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ESTIMATION OF GENETIC VARIABILITY FOR DUAL PURPOSE IN COWPEA (*VIGNA UNGUICULATA* (L.) WALP)

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Abstract

An experiment was conducted to estimate genetic variability, heritability and genetic advance expressed as per cent of mean, an investigation was carried out with 110 plants out of 1500 of F_2 population of MFC-09-12 x BL-2 and 90 out of 1500 plants of F_2 population of UPC-622 × EC-4216 in cowpea. Considerably high amount of variability was observed for the fifteen quantitative and qualitative characters under study. Environmental influence was minimum for the expression of most of the traits which is evident from narrow difference between phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) estimates. In both the populations, heritability in broad sense was high for most of the traits coupled with high genetic advance as per cent over mean indicated presence of additive gene action for the characters. Good number of superior segregants were isolated for seed yield and green fodder yield related traits from both the population. Highest number of superior segregants were isolated for stover yield per plant from MFC-09-12 × BL-2 cross while days to maturity from the cross of UPC-622 × EC-4216 in comparison to checks BL-1 and EC- 4216.

Key words: variability, dual purpose, F_2 population, superior segregants, heritability.

Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is of major importance to the livelihoods of millions of people in the tropics. Resource-poor small-holder farmers derive food, animal feed, cash and manure from the crop. Dual purpose cowpea has the potential to function as a key integrating factor in intensifying systems through supplying protein in human diets and fodder for livestock, as well as bringing N into the farming system through biological fixation. It has been suggested that cowpea varieties with semi-erect growth would be ideal for dual-purpose use (Singh *et al.*, 2003).

It is a highly self-pollinated crop and the procedures in use for cultivar development have followed the conventional methods of individual plant selection in naturally occurring or hybridization induced genetic variability, following the pedigree method of breeding (Allard, 1960). An important assumption underlying early generation selection generally adopted for self-pollinated species is that selection for a character in the early generation (F_2 or F_3) would be as effective as when practiced in the later generations assuming high heritability (Allard, 1960). An early and accurate appraisal of segregates has been of vital interest to most breeders of self pollinated species. Hence, there is a need for early generation testing and evaluation for better recovery of segregants (Moalafi *et al.*, 2010). Mahmud and Kramer, 1951 have indicated the two closely related problems *viz*., selection of those crosses which are most likely to give the highest proportion of superior segregates and evaluation of the potentialities of the segregates from those crosses. The success of any crop improvement programme depends on the magnitude of genetic variability and the extent to which the desirable trait is heritable. The presence of genetic variability in breeding material has been emphasized by Falconer (1960), as base for exercising central selection pressure. With this background an attempt was made to study the variability for dual purpose traits in F_2 populations of cowpea.

Material and methods

The released varieties and advanced breeding lines were evaluated for dual purpose traits. Based these traits, eight genotypes were selected and crossed in 8 × 8 half

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diallel fashion and 28 F_1's were generated. The 28 F_1's along with their parents and check evaluated in randomized block design with two replications. All the packages of practices followed to raise the crop. The F_1 plants were allowed for self pollination to generate F_2 seeds. Based on combining ability of twenty eight crosses and their parents for seed yield and green fodder yield related traits, two crosses *viz.,* MFC-09-12 × BL-2 and UPC-622 × EC-4216 were selected for estimation of genetic variability in F_2 generation. The F_2 seeds of cross MFC-09-12 × BL-2 and UPC-622 × EC-4216 along with their parents were sown at Indian Grassland and Fodder Research Institute, SRRS, Dharwad during *rabi*/summer 2014-15. There were two plots of size 65 m × 4 m accommodating approximately 1500 plants in each cross with a spacing of 45 cm × 15 cm. All packages of practices were followed to raise the crop. At first flowering stage, plants were harvested for green fodder yield leaving three nodes from base of the plant. It was followed by application of fertilizer and irrigation for regeneration of the crop. Observations *viz.,* number of pods per plant, number of seeds per pod, pod length (cm), test weight (g), seed yield per plant (g), days to maturity and stover yield per plant (g) were recorded on regenerated plant while, observations like plant height (cm), days to first flowering, number of primary branches per plant, number of secondary branches per plant, green fodder yield per plant (g), leaf to stem ratio, dry matter content (%) and crude protein content (%) were recorded prior to harvest. The crude protein content was estimated by the Kjeldahl method (Kjeldahl, 1883) determining total nitrogen content of the plant tissue. In order to estimate crude protein, total nitrogen content is multiplied with 6.26 since it is assumed that average protein content of pulse is 16 per cent and 100 divide by 16 gives 6.25.

Results and Discussion

Wide range of variation was observed among the selected F_2 populations for the characters under study compare to their

Table 1: Mean performance and variance in parents and F_2 population of MFC-09-12 × BL-2 cross for fifteen characters in cowpea.

Statistical parameters	Generation (Parental/F_2)	Plant height (cm)	No. of primary branches	No. of secondary branches	Leaf to stem ratio	Days to first flowering	Days to maturity	No. of pods per plant
Mean	MFC-09-12	96.10	5.40	4.20	1.41	71.40	111.60	12.80
	BL-2	101.60	4.20	4.00	1.31	73.80	116.60	14.40
	F_2 (MFC-09-12 × BL-2)	90.72	4.71	3.50	1.32	82.60	116.70	10.49
Range	F_2 (MFC-09-12 × BL-2)	23 to 210	2 to 8	0 to 11	0.52 to 2.72	65 to 96	98 to 130	4 to 40
Variance	MFC-09-12	587.60	1.30	5.20	0.04	5.80	14.30	4.70
	BL-2	461.77	0.70	3.50	0.07	9.20	40.30	15.30
	F_2 (MFC-09-12 × BL-2)	1831.72	2.10	6.50	0.19	66.30	56.60	42.70

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Statistical parameters	Generation (Parental/F_2)	No. of seeds per pod	Pod length (cm)	Test weight (g)	Seed yield per plant (g)	Green fodder yield per plant (g)	Dry matter content (%)	Stover yield per plant (g)	Crude protein content (%)
Mean	MFC-09-12	12.65	14.11	11.22	13.93	230.00	13.84	174.04	22.58
	BL-2	12.28	13.31	12.14	14.81	201.80	13.4	168.80	20.89
	F_2 (MFC-09-12 × BL-2)	12.28	13.8	12.46	13.24	142.57	13.89	181.30	23.57
Range	F_2 (MFC-09-12 × BL-2)	6.67 to 16.33	8.67 to 9.50	9.80 to 15.91	4 to 46.18	20 to 476	8.33 to 19.70	72 to 362	19.04 to 28.66
Variance	MFC-09-12	0.15	0.19	0.25	3.29	356.76	0.52	1805.71	0.69
	BL-2	0.96	0.54	0.47	6.52	513.20	0.62	860.80	1.61
	F_2 (MFC-09-12 × BL-2)	3.83	4.63	2.04	61.8	2562.54	6.25	5140.99	12.76

Table 2: Mean performance and variance in parents and F_2 population of UPC-622 × EC-4216 cross for fifteen characters in cowpea

Statistical parameters	Generation (Parental/F_2)	Plant height (cm)	No. of primary branches	No. of secondary branches	Leaf to stem ratio	Days to first flowering	Days to maturity	No. of pods per plant
Mean	UPC-622	93.00	4.60	4.20	1.52	70.80	112.80	12.80
	EC-4216	105.30	4.20	4.00	1.48	74.20	120.00	14.20
	F_2 (UPC-622 × EC-4216)	70.00	4.40	2.80	1.54	75.30	108.20	9.60
Range	F_2 (UPC-622 × EC-4216)	16 to 156	1 to 8	0 to 9	0.83 to 3.00	61 to 86	95 to 123	4 to 28
Variance	UPC-622	64.00	2.30	5.70	0.07	4.20	31.70	11.70
	EC-4216	127.33	1.70	1.50	0.01	5.20	15.50	16.20
	F_2 (UPC-622 × EC-4216)	855.89	1.80	5.30	0.18	30.90	35.90	28.40

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Statistical parameters	Generation (Parental/F_2)	No. of seeds per pod	Pod length (cm)	Test weight (g)	Seed yield per plant (g)	Green fodder yield per plant (g)	Dry matter content (%)	Stover yield per plant (g)	Crude protein content (%)
Mean	UPC-622	13.14	14.29	11.02	13.59	223.20	13.82	225.80	21.04
	EC-4216	13.34	14.19	10.10	13.87	217.60	13.94	147.00	20.45
	F_2 (UPC-622 x EC-4216)	11.9	14.25	11.82	11.29	152.50	14.71	161.91	24.77
Range	F_2 (UPC-622 x EC-4216)	5.50 to 17.00	8.00 to 21.67	9.24 to 15.90	4.18 to 36.23	90 to 320	8.33 to 22.58	66 to 302	15.16 to 29.57
Variance	UPC-622	0.21	1.00	0.28	8.32	499.20	1.29	704.20	0.88
	EC-4216	0.21	0.61	0.51	11.27	690.80	0.40	216.00	0.44
	F_2 (UPC-622 x EC-4216)	5.27	7.82	4.72	39.34	2479.70	11.02	2970.17	22.60

parents (tables 1 and 2). The present findings were in accordance with result of Moalafi *et al.,* 2010 which indicated significant difference among thirty F_2 populations of cowpea for days to fifty per cent flowering, days to pod maturity, pod length, number of pods per plant, 100-seed weight and grain yield thus indicating the presence of genetic variability among the seregating progenies. Dhole and Reddy (2011) reported variability for test weight and seed yield in F_2 population of mungbean. Interestingly it was noted that the mean performance of F_2 was higher than their respective parents for test weight, dry matter content, stover yield per plant and crude protein content in F_2 population of MFC-09-12 × BL-2 while for test weight, leaf to stem ratio, dry matter content and crude protein content in F_2 population of UPC-622 × EC-4216 indicating chances of recovering more number of superior segregants for these characters in both the populations. In addition to this, very interesting observation was that the value of upper range for most of the characters was double than mean value of F_2 populations which clearly indicates greater scope for isolation of more number of segregants for different characters.

Superior segregants were isolated for green fodder yield per plant, seed yield per plant, stover yield per plant and days to maturity (table 3) since these traits directly contributes to the dual purpose nature of cowpea. It was observed that maximum per cent of segregants were obtained for stover yield per plant in F_2 population of cross MFC-09-12 × BL-2 in comparison to BL-1 and EC-4216. Whereas in the cross UPC-622 × EC-4216, maximum per cent of segregants were obtained for days to maturity indicating development of early types from this population. Eleven plants each from both F_2 populations were identified superior for all these traits and advanced to next generation to develop dual purpose genotypes.

Genetic parameters were also calculated for these populations (tables 4 and 5). The PCV and GCV were high for plant height, number of secondary branches per plant, number of pods per plant, seed yield per plant,

Table 3: Superior segregants in F_2 population for various characters over checks.

Population	No. of plants	Green fodder yield /plant (g)	Seed yield per plant (g)	Stover yield per plant (g)	Days to maturity	No. of plants common for four characters
F_2 (MFC-09-12 × BL-2)	110	35 (32.11)a	27 (24.77)a	57 (52.29)a	36 (33.03)a	11 (10.00)
		18 (16.51)b	23 (21.10)b	49 (44.95)b	44 (40.37)b	
F_2 (UPC-622 × EC-4216)	90	31 (34.44)a	13 (14.44)a	38 (42.22)a	53 (58.89)a	11 (12.22)
		15 (16.67)b	10 (11.11)b	31 (34.44)b	46 (51.11)b	
BL-1 (check I)	-	155.20	16.23	157.60	114.40	
EC-4216 (Check II)	-	217.60	17.12	177.60	112.25	

* Values in parenthesis are percentage fig a - superior segregants scored over checks I b - superior segregants scored over checks II

Table 4: Estimation of genetic parameters for fifteen quantitative characters in F_2 population of MFC-09-12 × BL-2.

Characters	Mean	Range		PCV	GCV	h^2 (%)	GA	GAM (%)
		Min	Max					
Plant height (cm)	90.72	23.00	210.00	47.17	39.33	69.52	61.29	67.56
No. of primary branches per plant	4.71	2.00	8.00	30.78	23.90	60.28	1.80	38.22
No. of secondary branches per plant	3.50	0.00	11.00	73.02	51.43	49.61	2.61	74.62
Leaf to stem ratio	1.32	0.52	2.72	33.04	24.88	56.70	0.51	38.59
Days to first flowering	82.63	65.00	96.00	9.86	9.26	88.30	14.82	17.93
Days to maturity	116.72	98.00	130.00	6.45	4.91	58.04	8.99	7.71
No. of pods per plant	10.49	4.00	40.00	62.47	53.29	72.77	9.85	93.65
No. of seeds per pod	12.28	6.67	16.33	15.94	14.95	88.03	3.55	28.9
Pod length (cm)	13.80	8.67	19.50	15.60	15.05	93.15	4.13	29.93
Test weight (g)	12.46	9.80	15.91	11.46	10.58	85.27	2.51	20.13
Seed yield per plant (g)	13.24	4.00	46.18	59.38	53.35	80.72	13.07	98.74
Green fodder yield per plant (g)	142.57	20.00	476.00	48.21	35.59	54.51	77.18	54.13
Dry matter content (%)	13.89	8.33	19.70	17.99	16.54	84.53	4.35	31.33
Stover yield per plant (g)	181.30	72.00	362.00	39.55	32.09	65.83	97.24	53.63
Crude protein content (%)	23.57	19.04	28.66	15.15	13.79	82.88	6.10	25.87

Legends: GCV= Genotypic coefficient of variation h^2 = Heritability PCV= Phenotypic coefficient of variation GA= Genetic advance GAM= Genetic advance expressed in per cent mean

green fodder yield per plant, leaf to stem ratio and stover yield per plant in both the populations. Whereas, high PCV and GCV were recorded for number of primary branches per plant in F_2 of MFC-09-12 × BL-2 and dry matter content in F_2 of UPC-622 × EC-4216. Similar trend was observed by Mary and Gopalan (2006) for plant height, number of branches, number of leaves, leaf weight, stem weight and green fodder yield in cowpea. Higher magnitude of PCV, GCV, coupled with broad sense heritability and genetic advance in percentage over mean for number of pods per plant, 100- seed weight and seed yield per plant in F_2 population while seed yield per plant in F_3 population of cowpea reported by Salimath *et al*. (2007). Moderate PCV and GCV were recorded for pod length, number of seeds per pod, test weight and crude protein content. Mary and Gopalan (2006) also reported similar trend for leaf to stem ratio, crude protein content and dry matter yield in F_3 generation. Low PCV and GCV were recorded for days to first flowering and days to maturity. Interestingly narrow difference was observed for most of the characters indicating these characters were less influenced by environmental factors. Earlier reports of Mary and Gopalan (2006) indicated similar trend for plant height, number of branches, number of leaves, leaf length, leaf weight, stem weight, leaf to stem ratio, green fodder yield, dry matter yield and crude protein content in F_3 and F_4 populations of fodder cowpea. Salimath *et al*. (2007) also reported narrow range of variation between PCV and GCV for number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plant in F_2 and F_3 populations of cowpea.

The variability found in the F_2 populations of the evaluated crosses would provide greater scope for the recovery of superior segregants for dual purpose in

Table 5: Estimation of genetic parameters for fifteen quantitative characters in F_2 population of UPC-622 × EC-4216.

Characters	Mean	Range		PCV	GCV	h^2 (%)	GA	GAM (%)
		Min	Max					
Plant height (cm)	70.00	16.00	156.00	41.79	41.66	99.37	59.60	85.14
No. of primary branches per plant	4.37	1.00	8.00	31.04	11.96	14.85	0.41	9.45
No. of secondary branches per plant	2.79	0.00	9.00	82.14	58.07	49.98	2.35	84.16
Leaf to stem ratio	1.54	0.83	3.00	27.67	23.34	71.12	0.62	40.35
Days to first flowering	75.27	61.00	86.00	7.39	6.71	82.55	9.41	12.50
Days to maturity	108.22	95.00	123.00	5.54	1.79	10.42	1.28	1.18
No. of pods per plant	9.57	4.00	28.00	55.69	39.83	51.14	5.58	58.39
No. of seeds per pod	11.90	5.50	17.00	19.29	18.56	92.58	4.36	36.60
Pod length (cm)	14.25	8.00	21.67	19.63	18.50	88.85	5.09	35.76
Test weight (g)	11.82	9.24	15.90	18.37	17.74	93.25	4.17	35.30
Seed yield per plant (g)	11.29	4.18	36.23	55.56	49.76	80.20	10.31	91.35
Green fodder yield per plant (g)	152.53	90.00	320.00	32.65	29.67	82.57	84.29	55.26
Dry matter content (%)	14.71	8.33	22.58	22.57	21.72	92.60	6.30	42.84
Stover yield per plant (g)	161.91	66.00	302.00	33.66	31.08	85.26	95.26	58.83
Crude protein content (%)	25.14	15.16	29.57	19.19	18.90	97.00	9.50	38.35

Legends: GCV= Genotypic coefficient of variation h^2 = Heritability PCV= Phenotypic coefficient of variation GA= Genetic advance GAM= Genetic advance expressed in per cent mean

cowpea in further generations. The promising segregants identified from such population may be useful in the future plant breeding programmes.

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