Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Genetic variability studies in cowpea (*Vigna unguiculata* L.)

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Abstract
A field experiment was conducted to estimate the genetic variability and genetic divergence in Cowpea. Thirty-One genotypes were sown in a randomized block design with two replications, during *kharif* 2018 at Research farm, Department of Agricultural Botany, VNMKV, Parbhani. The objective of the experiment was to identify divergent to be used as donor parents in hybridization programmes. The observations were recorded on 12 characters *viz.,* Plant height (cm), number of primary branches per plant, days to 50% flowering, number of pods per plant, number of seeds per pod, mean pod weight (g), pod length (cm), pod width (cm), days to first pod harvest, 100 seed weight (g), pod yield per plant (gm), pod yield per hectare (Kg). Analysis of variance and mean performance for pod yield and its components revealed significant differences among all the genotypes for all the characters there by indicating presence of variability in genotypes studied. GA as per cent of mean, GCV and PCV values were at par with one another for most of the characters which indicated that the influence of the environment on the trait was vey negligible. The genotypic and phenotypic coefficient of variation were height (>20%) for the characters pod yield per hectare, plant height, number of primary branches per plant, pod length. Moderate (10-20%) for number of pods per plant, number of seeds per pod, 100 seed weight and low (<10%) for day to 50% flowering, mean pod weight, pod width, days to first pod harvest and pod yield per plant. The differences between PCV and GCV values were less indicating that these traits were less influenced by environment and could be improved by following phenotypic selection. High heritability was coupled with high genetic advance as per cent of mean was observed for all growth, flower attributes, earliness attributes and pod attributes except days to 50% flowering and pod width indicating that these characters were less influenced by environmental effects and these characters were governed by additive genes and selection will be rewarding for improvement of such traits.

Keywords: GCV, PCV, heritability, genetic advance

Introduction

Cowpea [*Vigna unguiculata* (L.)] is one of the most ancient a legume crop known to man. It is widely adopted and grown all over the world. Cowpea, which is commercially grown throughout India for its long green pods as a vegetable, seeds as pulses and foliage as fodder for milch animal. It is considered as one of the oldest legumes and referred as "Poor man's meat". Cowpea *(Vigna unguiculata)* has the largest usable protein content of all cultivated legumes and is arguably one of the most important plant protein source as a valuable and dependable commodity crop for farmer and grain traders (Nwosu *et al.,* 2013). In India, the cowpea is grown in an area of about 3.9 million ha with a production of 2.21 million tonnes having a productivity of 625 kg per ha compare to world India productivity is low, so still there is scope to improve the productivity of the cowpea. (Mohankumar, 2016). There are several diverse uses of cowpea due to which the varietal requirement in terms of plant type, pod type, maturity, pattern of use and growth are required to develop to suit the diverse regions of the country. Therefore, in cowpea selection and evaluation programme has become more complex and no single variety can be recommended to full fill the breeding objectives (Barrett, 1987). Thus, there is a growing need to develop suitable varieties for a specific region and or use. However, production is constrained by low and variable grain yield, grain quality, susceptibility to diseases and pests and the less availability of improved cultivars. Genetic variability is important to select characters, which are heritable unless and until there is large amount of variability present in the population, the breeder has little scope in breeding for high yielding varieties. Genetic association and path analysis play significant role to study inter-relationship contributing of each characters and thus simultaneously for bringing crop improvement. Thus, the present investigation aims to study genetic variability studies in cowpea among 31 vegetable cowpea genotypes at Department of Agricultural Botany, College of Agriculture Parbhani.

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Materials and Methods
The present investigation was undertaken to study genetic variability studies in thirty one genotypes of cowpea [*Vigna unguiculata* (L.)]. The experimental material consists of thirty one genotypes of cowpea including one check. All these thirty one genotypes were planted during *kharif* 2018. The experimental material was sown on 4 July, 2018 by dibbling two seeds per hill. Recommended agronomical and plant protection practices were followed regularly. The observations were recorded for the characters *viz*; day to 50% flowering, pod yield per hectare, plant height, number of primary branches per plant, pod length. Number of pods per plant, number of seeds per pod, 100 seed weight, mean pod weight, pod width, days to first pod harvest and pod yield per plants. Mean values of the five plants selected at random in each plot were used for statistical analysis. The data based on the mean of individual plants selected for observation were statistically analyzed using the method described by Panse and Sukhatme (1985) to find out overall total variability present in the material under study for each character and for all the population. The genotypic and phenotypic coefficient of variation (GCV and PCV) was calculated according to method suggested by Burton (1952) [4]. The genetic advance

was calculated for each character using the formula suggested by Johnson *et al.* (1955) [10]. Heritability (broad sense) was calculated according to the method suggested by Allard (1960) [1].

Results and Disussion
The data was subjected to analysis of variance to study the differences among thirty one genotypes for quantitative characters. The analysis of variance is presented in Table 1. The treatment mean sum of squares was found to be significant for all the twelve characters studied this indicates the presence of substantial amount of variation among these genotypes for the characters *viz.* Plant height(cm), number of primary branches per plant, days to 50% flowering, number of pods per plant, number of seeds per pod, mean pod weight (g), pod length (cm), pod width (mm), days to first pod harvest, 100 seed weight (g), pod yield per plant (g), pod yield per hectare (kg) was also noted significant. Thus considerable amount of genetic variability was present in the experimental material which can be exploited for improvement of pod yield and yield related attributes in cowpea. The character wise mean values are as follows:

Table 1: Analysis of variance for twelve quantitative traits

Sr. No	Character	Mean sum of squares		
		Replications (d.f=1)	Treatment (d.f=30)	Error (d.f=30)
1	Plant height (cm)	23.167	535.71**	24.93
2	No. of primary branches per plant	2.322	4.960**	1.064
3	Days to 50 % flowering	4.996	18.88**	6.806
4	Number of pods per plant	3.485	36.86**	5.581
5	Number of seeds per pod	0.542	7.189**	2.395
`6	Mean pod weight (g)	3.755	14.00**	3.202
7	Pod length (cm)	0.085	42.60**	6.833
8	Pod width (mm)	0.012	0.016*	0.004
9	Days to first pod harvest	0.109	21.93**	8.500
10	100 seed weight (g)	2.189	3.003**	0.969
11	Pod yield per plant (g)	54.25	32423.40**	2547.72**
12	Pod yield per hectare (kg)	67782.26	3689823.65**	144302.25

**Significant at 5% and 1% level

Variability parameters
The results with regard to mean, overall range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GA) for all the twelve characters are furnished in Table 2.

Genetic variability
Genetic variability is a pre-requisite in crop improvement programme. The breeder has to quantity the fixable and non-fixable components of variation for an effective selection programme. In the present study efforts are made to analyze the component of variability in the promising genotypes for future breeding work.

Table 2: Components of genetic variability for different characters in Cowpea genotypes.

Sr. No	Character	Range	General mean	Genotypic variance (σ²g)	Phenotypic variance (σ²p)	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic advance	Genetic Advance as % of mean 5%
1	Plant height (cm)	37.00 – 99.70	51.47	255.39	280.32	31.04	32.52	91.11	31.42	61.04
2	No. Of primary Branches/plant	4.40 – 11.10	6.41	1.94	3.01	21.74	27.03	64.66	2.31	36.01
3	Days to 50 per cent flowering	41.70 – 54.10	48.36	6.03	12.84	5.08	7.41	47.01	3.47	7.17
4	Number of Pods per Plant	23.50 – 41.20	33.50	15.64	21.22	11.80	13.75	73.70	6.99	20.87
5	Number of Seeds per Pod	10.50 – 17.60	14.18	2.39	4.79	10.91	15.43	50.01	2.25	15.90
6	Mean Pod Weight (g)	32.19 – 44.36	39.68	5.40	8.60	5.85	7.39	62.78	3.79	9.56
7	Pod length (cm)	14.25 – 32.00	19.94	17.88	24.72	21.20	24.93	72.36	7.41	37.16
8	Pod width (mm)	0.77 – 1.21	0.93	0.0062	0.01	8.41	11.12	57.15	0.12	13.09
9	Days to First Pod Harvest	45.95 – 58.45	53.87	6.71	15.21	4.81	7.24	44.14	3.54	6.58
10	100 seed weight (g)	9.09 – 15.60	12.50	1.01	1.98	8.06	11.26	51.19	1.48	11.88
11	Pod yield per plant (g)	133.90 -193.10	156.57	116.49	294.68	6.89	10.96	39.53	13.97	8.92
12	Pod yield per hectare (Kg/ha)	4766 – 14789	7708.61	8196916.88	9236187.47	37.14	39.42	88.75	5556.11	72.07

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, BS = Broad sense

Range of variability: In general a wide range of variability was observed for majority of the characters. Range of variability on the basis of mean values was more for the characters *viz.*, Plant height(37.00 – 99.70 cm), number of primary branches per plant(4.40 – 11.10), days to 50 per cent flowering (41.70 – 54.10), number of pods per plant (23.50 – 41.20), number of seeds per pod (10.50 – 17.60), mean pod weight(g) (32.19 – 44.36), pod length (cm) (14.25 – 32.00), pod width(mm) (0.775-1.210), days to first pod harvest (45.95 – 58.45), 100 seed weight (9.09 – 15.60), pod yield per plant (g) (133.90 – 193.10) and pod yield per hectare (kg) (4766 – 14789.00). Wide variation for different yield contributing characters in cowpea have been reported by several workers including, Baghizadeh *et al.* (2010) [2], Inuwa *et al.* (2012) and Shanko *et al.* (2014) [17].

Genotypic and phenotypic variances: Phenotypic variance (V$_p$) values were more than the genotypic variance (V$_g$) in all the characters (Table 03). High genotypic and phenotypic variances were observed for the characters pod yield per hectare. (G-8196916.88, P-9236187.47) followed by pod yield per plant (G-116.49, P-294.68), plant height (G-255.39, P-280.32). Similar trends regarding variability estimated were reported by Jogdhande and Kale (2017) and Nigude *et al.* (2004) [13]. The lowest genotypic and phenotypic variances were observed for characters pod width (G-0.0062, P-0.01), 100 seed weight (G-1.01, P-1.98), number of primary branches per plant (G-1.94, P-3.01), number of seeds per pod (G-2.39, P-4.79) and days to first pod harvest (G-6.71, P-15.21). Similar results regarding the genotypic and phenotypic variance were obtained by Patel *et al.,* (2018) [14]. Also Shanko *et al.,* (2014) [17] reported similar findings for number of primary branches per plant and 100 seed weight.

Genotypic and phenotypic coefficients of variation: The selection under field condition may be strongly influenced by the environment factors affecting the progress in the improvement programme. In the present studies, the genotypic coefficient of variation for all the characters was lower than the phenotypic coefficient of variation. However the differences between them were of lower magnitude except few characters. This relationship indicated that there was small effect of environment on these characters and phenotypic selection for such characters may be effective. In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for plant height (GCV-31.04%, PCV-32.52%), number of primary branches per plant (GCV-21.74%, PCV-27.03%), pod length (GCV-21.21%, PCV-24.93%), number of pods per plant (GCV-11.80%, PCV-13.75%) and number of seeds per pod (GCV- 10.91%, PCV-15.43%). Similar results were found by Patel *et al* (2018) [14], lnuwa *et al.* (2012), Shanko *et al.* (2014) [17], Kharde *et al.* (2014) [12] and Khanpara *et al.* (2015) [11]. The magnitude of variability is measured in terms of variance. But the variances of different characters having different scale of measurement are not directly comparable; hence they were converted into coefficient of variation like GCV and PCV. The magnitude of variability alone cannot provide any idea about the efficiency with which it can be exploited. In general, estimates of phenotypic coefficient of variation (PCV) were slightly higher than corresponding genotypic coefficient of variation (GCV) indicated the role of environment in the expression of characters. Similar findings were reported by Nigude *et al.* (2004) [13] and Pal *et al.* (2003). The low genotypic and phenotypic coefficient of

variations were observed for days to first pod harvest, days to 50 per cent flowering, mean pod weight, pod yield per plant, 100 seed weight and pod width. These results are in close agreement with those given by Inuwa *et al.* (2012), Girrano *et al.* and Shanko *et al.* (2014) [7, 17]. The characters which have less influence of environment may be improved by simple selection method such as mass selection or by pure line selection.

Heritability and genetic advance: The heritability estimates along with expected genetic advance are more useful in predicting yield under phenotypic selection than heritability estimates alone (Johnson *et al.* 1955) [10]. In the present study, the high broad sense heritability values were observed for the character plant height (91.11%), number of pods per plant (73.70%), pod length (72.36%), number of primary branches per plant (64.66%) and mean pod weight (62.78%). Moderate heritability was exhibited by pod width (57.10%), 100 seed weight (51.20%), number of seed per pod (50.00%), Days to 50 per cent flowering (47.00%) and days to first pod harvest (44.14%). These results are in close agreement with findings of Diwaker *et al.* (2017) [5], Inuwa *et al.*, (2012) [8] and Shanko *et al.* (2014) [17]. Bertini *et al.* (2009) [3] reported high heritability in cowpea for pod length. Similarly Suganthi and Murugan (2008) [18] recorded high heritability for number of seeds per pod and pod length. Diwaker and Sharma (2017) [5] also recorded high heritability for plant height and pod length in cowpea. The ultimate aim of studying the variability and heritability of any trait is to have an idea about the feasibility of selection. The improvement in the mean performance of progeny of the selected families over the base population is known as genetic advance, when expressed as per cent of mean is called genetic gain (Johnson *et al.* 1955) [10]. According to Johnson *et al.* (1955) [10] the expected genetic advance is categorized into less than 10% as low, 10-20% as moderate and more than 20% as high expected genetic advance. The high value of genetic advance (more than 20) recorded for the character plant height and pod yield per hectare. Low magnitude of genetic advance was observed for pod width. The results obtained are in confirmation with those of Pal (2003) and Santosh *et al.* (2002) [16] also found high genetic advance for plant height whereas Eswaran *et al.* (2007) [6] and Ramesh *et al.* (2014) [15] observed high heritability as well as high genetic advance for plant height and single plant yield in cowpea. The genotypic and phenotypic coefficients of variation were high (>20%) for the characters plant height, number of primary branches per plant, pod length, pod yield per hectare. Moderate (10-20 %) for number of pods per plant, number of seeds per pod, pod yield per plant and low for (<10%) days to 50 per cent flowering, mean pod weight and days to first pod harvest. The differences between PCV and GCV values were less, indicating that these traits were less influenced by environment and could be improved by following phenotypic selection. The high values of broad sense heritability of these characters expressed that they were least influenced by environmental factors. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

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