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Research Article

Genetic analysis and transgressive segregation for seed weight and seed yield in F_2 populations of mungbean

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Abstract:
Three F_2 populations of large x large (cross-I), small x large (cross-II) and medium x small (cross-III) seeded were evaluated along with their parents and F_1's to find out transgressive segregants and to estimate the heritability(h^2_{BS}), predicted selection response (*pR*) for seed weight and seed yield per plant in mungbean. For 100 seed weight, eight transgressive segregants (2.56%) were recorded only in the cross-I (range 8.52 to 9.29 g). For seed yield per plant, fifteen (4.79%) and one (0.0027%) transgressive segregants were recorded in the cross-I (range 7.95 to 11.93 g) and cross-III (15.01 g) respectively. The h^2_{BS} values were high in the cross-I (0.83) and cross-III (0.86) for 100 seed weight while for seed yield per plant it was the highest in cross-III (0.72) and the lowest in cross-II (0.54). The *pR* values were the highest in the cross-I (large seeded x large seeded) for 100 seed weight and seed yield per plant. The higher estimates of h^2_{BS} and *pR* in F_2 population of the cross-I for both the traits suggested that the selection will be more effective in the cross between large seeded genotypes and transgress more desirable transgressive segregants which were further confirmed by progeny test in F_3 generation.

Key words: Heritability, mungbean, response to selection, transgressive segregation

Introduction:

Mungbean (*Vigna radiata* L. Wilczek) is a short duration legume crop cultivated primarily for their dry seeds. Annual mungbean production in India is around 1.52 million tonnes from about 3.77 million ha area (Singh, 2010). The productivity (469 kg/ha.) of mungbean is less as compared to other pulse crops due to various reasons like biotic and abiotic stresses and poor agronomical practices. There is an urgent need to increase production and productivity for food and nutritional security. Among the yield contributing traits, seed weight, measured as mass per seed is a very important trait not only for increasing seed yield but also to improve seed quality. Demand for large seed mungbean in the market is increasing because large seed possesses better milling quality and higher recovery of dhal. Seed weight in mungbean is ranging from 2.44 to 9.19 g per 100 seeds (Yimram *et al*., 2009). Mungbean cultivars can be classified in to small (<3g/100 seeds), medium (3 to 5g/ 100 seeds) and large (>5g/100 seeds) seed size. Mungbean cultivars with large seed size are limited. The increasing interest in adapted mungbean cultivar that fit into specific market has made breeding for seed weight a major objective of some breeding programme.

Small seed size appears to be partially dominant to large seed size (Sen and Murty, 1960; Fatokun *et al*., 1992). But most of the literature suggested the polygenic inheritance with additive and non additive gene action for seed size (Singh and Jain, 1971; Singh and Singh, 1974; Singh and Singh, 1996; Khattak *et al*., 2002; Sarwar *et al*., 2004). Seed size is highly heritable which also reflected in high genetic advance (Yohe and Poehlman, 1975; Khairnar *et al*., 2003; Rahim *et al.,* 2008; Srivastava and Lavanya, 2008). Previous studies on heritability and genetic advance for seed size and seed yield were mostly concentrated on the genotypes and not on segregating populations. Information on the association between the genetic parameters of seed weight and selection in segregating populations should help to predict beneficial cross combinations to accelerate the development of large seed genotypes without compromising the yield. Production of transgressive segregants for yield and its components like seed size plays a vital role in breeding programme. Although transgressive segregants includes lines which fall out side the range of performance of either parents, but only those being superior to better parent are of practical value. Therefore, a breeder is more concerned with obtaining higher frequency of transgressive segregants in segregating population as it provides him a better scope for exercising selection to improve productivity.

Hence, present study was conducted in three F_2 populations to find out transgressive segregants, to determine the magnitude of genotypic variability, heritability, selection differential, predicted selection response for 100 seed weight and seed yield per plant.

Material and Methods:

Five genotypes viz., Rsel-246, JL-781, SML-668 (large seed size >5g/100 seeds), Kopergaon (medium seed size 3-5g/100 seeds) and Samrat (small seed size <3g/100 seeds) were selected on the basis of contrasting characters from different genetic background for 100 seed weight and other yield contributing traits. Three crosses were attempted by using five parents viz., Rsel-246 x JL-781 (large x large) (cross-I), Samrat x SML-668 (small x large) (cross-II) and Kopergaon x Samrat (medium x small) (cross-III). The three F_2 populations were developed by selfing each F_1 plant. All the seeds harvested from F_1 plants were sown as F_2 without replication while five parents and three F_1's were replicated thrice in Summer-2009 at Gamma Field Facility Section, Trombay, Mumbai. Each plot consisted of 3m row length with spacing 30 x 10 cm. All recommended package of practices were followed throughout the growth period. Observations on 100 seed weight and seed yield per plant were recorded on twenty and ten randomly selected plants from each parents and F_1 respectively and all the plants of the three F_2 populations. Mean, range, phenotypic and genotypic variance, coefficient of variation and standard deviations were computed following standard statistical methods (Panse and Sukhatme, 1985). Genetic parameters viz., realized selection differential (*rS*), predicted selection differential (*pS*), heritability in broad sense (h^2_{BS}) and predicted selection response (*pR*) were estimated for 10% selection intensity (*i*) following the standard procedure (Sharma, 1996). The limiting value of standard variates corresponding to range of parental means at 5% probability level was calculated so that the segregants beyond this limiting value would be transgresants. Transgressive segregants showing significant deviation only in the desirable direction were considered for drawing inferences about transgression. The frequency distribution polygon was obtained by plotting class values as abscissae and class frequency as ordinates.

In summer-2010, twenty four trasgressive segregants recorded in F_2 were grown to test their performance in F_3 generation in plant to row progeny with two replications. The mean of ten randomly selected plants from each F_3 families of transgressive segregants were compared with their performance in previous year in F_2 generation for 100 seed weight and seed yield per plant by using Fisher's 't' test at n_1+n_2-2 d.f.

Result and Discussion

Apart from the manipulation of mating system in seed propagated plants, selection is a potential force of altering the genetic properties of the population in point. The estimates of genetic parameters provide useful information for selection and improvement of yield and yield contributing traits. However, these estimates obtained from each cross may be unique in varying degree and not be applicable to the other population. In the present experiment in mungbean, impact of favouring large seed size and seed yield per plant was examined in terms of different genetic parameters. Analysis of seed weight in the F_2 generation of three crosses showed a continuous distribution which confirms the earlier result that seed weight is a quantitative character (Singh and Jain, 1971; Singh and Singh, 1974; Singh and Singh, 1996; Khattak *et al*., 2002, Sarwar *et al*., 2004). The frequency distribution polygon for 100 seed weight and seed yield per plant clearly showed the differences in three F_2 populations for frequencies and class values (Fig.1 & 2). The range was the widest for 100 seed weight and seed yield per plant in all three F_2 populations as compared to their respective parents and F_1's because segregational variability was most prevalent (Table-1 & 2). For 100 seed weight range was the widest in the cross-I (3.48 – 9.29 g), while for the seed yield per plant it was widest in the cross-III (0.32 – 15.01 g). The superior parent JL-781 of the cross-I had 7.13 g for 100 seed weight, while F_2 population on an average had 6.62 g. The difference between the means of superior parent, F_1 and F_2 population was very less in the cross-I. Therefore, predominance of positive genes in F_2 was quite obvious. Such an F_2 population was naturally commensurate with occurrence of transgressive segregation. A total of eight transgressive segregants (2.56%) was recorded in the cross-I, which ranged from 8.52 to 9.29 g for 100 seed weight. No transgressive segregants were obtained in cross-II and cross-III for 100 seed weight (Table 3). Among the F_2 populations, the mean seed yield per plant was highest in the cross-I (3.89 g) followed by the cross-III (2.74 g) and the cross-II (1.88 g). For seed yield per plant, fifteen (4.79%) and one (0.0027%) transgressive segregants were recorded in the cross-I (range 7.95 to 11.93 g) and the cross-III (15.01 g) respectively. Transgressive segregants were also reported in mungbean for various characters (Kataraki and Kajjidoni, 2006). Changes in means were closely followed by alteration in variances. As shown in parents, variances were less for both traits, suggesting thereby homogeneity within parents. But it abruptly increased in F_2 population due to release of segregational variability. Since coefficient of variation is associated directly with mean and deviation, this offers a comparable rate of change in variation. The Coefficient of variation for 100 seed weight (22.14) and seed yield per plant (60.88) were the highest in the cross-III. The mean of selected 10 % plants (*Xp*) for 100 seed weight (8.27 g) and seed yield per plant (8.02 g) were the highest in the cross-I, which is ultimately reflected in realized selection differential (*rS*) in the same generation for 100 seed weight (1.65 g) and seed yield per plant (4.13 g) in the same cross (Table-2).

Heritability determines the resemblance between relatives (Falconer, 1989). The heritability in broad sense (h^2_{BS}) indicates whether selection should operate or not. For 100 seed weight, h^2_{BS} values were high in the cross-I (0.83) and the cross-III (0.86) and the lowest in the cross-II (0.67). For seed yield per plant the values of h^2_{BS} were high in the cross-III (0.72) followed by the cross-I (0.68) and the cross-II (0.55) (Table-2). High heritability for 100 seed weight was also reported earlier (Imrie *et al.*, 1985; Frey, 1980; Humphry *et al.*, 2005). The low heritability estimates for 100 seed weight and seed yield per plant in the cross-II was not similar to that of other two populations. This cross was between small seeded Samrat and large seeded SML-668 hence can not be directly compared with other two crosses. The obvious explanation for different heritability values obtained among the crosses was that the parents have different genotypes with respect to this trait. However, it is not totally unexpected since the performance of progeny would vary depending on the other line in combination. The data regarding the magnitudes for a trait would vary from cross to cross. The heritability values also reflected in estimates of predicted response (*pR*). The greater predicted response to selection was estimated for 100 seed weight and seed yield per plant in F_2 population of the cross-I and the cross-III. The per cent proportion of *pR* in *Xp* (*pR %*) was the highest in F_2 population of the cross-III for 100 seed weight (27.39 %) as well as seed yield per plant (34.21%) (Table-2).

The transgressive segregants recorded in the cross-I had very high mean for 100 seed weight (8.76 g) and seed yield per plant (8.88 g) (Table 3). These transgressive segregants were very promising as the difference in mean performances of F_2 (6.62 g) and F_1 (6.71 g) for 100 seed weight seems to be governed by additive genes. It indicated that beneficial cross combinations can accelerate the development of large seed genotypes without compromising on the yield. The higher estimates of heritability and predicted selection response in F_2 population of the cross-I for seed weight and seed yield per plant suggested that the cross between large seed genotypes will transgress more desirable transgressive segregants as compared to the crosses between small x large and medium x small seed size. The selection for 100 seed weight will be more effective in the same cross as compared to other two crosses. The reason for this might be that the additive gene action is predominant for 100 seed weight (Singh *et al*., 2006). These results were further confirmed by progeny test of transgressive segregants in F_3 generation for 100 seed weight and seed yield per plant. The differences in mean of F_3 families of transgressive segregants (8.27 g) and their mean recorded in F_2 generation (8.76 g) was non-significant (Table 4). It indicated that there is no significant reduction in mean performance in F_3 generation for 100 seed weight which is implication of high heritability and genetic advance in cross-I. On the contrary, the difference between F_2 mean of sixteen transgressive segregants (9.27 g) and mean of their F_3 families (5.89 g) for seed yield per plant was significant (Table 4). It might be the result of low heritability and non additive gene action in early segregating generation for seed yield per plant.

In the present investigation, the positive relation in different genetic parameters like heritability, genetic advance with transgressive segregants for seed weight and seed yield based on different crosses suggested that this information has important implication for prediction of desirable combination. High heritability and predicted selection response in the cross between large seed genotypes suggested that crosses between large seed size genotypes of different genetic background will produce better transgressive segregants for large seed size. Although large seed size genotypes had desirable genes for seed size, still there is scope to accumulate more desirable genes by inter-mating these genotypes of different genetic background and to select better progenies in segregating populations.

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Table 1: Estimates of mean, range, variance, standard deviation and coefficient of variation for parents and F_1

Traits	Statistical/ genetic parameters	Rsel-246	JL-781	F_1 Rsel-246 X JL-781 (cross-I)	Samrat	SML-668	F_1 Samrat x SML-668 (cross-II)	Kopergaon	F_1 Kopergaon x Samrat (cross-III)
100 seed weight (g)	Mean	6.71	7.13	6.71	3.08	6.19	4.99	4.89	4.90
	Range	6.03– 7.31	6.17 - 7.8	6.20-6.85	2.74 - 3.52	5.25 - 7.2	4.22-5.68	4.42 - 5.17	4.07-5.89
	Vp	0.18	0.114	0.057	0.10	0.23	0.34	0.14	0.21
	S.D.	0.42	0.34	0.24	0.32	0.48	0.58	0.37	0.46
	C.V. (%)	6.26	4.77	3.58	8.47	7.75	11.63	7.56	9.39
Seed yield per plant (g)	Mean	4.32	4.74	6.62	3.43	4.19	3.12	4.29	3.63
	Range	2.79 - 5.64	3.26 - 6.53	4.71-7.99	2.03 -4.61	3.16 - 5.62	2.42-3.86	3.01 - 6.27	2.42-5.28
	Vp	1.25	1.13	0.97	0.38	0.57	0.28	1.18	0.59
	S.D.	1.11	1.06	0.99	0.61	0.75	0.52	1.08	0.77
	C.V. (%)	25.88	22.43	14.95	17.78	17.90	16.67	25.32	21.16

* *Vp- phenotypic variance*, S.D.- standard deviation, C.V.- coefficient of variation

Table 2: Estimates of statistical and genetic parameters for F_2 populations

Statistical/ genetic parameters	Rsel-246 x JL-781 (Cross-I)		Samrat x SML-668 (Cross-II)		Kopergaon x Samrat (Cross-III)	
	100 seed wt. (g)	Seed yield/ Plant (g)	100 seed wt. (g)	Seed yield/ Plant (g)	100 seed wt. (g)	Seed yield/ Plant(g)
F_2 population size	313		371		369	
Mean of F_2 population ($\bar{X}$o)	6.62	3.89	4.71	1.88	4.29	2.74
Range	3.48 - 9.29	0.83 - 11.93	2.29 - 7.15	0.23 - 6.88	1.73 - 5.87	0.32 -15.01
Vp (phenotypic variance)	0.86	3.69	0.52	1.04	0.91	2.78
S.D.(standard deviation)	0.93	1.92	0.72	1.11	0.95	1.67
C.V. (%) (coefficient of variation)	14.10	49.44	15.29	59.04	22.14	60.88
$\bar{X}$p (mean of selected 10% plants)	8.27	8.02	5.99	4.07	5.22	6.15
V_E (Vp_1+Vp_2)/2(Environmental variance)	0.15	1.19	0.17	0.48	0.12	0.78
Vg (Vp - V_E) (genotypic variance)	0.71	2.50	0.35	0.56	0.79	2.0
rS (Realized selection differential) ($\bar{X}$p - $\bar{X}$o)	1.65	4.13	1.28	2.19	0.93	3.41
pS (predicted selection differential g/100 seeds)	1.63	3.36	1.26	1.94	1.66	2.92
h^2_{BS} (Vg/Vp) (heritability in broad sense)	0.83	0.68	0.67	0.54	0.86	0.72
pR or GA (predicted / expected selection response)	1.33	2.28	0.84	1.04	1.43	2.10
pR % (% proportion of pR in $\bar{X}$p= pR/$\bar{X}$p x 100)	16.13	28.49	14.09	25.77	27.39	34.21

Table 3: Frequency, threshold and normal deviation value for transgressive segregants in F_2 populations

Parameters	Transgressive segregants					
Population (F_2)	Rsel-246 x JL-781 (Cross-I)		Samrat x SML-668 (Cross-II)		Kopergaon x Samrat (Cross-III)	
Character	100 seed wt. (g)	Seed yield/ Plant (g)	100 seed wt. (g)	Seed yield/ Plant (g)	100 seed wt. (g)	Seed yield/ Plant (g)
Threshold value	7.8	6.48	7.13	5.66	5.3	5.92
N.D. value	0.68	1.35	0.59	3.41	0.79	4.28
Frequency	8	15	-	-	-	1
% transgressive segregants	2.56	4.79	-	-	-	0.0027
Range	8.52 - 9.29	7.95 - 11.93	-	-	-	15.01
Mean	8.76	8.88	-	-	-	15.01

Table 4: Mean performance of F_3 families of transgressive segregants for 100 seed weight and seed yield per plant

Character/cross	Sr. no.	F_2 generation (g)	F_3 family mean(g)	t cal.	t tab. (5%) at (n1+n2 -2) d.f.
Transgressive segregant for 100 seed weight (g) in cross Rsel-246x JL-781	1	9.29	8.69	2.123	2.145
	2	8.98	9.06		
	3	8.96	9.33		
	4	8.64	8.82		
	5	8.60	8.01		
	6	8.58	7.37		
	7	8.52	7.11		
	8	8.52	7.75		
	mean	8.76	8.27		
Transgressive segregant for seed yield per plant (g) in cross-I(Rsel-246x JL-781)	1	11.93	8.37	78.89	2.04
	2	10.16	8.10		
	3	9.54	7.93		
	4	9.04	5.38		
	5	8.91	6.25		
	6	8.90	3.02		
	7	8.84	4.02		
	8	8.55	6.73		
	9	8.54	4.36		
	10	8.48	6.3		
	11	8.12	4.2		
	12	8.11	5.94		
	13	8.10	4.15		
	14	8.08	4.34		
	15	7.95	5.26		
Transgressive segregant for seed yield per plant (g) in cross -III (Kopergaon x Samrat)	1	15.06	9.89		
	mean	9.27	5.89		

Fig.: 1. Frequency distribution polygon for 100 seed weight in three F_2 populations in mungbean

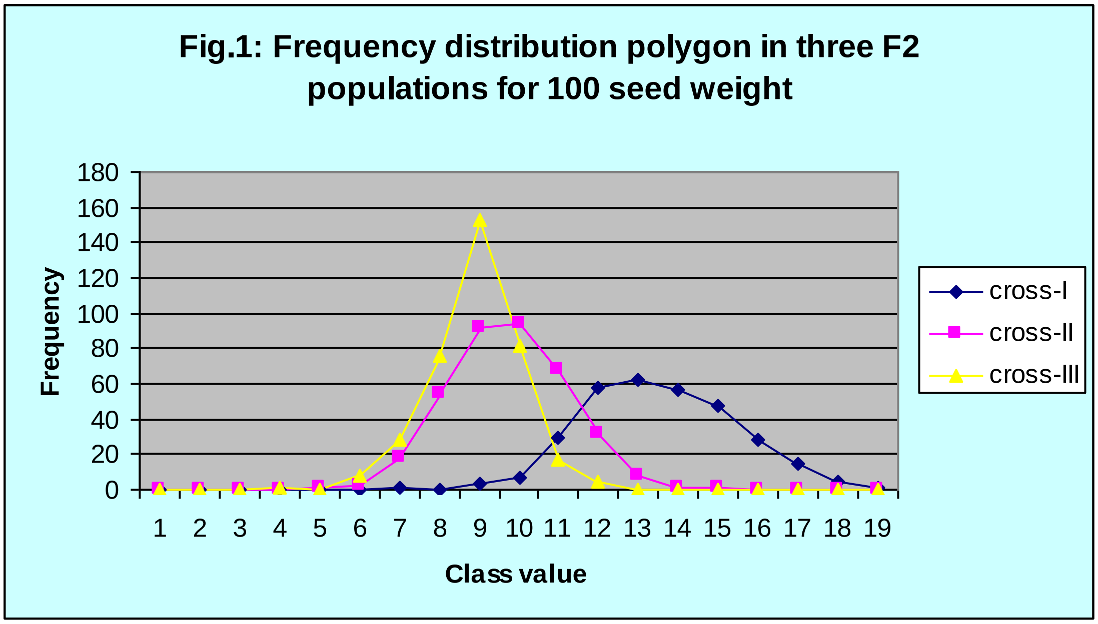

Fig.: 2. Frequency distribution polygon for seed yield per plant in three F_2 populations in mungbean