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Variability Studies in F_2, M_2 and F_2M_2 Populations of Cowpea (*Vigna unguiculata* L. Walp.)

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Abstract

Cowpea (*Vigna unguiculata* L. Walp.) is one of the important multipurpose grain legume cultivated throughout the world in arid and semi-arid tropics. Variability in cowpea is reported to be meager and the extent of variability released by hybrridization has been often reported to be inadequate. As variability is the prerequisite for improvement of crop, so in the present study, an investigation was carried out to compare the variability generated through hybridization, mutation and combination of both. One locally adopted cultivar C-152 was crossed with selected genotypes, KM-3 and KM-5. After hybridization, mutation and combination of both, the F_2, F_2M_2 and M_2 populations were evaluated for variability parameters. Reduction in the mean value for the most of the yield attributing traits was noticed in irradiated populations compared to hybridized population. Generally a wider range and higher upper limit of range values in the positive direction were observed in F_2M_2 compared to their corresponding F_2 populations indicating the effectiveness of mutation on hybridized population in creating the transgressive segregants which would allow the breeder to select for rare genotypes. The GCV, heritability and GAM values were less in F_2M_2's compared to their corresponding F_2's for plant height, number of primary branches per plant, number of pods per cluster and seed yield per plant. For other traits GCV, heritability and GAM values were higher in F_2M_2's compared to their corresponding F_2 populations.

Key words : *Vigna unguiculata*, Cowpea, Hybridization, Mutation, Variability.

Amongst the grain legumes grown in world, cowpea (*Vigna unguiculata* L. Walp.) is of immense importance as a multipurpose grain legume crop extensively cultivated in arid and semi-arid tropics. Cowpea fits well in different cropping systems and seasons due to its relative short duration, drought tolerance and photo-insensitive nature. Lack of sufficient genetic variability for economically important characters is one of the reasons attributed for the lack of yield improvement in cowpea. Besides being predominantly self pollinated, inherent variability in cowpea is much circumscribed by vulnerability of their flowers to artificial manipulation which renders production of large scale variability through hybridization and intermating a laborious exercise. The extent of variation released by hybridization in cowpea has been often reported to be inadequate. Under such circumstances induced mutagenesis, as an alternative or as a supplement to hybridization offers opportunities to improve the locally adopted varieties with regard to specific traits. Recent studies also have shown that the possible application of this technique in improving polygenic traits. Mutation studies by using gamma rays and chemical mutagens both singly and in combination showed significant increase in seed yield in greengram.C-152 cultivar which is a standard variety of southern India known for its seed quality lacks many economically important traits besides being indeterminate in growth habit. In the germplasm evaluation conducted at Department of Genetics and Plant Breeding, University of Agriculture Sciences, Dharwad, two entries viz., KM-3 and KM-5 were identified as promising genotypes with distinct growth habit associated with specific productivity related traits. These two promising genotypes along with a standard variety, C-152 were used in the present study. By considering all these points, the present study was made to create and evaluate

Table 1. Genetic variability parameters for important yield component traits in F_2 populations of cowpea.

	F_2 (C-152 × KM-3)						F_2 (C-152 × KM-5)					
Traits	Mean	Range	PCV	GCV	h^2_b (%)	GAM (%)	Mean	Range	PCV	GCV	h^2_b (%)	GAM (%)
Clusters per plant	8.51	2-26	41.28	31.69	58.92	50.11	10.12	2-27	49.05	43.49	78.63	79.45
Pods per cluster	1.67	1-3.33	28.83	22.81	62.61	37.18	1.65	1-3.3	23.85	17.09	51.36	25.23
Pods per plant	14.14	3-34	46.64	36.95	62.76	60.29	16.48	1- 42	50.81	43.49	73.28	76.70
Pod length (cm)	14.82	11.4-18.2	8.56	7.37	74.1	13.07	14.89	10.4-21	9.47	7.18	57.46	11.21
Seeds per pod	12.16	5.8-15.4	12.49	11.33	82.4	21.19	13.32	8.2-21	15.14	13.79	83.04	25.89
Hundred seed weight (g)	10.75	6-14.34	13.61	13.03	91.63	25.69	10.99	6.48-14.92	12.6	12.04	91.31	23.69
Seed yield per plant (g)	16.39	3.73-45.38	50.82	41.16	65.60	68.67	21.16	3.34-58.18	42.78	33.68	61.97	54.61

variability generated by different approaches namely, hybridization, mutation and combination of both to generate better segregating populations which would serve as potential base population for further varietal development.

Methods

Three inbred lines maintained through continuous selfing were used in this experiment, among them, one was locally adopted variety C-152, grown popularly in southern India known for its seed quality but lacks the traits like sufficient pod numbers and pod length. Other two lines were KM-3 and KM-5 known for their pod length and pods per plant respectively. The cultivar C-152 was used as common female parent and KM-3 and KM-5 were used as male parents. One thousand seeds of C-152 and F_1seeds of each cross (C-152 × KM-3 and C-152 × KM-5) were treated with 25 KR gamma radiation at Baba Atomic Research Center, Mumbai. All three populations viz., M_1 of C-152 and F_1M_1 of C-152 × KM-3 and C-152 × KM-5 were selfed to obtain M_2 and F_2M_2 seeds. All ten populations comprising of two single crosses (F_1's), F_2 and F_2M_2 populations of two crosses and M_2 of C-152 along with three parents were space planted at botany garden of Agriculture College, Dharwad during *rabi*-summer of 2000-01 at a distance of 45 cm between rows and 10 cm within the rows. Observations on important yield component characters were recorded on 200 plants in each F_2, 300 plants from each F_2M_2 and M_2 and 15 plants from each parent and single crosses. Estimates of mean, range, phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), Heritability in broad sense and genetic advance as per cent of mean (GAM) were computed by following standard method.

Results and Discussion

The comparison of mean performance of different traits between F_2, F_2M_2 and M_2 populations indicated that the mean values in general were relatively higher in F_2 compared to M_2 and F_2M_2 for most of the characters which is in line with the earlier reports of Virupakshappa et al. (1) and Mahishi (2). Negative shift in the mean values following mutagen treatment has been reported as general phenomenon and attributed to the occurrence of deleterious or harmful mutations, which are supposed to occur more frequently in early generations than later generations. Irradiated populations of hybrids (F_2M_2's) exhibited wider range than the F_2 populations for all the characters studied (Tables 1 and 2) except for pod length and seeds per pod in F_2M_2 of cross C-152 × KM-5. An increase in range in F_2M_2 relative to their corresponding F_2 populations was reported by earlier as Swamy (3) in sesame and Rooplakshmi (4) in blackgram. An upper limit of range was found to increase in F_2M_2 populations compared to F_2 of the both crosses for all the characters studied except pod length and seeds per pod in F_2M_2 of cross C-152 × KM-5. Virk et al. (5) and Katoch et al. (6) reported increase in variability may be the result of irradiation bringing about mutations in the minor genes governing polygenically inherited characters or by increasing the frequency of crossing over between genes governing closely related traits. This shows that irradiation has been useful to enhance the variability over hybridization alone. Therefore, it would offer better scope for the breeders to isolate transgressive segregants for the group of important characters like pods per plant, higher

Table 2. Genetic variability parameters for important yield component traits in F_2M_2 populations of cowpea.

	F_2M_2 (C-152 × KM-3)						F_2M_2 (C-152 × KM-5)					
Traits	Mean	Range	PCV	GCV	h^2_b (%)	GAM (%)	Mean	Range	PCV	GCV	h^2_b (%)	GAM (%)
Clusters per plant	8.87	3-27	43.68	35.53	66.17	59.54	8.9	2-28	53.22	46.55	76.53	83.9
Pods per cluster	1.57	1-3.45	21.42	10.27	22.98	10.14	1.64	1-3.75	23.81	16.89	50.32	24.68
Pods per plant	13.89	1-43	48.04	38.32	63.62	62.96	14.55	3-54	58.13	49.94	73.81	88.38
Pod length (cm)	14.65	8.4-19.2	10.13	9.12	81.08	16.92	14.61	10-18.8	10.22	8.05	62.04	13.07
Seeds per pod	11.8	3.4-17.7	17.86	17.02	90.87	33.43	12.08	5.8-17	17.14	15.71	83.93	29.64
Hundred seed weight (g)	10.41	4.9-16.1	14.07	13.47	91.64	26.56	10.76	6.22-18.08	14.97	14.49	93.58	28.87
Seed yield per plant (g)	15.09	2.6-53.45	53.46	42.54	63.32	69.74	16.9	3.62-61.44	54.85	43.78	63.70	71.98

hundred seed weight and higher seed yield per plant than in simple hybridization program. Further, M_2 of C-152 exhibited narrow range for almost all the characters with lower range of upper limit compared to both F_2 and F_2M_2 suggesting the inefficiency of mutation, when used alone in creating wide range for the characters (Tables 1 to 3). Phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) values showed wide variation for most of the characters in all five segregating populations. Similar results were reported by Paramasivan and Rajasekharan (7) in greengram. In general irradiated populations revealed highest PCV and GCV for seed yeld per plant, number of pods per plant and number of clusters per plant indicating that there is greater scope for selection for improvement of these characters in desirable direction. No definite trend was observed regarding magnitude of PCV and GCV within and among F_2 and F_2M_2 populations (Tables 1 and 2). Among F_2 populations, the cross C-152 ×KM-3 recorded highest PCV and GCV for number of pods per cluster, while the cross C-152 × KM-5 showed highest PCV and GCV for number of clusters per plant, number of pods per plant. The important seed yield contributing traits such as number of clusters per plant and number of pods per plant recorded larger differences between PCV and GCV values in F_2, M_2 and F_2M_2 populations indicating the greater role of environment in expression of these traits. However, the effect of environment was low on hundred seed weight and number of seeds per pod in all populations. The PCV and GCV values in case of M_2 of C-152 were on par with F_2 for some traits and F_2M_2 for some other traits indicating the non-cumulative effect of mutation in F_2M_2. Since the effective dosages of mutagens may vary from genotype to genotype and also the extent of variability generated for particular character is dependent on the genetic architecture of quantitative loci, it is difficult to draw any general conclusion on this respect.

In the present study increased heritability was observed in the F_2M_2's relative to their F_2 populations for number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and hundred seed weight whereas, for number of pods per cluster, the F_2 population exhibited higher heritability. However, few crosses had also exhibited decline in heritability. Saini and Sharma (8) observed increase in magnitude of heritability in mutagen treated hybrid populations of rice. Change in heritability towards higher side is probably due to the increased proportion of genetic variance to total phenotypic variance, occurring due to cryptic genetic changes brought about by mutations.

High heritability values of more than 90% have been observed or hundred seed weight in all segregating populations and for number of seeds per pod in F_2M_2 of cross C-152 ×KM-3. The highest heritability estimates of as high as 95.50% was observed in M_2 of C-152 indicating whatever the variations occurred due to mutations are mainly genetic and less influenced by environment. High heritability estimates have been reported earlier (9—13). The heritability in broad sense for seed yield and other important yield component traits such as number of pods per plant, number of clusters per plant and pod length were low to moderate. Thus improvement for yield through above components should be based not only on simple selection but also on progeny test as cowpea is considered as highly plastic as for as the expres-

Table 3. Genetic variability parameters for important yield component traits in M_2 population of cowpea variety C-152.

	M_2 of C-152					
Traits	Mean	Range	PCV	GCV	h^2_b (%)	GAM (%)
Cluters per plant	9.09	1-26	49.52	43.41	76.85	78.39
Pods per cluster	1.44	1-3.75	24.46	9.89	16.34	8.24
Pods per plant	12.87	2-33	49.64	36.82	55.01	56.26
Pod length (cm)	13.77	9.8-17.2	10.35	9.56	85.3	18.19
Seeds per pod	11.64	6.4-15.6	15.84	15.44	95.01	30.99
Hundred seed weight (g)	10.23	5.16-13.42	14.45	14.13	95.55	28.45
Seed yield per plant (g)	13.57	0.93-37.58	54.98	41.76	57.69	65.34

sion of morphological characters are concerned. In M_2 of C-152, low heritability was observed for number of pods per cluster and number of pods per plant compared in F_2 and F_2M_2 populations (Tables 1to 3).

Genetic advance can however help to predict the extent of improvement that can be achieved for improving the different traits. A high genetic gain along with high heritability would suggest better scope for selection. The genetic advance was high for seed yield per plant and number of pods per plant in almost all populations as reported by Biradar et al. (13). Sawant, (14); Kalaiyarasi and Palanisamy (15). The high genetic advance coupled with moderate to high heritability for these traits suggest the importance of additive gene action for these traits, implying that the performance can be repeated through individual plant selection. Comparison of genetic advance as per cent of mean (GAM) value of all populations revealed higher advance for number of pods per plant, number of clusters per plant, seed yield per plant and moderate genetic advance with high heritability estimates for hundred seed weight. As observed in respect of heritability estimates, pods per plant, clusters per plant and seed yield per plant recorded higher estimates of genetic advance as per cent of mean .Therefore priority should be given to these traits while deciding selection strategies and selection based on these characters would prove useful in realizing better gains by selection.

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