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Genetic Variability Studies for Yield and Yield Components in Cowpea [*Vigna unguiculata* (L.) Walp]

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Authors Contribution

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Abstract

Experimental studies were conducted to evaluate 54 genotypes of cowpea for genetic variability, heritability and genetic advance among varieties for 17 characters under study. The estimates of phenotypic coefficient of variation for all parameters were higher than that of the genotypic coefficient of variation suggest that there was an environmental influence on the performance of the genotypes. A high heritability value coupled with high genetic advance as per cent has been noticed in the parameters like number of nodes per plant, seed yield, biomass per plant, haulm yield, number of branches per plant, number of seed per pod, peduncle length, pod length, plant height, 100 seed weight, NDVI, Cu, Mn, Zn and Fe, content indicate the presence of a weak or slight environmental influence and prevalence of additive gene action in gene expression. Characters namely days to 50 per cent flowering and SPAD recorded a high heritability with low and moderate genetic advance, respectively suggesting the prevalence of non additive gene action. The information on genetic variability among the cowpea genotypes studied showed that there is sufficient genetic variation for all the traits and considerable progress in cowpea breeding could be achieved by exploiting these traits.

Keywords : Cowpea, Variability, Heritability, Genetic advance

Cowpea [*Vigna unguiculata* (L.) Walp], an autogamous leguminous crop belongs to the leguminosae family (Mackie and Smith, 1935) with a chromosomal number of 2n = 2x = 22 (Darlington and Wylie, 1955). It is known as Lobia, Southern pea, Blackeye pea, Chawalie and Mulatto-Gelato in different parts of the world. This pulse crop is rich in protein, vitamins and minerals and is primarily used for grain, vegetable, animal feed as well as green manure crop. The nutritive value of 100 g, Dietary Fiber (10.6 g), Folates (633 g), Niacin (2.075 mg), Pantothenic acid (1.496 mg), Pyridoxine (0.357 mg), Riboflavin (0.226 mg, Thiamin (0.853 mg) and Vitamin-C (1.5 mg) (USDA National Nutrient data base). Fresh seeds of cowpea are consumed as a vegetable and dried seeds used to make dal, flour, biscuits, and a variety of other foods. For animals, it's an excellent source of protein and other essential minerals. Further, cowpea is one of the most adaptable, drought-tolerant, and versatile pulse crop. The worlds total pulse production area is 78 million hectares, with a yield of 70 million tonnes and a productivity of 908 kg per hectare (Anonymous, 2012). This crop is most commonly grown in semi-arid and arid regions worldwide. Though cowpea is one of the vigorously growing drought tolerant pulse, its low productivity is one of the basic constraints. Cowpea exhibits considerable amount of morphological diversity. However, the growth circumstances and grower preferences for each variety differ from region to region (Padulosil, 1997). Availability of heterogeneity in the breeding material would increase the probability of evolving desired genotypes. The higher the genetic variability, the more likely it is that superior genotypes will be selected. The genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide an indication of the level of variability existing in a genetic population. Estimates of genetic characteristics, such as heritability and genetic advance, aid the plant breeder in selecting elite genotypes from various genetic populations. Genetic divergence across parents is essential for selection, as the segregating generations have greater variation that can be utilized in selecting superior genotypes (Nimbalkar *et al.,* 2017). With these considerations the present investigation was conducted to assess the genetic variability, heritability and genetic advance of cowpea genotypes.

MATERIAL AND METHODS

The experimental material, comprised of 54 genotypes of cowpea including 4 checks, were grown during *rabi* 2021 in a Randomized Complete Block Design with three replications at L block, GKVK, UAS, Bangalore. Data were recorded on five randomly selected plants for days to 50 per cent flowering, plant height, number of branches per plant, biomass per plant, number nodes per plant, pod length, peduncle length, number of seeds per pod, 100 seed weight (g), Seed Yeild (Kg/ha), haulm yield per plant, micronutrients (Cu, Zn, Fe, Mn), Soil Plant Analysis Development (SPAD) and Normalized Difference Vegetation Index (NDVI). The genetic and PCV were calculated according to Burton and Devane (1953), Heritability according to Hanson *et al.* (1956) GA as per Robinson *et al.* (1949).

RESULTS AND DISCUSSION

Genetic Parameters

The major genetic parameters, such as analyses of variance, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability and genetic progress, were recorded and calculated across 54 genotypes (Fig. 1) for 17 different characters. This research demonstrated that was slightly larger than the indicating the apparent relationship between two traits not just attributable to genetics but partly to the environment favorable influence (Fig: 3).

Analysis of Variance

The analyses of variance revealed that genotype-based mean of squares for all characters were significant (Table 1). It demonstrated that there is a high degree of genetic heterogeneity among the genotypes studied. Quantifying the genetic diversity

Fig. 1 : Field evaluation of cowpea genotypes

Fig. 2 : Comparison of cowpea genotypes with checks

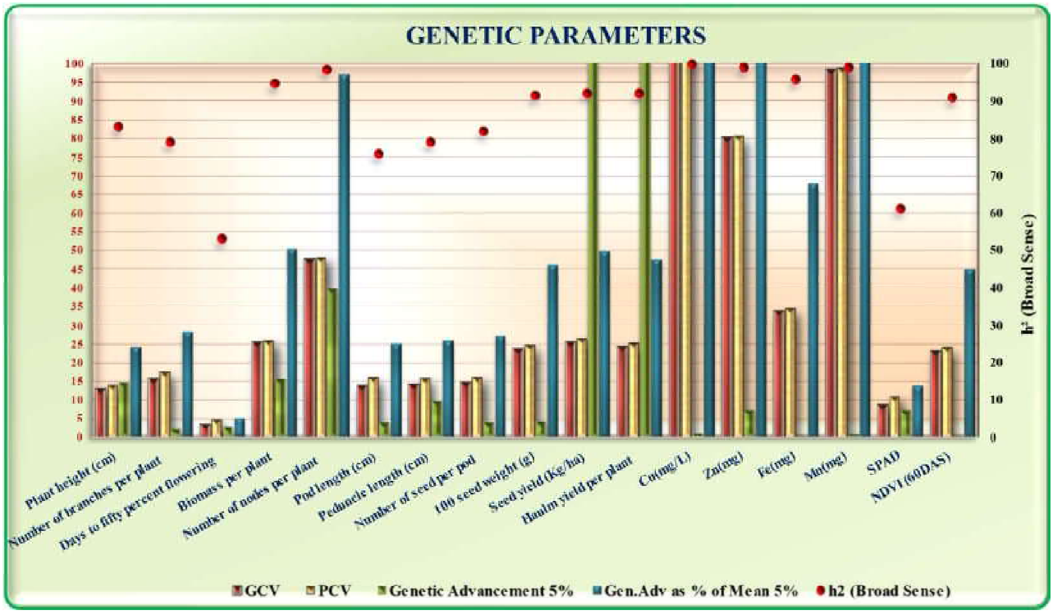

Fig. 3 : Genetic variability parameters for yield and yield component character

TABLE 1

Analysis of variance of various characters

Source Degrees of freedom	Replication 2	Treatment 54	Error 108
Plant height (cm)	10.1080	188.344 **	11.89
Number of branches per plant	0.1260	3.734 **	0.302
Days to fifty percent flowering	10.497 *	11.407 **	2.602
Biomass per plant	3.9790	181.379 **	3.44
Number of nodes per plant	8.0550	1138.902 **	6.775
Pod length (cm)	0.5640	15.123 **	1.456
Peduncle length (cm)	13.650	87.293 **	7.115
Number of seed per pod	1.4690	13.057 **	0.892
100 seed weight (g)	0.0980	13.7 **	0.419
Seed yield (Kg/ha)	15044.1150	585606.527 **	16709.542
Haulm yield per plant	7764.410	1320145.382 **	37490.64
Cu(mg/L)	0.0010	0.497 **	0
Zn(mg)	0.649 **	35.523 **	0.122
Fe(mg)	00	0.068 **	0.001
Mn(mg)	00	0.3 **	0.001
SPAD	1.2340	68.834 **	12.085
NDVI (60DAS)	00	0.056 **	0.002

Where,*and** significant level of 5% and 1%, respectively of a population is crucial for breeding programmes as it reveals the genetic composition of the population.

Genotypic and phenotypic coefficients of variation are beneficial in detecting the amount of variability present in the available genotypes for different characters. In general, if the phenotypic coefficient of variation for all the characters is higher than that of genotypic coefficient of variation, it indicates the influence of various environmental parameters in the expression of genes or characters.

Genotypic Coefficient of Variation (GCV)

Genotypic coefficient of variation (GCV) ranged from 3.354 to 154.63 (Table 2). Highest GCV was recorded for Cu (154.63) followed by Mn (98.37), Zn (80.12), number of nodes per plant (47.56), Fe (33.64), seed yield (Kg/ha) (25.23), biomass per plant (25.11), haulm yield per plant (24.02), 100 seed weight (23.40) and NDVI (22.80), indicating the availability of rich genetic variability for these attributes in the present experimental material. Number of branches per plant (15.385), number of seed per pod (14.49), peduncle length (14.00), pod length (13.79), plant height (12.78) and SPAD (8.47) exhibited moderate GCV. Whereas, SPAD (8.47) and days to fifty percent flowering (3.35), exhibited low magnitude of GCV.

Phenotypic Coefficient of Variation

The phenotypic coefficient of variation (PCV) ranged from 11.67 (crop duration) to 52.12 (pod weight). Highest PCV was recorded for pod weight (52.12) followed by seed yield per plant (31.72), number of pod clusters per plant (31.36), number of pods per plant (27.21), number of primary branches per plant (26.92), 100 seed weight (24.13), pod length (23.81) and number of pods cluster (21.32). Length of main stem (18.94), pod girth (18.85), days to 50 per cent flowering (16.44), number of seeds per pod (12.84) and crop duration (11.67) exhibited moderate PCV. Further, none of the characters exhibited low PCV in the present study.

GCV and PCV values are in close agreement with the findings for 100-seed weight and grain yield (Manggoel *et al.,*2012); for pod length and 100-seed weight (Ajayi *et al.,* 2014); for seed yield per plant , pod length and 100 grain weight (Selvakumar *et al.,* 2015); for pod length (Khandait *et al.,* 2016); for number of pod per plant and pod length (Rajput, 2016); and for number of seeds per pod (Srinivas *et al.,* 2017). Selection will be successful for characters with small differences in GCV and PCV estimates since these characters have little environmental influence.

Heritability and Genetic Advance

Crop improvement in any species depends on the quantum of available genetic variability, which reflects the heritable portion of variability in the species. The high heritability of any character will give greater genetic advance under selection and accordingly a breeder will make breeding strategies. Genetic advance gives the magnitude of improvement per generation in the base population by selection. Heritability and genetic advance would help in determining the influence of various environmental factors in the expression of characters and the extent to which improvement is possible after artificial selection. The estimates of genetic variation and heritability would provide a better idea about the efficiency of artificial selection (Burton, 1953).

In the present study, a high estimate of broad sense heritability was observed for all the characters. The broad sense heritability ranged from 53 per cent (days to 50% percent flowering) to 99.85 per cent (Cu) (Fig.3).

Heritability estimates alone cannot provide any reliable information regarding the amount of genetic progress that would result from the artificial selection. Therefore, heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Singh and Chaudhary, 1985).

Genetic advance is a measure of predetermined progress under artificial selection program and genetic advance as per cent of mean (GAM) ranged between 5.03 per cent (days to 50% flowering) to 318.29 per cent (Cu). The high broad sense heritability coupled

TABLE 2

Estimates of genetic variability parameters for yield and yield component character

Characters	Var Environmental	ECV	Var Genotypical	GCV(%)	Var Phenotypical	PCV (%)	h2 (Broad Sense)	Genetic Advancement	Genetic Advancement as % of Mean (GAM)
Plant height (cm)	11.89	5.75	58.818	12.788	70.708	14.021	83.185	14.409	24.027
Number of branches per plant	0.302	7.909	1.144	15.385	1.446	17.299	79.096	1.959	28.186
Days to fifty percent flowering	2.602	3.158	2.935	3.354	5.537	4.607	53.008	2.569	5.03
Biomass per plant	3.44	6.048	59.313	25.112	62.753	25.829	94.518	15.424	50.292
Number of nodes per plant	6.775	6.374	377.376	47.568	384.151	47.993	98.236	39.663	97.123
Pod length (cm)	1.456	7.799	4.556	13.795	6.012	15.847	75.779	3.828	24.738
Peduncle length (cm)	7.115	7.224	26.726	14	33.841	15.753	78.974	9.464	25.629
Number of seed per pod	0.892	6.795	4.055	14.49	4.947	16.004	81.971	3.756	27.024
100 seed weight (g)	0.419	7.204	4.427	23.404	4.846	24.488	91.344	4.142	46.079
Seed yield (Kg/ha)	16709.542	7.49	189632.33	25.233	206341.87	26.321	91.902	859.975	49.83
Haulm yield per plant	37490.64	7.115	427551.58	24.028	465042.22	25.059	91.938	1291.545	47.46
Cu(mg/L)	0	5.999	0.165	154.63	0.166	154.746	99.85	0.837	318.298
Zn(mg)	0.122	8.155	11.8	80.129	11.923	80.543	98.975	7.04	164.217
Fe(mg)	0.001	7.1	0.022	33.642	0.023	34.383	95.736	0.302	67.81
Mn(mg)	0.001	9.912	0.1	98.372	0.101	98.87	98.995	0.647	201.625
SPAD	12.085	6.775	18.917	8.477	31.001	10.852	61.019	6.999	13.641
NDVI (60DAS)	0.002	7.225	0.018	22.807	0.02	23.924	90.879	0.264	44.79

with high GAM recorded for all traits except for days to 50 per cent flowering and SPAD reading. Similar trend of heritability and GAM for pod length, number of seeds per pod, days till 50 per cent flowering and total seed weight per pod were reported by Manggoel *et al.* (2012) and comparable results for pod length, 100 seed weight, and seeds per pod by Adewale *et al.* (2010).

The high broad sense heritability coupled with high GAM indicated the role of additive gene effects for plant height, number of branches per plant, biomass per plant, number of nodes per plant, pod length, peduncle length, number of seed per pod, 100 seed weight, seed yield, haulm yield per plant, Cu, Zn, Fe, Mn and NDVI and reveals the presence of minor environmental influence and pervasiveness of additive gene action in gene expression of these characters. A high heritability combined with high genetic advance is an indication of additive gene action and selection based on these parameters would be more rewarding (Johnson *et al,* 1955). This suggests the importance of these characters through selection. Corroborative findings were reported by (Suganthi and Murugan, 2008) for seed yield per plant.

All the characters exhibited high genetic advance (as% of mean) except SPAD (13.64%) that exhibited moderate genetic advance; and days to 50 per cent flowering that exhibited low genetic advance (5.03%). improvement in these characters can be achieved by hybridization.

A significant variation for all the 17 characters studied in the experiment indicates the presence of variability in the genotypes and suggests scope for improvement. High estimates of GCV, heritability coupled with genetic advance for components traits of yield *viz.*, biomass per plant, number of nodes per plant, 100 seed weight, seed yield, haulm yield per plant, Cu, Zn and Mn content indicate the pervasiveness of additive gene action and clearly paves the way for cowpea improvement in terms of quantity and quality by artificial selection. Further, high heritability and a low genetic advance recorded for the days to 50 per cent flowering and moderate genetic advance recorded for SPAD suggests the prevalence non additive gene action. Further improvement in these characters can be achieved by hybridization.

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