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STUDY OF GENETIC VARIABILITY PARAMETERS IN COWPEA (*VIGNA UNGUICULATA* L. WALP.) GERMPLSAM LINES

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ABSTRACT
A genetic variability study is carried out with a set of 196 cowpea genotypes and analysis of variance revealed significant differences among the genotypes tested for all the nine characters, justifying the selection of genotypes for the study. The genotypes exhibits considerable amount of genetic variation for all the characters and it indicated the good scope for selection of suitable basic material for further improvement. PCV values were of higher magnitude than GCV for all the characters under study. The estimates of PCV and GCV were high for number of pods per plant, pod length, plant height, number of branches per plant, test weight and seed yield per plant. High heritability and high genetic advance as per cent (GAM) of mean was observed for number of pods per plant, number of seeds per pod, pod length, plant height, number of branches per plant, test weight and seed yield per plant. These characters are governed by additive gene action and one should go for direct selection for these traits to improve in future.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.), an annual legume among pulses, is one of the most ancient crops known to man. All parts of the plant in cowpea are used as nutritious food, providing protein, vitamins (notably vitamin B) and minerals. The largest production is in Africa, with Nigeria and Niger predominating, while Brazil, Haiti and India have significant production. However, the per capita availability of pulses has been come down considerably. Many reasons could be attributed for low production of pulses. Some of the main reasons are non-availability of high yielding varieties, short duration plant types and resistant cultivar for biotic and a biotic stresses. Development of high yielding early varieties and study on biotic and abiotic stresses has to receive much attention in cowpea research.

Before initiating crop improvement program in any crop, breeder should thoroughly evaluate, screen and understand the genetic architecture of the germplasm he is handling. Estimation of genetic variability parameters is the foremost step to be adopted in the source population, if the breeding program is aimed at improving economically important traits. The success of a crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability and select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather and Jinks, 1983).

Variability is the key factor for any selection program, which can be generated through various ways. To achieve or create variability, addition of some more diverse genotypes with the available collection is necessary or creation of new variability by other means is very much needed. The morphological observations recorded in the field usually will be the sum total of genotypic as well as environmental effects. Hence, the diversity obtained from the field data should be verified to ensure that the variability present is at genotypic level. Hence, in the present study a set of 196 cowpea genotypes were used to study the genetic variability parameters for yield and yield attributing traits.

MATERIALS AND METHODS

Plant material

The present study comprised a set of 196 diverse cowpea genotypes including released varieties maintained at the AICRP on Arid Legumes, GKVK, Bangalore. These genotypes of cowpea (Table 1) were sown during *Kharif* 2009 in Simple Lattice Design, in three meter long rows with spacing of 60 cm x 30 cm and standard agronomic practices were followed. Five plants selected at random were tagged from each genotype and observations on nine quantitative traits (days 50 per cent flowering, days to physiological maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, test weight and seed yield per plant) were recorded on these plants.

Biometrical analysis

Genetic variability parameter *viz.*, mean, variance (Cochran and Cox, 1957), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Burton and De Vane, 1953), heritability (h^2) (Hanson *et al.*, 1956) and Genetic

advance (GA) (Johnson *et al.*, 1955) among characters were calculated by following the standard procedures with the help of MSTATC, Statistica 2 and Genres software's.

RESULTS AND DISCUSSION

Analysis of variance revealed that the genotypes recorded highly significant variation for all the characters and it indicated the presence of sufficient variability for these characters (Table 2), thus there is a lot of scope for selection. One of the ways of assessing the variability is through examining the range of variation.

The range in the values reflects the extent of phenotypic variability in respect of the character, which includes genotypic, environmental and genotype environmental interaction components. In the present study the genotypes exhibited considerable amount of variation for nine characters *viz.,* days 50 per cent flowering, days to physiological maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, test weight and seed yield per plant (Table 3). Sawant (1994) recorded higher range for these characters, which was in accordance to the present study. The high range of values indicated the good scope for selection of suitable basic material for breeders for further improvement.

The mean values also play a major role in selecting suitable breeding lines and methods for the improvement of cowpea. In case of days to 50 per cent flowering and days to physiological maturity lower mean values enabled identification of several short duration genotypes. The lower mean values for these traits were observed in genotypes C 325, IC 402180 and IC 458411 and these genotypes can be used in niche areas where early varieties are needed or as parents in hybridization for the development of early duration and high yielding varieties.

Genetic variability is a basic information needed for the breeders to improve the crops by adopting appropriate method of selection based on variability that exist in the material. In this regard, it is necessary to partition the total variability into heritable and non-heritable components *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further to compute heritability and genetic advances for various metric traits.

Comparison of variability between two traits is possible with coefficient of variation as it is free of units. As expected, the PCV values were greater than the GCV values for all the characters indicating considerable influence of environment on the expression of these characters under field conditions (Table 3). The difference between PCV and GCV was more for seed yield per plant, pod length, number of branches per plant and number of pods per plant indicating the major role of environment on these characters. Earlier reports on cowpea by Anbu Selvam *et al.* (2000) and Awopetu *et al.* (2006) are in conformation with these results.

In general, the PCV and GCV were quite high for number of branches per plant, number pods per plant, pod length, plant height, test weight and seed yield per plant indicating greater scope for improvement of these characters by simple selection. Several earlier workers also reported high PCV and GCV for number of branches per plant (Marappa *et al.* 2007), number of pods per plant (Girish *et al.,* 2006, Meshram *et al.,* 2013), pod length (Mathura Rai *et al.,* 2004), plant hieght (Marappa *et al. 2007*), test wieght (Marappa *et al.* 2007; Omoigui *et al.*, 2006) and seed yield (Resmi *et al.,* 2004, Meshram *et al.,* 2013, Rakesh *et al.,* 2013, Ravishanker *et al.,* 2013,).However, number of seeds per pod showed moderate PCV and GCV values, while days to 50 per cent flowering and days to

Table 1: List of Cowpea genotypes along with their source of collection

S.no.	Source	Germplasm line
1	NBPGR, New Delhi	EC 458489, IC 402101, IC 402166, EC 458506, IC 249593, IC 402180 EC 472257, IC 249141, EC 170584, EC 472252, IC 202867(99), IC 1071, EC 458411, IC 402161, IC 2591054, IC 462099, IC 58905, EC 458473, IC 402182, IC 202777, IC 170574, EC 394779, IC 330996, IC 402166, IC 402164, EC 472250, IC 402114, EC 170584, EC 458402, EC 458442, EC 458470, IC 402172, IC 402048, IC 257428, IC 198326(38), EC 170585(B9), EC 402159, IC 249793, IC 402159, IC 402104, 402162, IC 202290, IC 402159, EC 458402, IC 202779, C 249593, EC 170578-1-1, EC 458418, EC 394779, EC 472252, IC 2591054, EC 458505, EC 394708, IC 402104, IC, 402174, IC 202782, IC 4506, EC 458425, IC 201©, EC 48475, IC 402125, IC 402098, EC 458417, IC 330996, EC 390287, EC 170584-1-1, EC 458440, TOME 77-4, IC 402175, IC 402101, IC 202781, IC 202797(97), IC 402098, EC 458480, EC 458483, EC 458489, EC 58473, EC 394839, IC 1061, IC, 402159, EC 458418, EC 394838, EC 458469, IC 1071, EC 394779, IC 249588, IC 402154, EC 458440, IC 202781, IC 198329(36), IC 253251, EC 472250, EC 458469, EC 458441, EC 458480, EC 394839, IC 10171, EC 458438, IC 249593, IC 402162, IC 249141, IC 206240, EC 458430, EC 472267, IC 402164, IC 402090, EC 458402, EC 458453, IC 402161, IC 402106, EC 472271, IC 49586, IC 25105, IC 202711(58), EC 458490.
2	IARI, New Delhi	V 24O, C 325, V 585, V 585, V 578 ©, C 720, C 24-1, V 16, V 578-17, C 517, V 578, C 33, V 604-7-29-3, C 458492, C 457, V 585©, C 1071.
3	GKVK, Bangalore	202804(83), 202854(97), C 131+CB-2, 202827(92), KBC 2, 27749(25), 202705(49), GENOTYPE 36, 198355(45), 201095(52), 97767(10), 202827(93), P 695, KBC 2, KM 5, C 152.
4	IITA, Nigeria	IT 97K 499-38, IT 97499-38, TVX 944.
5	Gujarat	GC 5, GC 3(C), GC 3, GC 4.
6	Hissar	HC 03-02, HC 9866.
7	-	NBC 14, NBC 30, CPD 31, NBC 32, NBC 40, CPD 19, NBC 6, NBC 42, NBC 41, NBC 38, NBC 39, NBC 2, NBC 33, NBC 7, NBC 19, NBC 27, ETC 27, CB 10, CPD 15, NB 12, NBC 10, NBC 51, NBC 9, NB 47, NBC 18, NBC 7, NBC 36, NBC 48, NBC 43, NBC 44, NBC 40, NBC 24, TC 201, TCM 44-1, APC 243-1-865, NBC 8, NBC 38, NBC 42

Table 2: Analysis of variance for nine quantitative characters in 196 cowpea genotypes during *Kharif* - 2009

Sources of variation	df	X1	X2	X3	X4	X5	X6	X7	X8	X9
Replications	1	0.09	40.84	8.62	1.75	60.67	10.14	0.21	0.43	60722.39
Genotypes(Unadjusted)	195	19.93*	72.73*	6.00*	37.08*	163.16*	4.07*	26.66*	16.81*	65691.40*
Blocks within Replications (adj.)	26	0.92	7.51	0.54	0.76	7.48	0.60	1.13	0.18	32457.05
Error(intra block)	169	1.80	46.35	3.25	5.24	28.32	1.53	17.30	8.35	70815.48

* indicates 5% level of significance

X_1 - Days 50 % Flowering, X_2 - Number of pods per plant, X_3 - Number of seeds per pod, X_4 - Pod length (cm), X_5 - Plant height (cm), X_6 - Number of branches per plant, X_7 - Test weight (gm), X_8 - Days to physiological maturity, X_9 - Seed yield per plant (gm)

Table 3: Estimation of mean and genetic variability parameters for nine characters in 196 cowpea genotypes

S.No	Characters	Mean ± SE	Range	PCV (%)	GCV (%)	h^2 (%)	GA M
1	Days to 50% flowering	55.79 ±0.23	47.00-62.00	5.83	5.82	99.88	11.98
2	Days to physiological maturity	88.81 ±0.24	84.00-107.00	3.89	3.88	99.66	7.99
3	Number of pods per plant	20.67 ±0.46	7.25-52.33	34.88	33.09	89.98	64.66
4	Number of seeds per pod	11.46 ± 0.13	6.00-17.66	18.44	16.58	80.86	30.72
5	Pod length (cm)	10.64 ±0.32	5.00-24.22	43.13	42.59	97.50	86.63
6	Plant height (cm)	28.02 ±0.66	12.00-52.75	34.78	34.32	97.40	69.78
7	Number of branches per plant	6.74 ±0.10	3.00 -13.33	24.47	22.59	85.25	42.97
8	Test weight (g)	14.70 ±0.32	7.20-31.50	31.12	31.08	99.71	63.93
9	Seed yield per plant (g)	34.11 ±1.00	9.60-92.05	44.62	41.64	87.09	80.05

physiological maturity exhibited low values.

Low PCV and GCV values were also reported for days to physiological maturity (Thiyagarajan, 1989), days to 50 per cent flowering (Apte *et al.*, 1987), while moderate PCV and GCV values were reported for number for seeds per pod (Vineeta Kumari *et al.,* 2003). But contradicting the present results, moderate to low PCV and GCV values were reported for plant height and branches per plant (Venkatesan *et al.,* 2007), pods per plant (Tyagi *et al.*, 2000), pod length and seed yield per plant (Rahul Chauhan *et al.*, 2003). High PCV and GCV were recorded for days to 50 per cent flowerig and days to physiological maturity by Henry *et al.* (2003) and Veneeta Kumari *et al.* (2003).The contradictory reports for similar traits from different studies might be due to various factors like genotypes and another environmental variations such as soil fertility, season, moisture availabilty etc.

In the present investigation, genetic advance estimates (Table 3) were medium to high (11.98 per cent to 86.63 per cent) for majority of the characters studied and low in case of days to physiological maturity (7.99 per cent). The characters like test weight, plant height, number of branches, number of pods per plant, pod length, seeds per pod and seed yield per plant exhibited high heritability along with high genetic advance. Days to 50 per cent flowering recorded maximum heritability (99.88) compared to other traits. Plant height exhibited maximum genetic advance (86.63 per cent) compared to the other characters. Days to 50 per cent flowering exhibited high heritability coupled with moderate genetic advance as per cent of mean. Whereas days to physiological maturity expressed high heritability coupled with low genetic advance as per cent of mean. Several earlier workers have also reported high heritability coupled with high genetic advance for plant height (Gireesh *et al.*, 2006), seed yield per plant (Sughanthi and Muragan, 2007), number of branches per plant (Malarvizhi and Rangasamy, 2005), number of pods per plant (Gireesh *et al.,* 2006), pod length (Rahul Chauhan *et al.*, 2003), test weight (Venkatesan *et al.*, 2007), seeds per pod (Vineeta Kumari *et al.,* 2003) and seed yield (Resmi *et al.*, 2004, Alok kumar *et al.,* 2013, Meshram *et al.,* 2013, Rakesh *et al.,* 2013, Ravishanker *et al.,* 2013, Binod kumar, 2013.). Some reports indicated high heritability and medium genetic advance for days to 50 per cent flowering (Awopetu *et al.*, 2006). High heritability and low genetic advance were reported for days to physiological maturity (Sarvamangala, 2004).

High heritability estimate indicates less influence of environment on respective characters. Hence, direct selection can be followed to improve early maturing genotypes. Low heritability (broad sense) indicates predominance of non-additive gene action indicating the scope for breeding. High estimates of GA coupled with substantial amount of heritability indicate that selection for such characters would result in the improvement of characters in the desired direction as the character is governed by additive genes. High heritability coupled with low genetic advance indicates non-additive gene action. The heritability exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. If, low heritability coupled with low genetic advance indicates such character was highly influenced by environment and selection would be ineffective for those traits.

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