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## Bamji Rukhsar C

Department of Genetics and  
Plant Breeding, JAU, Junagadh,  
Gujarat, India

## Pithia MS

Research Scientist (Chickpea),  
Pulses Research Station, JAU,  
Junagadh, Gujarat, India

## Lata Raval

Department of Genetics and  
Plant Breeding, JAU, Junagadh,  
Gujarat, India

## Patel Krina N

Associate Research Scientist,  
Department of Genetics and  
Plant Breeding, JAU, Junagadh,  
Gujarat, India

## Corresponding Author:

### Bamji Rukhsar C

Department of Genetics and  
Plant Breeding, JAU, Junagadh,  
Gujarat, India

## Genetic variability, heritability and genetic advance studies in cowpea (*Vigna unguiculata* (L.) Walp.)

Bamji Rukhsar C, Pithia MS, Lata Raval and Patel Krina N

### Abstract

The present investigation was carried out to access genetic variability, heritability and genetic advance with a set of forty two genotypes of cowpea. A high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for number of pods per plant, seed yield per plant, 100-seed weight, plant height and number of clusters per plant. High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for number of pods per plant, seed yield per plant, 100-seed weight, number of clusters per plant. This may be attributed to the preponderance of additive gene action and passes high selective value and thus, selection pressure could profitably be applied on these characters for their rationale improvement. Hence, these characters may be simultaneously selected for developing better quality high yielding genotypes of cowpea.

**Keywords:** Cowpea, genetic variability, heritability, genetic advance

### Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is a diploid species with  $2n = 2x = 22$  chromosomes. It is a self-pollinated crop, with natural cross-pollination of up to one percent. Cowpea belongs to class *Dicotyledonea*, order *Fabales*, family *Fabaceae*, subfamily *Faboideae*, tribe *Phaseoleae*, subtribe *Phaseolinae*, and genus *Vigna* (Pasquet, 2001) [9]. It is native of Central Africa. In Indian context, it is a minor pulse cultivated mainly in arid and semi-arid tracts of Rajasthan, Karnataka, Kerala, Tamilnadu, Maharashtra and Gujarat. It is early, multi-seasonal and multipurpose crop. It has multifarious uses like as fodder, cover crop and green manure and provides high quality protein in the form of vegetable and pulse to human diet. Its young leaves, pods and seeds contain vitamins and minerals which have fueled its usage for human consumption and animal feeding (Nielson *et al.*, 1997) [7]. It is considered as one of the oldest legumes and referred as “Poor man’s meat” because of its high protein (20-25%) source for human and livestock (Steele, 1972) [12]. It is a drought tolerant crop and thrives in warm weather (21- 35°C) and well adapted to the drier regions of the tropics, where other food legumes do not perform well. Bestowed with series of merits, cowpea is also known for some biological bottle necks of poor productivity due to inefficient plant types with less and slow conversion of dry matters to grain. Therefore, there is an urgent need to develop high yielding varieties in cowpea. For this, the knowledge on variability available in the population due to genetic and non-genetic causes is a key factor that determines the amount of progress expected from selection. Basic information on genetic parameters for economically important traits including seed yield is necessary for initiating a breeding programme. This coupled with estimates of heritability and genetic advance help the breeder to anticipate the extent of improvement possible in yield and other characters. Keeping this view in mind the present study was conducted for further use in the cowpea improvement programme.

### Materials and Methods

Forty two genotypes were selected to access genetic variability, heritability and genetic advance in cowpea. These genotypes were planted in Randomized block design with three replications. The material was grown at Pulses Research Station, Junagadh Agricultural University, Junagadh. A single row of 4 m length and plants were spaced at 45 x 10 cm. The recommended package of practices was followed for cultivation. In each replication, observations were recorded on five randomly selected competitive plants and their mean values were used for statistical analysis. The observations were recorded on 11 morphological characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of

primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight and seed yield per plant. Days to 50 per cent flowering and days to maturity were recorded on plot basis. Analysis of variance was carried out as per methodology given by Panse and Sukhatme (1985) [8]. Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated by the formula given by Burton and De Vane (1953) [4], heritability in broad sense ( $h^2$ ) and genetic advance given by Allard (1960) [2].

## Results and Discussion

The analysis of variance (Table 1) revealed that the mean squares due to genotypes were significant for 11 characters indicating the presence of sufficient amount of genetic variability among genotypes for seed yield per plant and other yield contributing traits. In a breeding programme, quantification of genetic variability of a population is a determining factor since it reveals the genetic structure of the populations.

The mean, range of variation, coefficient of range, phenotypic (PCV) and genotypic (GCV) coefficients of variation heritability (broad sense), genetic advance and genetic advance expressed as percentage of mean are presented in Table 2. The present experimental material showed high phenotypic range of variation for seed yield per plant followed by number of pods per plant, 100-seed weight, number of clusters per plant, number of pods per cluster and

number of seeds per pod. These results are in agreement with those of Ajayi *et al.* (2014) [1] and Havaraddi and Deshpande (2018) [5]. The results revealed that the phenotypic coefficient of variation was slightly higher than their corresponding genotypic coefficient of variation due to partly interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for number of pods per plant (41.34 and 40.48%), seed yield per plant (35.14 and 34.15%), 100-seed weight (29.46 and 29.31%), plant height (28.28 and 27.45%) and number of clusters per plant (27.25 and 26.97%) similar results were in accordance with Baranda *et al.* (2018) [3], Manju Devi and Jayamani (2018) [6] and Singh *et al.*, (2018) [11]. Whereas, low PCV and GCV was recorded for days to 50 per cent flowering (8.33 and 8.10%) and days to maturity (5.54 and 5.34%).

High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for number of pods per plant (95.90 and 81.64%), seed yield per plant (94.50 and 68.37%), 100-seed weight (99.00 and 60.07%), plant height (94.30 and 54.90%) and number of clusters per plant (98.00 and 54.98%) similar findings were in accordance with Sabale *et al.* (2018) [10] and Tatis *et al.* (2018) [13]. High heritability with moderate genetic advance as per cent of mean was recorded for days to 50 per cent flowering (94.62 and 16.23%) and days to maturity (93.10 and 10.61%).

**Table 1:** Analysis of variance showing mean squares for different characters in cowpea

Mean squares												
Source of variation	d.f.	Days To 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
Replications	2	18.627*	0.865	116.481	0.107	1.007*	0.001	7.722	0.705	0.310	0.225	0.983
Genotypes	41	81.007**	55.418**	679.699**	0.741**	15.449**	0.326**	118.919**	12.742**	8.380**	28.824**	38.565**
Error	82	4.359	3.849	39.073	0.192	0.316	0.066	4.917	0.985	2.204	0.295	2.136

\*, \*\* Significant at 5% and 1% levels, respectively

**Table 2:** Mean, Range of variation, coefficient of range, phenotypic (PCV) and genotypic (GCV) coefficients of variation heritability (broad sense), genetic advance and genetic advance expressed as per cent

Characters	Mean	Range	Coefficient of Range (%)	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability (Broad Sense) (%)	Genetic advance	Genetic advance expressed as percentage of mean
Days to 50 per cent flowering	62.39	52.67 - 73.00	16.18	8.33	8.10	94.62	10.13	16.23
Days to maturity	77.63	73.00 - 87.33	8.94	5.54	5.34	93.10	8.24	10.61
Plant height (cm)	53.23	36.57 - 106.20	48.77	28.28	27.45	94.30	29.23	54.90
Number of primary branches per plant	2.39	1.47 - 3.27	37.97	20.78	17.89	74.10	0.76	31.72
Number of clusters per plant	8.33	4.80 - 13.27	46.87	27.25	26.97	98.00	4.58	54.98
Number of pods per cluster	1.84	1.07 - 2.60	41.69	17.88	15.97	79.80	0.54	29.39
Number of pods per plant	15.23	7.00 - 31.70	63.82	41.34	40.48	95.90	12.43	81.64
Pod length (cm)	12.87	9.91 - 16.90	26.07	16.01	15.38	92.30	3.92	30.43
Number of seeds per pod	10.36	5.67 - 14.00	42.35	16.14	13.85	73.70	2.54	24.50
100-seed weight (g)	10.52	6.13 - 24.22	59.60	29.46	29.31	99.00	6.32	60.07
Seed yield per plant (g)	10.20	3.22 - 23.60	75.99	35.14	34.15	94.50	6.98	68.37

## Conclusion

From the study of genetic variability, heritability and genetic advance it can be concluded that phenotypic selection for number of pods per plant, seed yield per plant, 100-seed weight, number of clusters per plant, plant height, number of primary branches per plant, pod length, number of pods per cluster and number of seeds per pod would be more rewarding for improvement of seed yield in cowpea. Therefore, plant

breeder should focus his attention on above said characters in cowpea improvement programme.

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