Efficiency of breeding methods in early segregating generations in cowpea [*Vigna unguiculata* (L.) Walp.]

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Abstract

The segregating generations from the crosses C152 × APC412 and TVX944-02E × APC255 of cowpea [*Vigna unguiculata* (L.) Walp.] were advanced through pedigree, bulk and single seed descent (SSD) methods. The selection was made from F_2 based on seed yield per plant and advanced to F_3 and F_4 generations. The SSD populations matured early followed by bulk and pedigree populations. The shift in the means in positive direction were better achieved through pedigree method as compared to bulk and SSD methods in F_3 to F_4 generations for all the traits in both the crosses, whereas, in SSD and bulk populations the shift in the means were in either directions. The pedigree populations had high heritability estimates. The bulk and SSD populations had moderate to high value of heritability and genetic advance for most of the traits. For throwing superior segregants, the pedigree and SSD populations were equally efficient, but the bulk method turned out to be less efficient.

Key Words: Cowpea, pedigree, bulk, single seed descent, heritability, genetic advance.

Introduction

The poor average yields of cowpea [*Vigna unguiculata* (L.) Walp.] speak of the need for adopting appropriate method of handling segregating populations to ensure quick progress in the plant breeding programmes. In the genetic improvement of autogamous crops the selection methods followed after hybridization are pedigree, bulk and their modified versions. In the later years, the single seed descent (SSD) method [1] came into practice. In cowpea, there are very few studies where in, these methods are compared for their efficiency. These studies in general, concluded that the SSD method showed similar performance as that of pedigree method [2,3]. Ntare *et al.*, [4] also suggested that the SSD procedure has considerable merits and should be adopted when resources are limited. However, more and more such studies are required to confirm and generalise the relative efficiencies of different methods for cowpea. Keeping this in view, the present study was taken-up to compare the efficiency of pedigree, bulk and SSD methods in handling segregating generations derived from two crosses of cowpea.

Materials and methods

Two varieties of cowpea that are presently recommended for cultivation in Karnataka [C152 and TVX944-02E] were involved in the hybridization along with the new promising lines isolated from different trials. The crosses handled were C152 × APC412 (Cross 1) and TVX944-02E × APC255 (Cross 2).

In pedigree method, 30 plants selected from F_2, based on seed yield per plant were forwarded to F_3 in plant to row progenies. In bulk method, a random sample was drawn from F_2 population and forwarded to F_3 generation. To advance the material from F_2 and F_3 through SSD, two seeds were collected instead of single seed from each plant of F_2 population, to avoid loss of variability due to poor germination. After germination, only one seedling per hill was retained. By adopting same procedure, the pedigree, bulk and SSD populations of F_3 were followed to F_4 generation. This procedure was followed separately for raising replication 1 and 2 so that in each replication a representative sample of each treatment was included.

A random sample was taken from the produce of each plant selected, for pedigree method of advancing the generations for Replication-1 (Rep-) and then another random sample was taken separately for Rep-2, in which case we expected a representative sample of the seeds for R_1 as well as R_2. Similar procedure was followed for bulk and SSD methods also. When this procedure is followed, any treatment is (pedigree line or bulk or SSD populations) are supposed to be genetically same, in both the replications the differences between the replications treatments if any being due to environment. Further, the material from each cross was raised as a separate experiment in a Randomised Block Design with two replications. With in each replication, the 30 pedigree lines were randomised separately while the remaining treatments (Parents, SSD populations and bulk population) were grown in contiguous plots following pedigree lines and were randomized separately. The spacing adopted was 45 cm × 10 cm and the plants were raised in rows of

three meters length. The plot size was, one row (10 plants) for each pedigree line, five rows for each parent (150 plants) and eight rows each for bulk (240 plants) and SSD populations (240 plants). In each plot, 10 plants in each of the pedigree lines and parents and 100 plants each in SSD and bulk plot were chosen randomly for recording observations on six quantitative characters *viz.*, days to maturity, plant height (cm) number of pods per plant, number of seeds per pod, test weight (g) and seed yield per plant (g).

The data from pedigree lines (means of each line) was analysed as a replicated trial with 30 treatments and two replications, where as the data of both replications was clubbed in case of SSD and bulk populations for analysis (as an unreplicated trial). Raising of SSD and bulk populations, in each replication plots contiguous plots was only because pedigree lines were grown in replication line. The pedigree lines, SSD and bulk populations were compared for shift in mean and variance, heritability, genetic advance and for isolation of superior segregants. Heritability and genetic advance for pedigree lines was estimated from replicated data whereas for SSD and bulk populations these parameters were estimated by computing error variance as the average variance of parents.

Results and dissussion

The shift in mean, maintenance of variability, heritability, genetic advance and isolation of superior segregants were the parameters for which the methods were compared.

Shift in Mean : There was decline in the mean performance from F_2 to F_3 in all the three methods for all characters except for number of seeds per pod in cross 1 (Table 1 & 2) which indicated the predominance of non-additive gene action for these traits. The mean performance of days to maturity

indicated that the SSD population matured early followed by bulk and pedigree populations. The reduction in the mean performance for plant height was observed in all the three methods from F_3 to F_4 in both the crosses. Similar was the case with number of pods per plant except for bulk in cross 2. The positive shift in the mean performance for number of seeds per pod was greater in the SSD and bulk methods than in the pedigree method. This probably means that the superior of individual selections made in F_2 and F_3 characters was more due to environment than due to genotype. There were no significant difference among the methods means for test weight. In both the crosses from F_3 to F_4, the shift in mean performance for seed yield per plant in positive direction was achieved better through pedigree method than through bulk and SSD methods. This was probably due to the directional selection, which operated in pedigree method.

On the whole, in F_3, the bulk and SSD populations maintained high mean performance than pedigree, whereas, in F_4 generation the pedigree turned out to be superior to bulk and SSD methods with few exceptions. In bulk method, there was no change in mean performance from F_3 to F_4, whereas in SSD and pedigree methods the directional shift were observed for most of the traits. These results revealed that the bulk method was not maintaining high mean over generations, while the SSD performed better or equal to pedigree method. These results are in conformity with those of Virupakshappa [3] in cowpea. In bulk method, the random genetic drift due to inadequate sampling and/or natural selection are likely to reduce the genetic variability and alter the gene frequency in an undesirable direction, whereas in SSD method, the random genetic drift is supposed to be less as it preserves the whole range of variation by ensuring representation of every genotype [1].

Table 1. Means with standard errors for six quantitative traits in cross 1 (C152 x APC412)

Generation	Method	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Test weight (g)	Seed yield per plant (g)
F_2	-	90.53(0.24)	40.40(2.83)	15.14(l.15)	11.30 (0.22)	9.21 (0.14)	15.30 (1.32)
F_3	Pedigree	84.15(0.08)	21.82(l.12)	8.10 (1.10)	10.26 (0.38)	8.51 (0.38)	6.60 (0.80)
	Bulk	86.25(0.63)	19.46(l.36)	6.16 (0.37)	12.93 (0.36)	9.00 (0.28)	5.96 (0.51)
	SSD	80.50(0.66)	30.29(l.86)	9.79 (0.49)	12.25 (0.34)	8.45 (0.27)	9.14 (0.62)
t-test	P V$_s$B	*	NS	**	**	NS	NS
	P V$_s$S	**	**	**	**	NS	**
	B V$_s$S	**	**	**	NS	NS	**
F_4	Pedigree	85.51(2.07)	34.25(l.69)	11.84(l.04)	10.68 (0.66)	9.01 (0.44)	10.92 (1.11)
	Bulk	83.74(0.46)	29.67(0.95)	8.75 (0.36)	10.65 (0.18)	8.78 (0.10)	8.56 (0.32)
	SSD	81.25(0.46)	32.38(0.83)	9.25 (0.36)	11.46 (0.19)	9.38 (0.14)	8.86 (0.45)
t-test	PV$_s$B	NS	**	**	NS	NS	**
	P V$_s$S	**	NS	**	*	NS	**
	B V$_s$S	**	**	NS	**	**	NS

Note: Upper half of the F_3 and F_4 generations indicate method means and lower half indicates the t-test results.
P V$_s$ B: Pedigree V$_s$ Bulk: P V$_s$ S: Pedigree V$_s$ SSD- B V$_s$S: Bulk V$_s$ SSD Values in the parentheses : Standard Errors
** Significant at 1 % level; * Significant at 5% level; NS: Non-significant.

Table 2. Means with standard errors for six quantitative traits in cross 2 (TVX944 x APC255)

Generation	Method	Days to maturity	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Test weight (g)	Seed yield per plant (g)
F_2	-	88.67 (0.20)	35.27(l.12)	12.76(0.77)	11.77 (0.20)	10.62 (0.13)	15.97 (0.98)
F_3	Pedigree	86.66 (0.80)	23.10(l.63)	10.02(1.24)	11.01 (0.51)	9.16 (0.50)	10.43 (0.97)
	Bulk	85.50 (0.62)	27.02(l.35)	12.16(0.78)	11.65 (0.35)	9.05 (0.28)	12.22 (1.19)
	SSD	85.75 (0.62)	24.40(l.54)	11.79(l.04)	11.06 (0.34)	9.90 (0.34)	11.08 (0.62)
t-test	PVsB	**	**	NS	NS	*	*
	PVsS	**	NS	*	**	NS	NS
	BVsS	**	**	**	*	NS	**

Note: Upper half of the F_3 and F_4 generations indicate method means and lower half indicates the t-test results,
P V_s B: Pedigree V_s Bulk; P Vs S: Pedigree V_s S SD; B V_s S: Bulk V_s SSD Values in the parentheses: Standard Errors
**Significant at 1% level, *Significant at 5% level; NS: Non-Significant.

Maintenance of variability: As expected, the SSD and bulk methods were very efficient in preserving high phenotypic co-efficient of variability for all the traits except days to maturity whereas, the pedigree method turned out to be the least efficient in preserving the variability (Table 3 & 4). Similar results were obtained by Singh et al., [5] in mungbean and Arya et al., [6] in urdbean. Such results are quite expected as the SSD and bulk methods maintain high variability compared to pedigree, due to the presence of varied genotypes in unselected populations of segregating generations. Khalifa and Qualset [7] in wheat concluded that the increased variance was possibly the result of genetic differentiation due to inbreeding in successive generations of bulk population. In pedigree method, the directional shift in mean performance resulted in the reduction of variability.

Heritability and genetic advance : Heritability in broad sense showed that the pedigree advanced population had high heritability values, the bulk and SSD had moderate values for all traits with few exceptions (Table 3 & 4). These results are in conformity with Casali and Tigechelaar [8] and Singh et al., [9] in mungbean. In bulk method, extremely low values of heritability and genetic advance were observed for number of seeds per pod in F_4 of cross 2.

For heritability estimates, the pedigree method took the lead over bulk and SSD populations (Table 3 & 4). In pedigree method because of directed selection, the per cent of homozygotes is supposed to be higher then the per cent heterozygotes, which means that pedigree lines are supposed to be more susceptible to environment; however, as family means are considered for analysis, the environmental deviations of individual plants of each family are likely to get cancelled mutually resulting in a mean which is mostly due to the genotype and not environment [10]. Hence, the heritability values in pedigree method are likely to be high. The moderate to high values of heritability and expected genetic advance were observed in bulk and SSD methods for most of the traits with few exceptions. This indicated that the improvement of these traits through selection would be feasible. Though

Table 3. Estimates of phenotypic co-efficient of variation, heritability and genetic advance in cross 1 (C152 x APC412)

Character	Method	Phenotypic co-efficient of variation		Heritibility in broad sense (%)		Genetic advance as per cent of mean	
		F_3	F_4	F_3	F_4	F_3	F_4
Days to	Pedigree	4.43	5.74	90.79	64.44	8.28	7.62
maturity	Bulk	3.69	5.56	39.34	46.42	2.99	5.32
	SSD	4.14	5.69	44.79	45.52	3.81	5.34
Plant	Pedigree	24.90	16.87	91.43	81.30	46.90	28.26
height	Bulk	35.07	31.85	90.08	91.10	65.00	40.79
(cm)	SSD	30.74	25.69	94.67	87.89	59.92	46.52
Number	Pedigree	32.52	20.18	65.45	62.38	44.30	25.93
of pods	Bulk	47.44	41.60	60.77	61.81	59.25	22.03
per plant	SSD	25.22	39.20	45.08	61.36	23.39	49.60
Number	Pedigree	12.55	11.79	82.22	44.65	21.27	10.85
of seeds	Bulk	14.07	17.08	26.73	22.33	7.73	7.86
per pod	SSD	13.97	17.23	28.90	29.15	7.75	10.37
Test	Pedigree	11.60	8.65	68.92	36.06	16.48	6.43
weight (g)	Bulk	16.10	11.95	49.28	45.83	16.33	11.29
	SSD	16.31	15.77	43.94	66.06	14.67	21.47
Seeds	Pedigree	28.88	21.28	64.29	51.90	38.43	22.75
yield per	Bulk	42.94	38.31	26.71	40.65	23.48	32.08
plant (g)	SSD	54.60	42.09	62.47	54.26	50.32	47.06

the pedigree method had high heritability for most of the traits, it showed less expected genetic advance, compared to bulk and / or SSD methods for plant height, number of pods per plant and seed yield in F_3 and F_4 in both crosses because of less PCV than in the bulk and SSD populations for these characters. For the same reason, even for other characters, the genetic advance in pedigree was on per or was only slightly greater than in the SSD and bulk populations.

Isolating superior segregants : The success of any crop improvement program depends on the efficiency of selection methods, because of differences in the population size, per cent is considered instead of actual number of segregants, which ultimately lies in the isolation of superior segregants from segregating generations. The mean performance of top 15 per cent segregants and the percentage segregants superior to best parent with regard to seed yield per plant achieved through different selection methods are given in (Table 5). With regard to percentage of segregants

Table 4. Estimates of phenotypic co-efficient of variation, heritability and genetic advance in Cross 2 (TVX944 × APC255)

Character	Method	Phenotypic co-efficient of variation		Heritability in broad sense (%)		Genetic advance as per cent of mean	
		F_3	F_4	F_3	F_4	F_3	F_4
	Pedigree	2.32	6.42	77.41	74.50	3.71	9.86
	Bulk	3.62	5.23	43.40	57.99	3.23	9.25
	SSD	3.65	6.40	43.17	70.69	3.24	9.30
Plant	Pedigree	19.58	22.24	73.88	77.09	29.81	35.40
height	Bulk	25.06	22.46	89.94	90.62	50.03	41.94
(cm)	SSD	31.74	28.89	92.31	87.94	48.27	52.33
Number	Pedigree	33.70	20.40	72.64	73.84	50.39	31.03
of pods	Bulk	32.12	39.67	78.99	58.32	52.22	47.66
per plant	SSD	44.18	47.39	88.19	77.19	80.23	75.37
Number	Pedigree	11.94	10.85	68.82	64.51	16.94	10.43
of seeds	Bulk	15.11	12.83	41.77	5.99	12.61	1.43
per pod	SSD	15.58	18.13	39.22	63.12	12.56	23.59
Test	Pedigree	14.34	9.37	70.00	52.00	20.69	10.04
weight(g)	Bulk	19.07	16.87	47.98	47.80	18.78	16.61
	SSD	19.18	14.41	55.26	28.74	19.39	8.53
Seeds	Pedigree	34.66	20.95	85.53	84.78	61.11	36.59
yield per	Bulk	41.64	38.28	79.53	60.70	68.16	47.87
plant (g)	SSD	35.50	49.69	81.71	81.59	59.38	83.48

superior to best parent and seed yield per plant of top most segregants in F_3 generation, the SSD ranked first. In contrast, the pedigree method, surpassed the performance of other methods in F_4 of both the crosses, it might be because the directed selection leads to favourable genotypes in the later generations.

While calculating the percentage of segregants superior to best parent, the marginally superior segregants over best parent were also considered. But, it may not give the appropriate information from the practical point of view. Hence, it is worthwhile to compare the mean seed yield of top 15 per cent segregants obtained through different selection methods. For this parameter, the superiority of SSD method over pedigree was observed in cross 2, but in cross I both methods performed equally. The bulk method showed less efficiency, which could be probably attributed to random genetic drift, natural selection and competitive effects (11, 12). It indicated that the SSD method performed better or equally with pedigree method.

In general, the SSD method performed better than or on par with pedigree method, which indicated the preponderance of non-additive gene action than additive gene action. So, depending upon the nature of gene action, breeder may have to handle the segregating generations by SSD method or has to think of SSD method for early generations before operating selection in the subsequent generations. Further, SSD may be useful to handle large number of crosses for isolation superior segregants, because it demands less cost and resources unlike pedigree method.

Table 5. Isolation of superior segregants from F_3 and F_4 through pedigree, bulk and SSD methods in two crosses of cowpea

Cross	Method	Per cent segregants superior to best parent (APC412)		Mean seed yield of top 15% segregants		Seed yield per plant of top most segregants	
		F_3	F_4	F_3	F_4	F_3	F_4
Cross 1:	Pedigree	16.66	54.60	15.56	15.98	29.60	33.20
(C152 ×	Bulk	12.00	28.52	10.81	13.83	13.20	19.90
APC412)	SSD	20.00	31.25	14.05	15.42	42.20	18.20
Cross 2:	Pedigree	51.23	48.12	14.89	15.51	27.40	38.80
(TVX944	Bulk	43.00	42.80	12.32	14.23	18.90	22.40
-02E ×	SSD	47.35	45.81	16.46	20.00	34.50	30.40
APC255)							

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