

Genetic variability, heritability and genetic advance in vegetable cowpea [*Vigna unguiculata* (L.) Walp]

■ G.K. SAPARA, R.M. JAVIA AND M.V. POKAR

SUMMARY

Studies on genetic variability, heritability and genetic advance were carried out with forty genotype of cowpea [*Vigna unguiculata* (L.) Walp] for 12 traits. Significant differences among the genotypes for all the characters studied except pod width indicating existence of ample variability in the experimental material for all the characters. High to moderate range of variation was observed for important yield components. The estimates of genotypic and phenotypic co-efficient of variation were high for number of pods per plant, 100 fresh seed weight, plant height, 10 pod weights and green pod yield per plant. The values of phenotypic co-efficient of variation were higher than their genotypic co-efficients of variation for all the characters indicating the influence of environmental factors. High heritability along with high genetic advance expressed as percentage of mean and high genotypic co-efficient of variation was observed for number of pods per plant, 100-fresh seeds weight, 10-pods weight, green pod yield per plant, plant height indicating scope for improvement by selection and breeding programme.

Key Words : Cowpea, Genetic variability, Heritability, Genetic advance

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Cowpea [*Vigna unguiculata* (L.) Walp] is an important multi-purpose grain legume extensively cultivated in arid and semi-arid regions of the world as pulses, vegetable, fodder as well as green manure crops. Being short duration and photo-insensitive, it can be grown successfully through out the year, in all types of soils and varying climatic conditions. Cowpea is a protein rich crop, demands more attention especially in a country like India, where majority of the vegetarians suffer for protein malnutrition. It contains 24 per cent protein, 60 per cent carbohydrate and 2 per cent fat besides being good sources of vitamins and phosphorus. The market demand also changing and there are ample

opportunities for cowpea to develop into a most popular vegetable crop made available throughout the year.

Nature and magnitude of variability is the basic foundation of any breeding programme. The major function of heritability estimates is to provide information on transmission of traits from the parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effects in phenotypic variation, thereby aiding in selection. Estimates of heritability can be used to predict genetic advance under selection so that the breeder can anticipate improvement from different types and intensities of selection. Yield is a complex entity and depends on the expression of a number of traits known as yield components.

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MATERIAL AND METHODS

Forty vegetable cowpea genotypes were selected for the present investigation. Randomized Block Design with three replications was used. The materials were grown during summer season at vegetable research station Junagadh Agricultural University. A single row plot of 4.5 m length

and plant were kept between 60 and 30 cm, respectively. The recommended package of practices was followed for cultivation. The mean values of these observations were used to determine the range, mean, sum of square and test of significance. The mean values of five randomly selected plants were used for analysis of variance for all the characters using method described by Panse and Sukhatme (1984). Phenotypic and genotypic co-efficient of variation were worked out according to Burton (1952). Heritability in broad sense, which is the ratio of genotypic variance and phenotypic variance, was calculated by using the formula suggested by Allard (1960). The expected genetic advance under selection (Gs) at 5 per cent selection intensity was estimated by using formula suggested by Allard (1960).

The genetic advance expressed as percentage of mean was calculated as under:

$$\text{Genetic advance as percentage of mean} = \frac{\text{Genetic advance (GA)}}{\text{Mean of character (X)}} \times 100$$

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed significant

differences among the genotypes for all the characters studied. It indicates the presence of sufficient variability in the material investigated in the present study. Availability of sufficient variability in the material handled by the breeder is of immense importance for the success of any breeding programme. Wide range of phenotypic variation was observed for plant height, green pod yield per plant, 10-pod weight and number of pods per plant. Similar results were recorded by Pan *et al.* (2004) for fresh pod yield per plant, 10-pods weight, number of pods per plant and Venkatesan *et al.* (2003) for plant height, pod yield per plant and number of pods per plant. While moderate range of variation was registered for days to 50 per cent flowering, days to 1st pod picking, pod length and 100-seed weight. The characters *viz.*, number of primary branches per plant, pod width, number of fresh seeds per pod and fresh crude protein content exhibited low variation.

The genetic parameters *viz.*, genotypic and phenotypic co-efficients of variation, heritability in broad sense and genetic advance along with mean and range of different characters are presented in Table 2.

High phenotypic co-efficient of variation (PCV) was

Table 1: Analysis of variance for 12 characters in vegetable cowpea

Source	df	Green pod yield per plant (g)	Days to 50% flowering	Days to 1 st pod picking (vege-table)	No. of primary branches per plant	Plant height (cm)	Pod length (cm)	Pod width (cm)	No. of pods per plant	10-pods weight (g)	No. of fresh seeds per pod	100-fresh seeds weight (g)	Fresh pod crude protein content (%)
Replications	2	1802.26	6.3	211.57	0.196	428.43	0.086	0.0001	46.703	76.67	15.60	1.041	0.004
Genotypes	39	4225.98**	96.22**	121.60**	3.65**	8874.71**	21.84**	0.012	314.44**	590.34**	5.41**	86.41**	24.80**
Error	78	281.87	4.90	8.33	0.066	96.605	0.732	0.002	19.625	8.93	0.87	2.249	0.056

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2 : Phenotypic and genotypic co-efficients of variation, heritability (b.s.), genetic advance and genetic advance expressed as percentage of mean for 12 characters in 40 vegetable cowpea genotypes

Characters	Range of variation	Mean	Phenotypic co-efficient of variation (%)	Genotypic co-efficient of variation (%)	Heritability in broad sense (%)	Genetic advance	Genetic advance expressed as percentage of mean
Green pod yield per plant (g)	57.27 - 213.53	128.01	31.22	28.33	82.30	67.78	52.95
Days to 50% flowering	48.33 - 78.68	62.15	9.57	8.88	86.10	10.55	16.97
Days to 1 st pod picking (vegetable)	57.67 - 92.67	71.55	9.49	8.59	81.90	11.46	16.02
No. of primary branches per plant	3.13 - 7.93	5.49	20.46	19.12	94.80	2.19	39.89
Plant height (cm)	74.20 - 312.33	186.12	29.54	29.06	96.80	109.64	58.91
Pod length (cm)	11.95 - 24.07	17.65	15.79	15.03	90.60	5.20	29.46
Pod width (cm)	0.51 - 0.75	0.60	11.82	9.78	68.40	0.10	16.67
No. of pods per plant	7.49 - 53.07	28.12	38.61	35.25	83.40	18.64	66.28
10-pods weight (g)	22.00 - 85.00	48.32	29.47	28.81	95.60	28.04	58.03
No. of fresh seeds per pod	10.00 - 15.40	12.39	12.46	9.93	63.60	2.02	16.30
100-fresh seeds weight (g)	10.83 - 41.17	17.25	31.92	30.71	92.60	10.50	60.87
Fresh pod crude protein content (%)	15.40 - 26.13	21.10	13.66	13.61	99.30	5.90	27.96

observed for number of pods per plant followed by 100-fresh seeds weight, green pod yield per plant, plant height and 10-pods weight. Similar result were recorded by Selvam *et al.* (2000) for number of pods per plant, Venkatesan *et al.* (2003) for 100-seeds weight, Vardhan and Savithamma (1998) for green pod yield per plant, Nigude *et al.* (2004) for plant height and Narayankutty *et al.* (2003) for 10-pods weight. Certain characters like number of primary branches per plant, pod length, number of fresh seeds per pod, fresh crude protein content and pod width exhibited moderate values of this estimate. Nigude *et al.* (2004) also reported the moderate PCV for pod length and number of seeds per pod. Two character *viz.*, days to 50 per cent flowering and 1st pod picking showed narrow phenotypic co-efficient of variation (PCV).

High genotypic co-efficient of variation (GCV) was observed for number of pods per plant, 100-fresh seeds weight, plant height, 10-pod weight and green pod yield per plant. High GCV thereby suggesting that these characters could be improved genetically. Similar magnitude of these parameters were also found by Pal *et al.* (2003) for 10-pods weight, plant height, number of pods per plant and green pod yield per plant, Venkatesan *et al.* (2003) for 100-seeds weight and Pan *et al.* (2004) for 10-pods weight.

The co-efficient of variation does not offer full scope to estimate the heritable variation. The relative amount of heritable portion of variation is assessed with the help of heritability estimates and genetic advance expressed as percentage of the mean (genetic gain). The success of selection depends on the breeding value of a genotype recognized from its phenotypic expression. The degree of correspondence between phenotypic value and breeding value for a character is measured by heritability, which indicates reliability of the former as a guide to the later. The heritability expresses the proportion of total variance that is attributed to the average effect of genes and determines the degree of resemblance between relatives. It is a good index of transmission of characters from parents to their off-springs (Falconer, 1981). High values of heritability in broad sense are helpful in identifying the appropriate character for selection and enabling the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits (Johnson *et al.*, 1955).

Moderate to high estimates (>63%) of broad-sense heritability were noticed for all the character under studies. These results are in agreement with those of Nigude *et al.* (2004); Venkatesan *et al.* (2003) and Pan *et al.* (2004). High heritability estimates indicated that the characters were least influenced by the environmental effects. This also suggested that the phenotypes were the true representative of their genotypes of these traits and the selection based on phenotypic value could be reliable. In a crop improvement programme the highly heritable characters may be selected early in the programme and selection of characters with low

heritability may be postponed till they are close to complete homozygosis (Sakai, 1951). Characters showing high heritability values indicate that they have more number of additive factors (Panse, 1957).

High values of genetic advance expressed as per cent of mean were exhibited by number of pods per plant (66.28 %), 100-fresh seeds weight (60.87 %), plant height (58.91 %), 10-pods weight (58.03 %) and green pod yields per plant (52.95 %) (Table 2). High/moderate estimates of these parameters were also reported by Nigude *et al.* (2004), Narayankutty *et al.* (2003) and Pal *et al.* (2003). Whereas the remaining characters manifested moderate to low genetic advance as percentage of mean.

The investigation has shown that the most important economic character like green pod yield can be raised by 67.78g with a selection pressure of 5 per cent intensity and this improvement would be 52.95 per cent of the mean yield. Another important character number of pods per plant also showed the good scope of improvement. Number can be increased by 18.64 and 66.28 per cent of the mean of number of pods per plant. Good scope of improvement of 100-fresh seeds weight was also evident due to possibility of 10.50g increases with 60.87 per cent and plant height 109.64 cm increased with 58.59 per cent genetic advance expressed as percentage of mean. Also 10-pods weight was evident due to possibility of 28.04 increases with 58.03 per cent. There was ample scope of improvement of these characters which exhibited high values of genetic advance expressed as percentage of mean.

Number of primary branches per plant, pod length and fresh pod crude protein content exhibited moderate genetic advance (GA %).

Very high estimates of heritability in broad sense coupled with moderate/high genetic advance as percentage of mean were expressed by number of pods per plant, 100-fresh seed weight, plant height and 10-pods weight characters which might also be ascribed to additive gene action controlling the expression of the traits and substantial improvement for these traits could be achieved through direct selection. High estimates of heritability with low genetic advance as percentage of mean were observed for days to 50 per cent flowering, 1st pod picking, pod width and number of fresh seeds per pod. Similar results were reported by Selvam *et al.* (2000) for days to 50 per cent flowering, Pal *et al.* (2003) for pod width and seeds per pod. It may be inferred that these characters were conditioned by non-additive gene action and presence of high genotype x environment interaction (Munshi *et al.*, 1993). The heritability is being exhibited due to favourable influence of the environment rather than genotype and simple selection would not be rewarding. As such, progeny or family testing is to be practiced for improvement of these traits. However, these characters can be improved by selecting transgressive segregants from

segregating generations.

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