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Genetic variability, heritability and genetic advance studies in F₂ & F₃ populations of cowpea [*Vigna unguiculata* (L.) Walp]

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Abstract

The present research entitled “Genetic variability heritability genetic advance studies in F₂ and F₃ populations of Cowpea (*Vigna unguiculata* L. Walp)”. The experimental material comprising of three parent, two F₂ crosses and their respective F₃ populations were evaluated at Research Farm of the Department of Genetics and Plant Breeding, College of Agriculture, Latur, Maharashtra. During *kharif*-2021-22. The material was sown in RBD with three replications. Observations were recorded for ten yield contributing quantitative characters. The estimates of GCV and PCV were recorded high for yield per plant, number of pods per plant, plant height and primary branches per plant. Thus, these characters provide good source of variation and hence they are useful in crop improvement programme in cowpea. High heritability estimates along with high genetic advance were obtained for characters days to maturity and plant height. The character days to maturity showed the highest heritability followed by test weight and plant height. This suggests that these characters were governed by additive gene action and selection will effective. Therefore, there was scope for improvement of these characters in breeding programme. The lowest genetic advance along with high heritability was observed for number of primary branches per plant and number of seeds per plant.

Keywords: Cowpea, genetic variability, heritability, genetic advance, F₂ & F₃ populations

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important pulse crop, native to Central Africa, belongs to family *Leguminaceae*. The family *Leguminaceae*, sub family *Fabaceae*, contains 170 species in the genus *Vigna* (Verdcourt, 1970) [17]. Cowpea is mainly grown in tropical and subtropical regions in the world for vegetable and seed purpose and to lesser extent as a fodder crop. It is a most versatile pulse crop because of its smothering nature, drought tolerant characters, soil restoring properties and multi-purpose uses. As a pulse crop, cowpea fits well into most of the cropping systems.

On dry weight basis, cowpea grain contains 23.4% protein, 1.8% fat and 60.3% carbohydrates and it is rich source of calcium and iron Gupta (1988). It was grown in area of about 3.9 million ha with a production of 2.21 million tonnes having a productivity of 650 kg per ha. In Maharashtra, the Konkan region is contributing maximum area of 1300 ha and a productivity of 410 kg per hectare (Anonymous, 2014) [2]. This crop is grown in Maharashtra for as a grain, vegetable, and as fodder.

In India is having diversity in terms of environment, there is also diversity in term of uses of cowpea. Hence, the varietal requirements are also varies in term of plant type, pod type, days to maturity, pattern of use and growth to suit the diverse regions of the country. The present cultivars under cultivation are having low productivity, non-synchronous flowering and fruiting, a lack of response to high doses of inputs like fertilizer’s, irrigation, tillage, etc.

Since yield is a complex trait, it is impacted by a variety of polygene-controlled traits that contribute to yield as well as environmental influences. Success of any plant breeding programme will depend on variability existing in population. Hence study of genetic variability, heritability and genetic advance become important for effective selection and utilizations of genotypes in breeding programme. In autogamous crop like cowpea variability existing is limited. Hence, the efforts of the breeder are recombination breeding to develop high yielding pure line varieties by exercising selection in segregating generation. The recombination breeding involves hybridization, selection and critical evaluation. Early generation testing and selection have gained momentum in self-pollinated crops, as additive

genetic variances are more important.

Martials and Methods

The present investigation entitled “Genetic Variability, Heritability, and Genetic Advance studies in F₂ and F₃ populations of Cowpea (*Vigna unguiculata* L. Walp)” was carried out at Research farm of the Department of Genetics and Plant Breeding, College of Agriculture, Latur Maharashtra. The experimental material comprised of three parents of cowpea LC-1, GDVC-2, GC-6 and their F₂ and F₃ generations LC-1 was used as male parent. This material of Cowpea (*Vigna unguiculata* L.) was evaluated during Kharif-2021 for Genetic variability, Heritability and Genetic advance studies.

Seeds obtained from each individual F₂ plants were collected separately and forwarded to F₃ generation. During kharif-2021, F₃ were sown in four rows in three replications under natural field conditions by Randomized block design. Observations were recorded at flowering and physiological maturity on the yield and its attributes like, days to flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seeds weight (gm) and seed yield per plant (gm).

Statistical Analysis

The analysis of variance of the experimental design was carried out for yield and its contributing traits separately by following the procedure given by Panse and Sukhatme (1985) [16]. Heritability and Genetic Advance were measured as suggested by Singh and Chaudhary (1985) [15] and Allard (1960) [1]. Phenotypic co-efficient of variation were calculated by the formula of Burton (1952) [3]. In order to assess and estimate the variability among the populations, the statistical analysis was carried out using WINDOSTAT 8.1 package. Phenotypic and genotypic components of variance estimated by applying the formula as suggested by Snedecor and Cochran (1994) [18].

Formulae,

1. Genotypic variance (δ^2g) = $\delta^2t - \delta^2e/r$.
2. Phenotypic variance (δ^2p) = $\delta^2g + \delta^2e$.
3. Genotypic coefficient of variation (GCV %) = $\sqrt{\delta^2g/\bar{x}} \times 100$.
4. Phenotypic coefficient of variation (PCV %) = $\sqrt{\delta^2p/x} \times 100$.
5. Heritability (H) = $\delta^2g/\delta^2g + \delta^2e = \delta^2g/\delta^2p$.
6. Genetic advance = GA = $K \times \delta^2p \times H$.
7. Genetic advance % of mean = $G.A/X \times 100$.

Where,

H = Heritability in broad sense.

δ^2g = Genotypic variance.

δ^2e = Environmental variance.

δ^2p = Phenotypic variance.

K = Selection differential (value of K at 5% selection Intensity = 2.06).

X = Grand mean of character.

Result and Discussion

The mean replicated data was collected on the three parents, two inter varietal crosses of F₂ and their corresponding F₃ populations of cowpea. The data obtained was subjected to statistical analysis to find out Means, Variance, Genetic

Variability, Heritability and Genetic Advance among the different characters under study.

The mean sum of squares due to the genotypes was highly significant for all the characters under study. This showed considerable amount of variation for all the characters. The genotypic and error mean sum of squares were used further for analysis of genotypic and phenotypic variances. The mean performance of parents (LC-1, GDVC-2 and GC-6), F₂ and F₃ crosses are days to 50% flowering ranged from 39.04 days to 44.03 days, days to maturity 60.18 to 73.90 days, plant height 33.53 to 52.03 cm, primary branches/plant 2.60 to 3.51, secondary branches/plant 8.74 to 10.97, number of pods/plants 9.50 to 20.66, pod length 10.67 to 12.71 cm, number of seeds/pods 10.74 to 12.66, 100 seed weight 7.77 to 9.58 gm and grain yield/plant 11.90 to 23.56. Wide range of variability was also reported by Khan *et al.* (2015) [8], Khanpara *et al.* (2015) [9], Bhadru and Navale (2012) [4] in cowpea for above trait.

The total variation among the genotypes was partitioned into three components viz., genotypic, phenotypic and environmental variance. The phenotypic variance ranged from 0.10 (primary branches per plant) to 50.31 (plant height). The genotypic variance ranged from 0.09 (primary branches per plant) to 47.60 (plant height) and the environmental variance ranged from 0.01 (primary branches per plant) to 2.70 (plant height). In general, phenotypic variances were higher in magnitude than genotypic variance for all characters. The phenotypic variance was found to be high for plant height (50.31) followed by grain yield per plant (23.68), days to maturity (23.36) and number of pods per plant (20.95) whereas secondary branches per plant (0.70), number of seed per pod (0.70), 100 seeds weight (g) (0.49), pod length (cm) (0.42) and primary branches per plant (0.10) showed low estimate of phenotypic variance. These findings confirmed the previous reports of Thorat and Gadewar (2013) [16], Nkoana *et al.* (2019) [13], Nwosu *et al.*, (2013) [11], Gerrano *et al.*, (2019) [6] and Kamara *et al.* (2006) [9].

The estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variation (GCV) are presented in Table No: 3. the high PCV was recorded for the character number of pods per plant (30.57%) followed by seed yield per plant (29.37%) it also recorded by Joshi *et al.* (1998) [7] and Pandiyan *et al.* (2020) [15]. Lower estimates of phenotypic coefficient of variation were recorded for the characters days to 50% flowering (4.20%) and pod length (6.24%). Highest magnitude of GCV was recorded in number of pods per plant (29.10%), grain yield per plant (28.50%) and plant height (17.44%). The low GCV was exhibited by characters days to 50% flowering (3.94%), number of seed per pod (5.19%), pod length (5.32%) and days to maturity (7.00%) Such findings are also observed by Nair *et al.* (2018) [10] and Ravish *et al.* (2020) [13].

The estimate of broad sense heritability, genetic advance and genetic advance as per cent of mean (%) was presented in the Table No: 3. The range of heritability was from days to maturity (98.64%) to number of seed per pod (54.24%). High heritability recorded for the characters days to maturity (98.64%), 100 seed weight (94.84%), plant height (cm) (94.63%). The moderate heritability was recorded by the number of seed per pod (54.24%). Shinde *et al.* (2021) [14] also reported broad sense heritability for cross GDVC-2 × LC-1 and GC-6 × LC-1, which was ranged from 96.32% to 61.14% and 65.20% to 94.14% respectively. The range of

genetic advance was from 0.57 to 13.83. Plant height (13.83), which was estimated highest genetic advance among the characters under study. Low magnitude of genetic advance was observed for characters primary branches per plant (0.54), number of seed per pod (0.93), Pod length (1.107), 100 seed

weight (1.37), Secondary branches per plant (1.45) Shinde *et al.* (2021) [14] also reported genetic advance for cross GDVC-2 × LC-1 and GC-6 × LC-1, which ranged from 1.10 to 15.77 and 0.96 to 12.06, respectively.

Table 1: Analysis of variance (ANOVA) for seed yield and yield components traits in cowpea

Source of variance	d.f.	Days to Flowering	Days to maturity	Plant Height (cm)	Primary Branches/plant	Sec. Branches/plant	No. of pods/plant	Pods length (cm)	No. of seeds/pod	100 seed weight	Yield per plant
Replication	2	0.175	0.031	1.305	0.019	0.135	1.05	0.855	0.101	0.028	0.837
Treatment	6	8.261**	69.930**	145.5**	0.277**	1.889**	58.93**	1.3420**	1.461**	1.387**	72.77**
Error	12	0.363	0.326	2.703	0.012	0.105	1.963	0.150	0.320	0.026	1.299

Table 2: Estimates of phenotypic (σ_p), genotypic (σ_g) and environmental (σ_e) variance in F₂ generation of cowpea.

Sr. No.	Name of characters	Phenotypic variance (σ_p)	Genotypic variance (σ_g)	Environmental variance (σ_e)
1.	Days to 50% flowering	3.00	2.63	0.36
2.	Days to maturity	23.36	23.05	0.32
3.	Plant height(cm)	50.31	47.60	2.70
4.	Primary branches per plant	0.10	0.09	0.01
5.	Secondary branches per plant	0.70	0.59	0.11
6.	No. of pods per plant	20.95	18.99	1.96
7.	Pod length (cm)	0.42	0.27	0.15
8.	No. of seed per pod	0.70	0.38	0.32
9.	100 seeds weight (g)	0.49	0.47	0.03
10.	Grain yield per plant.	23.68	25.15	1.47

Table 3: Parameters of genetic variability for yield and yield contributing traits in cowpea

Sr. No.	Name of characters	GCV	PCV	ECV	Heritability (%)	Genetic advance	GAM (%)
1.	Days to 50% flowering	3.94	4.20	1.46	87.88	3.13	7.60
2.	Days to maturity	7.00	7.05	0.82	98.64	9.82	14.33
3.	Plant height (cm)	17.44	17.93	4.16	94.63	13.83	34.95
4.	Primary branches per plant	9.65	10.28	3.56	88.03	0.57	18.65
5.	Secondary branches per plant	7.66	8.31	3.23	84.96	1.45	14.55
6.	No. of pods per plant	29.10	30.57	9.36	90.63	8.55	57.07
7.	Pod length (cm)	5.324	6.247	3.32	72.632	1.107	9.346
8.	No. of seed per pod	5.19	7.05	4.72	54.14	0.93	7.86
9.	100 seeds weight (g)	7.96	8.16	1.85	94.84	1.37	15.94
10.	Grain yield per plant (gm)	28.50	29.37	7.09	94.17	9.73	56.97

References

- Allard RW. Principles of Plant Breeding. John Willey and Sons. Inc. New York; c1960. p. 36.
- Anonymous. Statistics, Directorate of Agriculture, Govt. of Rajasthan, Jaipur; c2014.
- Burton GW. Quantitative inheritance in grass pea. Proc. 6th Grassl. Cong. 1952;1:277-283.
- Bhadru D, Navale PA. Genetic variability parameters in F₂ and F₃ populations of cowpea (*Vigna unguiculata* L.). Legume Research. 2012;35(1):75-77.
- Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 1959;51:515-518.
- Gerrano AB, Gwata ET. Agronomic performance and genetic variability of cowpea (*Vigna unguiculata*) accessions Legume Research. 2019;42(6):757-762.
- Gupta YP. Pulse crops. In: Nutritive Value of Pulses, Ed., Baldev B, Ramanujam S and Jain HK; c1988. p. 563.
- Joshi SN, Bapna CS, Kabaria MM. Correlation studies on yield and agronomic characters in cowpea. Indian Journal of Agronomy. 1998;17(1):321-324.
- Kamara AY, Omoigui LO, Ishiyaku MF. Genetic variability and heritability studies of some reproductive traits in cowpea (*Vigna unguiculata* (L.) Walp.). African Journal of Biotechnology. 2006;5(13):684-688.
- Khan H, Viswanatha KP, Sowmya HC. Study of genetic variability parameters in cowpea (*Vigna unguiculata* L. Walp.) germplasm lines. The Pharma Innovation Journal. 2015;9(12):275-278.
- Khanpara SV, Jivani LL, Vachhani JH, Kachhadia VH. Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. Electronic Journal of Plant Breeding. 2015;7(2):0975-928.
- Nair KR, Desai SS, Sawardekar SV, Burudkar MM. Study of genetic variability parameter in F₂ generation of interspecific hybrids in cowpea [*Vigna unguiculata* L. Walp]. International journal on pure and applied biosciences. 2018;6(1):954-958.
- Nkoana DK, Abe SG, Gwata ET. Agronomic performance and genetic variability of cowpea (*Vigna unguiculata* L.) accessions. Legume Research. 2019;42(6):757-762.
- Nwosu DJ, Olatunbosun BD, Adetiloye IS. Genetic variability, heritability and genetic advance in cowpea genotypes in two agro-ecological environments. Greener Journal of Biological Sciences. 2013;3(5):202-207.

15. Pandiyan M, Vaithilingan M, Krishnaveni A, Sivakumar P, Sivakumar C, Jamuna E. Genetic variability studies on cowpea genotypes. *International Journal of Current Microbiology and Applied Sciences*. 2020;9(1):2319-7706.
16. Panse VG, Sukhatme PV. *Statistical method for Agril, workers ICAR, New Delhi, India; c1985*.
17. Ravish P, Satyawar AS, Satyapal D, Preeti RK. Genetic variability and association studies in cowpea (*Vigna unguiculata* L.) for seed yield and related traits. *Forage Research*. 2020;46(3):232-235.
18. Snedecor GW, Cochran WG. *Statistical methods*. 8th edition, Iowa state university press, Ames, Iowa, USA; c1994.
19. Shinde RJ, Toprope VN, Sargar PR, Gavali RG. Heritability and genetic advance as indices for yield and yield components selection in cowpea (*Vigna unguiculata* L. Walp). *International Journal of Plant and Environment*. 2021;7(4):297-299.
20. Singh RK, Chaudary BD. *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi, India; c1985. p. 56.
21. Thorat A, Gadewar RD. Variability and correlation studies in cowpea [*Vigna unguiculata* L. Walp]. *International Journal for Environmental Rehabilitation and Conservation*. 2013;1(2):44-49.
22. Verdcourt B. Studies on the leguminosae papilionaceae for flora of east. *Tropical Africa IV Review Bulletin*. 1970;24:507-509.