

Study of Simple Measures of Genetic Variability Parameters in F_{2:3} Populations of Cowpea (*Vigna unguiculata* L. Walp.)

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ABSTRACT: Two F_{2:3} populations of cowpea were evaluated for 10 different quantitative traits during summer 2021 to study genetic variability parameters. Analysis of variance revealed significant differences among all the segregants of the population for most of the traits studied. High phenotypic coefficient of variance and genetic coefficient of variance were recorded for plant height, number of primary branches/plant, dry matter/plant and seed yield/plant in F_{2:3} population of VBN-1 × RC-19; number of primary branches/plant, number of pods/plant, dry matter/plant and seed yield/plant in F_{2:3} population of KBC-9 × PGCP-6. High heritability and GAM were recorded for plant height, number of primary branches/plant, number of pods/plant, pod length, number of seeds/pod, dry matter/plant and seed yield/plant in the F_{2:3} population of VBN-1 × RC-19; plant height, number of primary branches/plant, number of pods/plant, number of seeds/pod, dry matter/plant and seed yield/plant. This indicates the scope for improvement of these characters through selection.

Keywords: Cowpea, genetic coefficient of variance, phenotypic coefficient of variance, heritability, variability.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.) is a warm-season, annual, self-pollinated diploid grain legume with a 620 Mb genome size (Munoz *et al.*, 2017). It is commonly known as Lobia. Cowpea has been named so because of its use as cattle feed. It is commonly known as Lobia. It is also known by its different vernacular names *viz.*, Rawan (Hindi), Chavali (Marathi) and Barbate (Bengali). Some of the cowpea cultivars grown for their immature pods or vegetable purpose are known as Asparagus bean, snake bean or yard long bean and when they are grown for dry seeds, it is also known as black eyed pea, kaffir pea and southern pea.

Its dry edible grains are rich in protein (20–32%) with high amounts of essential amino acids (lysine and tryptophan), minerals (zinc, iron, calcium), vitamins (thiamine, folic acid and riboflavin) and fibre (6%) with low fat (<1%) (Sebetha *et al.*, 2014; Boukar *et al.*, 2015). Cowpea is a multifunctional legume grown for food, fodder, vegetables and green manure (Timko and Singh, 2008; Gonçalves *et al.*, 2016). Cowpea can be cultivated in subtropical, semitropical, and desert environments. It grows well on poor soil with a wide range of soil pH and it is resistant to high temperatures and low water constraints, thus it is an excellent choice for resource-limited small-scale farmers to sustenance (Carvalho *et al.*, 2017).

The development of an effective crop improvement programme depends upon the existence of genetic variability. Genetic variability is the measure of the tendency of distinct genotypes in a population to vary from each other. Variability depends on genetic factors, environmental factors (edaphic and climatic), and bioactive compounds (caused by physiological factors). The degree to which the variability of a quantitative character is transmitted to the progeny is referred to as heritability. It provides valuable biometrical concepts and has been considered to be an index of the effectiveness of selection because it helps in proportioning the total variation into heritable and environmental effects (Johnson *et al.*, 1955; Khan *et al.*, 2015).

MATERIALS AND METHODS

The experimental material consisted of 100 and 70 F₃ family rows derived from crosses VBN-1 × RC-19 (cross I) and KBC-9 × PGCP-6 (cross II), respectively. These F₃ family rows were evaluated during summer 2021 using Augmented Block Design with five checks (C-152, KBC-2, KBC-9, PGCP-6 and IT-803695-1) replicated five times and parents at the Department of Genetics and Plant Breeding, College of Agriculture, Kalaburagi. Each F₃ progeny family was sown in rows with a length of 4 meters and a spacing of 45 cm × 10 cm. Five competitive plants selected randomly from

each family row were used to record observation on ten traits viz., days to initiation of flowering, days to physiological maturity, plant height (cm), number of primary branches/plant, number of pods/plant, number of seeds/pod, pod length, test weight (g), dry matter/plant (g), seed yield/plant (g). The mean data of all traits were recorded and utilized for statistical analysis viz., genetic coefficient of variation (%), phenotypic coefficient of variation (%), heritability (%) (broad sense), genetic advance and genetic advance as per cent mean (%).

RESULTS AND DISCUSSION

Analysis of variance revealed that most of the segregants recorded significant variation for most of the traits, and it indicated the presence of sufficient variability for these characters (Table 1 and 2). ANOVA revealed that all segregants of both the populations were significantly different for all the traits studied. Similarly, the effects due to block, due to treatment, and due to check and variety were also significant for most of the traits studied, except days to maturity in the F_{2:3} population of KBC-9 × PGCP-6. This indicated that there is a significantly higher level of variability present among the segregating populations for all the yield-related characters studied. Similar findings were also observed by Verma *et al.* (2019), Nair *et al.* (2018) and Khan *et al.* (2015). Estimates of variability components viz., mean, range, genotypic coefficient of variation (GCV),

phenotypic coefficient of variation (PCV), heritability (h²) and genetic advance as per cent of mean (GAM) for all the yield contributing traits are presented in Table 3 for F_{2:3} population of VBN-1 × RC-19 (Fig. 1 and Fig. 2) and Table 4 for F_{2:3} population of KBC-9 × PGCP-6 (Fig. 3 and Fig. 4). Higher phenotypic coefficient of variation values than that of genotypic coefficient of variation values indicated the influence of environment on all traits. But, narrow differences between PCV and GCV values were observed for all the traits.

High PCV and GCV were recorded for plant height (21.06%, 20.46%), number of primary branches/plant (28.27%, 27.23%), dry matter/plant (22.45%, 21.98%) and seed yield/plant (27.47%, 26.66%) in F_{2:3} population of VBN-1 × RC-19; number of primary branches/plant (31.89%, 31.18%), number of pods/plant (27.31%, 26.73%), dry matter/plant (24.53%, 23.42%) and seed yield/plant (31.77%, 31.37%) in F_{2:3} population of KBC-9 × PGCP-6 suggesting that sufficient amount of variability is present among the segregants which can be further used in crop improvement programme. Similar findings were observed by Nair *et al.* (2018), Sheela (2017), Mahesh *et al.* (2017), Bhadru and Navale (2012), Khan *et al.* (2015), Meenatchi *et al.* (2019), Sabale *et al.* (2018), Shanko *et al.* (2014) and Khan *et al.* (2013).

Table 1: Analysis of variance in F_{2:3} segregating generation of cross VBN-1 × RC-19.

	DF	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
Block	4	169.22**	129.83**	258.35**	0.57 **	14.37**	9.55**	11.40 **	1.69 *	104.36 **	49.33 **
Check	6	93.77	95.54*	3.95**	31.74**	485.35**	35.00**	94.40**	161.28**	232.21**	10.62**
Entries	106	90.34**	96.69**	164.56**	1.51**	11.58**	6.92 **	6.44 **	3.05 **	81.88 **	42.03 **
Genotype	99	50.89*	64.07**	154.62**	1.30**	8.10**	5.23 **	5.22 **	1.81 **	74.71 **	37.57 **
Checks vs. Genotype	1	457.14**	3.85	39.39*	0.32*	12.00**	30.89**	22.87 **	70.59 **	184.92 **	20.49 **
Error	24	23.26	16.59	6.67	0.07	1.04	0.82	0.65	0.56	2.36	1.70

Note: * Significance at 0.05% of probability ** Significance at 0.5 % of probability

Where, X₁=Days to initiation of flowering, X₂=Days to physiological maturity, X₃=Plant height, X₄=Number of branches/plant, X₅= Number of pods/plant, X₆= Pod length, X₇= Number of seeds/pod, X₈=Test weight, X₉=Total dry matter content/plant, X₁₀=Seed yield/plant

Table 2: Analysis of variance in F_{2:3} segregating generation of cross KBC-9 × PGCP-6.

	DF	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀
Block	4	90.42**	208.14*	170.68**	2.02**	12.39**	1.42	5.14**	0.05	125.35**	63.92**
Check	6	45.60*	53.65	0.66**	6.47**	170.03**	5.6 **	35.09**	12.99 **	29.69**	5.29**
Entries	76	52.76**	67.28	114.88**	1.46**	13.80**	2.93**	3.24**	1.43**	62.89**	31.96**
Genotype	69	42.88**	50.69	111.08**	1.57**	11.00**	2.88**	3.08**	0.99**	66.24**	33.55**
Checks vs. Genotype	1	167.94**	512.24**	75.58*	0.01	146.43**	1.73	6.24**	13.27**	71.38**	33.37**
Error	24	14.39	58.47	10.72	0.05	0.32	0.81	0.38	0.41	4.15	0.58

Note: * Significance at 0.05% of probability ** Significance at 0.5 % of probability

Where, X₁=Days to initiation of flowering, X₂=Days to physiological maturity, X₃=Plant height, X₄=Number of branches/plant, X₅= Number of pods/plant, X₆= Pod length, X₇= Number of seeds/pod, X₈=Test weight, X₉=Total dry matter content/plant, X₁₀=Seed yield/plant

Table 3: Estimation of mean and genetic variability parameters in F_{2:3} segregating generation of cross VBN-1 × RC-19.

Sr. No.	Character	Mean	Range		Coefficient of variation		h ² _(bs) (%)	GAM at 5% mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1.	Days to initiation of flowering	61.85	49.00	76.00	10.81	7.45	47.48	10.58
2.	Days to physiological maturity	97.86	83.00	116.00	7.42	6.14	68.54	10.48
3.	Plant height (cm)	51.95	19.00	74.00	21.06	20.46	94.41	40.96
4.	Number of branches/plant	3.54	2.00	6.00	28.27	27.23	92.73	54.02
5.	Number of pods/plant	13.63	6.00	18.00	18.53	16.96	83.79	31.99
6.	Pod length (cm)	14.16	9.34	18.84	14.36	12.87	80.31	23.76
7.	Number of seeds/pod	12.58	8.00	17.00	16.08	14.77	84.38	27.95
8.	Test weight (g)	9.67	7.90	14.00	12.87	10.17	62.50	16.58
9.	Total dry matter content/plant (g)	33.59	16.43	54.90	22.45	21.98	95.88	44.35
10.	Seed yield/plant (g)	19.55	8.82	35.21	27.47	26.66	94.14	53.29

Table 4: Estimation of mean and genetic variability parameters in F_{2:3} segregating generation of cross KBC-9 × PGCP-6.

Sr. No.	Character	Mean	Range		Coefficient of variation		h ² _(bs) (%)	GAM at 5% mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to initiation of flowering	67.77	52.00	77.00	8.58	6.52	57.73	10.20
2	Days to physiological maturity	103.45	86.00	117.00	7.02	2.23	10.10	1.46
3	Plant height (cm)	49.19	27.67	73.67	18.19	16.86	86.60	32.32
4	Number of branches/plant	3.28	2.00	6.00	31.89	31.18	95.58	62.79
5	Number of pods/plant	10.00	4.00	17.00	27.31	26.73	95.79	53.89
6	Pod length (cm)	12.56	9.00	17.50	11.94	9.53	63.67	15.66
7	Number of seeds/pod	10.43	7.00	15.00	14.43	13.14	82.91	24.64
8	Test weight (g)	11.25	7.90	14.00	7.94	5.59	49.44	8.09
9	Total dry matter content/plant (g)	28.11	16.62	59.76	24.53	23.42	91.16	46.06
10	Seed yield/plant (g)	15.31	7.21	34.90	31.77	31.37	97.52	63.82

Moderate PCV and GCV were recorded for the number of pods/plant (18.53%, 16.96%), pod length (14.36%, 12.87%), number of seeds/ pod (16.07%, 14.77%) and test weight (12.87%, 10.17%) in F_{2:3} population of VBN-1 × RC-19; plant height (18.19%, 16.86%) and number of seeds/pod (14.43%, 13.14%) in F_{2:3} population of KBC-9 × PGCP-6. Similar findings were also recorded by Sabale *et al.* (2018) and Dinesh *et al.* (2017a). Low PCV and GCV were recorded for days to physiological maturity (7.42%, 6.14%) in F_{2:3} population of VBN-1 × RC-19; days to initiation of flowering (8.58%, 6.52%), days to physiological maturity (7.02%, 2.23%) and test weight (7.94%, 5.59%) in F_{2:3} population of KBC-9 × PGCP-6. Similar findings were also recorded by Sabale *et al.* (2018) and Dinesh *et al.* (2017a). This indicates the presence of low genetic variability and non additive gene action for these traits. Hence, there is a limited scope for selection for traits with low variability. *i.e.*, selection is not effective for these traits.

High heritability and GAM were recorded for plant height (94.41%, 40.96%), number of primary branches/plant (92.73%, 54.02%), number of pods/plant (83.79%, 31.99%), pod length (80.31%, 23.76%), number of seeds/ pod (84.38%, 27.95%),

dry matter/plant (95.88%, 44.35%) and seed yield/plant (94.14%, 53.29%) in F_{2:3} population of VBN-1 × RC-19; plant height (86.60%, 32.32%), number of primary branches/plant (95.58%, 62.79%), number of pods/plant (95.79%, 53.89%), number of seeds/ pod (82.91%, 24.64%), dry matter/plant (91.16%, 46.06%) and seed yield/plant (97.52%, 63.82%). Similar findings were reported by Verma *et al.* (2019), Meenatchi *et al.* (2019), Khan *et al.* (2013), Nair *et al.* (2018), Sheela (2017), Sabale *et al.* (2018), Mahesh *et al.* (2017), Bhadru and Navale (2012), Dinesh *et al.* (2017a), Dinesh *et al.* (2017b) and Khan *et al.* (2015). This indicates that the character is least influenced by the environment due to the presence of additive gene action. Here, selection based on phenotypic values for these traits could be more reliable.

Moderate heritability and GAM were recorded for days to initiation of flowering (47.48%, 10.58%) in F_{2:3} population of VBN-1 × RC-19; days to initiation of flowering (57.73%, 10.20%) in F_{2:3} population of KBC-9 × PGCP-6 indicating the presence of additive and non-additive gene action. Similar findings were recorded by Nair *et al.* (2018) and Verma *et al.* (2019). High heritability and moderate GAM were reported for

days to physiological maturity (68.54%, 10.48%) and test weight (62.5%, 16.58%) in F_{2:3} population of VBN-1 × RC-19 indicating the influence of additive and non-additive gene action and less influence of the environment for expression of the trait. Low heritability and GAM were reported for days to physiological maturity (10.10%, 1.46%) in F_{2:3} population of KBC-9 × PGCP-6 which indicates high environmental influence on this trait. Hence, selection will be difficult due to the masking effects of the environment on genotypic effects.

Estimates of PCV, GCV, heritability and genetic advance as per mean were moderate to high for days to physiological maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight, dry matter per plant and seed yield per plant for both the F_{2:3} populations except days to initiation of flowering and days to physiological maturity in F_{2:3} populations of VBN-1 × RC-19; days to initiation of flowering, days to physiological maturity and test weight in F_{2:3} populations of KBC-9 × PGCP-6, this indicating that these traits are predominantly governed by additive genetic variance and parents are diverse with respect to most of the traits studied. Hence, there is a scope for selection for these traits with moderate to high variability. *i.e.*, selection is effective for these traits.

Moderate PCV and low GCV were observed for days to initiation of flowering in F_{2:3} populations of VBN-1 × RC-19. While, Low PCV and GCV were observed for days to physiological maturity in F_{2:3} populations of VBN-1 × RC-19; days to initiation of flowering, days to physiological maturity and test weight in F_{2:3} populations of KBC-9 × PGCP-6, indicating the presence of low genetic variability and non additive gene action for these traits. Hence, there is a limited scope for selection for traits with low variability. *i.e.*, selection is not effective for these traits.

CONCLUSION

High phenotypic coefficient of variance and genetic coefficient of variance were recorded for plant height, number of primary branches/plant, dry matter/plant and seed yield/plant in F_{2:3} population of VBN-1 × RC-19. High heritability coupled with medium genetic advance as per cent of mean indicated the presence of both additive and non-additive gene actions for the inheritance of these characters and high genotype × environment interaction.

FUTURE SCOPE

These characters could be improved suitably by modified selection procedure for mixed effects of additive and non additive gene actions like cyclic hybridization followed by selection. These characters and simple selection helps in development of high yielding cowpea genotypes.

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Conflict of Interest. None.

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