SELECTION CRITERIA IN F_3 AND F_4 POPULATION OF MUNGBEAN (*VIGNA RADIATA* (L.)WILCZEK)

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Abstract

Five cross combinations of mungbean viz., NM 92 x NM 51,NM 92 x Pusa Baisakhi, NM 92 x NM 93, NM 92 x CV. 6601 and CV. 6601 x NM 92 in F_3 and F_4 generations were studied for genetic parameters and direct and indirect effects of different morphological traits on yield. Based on results of genetic parameters, populations of CV. 6601 x NM 92 and NM 92 x Pusa Baisakhi for pods per plant and NM 92 x CV. 6601 for 100 seed weight in F_3 and NM 92 x CV. 6601, NM 92 x NM 93, and CV. 6601 x NM 92 in F_4 showed additive type of genes as the said traits in these particular cross combinations contain high heritability values combined with high genetic advance. Population of NM 92 x Pusa Baisakhi, NM 92 x NM 51, NM 92 x NM 93 and NM 92 x CV. 6601 in F_3 and NM 92 x CV. 6601, NM 92 x Pusa Baisakhi, CV. 6601 x NM 92 and NM 92 x NM 51 in F_4 showed positive direct effects for branches per plant, pods per plant, 100 seed weight and seeds per pod.
Present studies revealed that during selection, pods per plant may be used as selection criteria followed by 100 seed weight, seeds per pod and branches per plant, whereas selection of single stem plants should be discouraged and preference must be given to medium tall plants having profused branching habit alongwith more number of pods, seeds per pod and bold seed size.

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is an important short duration pulse crop of Pakistan and in other South Asian countries where the diet is mostly cereal based. It is highly prized for its rich protein content (24%) with excellent digestibility (Rachie & Robert, 1974). It is consumed as dhal or boiled dry beans. It is also used as fodder for livestock or incorporated in the soil for enriching organic matter. In Pakistan, mungbean is planted on an area of about 220100 ha with an annual production of 104500 tons having an average seed yield of 475 kg ha^{-1} (Anon., 2000), which is very low. Seed yield per unit area may be increased substantially through the evolution of high yielding genotypes having desired combination of yield components. Knowledge of genetic parameters is very important for breeding ideotypes with special emphasis on certain characters. If the understanding of genetic behaviour of traits at an early segregating generation is known, the ideotype based selection may be carried out. Selection based on yield components is advantageous if different yield related traits have been well documented (Johnson *et al.,* 1955; Panse, 1957; Tickoo *et al.,* 1988 Poehlman, 1991; Singh *et al.,* (1995). Earlier, Sharma (1999) observed high genetic advance coupled with high herirtability and genotypic coefficient of variation in 42 diverse genotypes of cowpea in case of plant height, indicating a preponderance of additive gene effects for this trait. Moderate genotypic coefficient of variation and genetic advance estimates were observed for the other traits.

Seed yield being a complex and multifacet character, is an ultimate expression of different factors. The knowledge of interrelationship among various developmental and productive traits is necessary for framing an effective breeding programme. Path

coefficient is used in assessing the real contribution of various component characters towards seed yield so that direction for desired improvement may be developed. Research workers have achieved significant results by employing these biometrical techniques. In two separate studies Aslam *et al*., (2002) and Saifulla & Hassan (2002) observed positive association of pods per plant and seeds per pod with seed yield in mungbean genotypes of diverse origin. Hameed *et al., (*2002) observed highly significant correlation of seed yield with plant height, pods per plant, pod length and seeds per pod, and significant with 100 seed weight in mungbean.

Present study was undertaken to search out the importance of different characters in five mungbean cross combinations of diverse nature, through the estimation of genetic parameters and path analysis, so that the suitable selection criterion may be framed out for developing ideotypes possessing high yield potential.

Materials and Methods

The experimental material comprised of five different F_3 and F_4 cross combinations of exotic and indigenous varieties/ breeding lines viz. NM 92 x NM 51, NM 92 x Pusa Baisakhi, NM 92 x NM 93, NM 92 x CV.6601 and CV.6601 x NM 92. A cultivar CV.6601 is an indigenous first approved mungbean variety in Pakistan, with more plant height, longer and non-synchronous maturity period alongwith small seed size. Pusa Baisakhi is an exotic (Indian origin) variety with small seed size and medium maturity period. NM 51, NM 92, and NM 93 are bold seeded varieties derived from both cross breeding and mutation breeding techniques either directly or indirectly at NIAB, Faisalabad. These elite lines possess short plant type, synchronous pod maturity, short reproductive period and bold seed size.

To raise F_3 population, single plants randomly selected from F_2 population were planted during summer 1998 at NIAB, Faisalabad as plant progeny rows having 4 meter length in four repeats keeping plant to plant and row to row distance of 10 and 30 cm, respectively. At maturity 40 guarded plants were randomly taken for recording data on various morphological traits i.e., plant height, branches per plant, pod length, seeds per pod, pods per plant, cluster per plant, 100 seed weight and seed yield per plant. Seeds collected from F_3 single plants were used to raise F_4 generation in the next summer season during 1999 in the similar fashion as for F_3. At maturity data on similar morphological attributes were recorded as in F_3. Data recorded from both F_3 and F_4 generations were statistically analyzed separately for computation of genetic parameters i.e., genotypic variance, phenotypic variance, heritability (bs) and genetic advance (Singh & Chaudhary 1985). Correlation coefficient and path analysis of different characters keeping seed yield as dependent variable was also performed (Steel & Torrie 1980; Singh & Chaudhary, 1985).

Results and Discussion

Genetic parameters (F_3)

Genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation was higher for plant height in case of NM 92 x CV 6601 cross combination. This cross combination also showed 67.2% heritability alongwith 14.4% genetic advance (Table 1).

Table 1. Genetic parameters in F$_3$ generation of mungbean.

Character	C.C*	Mean	G.V	G.C.V	P.V	P.C.V	H^2(bs)	G.A
Plant height (cm)	1	66.2	18.5	6.5	96.1	9.1	51.2	13.3
	2	68.2	17.7	6.2	29.8	8.0	59.6	8.4
	3	53.6	1.5	2.3	13.4	6.8	11.1	1.33
	4	56.0	31.3	10.0	46.6	12.2	67.2	14.4
	5	57.5	19.6	7.7	32.2	9.9	60.9	10.6
Branches/plant	1	2.2	0.1	12.8	0.7	37.9	11.5	7.7
	2	1.8	0.02	7.1	0.5	39.1	3.3	2.3
	3	1.5	0.3	34.7	0.5	47.3	53.8	44.6
	4	1.6	0.2	31.5	0.8	56.7	30.9	30.9
	5	1.8	0.2	24.0	0.4	36.7	42.7	27.4
Clusters/plant	1	13.3	5.5	17.6	10.5	24.4	52.0	22.4
	2	8.4	3.7	23.0	5.3	27.6	69.6	33.8
	3	8.3	6.6	31.2	7.7	33.7	85.8	50.9
	4	7.3	3.7	26.4	5.0	30.4	75.6	40.5
	5	10.8	12.6	32.9	14.0	34.7	89.9	54.9
Pods/plant	1	26.1	28.2	20.4	71.6	32.5	39.3	22.5
	2	21.6	23.1	22.3	29.2	25.1	79.1	34.8
	3	23.9	2.4	6.5	9.2	12.7	26.1	5.8
	4	29.1	39.1	21.5	577.8	82.7	0.7	0.1
	5	27.8	72.3	30.6	80.2	32.2	90.2	51.3
Pod length (cm)	1	8.7	0.04	2.3	0.5	7.8	8.9	1.2
	2	8.6	0.04	2.2	0.2	5.6	15.7	1.6
	3	9.5	0.1	3.3	0.4	6.9	22.7	2.7
	4	8.9	0.002	0.5	0.3	6.0	0.6	0.1
	5	9.3	0.1	4.0	0.5	7.4	29.4	3.9
Seeds/pod	1	12.3	0.01	2.6	0.5	5.7	19.1	1.9
	2	11.9	0.1	3.2	0.5	6.1	27.7	3.0
	3	11.7	0.3	4.4	0.7	6.9	40.6	5.0
	4	11.9	0.07	2.2	0.5	5.8	13.9	1.4
	5	11.7	0.03	1.4	0.4	5.4	0.68	0.1
100 seed weight (g)	1	4.1	0.1	7.7	0.2	11.4	45.7	9.2
	2	4.2	0.02	3.1	0.2	9.8	9.9	1.7
	3	5.1	0.02	2.9	0.1	7.4	15.3	2.0
	4	4.1	0.01	2.7	0.2	11.9	5.0	1.0
	5	5.1	0.1	6.1	0.1	7.3	77.10	9.9
Seed yield per plant(g)	1	10.3	18.1	41.5	19.6	43.2	92.2	70.1
	2	7.5	1.1	14.3	2.1	19.3	55.2	18.7
	3	8.1	1.8	16.6	2.9	21.3	61.0	22.9
	4	6.6	1.5	18.2	2.9	25.5	50.9	22.9
	5	10.4	14.0	36.0	16.0	38.4	87.0	59.4

*C.C.= Cross combinations
1. NM 92 X NM 51   2. NM 92 x Pusa Baisakhi,
3. NM 92 x NM 93   4. NM 92 x CV. 6601
5. CV. 6601 x NM 92

Cross combinations NM 92 x NM 93 and NM 92 x CV. 6601 showed high degree of genotypic and phenotypic coefficient of variations in branches per plant. High heritability (53.8%) alongwith high genetic advance (44.6%) was estimated in NM 92 x NM 93 cross combination. Clusters per plant and pods per plant showed genotypic and phenotypic coefficient of variation ranging from 17.6-32.9 and 6.5-30.6 respectively in all the cross combinations. Heritability values in cluster per plant ranged from 52.0 to 89.9. In pods per plant, the highest heritability values (79 and 90%) were noted in cross combination NM 92 x Pusa Baisakhi and CV 6601 x NM 92 alongwith high genetic advance of 34.8 and 51.3%, respectively.

Pod length and seeds per pod showed very low genotypic and phenotypic variations resulting in less heritability and genetic advance values in almost all the cross combinations. The maximum heritability of 40.6% in case of seeds per pod alongwith highest genetic advance (5%) was noted in NM 92 x NM 93 cross combination. Heritability from 46 to 77% along with 9 - 10% genetic advance was observed in NM 92 x NM 51 and CV. 6601 x NM 92 respectively for 100 seed weight.

Seed yield showed highest heritability values combined with more values of genetic advance in all cross combinations. The maximum heritability (92%) alongwith highest genetic advance (70%) was obtained in NM 92 x NM 51 cross combination. Branches per plant showed non additive type of variation in four cross combinations except the first cross combination. Pods per plant and cluster per plant showed more additive type of variation in almost all the combination while the characters like pod length and seeds per pod seemed to be governed by non-additive type (epistatis or interaction) of genes. There was non-additive type of genes in NM 92 x NM 51 and NM 92 x CV 6601 in case of 100 seed weight.

Additive type of genes may be exploited more efficiently by selecting genotypes on the basis of seed yield in all cross combinations as they all possessed very high degree of heritability and genetic advance. Johnson *et al.*, (1955) and Panse (1957) have also mentioned the importance of additive type of genes. They further stated that a high genetic advance accompanied with high heritability estimates offered a most effective criterion of selection.

Genetic parameters (F$_4$)

Mean plant height in F$_4$ ranged from 38.0 to 58.8 cm. Genotypic and phenotypic variance was lowest (10.3-13.6) in NM 92 x NM 51 cross combination and highest (70.6-120) in NM 92 x CV 6601. However the differences of genotypic coefficient of variation and phenotypic coefficient of variation were narrow. Heritability was more than 50% in all cross combinations with maximum value (88.7%) in NM 92 x Pusa Baisakhi. Highest genetic advance (19%) was found in cross combinations NM 92 x CV. 6601 and CV. 6601 x NM92. The differences among the genotypic and phenotypic variances for branches per plant were very narrow. The heritability was also low with maximum value of 25% in NM 92 x CV 6601. However this cross combination showed high genetic advance of 28% (Table 2). This high genetic advance is based on high heritability and high phenotypic variance. It indicates that in this cross combination the character branches per plant is governed by additive type of genes to more extent as compared to other cross combinations under study. The difference in genotypic and phenotypic variances for cluster per plant were also high. Heritability values ranged from 5-36% with maximum genetic advance of 24.9% in NM 92 x CV 6601 cross combination (Table 2).

Table 2. Genetic parameters in F$_4$ generation of mungbean

Character	C.C*	Mean	G.V	G.C.V	P.V	P.C.V	H^2(bs)	G.A
Plant height (cm)	1	46.4	10.3	6.9	13.6	8.0	76.0	10.6
	2	38.0	55.2	19.6	62.2	20.8	88.7	16.6
	3	42.4	12.6	8.4	21.0	10.8	60.0	11.4
	4	58.8	70.6	14.3	120.2	18.7	58.7	19.3
	5	55.9	58.1	13.6	89.8	17.0	64.6	19.1
Branches/plant	1	1.8	0.1	16.9	1.2	62.2	7.4	8.1
	2	1.7	0.1	19.3	0.8	52.9	13.4	12.5
	3	1.6	0.1	9.2	1.1	65.8	2.0	2.3
	4	2.1	0.5	28.7	1.8	57.3	25.1	28.1
	5	2.4	6.7	10.8	1.3	46.7	5.3	4.1
Clusters/plant	1	7.5	1.9	18.2	9.8	41.8	18.9	13.9
	2	6.6	1.7	19.8	4.6	32.8	36.4	21.1
	3	8.2	0.8	10.8	5.7	29.3	13.6	7.0
	4	9.0	4.4	23.5	12.2	30.1	36.2	24.9
	5	8.4	0.5	8.4	8.8	35.5	5.6	3.1
Pods/plant	1	25.1	13.3	14.5	69.2	33.4	19.0	11.2
	2	23.7	14.6	16.1	52.5	30.6	27.8	15.0
	3	27.6	18.6	15.6	22.3	17.1	83.8	25.9
	4	26.1	89.5	36.2	168.3	49.7	53.2	27.5
	5	29.4	53.24	24.82	64.9	27.40	82.0	39.56
Pod length (cm)	1	9.4	0.1	3.4	0.4	6.6	25.6	3.0
	2	9.0	0.3	5.8	0.7	9.6	36.3	6.1
	3	8.6	0.1	1.6	0.8	10.6	2.4	0.5
	4	7.9	0.5	9.1	1.0	12.4	53.8	11.8
	5	8.5	0.03	2.03	0.8	11.1	3.3	0.6
Seeds/pod	1	11.8	0.3	4.4	1.2	9.4	22.2	3.7
	2	11.7	0.6	6.9	1.3	9.8	49.0	8.4
	3	10.6	0.2	3.8	1.8	12.7	8.9	2.0
	4	10.5	1.2	10.5	1.8	12.9	66.4	15.1
	5	11.5	0.19	3.96	0.49	6.27	4.0	4.29
100 seed weight (g)	1	4.9	0.3	10.9	0.7	16.6	42.9	12.6
	2	4.3	0.2	10.4	0.5	16.0	42.1	11.9
	3	5.4	0.2	7.8	0.3	10.0	61.7	10.8
	4	3.3	0.4	19.2	0.7	26.2	53.7	24.7
	5	3.7	0.1	6.6	0.4	16.0	16.8	4.7
Seed yield per plant (g)	1	10.4	2.8	16.1	19.6	42.5	14.4	10.8
	2	8.4	0.8	10.5	7.1	31.8	10.9	6.1
	3	11.62	10.1	27.3	11.3	28.9	89.2	45.3
	4	5.2	8.9	57.9	17.2	80.5	51.8	73.4
	5	5.6	0.1	6.3	10.1	57.1	1.2	1.0

* C.C. = Cross combination
G. V = Genotypic variance   G. C. V. = genotypic coefficient of variation
P. V = Phenotypic variance   P. C. V. = Phenotypic coefficient of variation
H^2(bs) = Heritability broad sense G. A. = Genetic Advance

Pods per plant showed a high degree of variances both in phenotypic and genotypic values ranged from 22.3-168.3 and 13.3-89.5 respectively. These high differences in pods per plant indicates the presence of a range of variation in the population under study, furthermore, being a quantitative character it is affected by the environment to a greater extent. Moreover, the genetic differences among the cross combinations are also high due to different genetic make up of the exotic and local parents. The heritability values were also encouraging ranging from 53-83 in NM 92 x NM 93 and NM 92 x CV.6601, respectively. In these two cross combinations, the values of genetic advance were also high (25-39%). In case of pod length and seeds per pod, NM 92 x CV.6601 showed high degree of variation as compared to other cross combinations. Heritability and genetic advance was also high in this cross combination. Generally very low variation existed in this character.

Genotypic and phenotypic coefficient of variation in case of 100-seed weight showed high range of differences in the entire cross combinations. The highest heritability (61.70%) was estimated in NM 92 x NM 93 followed by NM 92 x CV.6601 (53.70%). This high heritability is due to high value of genotypic variance as compared to phenotypic variance. Furthermore the 100 seed weight is not affected too much as compared to other quantitative characters by the environment. The maximum genetic advance (24.70%) was observed in NM 92 x CV.6601.

Genotypic and phenotypic coefficient of variation in case of seed yield per plant were 57.9% and 80% respectively in NM 92 x CV.6601 (Table 2). The highest heritability (89.20%) was observed in NM 92 x NM 93 followed by NM 92 x CV.6601 (51.80%). The maximum genetic advance (73.39%) was computed in NM 92 x CV.6601 followed by NM 92 x NM 93 (45.26%).

Panse (1957), Rajput *et al.,* (1987) and Sadiq *et al.,* (2000) have reported that if heritability is mainly due to non-additive genetic effect, the genetic gain would be low, whereas, if heritability is due to additive gene effect, a high genetic advance may be expected. In this study we found that cross combinations NM 92 x NM 51, NM 92 x CV.6601 and CV.6601 x NM 92 were possessing more additive type of genes in case of plant height. Additive type of variance was also observed in NM 92 x NM 51 for branches per plant. NM 92 x CV.6601 showed additive type of variance in case of pods per plant, cluster per plant, pod length, seeds per pod, 100-seed weight and seed yield. Cross combination NM 92 x NM 93 also mainly governed by additive type of genes in case of pods per plant and seed yield.

Direct and indirect effects (F$_3$)

Cross combination NM 92 x NM 51 and NM 92 x NM 93 showed positive direct effects in case of plant height but only NM 92 x NM 93 showed positive genotypic correlation (Table 3). All cross combinations except NM 92 x NM 51 showed positive indirect effects of plant height via pods per plant. Positive indirect effects of plant height via seeds per pod were also noted in all cross combinations.

Three cross combinations viz., NM 92 x Pusa Baisakhi, NM 92 x NM 93, and NM 92 x CV.6601 showed positive direct effects combined with positive genotypic correlation coefficients in branches per plant. Positive indirect effects to some extent were observed via seeds per pod and 100 seed weight in at least three cross combinations (Table 3). CV.6601x NM 92 showed the highest value of indirect positive effects via pod length and seeds per pod (1.20 and 1.72) respectively. It indicates that seed yield can be

Table 3. Direct and indirect effects in F$_3$ generation of mungbean.

Character	C.C.[a]	Plant height	Branches /plant	Clusters /plant	Pods /plant	Pod length	Seeds /pod	100 seed weight	Rg[**]
height (cm)	1	0.38	-0.02	0.14	-0.17	-0.01	0.22	-0.05	-0.10
	2	-0.62	-0.09	-0.15	0.14	-0.16	0.26	-0.15	-0.77
	3	0.28	-0.02	-0.98	0.22	0.01	0.37	-0.43	0.55
	4	-0.40	-0.04	0.01	0.06	-0.14	0.10	0.03	-0.37
	5	-2.68	0.01	0.01	0.04	1.20	1.72	-0.37	-0.07
ches/plant	1	0.05	-0.13	0.01	0.23	0.13	0.16	0.06	0.50
	2	0.44	0.13	0.39	-0.41	0.20	-0.08	-0.002	0.66
	3	-0.005	1.36	-0.82	-0.04	-0.02	0.21	0.02	0.71
	4	0.14	0.11	-0.01	0.35	-0.24	0.005	0.08	0.43
	5	-0.23	0.16	-0.45	-0.11	1.38	-1.66	0.60	-0.30
ers/plant	1	-0.15	0.004	-0.34	0.49	0.23	0.13	0.09	0.46
	2	0.12	0.06	0.81	-0.24	-0.08	-0.26	-0.12	0.28
	3	0.24	0.98	-1.14	-0.01	-0.02	0.27	0.02	0.34
	4	0.08	-0.02	-0.05	-0.16	0.10	-0.06	-0.03	-0.11
	5	0.08	0.24	-0.31	-0.15	-0.20	0.33	0.65	0.64
plant	1	-0.24	-0.02	-0.14	1.21	0.03	-0.01	-0.08	0.74
	2	-0.41	-0.23	-0.88	0.22	-0.22	0.29	0.16	-1.06
	3	-0.32	0.26	-0.08	-0.19	-0.04	-0.11	0.28	-0.21
	4	-0.05	0.08	0.02	0.50	0.01	-0.02	0.20	0.74
	5	0.37	0.07	-0.17	-0.27	0.21	0.06	0.68	0.97

Table 3 (Cont'd.)

Character	C.C.*	Plant height	Branches /plant	Clusters /plant	Pods /plant	Pod length	Seeds /pod	100 seed weight	Rg**
length (cm)	1	-0.01	-0.04	-0.20	0.11	0.39	0.31	0.07	0.63
	2	-1.91	-0.49	1.26	0.95	-0.05	-1.50	-1.43	-3.17
	3	0.01	-0.21	0.17	0.07	0.12	-0.17	-0.32	-0.33
	4	-0.28	0.14	0.03	-0.02	-0.20	0.09	0.30	0.06
	5	2.07	-0.15	-0.04	0.04	-1.54	-0.37	0.06	0.07
s/pod	1	0.36	-0.09	-0.19	-0.07	0.52	0.24	0.09	0.85
	2	-0.48	-0.03	-0.63	0.19	0.23	0.33	0.15	-0.23
	3	0.20	0.54	-0.59	0.04	-0.04	0.52	0.01	0.68
	4	-0.47	0.01	0.03	-0.12	-0.19	0.09	-0.06	-0.70
	5	-2.03	-0.12	-0.04	-0.01	0.25	2.26	-0.07	0.23
seed weight (gm)	1	0.08	0.04	0.15	0.46	-0.14	-0.11	-0.21	0.27
	2	0.54	-0.002	-0.57	0.20	0.41	0.29	0.18	1.05
	3	-0.14	0.03	-0.03	-0.07	-0.05	0.01	0.83	0.58
	4	-0.05	0.03	0.01	0.34	-0.20	-0.02	0.30	0.41
	5	2.04	0.20	-0.41	-0.38	-0.020	-0.34	0.48	1.39

C.C.* = Cross combination ** rg= Genotypic correlation
1. NM 92 X NM 51 4. NM 92 x CV. 6601
2. NM 92 x Pusa Baisakhi 5. CV. 6601 x NM 92
3. NM 92 x NM 93

improved indirectly by selection of these characters. All cross combinations except NM 92 x Pusa Baisakhi showed negative indirect effects for clusters per plant. Positive indirect effects of clusters per plant were shown via plant height, branches per plant, pod length, seeds per pod and 100 seed weight in majority of the cross combinations (Table 3). Significance of direct and indirect effects had been well documented by scientists working on different legume crops. Singh & Phul (1999), studying 30 genotypes of soybean for six yield related traits observed the positive direct effects of pods per plant on seed yield and explained that this is the most important yield component. High positive correlation and high positive direct effect of green pod yield per plant were noted in pole French bean (*Phaseolus vulgaris*) field experiments (Nandi *et al*., 1999). Study on 20 chickpea elite genotypes indicated the importance of number of pods per plants and 100 seed weight by showing highly positive genotypic as well as phenotypic correlation with seed yield. Number of pods had maximum positive direct effect on seed yield. The other traits of economic importance also exhibited indirect effects through number of pods on seed yield (Saleem *et al*., 2002). Studying 63 genotypes (45 F$_1$ and 18 parents) of mung bean in eight environments, Vikas *et al*., (1999), observed higher values of genotypic correlations as compared to phenotypic correlations. Seed yield showed positive association with number of clusters, number of pods per plants, seeds per pod, 100 seed weight and harvest index. The path analysis revealed that seed yield was influenced directly by biological yield and harvest index in most of the environments and plant height, number of cluster per plant, number of pods per plants and 100 seed weight in few environments.

In the present study, NM 92 x NM 51 showed highest values (1.21) of direct positive effect for pods per plant followed by NM 92 x CV. 6601 (0.50) and NM 92 x Pusa Baisakhi (0.22). Cross combinations NM 92 x NM 51 and NM 92 x CV. 6601 also showed positive genotypic correlation. Pods per plant showed indirect positive effects via branches per plant, pod length and 100 seed weight.

Positive direct effects in case of pod length were noted only in two cross combinations viz., NM 92 x NM 51 and NM 92 x NM 93, of which only NM 92 x NM 51 showed positive genotypic correlation coefficient value. Contrary to this, seeds per pod showed positive direct effects in all cross combinations with highest value of 2.26 in cross combination of CV. 6601 x NM 92. The genotypic correlation values of three cross combinations viz., NM 92 x NM 51, NM 92 x NM93 and CV. 6601 x NM 92 were also positive. Seeds per pod also exhibited positive indirect effects via pod length in three cross combinations. All cross combinations except NM 92 x NM 51 showed positive direct effects alongwith positive genotypic correlation in case of 100 seed weight (Table 3). On the basis of positive direct effects combined with positive values of genotypic correlation coefficients, population of this nature may be exploited through direct selection of plants, bearing more number of branches, pods and 100 seed weight.

Direct and indirect effects (F$_4$)

Cross combination NM 92 x NM 93 only showed positive direct effect but negative correlation coefficient value in case of plant height (Table 4). Plant height showed positive indirect effects via branches per plant, clusters per plant and pod length in at least four cross combinations.

Direct positive effect in branches per plant was shown by NM 92 x Pusa Baisakhi, NM 92 x NM 93 and CV.6601 x NM 92. Highly positive indirect effect were noted with plant height in NM 92 x NM 51 and NM 92 x NM 93. Branches per plant showed maximum (11.73) positive indirect effect via cluster per plant.

Table 4. Direct and indirect effects in F_4 generation of mungbean.

Character	C.C.*	Plant height	Branches /plant	Clusters /plant	Pods /plant	Pod length	Seeds /pod	100 seed weight	Rg**
Plant height (cm)	1	-5.79	0.74	1.43	-0.32	2.04	0.79	0.65	-0.46
	2	-0.60	0.04	0.25	1.12	0.03	-0.09	-0.40	0.35
	3	0.64	0.47	-0.46	-0.02	-0.99	0.12	-0.02	-0.26
	4	-0.28	-0.04	0.03	-0.38	0.69	-0.47	-0.34	-0.78
	5	-3.36	0.98	2.28	-0.39	1.77	1.92	-4.30	-0.99
Branches/plant	1	6.68	-0.64	-3.35	0.88	-1.71	-0.35	-0.64	0.68
	2	-0.53	0.04	0.30	2.10	0.03	-0.12	-0.54	1.28
	3	0.94	0.32	-0.75	-0.11	-1.42	2.65	-0.03	1.61
	4	-0.02	-0.45	0.02	0.05	0.03	-0.05	0.03	-0.38
	5	-0.29	10.82	11.73	-1.94	6.10	-23.99	-3.04	-0.56
Clusters/plant	1	4.89	-1.34	-1.69	0.56	-1.06	-0.25	-0.55	0.56
	2	-0.42	0.04	0.36	1.54	0.01	-0.09	-0.52	0.92
	3	0.81	0.67	-0.37	-0.06	-1.60	1.07	-0.02	0.51
	4	0.09	0.11	-0.09	0.57	-0.11	0.18	0.11	0.88
	5	-0.82	14.10	9.06	1.33	-7.92	-19.44	-3.82	-7.52
Pods/plant	1	3.51	-1.06	-1.77	0.53	-0.24	-0.01	-0.38	0.59
	2	-0.37	0.05	0.30	1.82	0.02	-0.08	-0.50	1.24
	3	0.10	0.29	-0.19	-0.12	0.49	0.13	-0.01	0.70
	4	0.17	-0.04	-0.09	0.61	-0.08	0.16	0.07	0.80
	5	-0.36	-6.11	3.48	3.46	0.57	-3.54	-0.03	-1.80

Table 4 (Cont'd.)

Character	C.C.*	Plant height	Branches /plant	Clusters /plant	Pods /plant	Pod length	Seeds /pod	100 seed weight	Rg**
Pod length (cm)	1	-4.50	0.42	0.68	-0.05	2.62	1.18	0.35	0.69
	2	-0.51	0.03	0.15	1.05	0.03	-0.12	-0.38	0.26
	3	0.80	0.57	-0.73	0.07	-0.80	0.36	-0.02	0.26
	4	0.22	0.01	-0.01	0.05	-0.85	0.50	0.39	0.32
	5	1.44	-16.62	17.96	-0.50	-3.99	-0.77	-8.19	-10.68
Seeds/pod	1	-4.66	0.23	0.44	-0.01	3.16	0.98	0.58	0.72
	2	-0.39	0.04	0.25	1.12	0.03	-0.13	-0.42	0.50
	3	0.18	2.02	-0.93	-0.04	-0.68	0.43	0.01	0.99
	4	0.23	0.04	-0.03	0.17	-0.73	0.57	0.27	0.51
	5	-0.31	12.83	8.65	0.60	-0.15	-20.35	-0.76	1.14
100 seed weight (g)	1	4.82	-0.52	-1.18	0.26	-1.16	-0.72	-0.78	0.71
	2	0.45	-0.04	-0.35	-1.73	-0.03	0.11	0.53	-1.07
	3	-0.44	-0.40	0.29	0.01	0.80	0.14	0.02	0.42
	4	0.16	-0.02	-0.01	0.07	-0.52	0.27	0.57	0.47
	5	3.52	-8.34	-8.72	-0.02	8.24	3.87	3.97	2.53

* C.C. = Cross combination
1. NM 92 X NM 51
2. NM 92 x Pusa Baisakhi
3. NM 92 x NM 93

** rg= Genotypic correlation
4. NM 92 x CV. 6601
5. CV. 6601 x NM 92

Two cross combinations viz., NM 92 x Pusa Baisakhi and CV. 6601 x NM 92 showed positive direct effects for cluster per plant with the highest value (9.06) in CV.6601 x NM 92. However this high value of direct effect carried negative genotypic correlation as compared to positive correlation in NM 92 x Pusa Baisakhi. Positve indirect effects were observed via plant height and branches per plant in most of the cross combinations (Table 4).

All cross combinations except NM 92 x NM 93 showed positive direct effects in pods per plant. Genotypic correlation was positive in four cross combinations except CV. 6601 x NM 92. Indirect effects were positive via plant height in three cross combinations with highest value of 3.51. Only two first cross combinations viz., NM 92 x NM 51 and NM 92 x Pusa Baisakhi showed positive direct effect in pod length alongwith positive correlation coefficient (Table 4). Indirect positive effects were more pronounced via branches per plant, clusters per plant, pods per plant and seeds per pod.

Three cross combinations viz., NM 92 x NM 51, NM 92 x NM 93, and NM 92 x CV. 6601 showed positive direct effects in seeds per pod combined with positive values of genotypic correlation coefficient. Indirect effects via pod length were only visible in two cross combinations. Positive direct effects of 100 seed weight were observed in four cross combinations except NM 92 x NM 51 with almost positive correlation values except in NM 92 x Pusa Baisakhi.

Overall in F_4, pods per plant, 100 seed weight, seeds per pod, and branches per plant showed positive direct effects alongwith positive genotypic correlation coefficient values. These results were also cross specific. Pods per plant showed positive response where NM 92 was combined with local cultivars CV.6601 or Pusa Baisakhi viz., NM 92 x Pusa Baisakhi and CV.6601 x NM 92. It was also positive in NM 92 x NM 51. 100 seed weight and seeds per pod was more pronounced positively in NM 92 x NM 93, NM 92 x CV.6601 and CV.6601 x NM 92.

Studying 400 F_2 germplasm plants of mung bean from each of four crosses, Singh *et al*., (1995) observed positive correlation of 100 seed weight with seed yield which was also cross specific. Pods per plant was the only character, which showed positive correlation with seed yield in all the selection groups. Correlation of seed yield with other characters was dependent on selection groups as well as cross combinations. Singh & Chaudhary (1985) explained that if direct effect value is almost equal to correlation coefficient, the direct selection will be effective. If the correlation is positive but the direct effect is negative or negligible, the character may be selected indirectly based on high indirect effects. Singh & Kakar (1997) describing the third situation i.e., correlation negative with positive direct effect, mentioned the use of a restricted simultaneous selection model to be followed. These restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effects.

Byregowda *et al.,* (1997) observed high heritability associated with high genetic advance for grain yield and pods per plant in greengram and assumed that main cause was the additive type of gene action. They also noted highest direct effects of pods per plant, seeds per pod and 100 seed weight on grain yield and mentioned that due importance should be given to these traits while making selection for increased seed yield in green gram.

In the present studies, in majority of the cross combinations, pods per plant showed the highest degree of heritability combined with maximum genetic advance both in F_3 and F_4 generations followed by 100 seed weight. High heritability alongwith high genetic advance was also observed for cluster per plant and seed yield.

Both F_3 and F_4 generations exhibited highest positive direct effects combined with positive genotypic correlation in pods per plant, 100 seed weight, branches per plant and seeds per pod. The pattern of behaviour of these traits in respect of direct effects was almost at par in both F_3 and F_4 populations, however, it was more close for pods per plant and 100 seed weight.

Results of present study revealed that while making selection, pods per plant should be given more emphasis followed by 100 seed weight, seeds per pod and branches per plant and preference must be given to medium tall plant.

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