.85	9.00	48.00	36.48	36.98	97.32	16.2	74.15

Table 2 Variability parameters for twelve quantitative characters in F<sub>2</sub> generation derived from the cross UAHS 47 × UAHS 34 of cowpea

Characters	Mean	Range		GCV (%)	PCV (%)	h <sup>2</sup> (%)	GA	GAM
		Min	Max					
X <sub>1</sub> : Days to 50% flowering	40.43	40.00	50.00	13.15	13.84	90.26	10.4	25.73
X <sub>2</sub> : Days to maturity	74.04	70.00	82.00	3.33	3.78	77.73	4.49	6.06
X <sub>3</sub> : Plant height (cm)	40.96	30.00	85.00	21.75	21.96	98.14	18.19	44.4
X <sub>4</sub> : No. of Primary branches	4.02	2.00	8.00	25.17	32.16	61.26	1.63	40.59
X <sub>5</sub> : No. of Secondary branches	7.73	2.00	9.00	19.93	25.45	61.28	2.48	32.14
X <sub>6</sub> : No. of Clusters per plant	6.86	3.00	20.00	26.54	32.3	67.48	3.08	44.91
X <sub>7</sub> : No. of Pods per plant	11.87	4.00	32.00	26.58	29.73	79.95	5.81	48.97
X <sub>8</sub> : No. of Pods per cluster	2.13	2.00	4.00	19.26	28.46	45.79	0.57	26.85
X <sub>9</sub> : Pod length (cm)	13.98	9.00	21.00	15.04	17.76	71.66	3.66	26.22
X <sub>10</sub> : No. of Seeds per pod	11.46	6.00	22.00	15.23	19.4	61.63	2.82	24.63
X <sub>11</sub> : Test weight (g)	9.68	7.00	18.00	21.08	23.47	80.66	3.77	39.00
X <sub>12</sub> : Seed yield per plant (g)	16.4	7.00	36.00	19.93	25.45	61.28	2.48	32.14

In the cross UAHS 47 × UAHS 34 high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for plant height, number of primary branches, number of clusters per plant and seed yield per plant [8]. Number of secondary branches reported moderate GCV and high PCV in both F<sub>2</sub> and F<sub>3</sub> generation of this cross [12]. Moderate GCV and PCV were observed for the traits like days to 50% flowering, pod length and number of seeds

per pod were on par with [13]. Number of pods per plant and test weight showed high GCV and PCV in F<sub>2</sub> where as in F<sub>3</sub> moderate GCV and PCV [8]. Low GCV and PCV were reported for days to maturity in both generation of this cross were similar to the results of [10].

Heritability (h<sup>2</sup>) as a ratio of genotypic to phenotypic variance indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. Plant

height recorded highest heritability in  $F_2$  and  $F_3$  generation of both crosses followed by seed yield per plant and number of pods per plant in  $F_2$  and  $F_3$  of cross UAHS 58  $\times$  North bold showed high heritability in  $F_2$  and  $F_3$  generation of the cross UAHS 47  $\times$  UAHS 34 [14]. The higher values of  $h^2$  in generally are the reflection of closed value of respective phenotypic and genotypic variances and also indicate that selection of this character is useful in improving plant type. Heritability by itself does not provide indication of the amount of genetic progress that would results from selecting the best individuals rather it depends on the amount of genetic

variance. Therefore, genetic advance and genetic advance over mean gain importance in providing an idea of the amount of progress that can be achieved by selection. The higher genetic advance over mean was observed for seed yield and plant height in  $F_2$  and  $F_3$  generation of cross UAHS 58  $\times$  North bold where as in the cross UAHS 47  $\times$  UAHS 34 plant height and number of clusters per plant showed high genetic advance over mean in both  $F_2$  and  $F_3$  generation. Except the traits days to 50% flowering and days to maturity showed higher genetic advance over mean in  $F_2$  and  $F_3$  generation of both the crosses [15].

Table 3 Variability parameters for twelve quantitative characters in  $F_3$  generation derived from the cross UAHS 58  $\times$  North bold of cowpea

Characters	Mean	Range		GCV (%)	PCV (%)	$h^2$ (%)	GA	GAM
		Min	Max					
X <sub>1</sub> : Days to 50% flowering	46.85	41.00	54.00	4.63	5.79	64.01	3.57	7.63
X <sub>2</sub> : Days to maturity	76.17	72.00	84.00	2.78	3.27	71.94	3.7	4.85
X <sub>3</sub> : Plant height (cm)	42	30.00	60.00	15.26	15.45	97.61	13.05	31.07
X <sub>4</sub> : No. of Primary branches	4.93	2.00	7.00	17.27	21.98	61.79	1.31	27.98
X <sub>5</sub> : No. of Secondary branches	5.86	2.00	9.00	19.41	20.08	64.96	1.89	32.75
X <sub>6</sub> : No. of Clusters per plant	7.67	3.00	25.00	21.91	27.1	65.32	2.79	36.48
X <sub>7</sub> : No. of Pods per plant	15.04	9.00	43.00	23.29	24.22	92.46	6.94	46.14
X <sub>8</sub> : No. of Pods per cluster	2.2	1.00	4.00	15.8	25.06	39.75	0.47	20.52
X <sub>9</sub> : Pod length (cm)	11.08	6.50	19.00	12.28	14.38	72.96	2.39	21.62
X <sub>10</sub> : No. of Seeds per pod	11.11	6.00	16.00	14.05	15.94	77.72	2.83	25.53
X <sub>11</sub> : Test weight (g)	10.48	7.00	21.00	19	21.37	79.09	3.65	34.82
X <sub>12</sub> : Seed yield per plant (g)	20.6	11.20	33.40	25.91	26.29	97.1	10.83	52.6

Table 4 Variability parameters for twelve quantitative characters in  $F_3$  generation derived from the cross UAHS 47  $\times$  UAHS 34 of cowpea

Characters	Mean	Range		GCV (%)	PCV (%)	$h^2$ (%)	GA	GAM
		Min	Max					
X <sub>1</sub> : Days to 50% flowering	41.43	38.00	50.00	11.88	12.49	90.18	3.29	19.96
X <sub>2</sub> : Days to maturity	75.04	70.00	82.00	3.05	3.52	75.04	4.09	5.45
X <sub>3</sub> : Plant height (cm)	41.09	30.00	85.00	20.11	20.33	97.85	16.84	40.98
X <sub>4</sub> : No. of Primary branches	4.27	3.00	7.00	20.45	26.29	60.47	1.40	32.76
X <sub>5</sub> : No. of Secondary branches	5.96	3.00	9.00	18.82	24.06	61.16	1.80	30.32
X <sub>6</sub> : No. of Clusters per plant	7.37	4.00	20.00	24.78	31.33	62.56	2.97	40.38
X <sub>7</sub> : No. of Pods per plant	12.92	5.00	32.00	22.03	25.21	76.34	5.11	39.65
X <sub>8</sub> : No. of Pods per cluster	2.19	2.00	4.00	16.62	26.31	39.93	0.47	21.65
X <sub>9</sub> : Pod length (cm)	13.98	9.00	21.00	13.54	16.52	67.24	3.20	22.88
X <sub>10</sub> : No. of Seeds per pod	11.46	6.00	20.00	14.52	19.54	55.21	2.54	22.23
X <sub>11</sub> : Test weight (g)	9.81	7.00	21.00	16.66	19.53	72.78	2.87	29.28
X <sub>12</sub> : Seed yield per plant (g)	16.50	7.00	36.00	12.15	15.23	63.63	3.29	19.96

## SUMMARY

Variability studies in  $F_2$  and  $F_3$  generation of two cowpea crosses reported that high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for plant height, number of clusters per plant, number of pods per plant and test weight. High heritability coupled with high genetic advance percent mean was observed for plant height, number of clusters per plant,

number of pods per plant and test weight. Hence selection for these traits helps in improving yield. In the cross UAHS 58  $\times$  North bold family number 396 exhibited highest seed yield per plant and in UAHS 47  $\times$  UAHS 34 families 74 exhibited highest seed yield. The crosses were thrown the best transgressive families with improved seed size which has the major concern and superior families recovered from two crosses need to be forwarded to  $F_4$  and up to  $F_8$  generation through pedigree method then further released as a variety.

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