

## Studies on Genetic Variability and Heritability for Different Traits in Cowpea [*Vigna unguiculata* (L.) Walp]

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### ABSTRACT

The present investigation entitled was carried out at experimental farm of Department of Horticulture, AKS University, Satna (M.P.) during Kharif season of year 2019-20. The experiment was conducted in Randomized Block Design having 12 treatments i.e. 12 genotypes of Cowpea in three replications. Twelve diverse varieties of Cowpea collected from different sources and all the genotypes are grown with three replications in 2.4 m<sup>2</sup> plot and the plant keeping 60 x 25 cm maintained between Row and Plant distance. They were evaluated for growth yield and quality attribute for all the traits. High heritability (77.44%) coupled with high genetic advance (52.08) observed for green pod yield per plant, very high heritability (94.47%) for plant height at final harvest indicated that phenotypic selection would be effective for genetic improvement in these traits. High magnitude of phenotypic GCV and PCV (i. e. >20 per cent) were observed for Economic yield (kg/plot) (71.97 per cent and 81.76 per cent, respectively), followed by Biological yield (kg/plot) (61.59 and 79.96 per cent, respectively). whereas, the moderate magnitude of GCV and PCV (10-20 per cent) were observed for Harvest index (19.78 and 35.53 per cent), respectively) and Plant height (19.52 and 25.86 per cent), respectively. The low magnitude GCV (<10 per cent) was also observed for the character Number of primary branches/plant (8.60 and 14.49 per cent, respectively) Days to 50% flowering (5.10 and 6.88 per cent, respectively), Days to 1<sup>st</sup> flowering (1.22 and 2.10 per cent, respectively).

**Keywords:** Cowpea, Heritability, Genetic Variability, Genetic Advance.

### INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) is a large seeded legume developed for its protein-rich green pods, and grains, by the resource

poor farmers from underdeveloped and developing African and Asian nations. Cowpea belongs to family Fabaceae, and *Vigna* type.

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Sort Vigna is a pantropical class consisting of eight subgenera and approximately 150 genera, a large portion of which is found in Asia and Africa. Only seven kinds of Vigna are delivered as pulse crops, two sorts of African subgenus Vigna, *Vigna unguiculata* and *Vigna subterranea*, and five Asian subgenera *Ceratropis*, *Vigna radiata*, *Vigna mungo*, *V. aconitifolia*, *V. angularis*, and *V. umbellata*. *Vigna unguiculata*, *V. mungo* and *Vigna radiata* are amongst the widely developed yields. *Unguiculata Vigna L.* Walp originated in Africa and happens in dry semi-bone tropics spanning portions of Asia, Africa, Southern Europe, the Southern United States, and Central and South America (Singh, 2005, & Timko et al., 2007). India is the most dynamic cowpea-producer in Asia. With a cumulative yield of 3.2 million tons (Egbadzor, 2014). Cowpea has delivered over 11.2 million hectares worldwide.

Cowpea plants are impenetrable to drought, high temperatures and soil toxicity, and their ability to fix air nitrogen contributes to quick development in tropical climates with low rainfall, high temperatures and low fertility soils (Ortiz, 2003). Cowpea is grown throughout India in both summer and rainy season. It is cultivated for green peas, dry seeds, and forage. Dry seeds are rich in protein therefore, it is called as vegetable meat. Once developed for dry beans, it's called "black eye pea" or "kaffir pea" or "southern bean." Sortiments of green cases are known as catjang bean, asparagus bean, or yard long bean. This is also utilized as green manure crop. Characterization of the available germplasm is a crucial initial advance in promoting breeding efforts; particularly in selecting suitable parental material, it benefits a plant raiser.

To increase the yield potential of an existing harvest, it is critical to consider the variability in the formulation and acceleration of the breeding procedure the resulting heritability, genetic progression and coefficient of genotypic and phenotypic variation within a yield would propel the selection of better genotypes relative to the

proportion of genetic variability Since various economic qualities are quantitative in nature and highly influenced by the environment, breeding accomplishment is driven by the combination of genetic and non-genetic variations; if the relatives inherit selection prevalence, it is useful to partition the total variability into heritable and non-heritable components for overview. The best possible selection of genotypes for desirable traits is determined by heritability tests, along with genetic development. The point of the current investigation was therefore to establish the genetic variation in the cowpea genotypes and to isolate it into heritable and non-heritable constituents.

### MATERIALS AND METHODS

To estimate genetic variability and heritability studies, field experiment was conducted in *kharif* 2019. The seeds of 12 genotypes were planted in Randomized Block Design (RBD) with three replications are presented in Table 1. In this experiment, fourteen characters viz., Plant height (cm), Number of primary branches/plant, Days to 1<sup>st</sup> flowering, Days to 50% flowering, Number of pods/plant, Green pod length (cm), Dry pod length (cm), Economic yield (kg/plot), Biological yield (kg/plot), Number of seeds /pod, 100 Seed weight (g), Pod yield /plant (kg) and Harvest index.

Finally, data was subjected to statistical analysis by applying statistical procedure for study of genetic variability, genotypic and phenotypic variance, coefficient of variance, heritability, genetic advance for all thirteen characters whereas, coefficient and clustering pattern was studied on the basis of observations taken at the time of harvesting for thirteen characters. The data collected from various observations recorded in the field were to statistical of analysis by standard analysis of variance technique. (Panse & Sukhatme, 1967).

Cowpea's genetic overhaul rehearsals aim to develop tolerant dry season using viable phosphorus, bacterial blight, and healthy infection lines by leveraging available genetic

assets and deploying back and forth breeding tools that will boost genetic gain by sub-Saharan African farmers when established. Variance to the phenotypes variance and is expressed in percentage and calculated as per the formula suggested by Burton and Devance, (1953).

Genetic variability parameters were calculated according to Johnson et al. (1955), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and genetic development in level of mean. In the broadest sense, heritability was calculated according to Lush's (1940) technique.

### RESULTS AND DISCUSSION

The result obtained showed that phenotypic coefficient of variance was in general higher than the genotypic coefficient of variance for all the characters. It is due to presence of substantial influence of environmental factors besides the genetic variation for expression of these traits are summarised and presented in Table 2. High magnitude of phenotypic GCV and PCV (*i. e.* >20 per cent) were observed for Economic yield (kg/plot) (71.97 per cent and 81.76 per cent, respectively), followed by Biological yield (kg/plot) (61.59 and 79.96 per cent, respectively). whereas, the moderate magnitude of GCV and PCV (10-20 per cent) were observed for Harvest index (19.78 and 35.53 per cent), respectively and Plant height (19.52 and 25.86 per cent), respectively. The low magnitude GCV (<10 per cent) was also observed for the character Number of primary branches/plant (8.60 and 14.49 per cent, respectively) Days to 50% flowering (5.10 and 6.88 per cent, respectively), Days to 1<sup>st</sup> flowering (1.22 and 2.10 per cent, respectively). In the present study, heritability estimate in broad sense was calculated for tuber yield and its components. The obtained value of heritability for each character was grouped into high (> 61 per cent), moderate (31 to 60 per cent) and low (< 30 per cent). Estimate of heritability was recorded high for the character Pod yield /plant (kg) (79.97 per cent) followed by Economic yield (kg/plot) (77.48 per cent), Number of seeds /pod (69.56

per cent) and Green pod length (cm) (67.38 per cent) exhibited the moderate heritability. However, low heritability was observed in Harvest index (31.01 per cent), Days to 1<sup>st</sup> flowering (33.69 per cent) and Number of primary branches/plant (35.21 per cent). These findings are in accordance with the findings by Gerrano et al. (2015), Sound Magashie (2017) and Gupta et al. (2019).

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Genetic advance was worked out as percentage of mean for pod yield and its components which is presented in Table- 4.7 and Fig 9. Genetic advance is important to find out the genetic gains likely to be achieved in the next generation. These are classified as high (> 20 per cent), medium (10 to 20 per cent) and low (0-10 per cent). The success of genetic advance under selection mainly depends upon genetic variability, heritability and selection intensity. Highest estimates of genetic advance as percentage of mean were obtained for characters namely Economic yield (130.50 per cent), Pod yield /plant (98.36 per cent). The high value of genetic advance for these traits showed that these characters are governed by additive genes effect and selection will be rewarding for the further improvement of such traits. However, the low genetic advance as percent of mean was observed for the characters such as Number of primary branches/plant (10.51 per cent), Days to 50% flowering (7.79 per cent) and Days to 1<sup>st</sup> flowering (1.46 per cent). This indicates the presence of non-additive gene effects. In agreement to the above results, Owusu et al. (2018) recorded the high heritability and genetic advance for high grain yield.

Based on overall findings of mean performance for various yield and its attributing traits, cowpea genotypes *viz.* Ankur Gomati (vu-89), Arka Garima, Lobia -VU- 5, Betul White and Cowpea (Gayatri V.U- 99) possessed highest plant height, Ankur Gomati (VU-89) and Arka Garima possessed highest plant height (at Flowering). The genotypes *viz.* Ankur Gomati (vu-89), Arka Garima, Lobia -

VU- 5, Betul White and Cowpea (Gayatri V.U- 99) had maximum Number of primary branches/plant. The genotypes namely Ankur Gomati (vu-89), Arka Garima, Lobia -VU- 5, Betul White and Cowpea (Gayatri V.U- 99) had maximum Days to 1<sup>st</sup> and flowering Days to 50% flowering, whereas Ankur Gomati (vu-89) and Arka Garima had highest Number of pod/plant. The above findings indicate that the characters with high magnitude of GCV and PCV *viz*: Economic yield (kg/plot), Biological yield (kg/plot) can be utilized for improvement as the population possesses considerable variability for these characters. However, the moderate GCV and PCV as recorded for the traits *viz*. Harvest index and Plant height indicates the existence of some variability in the population for these characters. Therefore, selection for above traits can also be beneficial for improvement. High heritability recorded for number of Pod yield /plant, Economic yield (kg/plot), Number of seeds /pod and Green pod length (cm) indicated that these characters are less influenced by environmental fluctuations and governed by the additive gene effects that are substantially contributing towards the expression of these traits. However, rest of the traits seems to be governed by non additive gene effects. Hence, selection for these traits will lead to accumulation of more desirable genotypes. The analysis of variance indicated the existence of sufficient amount of variability

among genotypes for all the characters. The phenotypic variance was in general higher than the genotypic variance for all the characters. Among different yield attributing characters studied, Number of pod/plant had the highest magnitude of PCV (44.85 per cent) and GCV (30.49 per cent). The estimates of heritability revealed that characters namely, Economic yield (kg/plot) followed by Number of seeds /pod, 100 Seed weight (g) and Green pod length (cm) were recorded with high heritability. The highest genetic advance as percentage of mean was recorded for Economic yield (kg/plot) and Pod yield /plant (kg). Ishiyaku et al. (2005) reported similar findings for 100-seed weight.

On the basis of the results the phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied which suggests that the phenotypic expression of characters is largely influenced by the prevailing environmental conditions. The estimates of heritability were recorded high for the characters *Viz*, Economic yield (kg/plot) followed by Number of seeds /pod, 100 Seed weight (g) and Green pod length (cm) indicating that these characters are governed by additive gene effect and are less influenced by environment and hence, selection for these characters, if found positively associated with yield will be beneficial in improvement of Cowpea.

**Table 1: Estimates of GCV, PCV, Heritability and Genetic Advance in different genotypes of Cowpea**

S. No.	Parameters	GCV (%)	PCV (%)	Heritability (H <sup>2</sup> b) %	Genetic Advance K=20.6	Genetic Advance as % of mean
1.	Plant height (cm)	19.52	25.86	56.99	1.92	30.36
2.	Number of primary branches/plant	8.60	14.49	35.21	0.73	10.51
3.	Days to 1 <sup>st</sup> flowering	1.22	2.10	33.69	0.63	1.46
4.	Days to 50% flowering	5.10	6.88	55.01	5.75	7.79
5.	Number of pod/plant	30.49	44.85	46.22	1.91	42.71
6.	Green pod length (cm)	15.89	19.36	67.38	4.77	26.88
7.	Dry pod length (cm)	15.72	20.75	57.40	4.21	24.54
8.	Economic yield (kg/plot)	71.97	81.76	77.48	0.29	130.50
9.	Biological yield (kg/plot)	61.59	79.96	59.33	0.54	97.73
10.	Number of seeds /pod	21.89	26.24	69.56	4.44	37.60
11.	100 Seed weight (g)	25.64	31.16	67.71	2.84	43.46
12.	Pod yield /plant (kg)	53.39	59.71	79.97	0.26	98.36
13.	Harvest index	19.78	35.53	31.01	0.08	22.69

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