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Generation mean analysis to estimate the genetic parameters for yield improvement and inheritance of seed colour and lusture in mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

In the present study, generation mean analysis and chi-square test were undertaken to estimate the nature and magnitude of gene action for yield and its component traits; and inheritance pattern of seed colour and lustre in two crosses of mungbean *viz* Sona/ DMS 03-17-2 and Sona/ DMS 01-34-2. Scaling and joint scaling tests revealed the presence of one or more kinds of epistatic effects for almost all the agro-morphological traits. The selection of elite lines from delayed generations and subsequent inter mating might be useful approach to recover/ develop the high yielding mungbean lines. The elite lines recovered from crosses Sona/ DMS 03-17-2 and Sona/ DMS 01-34-2 might be superior in terms of early maturity with more number of branches, pods high seed index, biomass and yield. Likewise, crosses *i.e.* Sona/ DMS 03-17-2 for average intermodal length; Sona/ DMS 01-34-2 for NSP; may give opportunity to isolate transgressive segregants in advanced generations. There was also a possibility to recover the yellow and shiny seeded mungbean lines due to its monogenic inheritance of seed coat colour and lusture.

Key words: Epistasis, GMA, Gene effect, Inheritance, Mungbean, Transgressive segregants.

INTRODUCTION

Due to complex inheritance of seed yield and its component traits, development of high yielding mungbean varieties may be possible by studying the nature and magnitude of genetic variability present in the available stocks for different traits. The adequate information on extent of variability parameters may be helpful in the development of promising varieties through identification of yield determinants. The choice of efficient breeding programmes depends on knowledge of gene action involved in expression of yield and its component traits. Several researchers Ullah *et al.* (2011); Singh *et al.* (2014a, b) studied the genetic parameters and found additive type of gene action in governing the seed yield per plant (SYP), whereas Mehandi *et al.* (2013); Bisht *et al.* (2014) observed both additive and non-additive type of gene action. Patil *et al.* (2011) performed the combining ability analysis and suggested the importance of both additive and non-additive type of gene action for SYP and its other related traits. But these methods give general idea about inheritance of traits and some time misleads. Therefore, generation mean analysis was used in present study, which may give more reliable results about inheritance of traits due to individual cross analysis.

To detect the inheritance pattern, selection of parents to develop the populations for study is also an important step. Characterization of germplasm helps to form trait specific groups and gives the idea about those traits, which may be used to distinguish the genotypes from each other. Piyada *et al.* (2010) also gave emphasis on morphological characterization to assess the variability for classifing the crop germplasm. Some of the agro-morphological traits may be used as morphological markers in crop improvement. Physical parameters indicating seed quality such as seed colour and seed luster are important as morphological marker and affect the market quality. Consumers prefer the green/ yellow, shiny and bold seeds over spotted/ black, dull and small seeds. Seed colour also indicates the phytic acid (PA) content. Tajoddin *et al.* (2011) reported that yellow seeded mungbean had low phytic acid content and may be used as a donor for quality improvement of mungbean seeds. Sompong *et al.* (2010) reported that two major genes at two different loci govern this trait. They also found the transgressive segregation for phytic acid in F_2 population revealing modifying gene action among progenies of normal phytic acid mungbean lines. Thus, crossing among yellow seeded mungbean lines and/ or yellow seeded with green seeded mungbean lines may give opportunity to develop the varieties with desirable amount of phytic acid content. Grouping of genotypes based on these morphological traits can be easily done by naked eye and

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used in mungbean breeding program for improving the seed physical quality. Keeping the above facts in mind, the present experiment was conducted (1) to test suitability of additive-dominance model and (2) to estimate genetic parameters such as gene effects using six basic generations and (3) to study the inheritance pattern of seed colour and lustre in mungbean.

MATERIALS AND METHODS

Genetics of seed yield and other traits of mungbean were studied using the F_1, F_2, $BC_{1.1}$ and $BC_{1.2}$ of a cross between Sona (a small, yellow and dull seeded line) as female parent (P_1) and DMS 03-17-2 and DMS 01-34-2 (bold, green and shiny seeded line) as male parents (P_2). The experiment was laid out in randomized complete block design (RCBD) with three replications during *kharif*, 2013. These parents were selected from previous experiment conducted during summer, 2012 (Singh *et al.*, 2014a) and crossed to obtain the crosses during *kharif*, 2012. The F_1 seeds were subjected to back crossing and selfing during summer, 2013. Ten competitive random plants from P_1, P_2 and F_1; 15 from $BC_{1:1}$ and $BC_{1:2}$ and 60 from F_2 population were randomly selected from each family in each replication, to record the observations for agro-morphological traits *viz.*, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, seed index, biological yield per plant, harvest index and seed yield per plant. The traits *viz.*, days to first flower open and days to maturity were computed on plot basis. The observed means of the six generations and their standard errors were used to estimate the mid-parent [m], additive [d] and dominance [h] gene effects using the joint scaling test of Mather and Jinks (1982). The adequacy of the simple additive-dominance model (mean, additive, and dominance effects) was determined by χ^2 test. Where the simple model proved to be inadequate, additive×additive [i], additive×dominance [j] and dominance×dominance [l] were added to the model, as proposed by Mather and Jinks (1982). The significance of genetic parameters (m, [d], [h], [i], [j] and [l]) were tested using *t*-test. The data were subjected to generation mean analysis by using statistical package WINDOSTAT 9.1 version. To confirm the inheritance pattern of seed colour and luster, the F_2, $BC_{1:1}$ and $BC_{1:2}$ were subjected to χ^2 test.

RESULTS AND DISCUSSION

The generation performance for crosses Sona/ DMS 03-17-2 and Sona/ DMS 01-34-2 are presented in Table 1. For Sona/ DMS 03-17-2; among all six generations, female parent (P_1) was found superior than other generations for days to first flower open (early), pod length and number of seeds per pod, whereas, male parent (P_2) was found superior for number of pods per plant, seed index, biological yield per plant, harvest index and seed yield per plant. The F_1 was found superior for most of the agro-morphological traits *viz.*, days to maturity (early), plant height (short), number of secondary branches per plant and number of nodes on main stem, indicating the heterotic response. However, number of primary branches per plant was found superior in F_2 generation over both male and female parent. $BC_{1:1}$ and $BC_{1:2}$ showed greater mean for average inter-nodal length (short) and number of primary branches per plant, respectively. Likewise, for Sona/ DMS 01-34-2; female parent (P_1) was found superior for days to first flower open (early) and pod length over rest five generations, whereas, male parent (P_2) was noted as superior for number of nodes on main stem, average inter-nodal length (short) and seed index. The cross (F_1) exhibiting superiority over rest of the five generations for number of primary branches per plant, number of secondary branches per plant, pod length, harvest index and seed yield per plant. However, F_2 exhibited superiority over rest generations for biological yield per plant. F_2 also exhibited greater mean for seed yield per plant, number of pods per plant (over both P_1 and P_2); number of nodes on main stem, harvest index (over P_1); number of secondary branches per plant (over P2). The maximum mean value was exhibited by $BC_{1:1}$ for plant height (short), whereas, $BC_{1:2}$ for days to maturity (early), number of nodes on main stem and number of seeds per pod.

Significance of epistasis was detected by both type of (scaling and joint scaling) tests, (Table 2). A scale (days to maturity, number of primary branches per plant, number of nodes on main stem, pod length, seed index and harvest index), B scale (days to first flower open, days to maturity, plant height, pod length, number of seeds per pod and seed index), C scale (days to first flower open, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, seed index, biological yield per plant, harvest index and seed yield per plant) and D scale (days to first flower open, days to maturity, number of pods per plant, pod length, number of seeds per pod, seed index, biological yield per plant, harvest index and seed yield per plant) were found significant for all the agro-morphological traits given in parenthesis. Likewise, for Sona/ DMS 01-34-2; A scale (days to first flower open, plant height, number of primary branches per plant, number of secondary branches per plant, average inter-nodal length, number of pods per plant, pod length, seed index, biological yield per plant, harvest index and seed yield per plant), B scale (days to first flower open, days to maturity, plant height, number of primary branches per plant, average inter-nodal length, number of pods per plant, seed index, biological yield per plant, harvest index and seed yield per plant), C scale (days to first flower open, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, average inter-nodal length, pod length, seed index, biological yield per plant and seed yield per plant) and D scale (days to maturity, number of pods per plant, pod length, seed index, biological yield per

Table 1: Mean performance of P1, P2, F1, F2, B1 and B2 generations for fourteen agro-morphological traits in cross Sona/ DMS 03-17-2 (cross I) and Sona/ DMS 01-34-2 (cross II)

Traits	Cross	P1	P2	F1	F2	B1	B2
DFFO	I	33.33 ± 0.18	35.67 ± 0.23	36.67 ± 0.09	35.33 ± 0.04	34.67 ± 0.23	34.33 ± 0.09
	II	33.00 ± 0.15	35.67 ± 0.09	37.67 ± 0.32	37.67 ± 0.13	38.33 ± 0.32	37.67 ± 0.38
DM	I	68.33 ± 0.53	65.67 ± 0.09	59.67 ± 0.23	71.67 ± 0.13	62.33 ± 0.32	66.00 ± 0.15
	II	67.67 ± 0.38	65.33 ± 0.09	63.00 ± 0.46	70.33 ± 0.15	65.67 ± 0.18	62.67 ± 0.38
PH	I	47.98 ± 0.84	45.78 ± 0.94	42.49 ± 0.63	48.45 ± 0.59	46.30 ± 0.88	48.31 ± 1.26
	II	43.02 ± 0.66	42.65 ± 0.64	50.55 ± 0.79	44.01 ± 0.38	42.13 ± 0.68	43.63 ± 0.91
NPBP	I	1.97 ± 0.09	2.13 ± 0.12	2.27 ± 0.18	2.39 ± 0.07	2.60 ± 0.09	2.67 ± 0.21
	II	2.43 ± 0.21	2.33 ± 0.14	3.20 ± 0.22	2.42 ± 0.07	2.30 ± 0.14	2.20 ± 0.16
NSBP	I	2.53 ± 0.16	2.27 ± 0.16	2.60 ± 0.21	2.49 ± 0.09	2.40 ± 0.18	2.20 ± 0.16
	II	2.33 ± 0.21	1.93 ± 0.19	3.17 ± 0.21	2.16 ± 0.09	1.83 ± 0.17	2.13 ± 0.21
NMS	I	11.63 ± 0.25	10.43 ± 0.27	11.83 ± 0.30	11.16 ± 0.12	10.73 ± 0.27	11.23 ± 0.25
	II	10.43 ± 0.31	11.07 ± 0.23	10.27 ± 0.36	10.70± 0.12	10.37 ± 0.26	11.07 ± 0.28
AIL	I	4.37 ± 0.14	4.47 ± 0.17	4.51 ± 0.17	4.40 ± 0.06	4.25 ± 0.1	4.46 ± 0.18
	II	4.23 ± 0.14	3.91 ± 0.11	5.08 ± 019	4.21 ± 0.06	4.15 ± 0.13	4.03 ± 0.15
NPP	I	17.20 ± 0.70	20.90 ± 1.13	16.50 ± 0.96	13.67 ± 0.31	16.37 ± 0.86	18.07 ± 1.19
	II	14.37 ± 0.77	15.77 ± 0.53	26.13 ± 0.75	19.67 ± 0.77	17.00 ± 1.05	16.20 ± 0.94
PL	I	7.76 ± 0.11	6.63 ± 0.17	6.35 ± 0.11	7.55 ± 0.06	6.25 ± 0.03	7.31 ± 012
	II	7.72 ± 0.14	7.42 ± 0.14	6.59 ± 0.12	6.57 ± 0.05	6.40 ± 0.07	7.17 ± 0.14
NSP	I	11.70 ± 0.25	11.00 ± 0.30	10.90 ± 0.28	10.71 ± 0.12	10.87 ± 0.30	11.60 ± 0.21
	II	11.40 ± 0.29	10.97 ± 0.24	10.97 ± 0.32	11.37 ± 0.11	10.80 ± 0.24	11.50 ± 0.28
SI	I	2.62 ± 0.05	5.24 ± 0.07	3.36 ± 0.07	3.50 ± 0.03	4.46 ± 0.07	4.92 ± 0.05
	II	2.58 ± 004	5.18 ± 0.03	4.70 ± 0.03	3.32 ± 0.04	4.38 ± 0.10	5.04 ± 0.10
BYP	I	16.50 ± 0.60	20.13 ± 0.67	13.67 ± 0.85	12.31 ± 0.37	16.67 ± 1.05	19.13 ± 1.24
	II	17.93 ± 0.60	18.30 ± 0.73	17.43 ± 0.95	19.51 ± 0.65	13.50 ± 0.55	14.33 ± 0.82
HI	I	28.02 ± 0.61	32.63 ± 1.51	24.36 ± 0.98	25.37 ± 0.43	23.40 ± 0.76	30.79 ± 1.28
	II	25.85 ± 0.87	31.24 ± 1.13	38.37 ± 2.07	29.89 ± 0.87	23.22 ± 0.79	26.95 ± 1.17
SYP	I	4.59 ± 0.17	6.70 ± 0.48	3.28 ± 0.26	3.13 ± 0.11	4.00 ± 0.36	6.15 ± 0.59
	II	4.60 ± 0.019	5.86 ± 0.45	6.22 ± 0.17	5.95 ± 0.29	3.13 ± 0.16	3.81 ± 0.23

DFFO= Days to first flower open, DM= days to maturity, PH= plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP).

plant, harvest index and seed yield per plant) were found significant for the agro-morphological traits given in parenthesis. However, joint scaling test exhibited significant χ^2 values for all the agro-morphological traits studied with few exceptions (except number of nodes on main stem and number of seeds per pod in Sona/ DMS 03-17-2 and number of secondary branches per plant, average inter-nodal length and number of seeds per pod in Sona/ DMS 01-34-2), indicating the un-adequacy of simple additive dominance model. The respective agro-morphological traits for Sona/ DMS 03-17-2 (number of secondary branches per plant and average inter-nodal length) and Sona/ DMS 01-34-2 (number of nodes on main stem and number of seeds per pod) given in parenthesis have proved the adequacy of additive-dominance model for respective crosses. Besides the scaling test, joint scaling test also indicated the same conclusion. In present study, one or more kinds of epistatic effects were detected for all the agro-morphological traits (barring some exceptions) and it would have been biased, if they had been estimated using the procedure by assuming the absence of epistasis.

The [m] effect was found positive and significant for all the agro-morphological traits under study barring few exceptions (except number of pods per plant, seed index, biological yield per plant and seed yield per plant in Sona/ DMS 03-17-2) in both crosses (Table 3). Additive [d] gene effect was found positive and significant for number of nodes on main stem and pod length in Sona/ DMS 03-17-2 and for days to maturity in Sona/ DMS 01-34-2, whereas negative and significant [d] gene effect was found for days to first flower open, number of pods per plant, seed index, biological yield per plant, harvest index and seed yield per plant in Sona/ DMS 03-17-2 and for days to first flower open, number of nodes on main stem, seed index, harvest index and seed yield per plant in Sona/ DMS 01-34-2, indicating the involvement of additive gene action in the inheritance of these yield component traits in specific crosses. Dominance [h] gene effect was found positive and significant for number of secondary branches per plant in Sona/ DMS 03-17-, indicating the preponderance of dominance gene action in expression of number of secondary branches per plant may improved through combination breeding. Likewise, average

Table 2: Scaling and joint scaling test for adequacy of additive-dominance model of fourteen agro-morphological traits in cross Sona/ DMS 03-17-2 (cross I) and Sona/ DMS 01-34-2 (cross II)

Traits	Cross	A	B	C	D	m	[d]	[h]	χ^2
DFFO	I	-0.67 ± 0.50	-3.67 ± 0.30**	-1.00 ± 0.37**	1.67 ± 0.26**	37.83 ± 0.54**	-1.17 ± 0.15**	-8.83 ± 1.58**	189.34**
	II	6.00 ± 0.7**	2.00 ± 0.83*	6.67 ± 0.83**	-0.67 ± 0.56	33.00 ± 1.12**	-1.33 ± 0.09**	14.00 ± 3.17**	97.70**
DM	I	-3.33 ± 0.86**	6.67 ± 0.39**	33.33 ± 0.87**	15.00 ± 0.43**	97.00 ± 0.91**	1.33 ± 0.27**	-64.00 ± 2.48**	2245.69**
	II	0.67 ± 0.69	-3.00 ± 0.89**	22.33 ± 1.17**	12.33 ± 0.52**	91.17 ± 1.06**	1.17 ± 0.20**	-55.17 ± 2.90**	780.85**
PH	I	2.13 ± 2.04	8.35 ± 2.77**	15.05 ± 2.94**	2.28 ± 1.93	51.44 ± 3.92**	1.10 ± 0.63	-3.03 ± 1.54	31.24**
	II	-9.31 ± 1.70**	-5.94 ± 2.09**	-10.74 ± 2.38**	2.26 ± 1.37	47.35 ±2.78**	0.18 ± 0.46	-16.56 ± 7.65*	37.97**
NPBP	I	0.97 ± 0.27**	0.93 ± 0.47	0.94 ± 0.47*	-0.48 ± 0.27	1.09 ± 0.54*	-0.08 ± 0.07	4.03 ± 1.51**	14.60**
	II	-1.03 ± 0.41*	-1.13 ± 0.41**	-1.50 ± 0.58*	0.33 ± 0.26	3.05 ± 0.53**	0.05 ± 0.13	-2.68 ± 1.46	11.01**
NSBP	I	-0.33 ± 0.44	-0.47 ± 0.41	-0.02 ± 0.60	0.39 ± 0.29	3.18 ± 0.60**	0.13 ± 0.11	-2.16 ± 1.63	—
	II	-1.83 ± 0.44**	-0.83 ± 0.51	-1.96 ± 0.61**	0.36 ± 0.32	2.84 ± 0.65**	0.20 ± 0.14	-3.06 ± 1.82	19.32**
NMS	I	-2.00 ± 0.66**	0.20 ± 0.65	-1.11 ± 0.86	0.34 ± 0.44	11.72 ± 0.90**	0.60 ± 0.18**	-2.38 ± 2.49	13.10**
	II	0.03 ± 0.70	0.80 ± 0.71	0.77 ± 0.93	-0.03 ± 0.45	10.68 ± 0.91**	-0.32 ± 0.19	0.48 ± 2.56	—
AIL	I	-0.38 ± 0.39	-0.07 ± 0.43	-0.25 ± 0.47	0.10 ± 0.27	4.62 ± 0.54**	-0.05 ± 0.11	-0.76 ± 1.55	—
	II	-1.02 ± 0.35**	-0.93 ± 0.37*	-1.48 ± 0.48**	0.24 ± 0.24	4.55 ± 0.48**	0.16 ± 0.09	-1.91 ± 1.34	15.43**
NPP	I	-0.97 ± 2.09	-1.27 ± 2.80	-16.43 ± 2.64**	-7.10 ± 1.60**	4.85 ± 3.26	-1.85 ± 0.66**	23.62 ± 9.42*	5.44**
	II	-6.50 ± 2.36**	-9.50 ± 2.09**	-3.73 ± 3.55	6.13 ± 2.09**	27.33 ± 4.20**	-0.70 ± 0.47	-29.47 ± 10.57**	28.22**
PL	I	-1.62 ± 0.17**	1.64 ± 0.31**	3.09 ± 0.38**	1.54 ± 0.17**	10.27 ± 0.36**	0.56 ± 0.10**	-6.97 ± 0.89**	355.08**
	II	-1.50 ± 0.24**	0.32 ± 0.34	-2.04 ± 0.37**	-0.43 ± 0.19*	6.71 ± 0.38**	0.15 ± 0.10	-0.44 ± 1.08	59.65**
NSP	I	-0.87 ± 0.71	1.30 ± 0.58*	-1.68 ± 0.84*	-1.06 ± 0.44*	9.24 ± 0.90**	0.35 ± 0.19	4.21 ± 2.49	
	II	-0.77 ± 0.64	1.07 ± 0.69	1.17 ± 0.56	0.43 ± 0.42	12.05 ± 0.87**	0.22 ± 0.19	-1.65 ± 2.44	—
SI	I	2.94 ± 0.17**	1.24 ± 0.14**	-0.58 ± 0.19**	-2.38 ± 0.10**	-0.83 ± 0.21**	-1.31 ± 0.04**	13.13 ± 0.53**	567.34**
	II	1.48 ± 0.21**	0.20 ± 0.1	-3.88 ± 0.17**	-2.78 ± 0.16**	-1.68 ± 0.32**	-1.30 ± 0.03**	13.62 ± 0.91**	623.65**
BYP	I	3.17 ± 2.34	4.47 ± 2.70	-14.72 ± 2.43**	-11.18 ± 1.79**	-4.04 ± 3.60	-1.82 ± 0.45**	47.69 ± 10.31**	60.27**
	II	-8.37 ± 1.57**	-7.07 ± 2.04**	6.92 ± 3.36*	11.18 ± 1.63**	40.47 ± 3.30**	-0.18 ± 0.47	-60.83 ± 8.07**	64.00**
HI	I	-5.57 ± 1.91**	4.59 ± 3.13	-7.88 ± 3.06*	-3.45 ± 1.72*	23.43 ± 3.53**	-2.31 ± 0.82**	6.85 ± 0.92	19.10**
	II	-17.78 ± 2.74**	-15.70 ± 3.32**	-14.28 ± 5.58*	9.60 ± 2.24**	47.75 ± 4.53**	-2.70 ± 0.71**	-62.07 ± 11.34**	52.61**
SYP	I	0.13 ± 0.78	2.33 ± 1.30	-5.30 ± 0.86**	-3.88 ± 0.73**	-2.12 ± 1.48	-1.05 ± 0.25**	15.62 ± 4.32**	52.78**
	II	-4.56 ± 0.42**	-4.46 ± 0.67**	0.89 ± 1.31	4.95 ± 0.65**	15.13 ± 1.32**	-0.63 ± 0.24*	-27.83 ± 2.99**	170.01**

*= P<0.05, **= P<0.01, DFFO= Days to first flower open, DM= days to maturity, PH= plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP).

Table 3: Estimates of gene effects with SE of the fitted models for fourteen agro-morphological traits in cross Meha/ DMS Sona/ DMS 03-17-2 (cross I) and Sona/ DMS 01-34-2 (cross II)

Traits	Cross	m	[d]	[h]	[i]	[j]	[l]	Epistasis
DFFO	I	39.40 ± 0.44**	-0.78 ± 0.13**	-13.54 ± 1.29**	-5.01 ± 0.40**	—	10.81 ± 0.87**	D
	II	34.33 ± 0.09**	-1.33 ± 0.09**	10.28 ±0.61**	—	4.20 ± 0.99**	-6.95 ± 0.80	D
DM	I	95.74 ± 0.87**	—	-60.21 ± 2.36**	-30.00 ± 0.87**	-7.33 ± 0.70**	24.14 ± 1.57**	D
	II	89.50 ± 0.97**	1.49 ± 0.18**	-50.16 ± 2.61**	-22.70 ± 0.94**	—	23.66 ± 1.86**	D
PH	I	50.16 ± 0.73**	—	—	-3.25 ± 1.00**	—	-7.71 ± 1.10**	—
	II	48.21 ± 2.70**	—	-19.15 ± 7.39**	-5.38 ± 2.66*	—	—	—
NPBP	I	1.17 ± 0.43**	—	3.81 ± 0.39**	0.86 ± 0.43*	—	-2.71 ± 0.8**	D
	II	2.22 ± 0.08**	—	0.44 ± 0.21*	—	—	0.80 ± 0.25**	—
NSBP	I	2.43 ± 0.16**	—	0.15 ± 0.10*	—	—	—	—
	II	2.11 ± 0.14**	—	-1.11 ± 0.54*	—	—	0.33 ± 0.58**	D
NMS	I	10.94 ± 0.13**	0.61 ± 0.18**	—	—	-2.18 ± 0.82**	0.81 ± 0.36*	—
	II	10.68 ± 0.09**	-0.41 ± 0.17*	—	—	—		—
AIL	I	4.40 ± 0.05**	-0.08 ± 0.10*	—	—	—	—	—
	II	3.96 ± 0.48**	—	—	—	—	0.04 ± 0.0.20	—
NPP	I	—	-1.86 ± 0.60**	37.40 ± 1.49**	18.88 ± 0.64**	—	-20.90 ± 2.23**	D
	II	27.77 ± 4.18**	—	-30.77 ± 1.34**	-12.45 ± 4.16**	—	43.81 ± 6.62**	D
PL	I	8.69 ± 0.16**	0.63 ± 0.10**	-2.51 ± 0.24**	-1.66 ± 0.19**	-4.22 ± 0.57*	—	—
	II	6.57 ± 0.04**	—	—	0.99 ± 0.11**	-1.60 ± 0.44**		—
NSP	I	10.81 ± 0.17**	—	—	0.67 ± 0.30**	-1.84 ± 0.25**	—	—
	II	11.25 ± 1.33**	0.03 ±0.01*	—	—	—		—
SI	I	—	-1.32 ± 0.04**	10.83 ± 0.11**	3.97 ± 0.04**	1.50 ± 0.19**	-7.47 ± 0.16**	D
	II	1.72 ± 0.32**	-1.28 ± 0.03**	13.73 ± 0.91**	5.60 ± 0.32**	—	-7.31 ± 0.60**	D
BYP	I	—	-1.85 ± 0.43**	36.25 ± 1.60**	18.38 ± 0.45**	—	-22.59 ± .17**	D
	II	41.09 ± 3.21**	—	-62.68 ± 7.73**	-23.00 ± 3.18**	—	24.51 ± 7.88**	D
HI	I	25.31 ± 0.37**	-2.41 ± 0.80**	—	5.16 ± 0.90**	-9.01 ± 30**	—	—
	II	48.42 ± 4.41**	-2.91 ± 0.64**	-64.08 ± 10.93**	-19.82 ± 4.38**	—	54.03 ± 7.67**	D
SYP	I	—	-1.18 ± 0.24**	9.39 ± 0.50**	5.76 ± 0.24**	—	-6.12 ± 0.67**	D
	II	15.17 ± 1.30**	-0.65 ± 0.18**	-27.93 ± 2.90**	-9.92 ± 1.29**	—	18.99 ± 1.66**	D

*= P<0.05, **= P<0.01, DFFO= Days to first flower open, DM= days to maturity, PH= plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP), D= duplicate gene interaction.

inter-nodal length in Sona/ DMS 03-17-2 and number of nodes on main stem and number of seeds per pod in Sona/ DMS 01-34-2 exhibited simple additive gene action may improved through simple plant selection methods. [h] gene effect was found positive and significant for number of primary branches per plant, number of pods per plant, seed index, biological yield per plant and seed yield per plant in Sona/ DMS 03-17-2 and days to first flower open and for seed index in Sona/ DMS 01-34-2, whereas negative and significant for days to first flower open, days to maturity and pod length in Sona/ DMS 03-17-2 and for days to maturity, plant height, number of secondary branches per plant, number of pods per plant, biological yield per plant, harvest index and seed yield per plant in Sona/ DMS 01-34-2, indicating the involvement of dominance gene action. In Sona/ DMS 03-17-2 (days to first flower open, number of pods per plant, pod length, seed index, biological yield per plant and seed yield per plant) and Sona/ DMS 01-34-2 (days to first flower open, days to maturity, seed index, harvest index and seed yield per plant); both [d] and [h] components were significant for respective traits given in parenthesis, proving the equal importance of additive and dominance gene action.

The [h] gene effects were greater than the [d] gene effects for all agro-morphological traits in both crosses, indicated the importance of dominance gene effects for yield and its related agro-morphological traits. The contribution of dominance gene effects varied with to cross and traits. Similar result was also observed earlier by Gawande *et al.* (2005) and Azizi *et al.* (2006). The negative and positive sign of [h] gene effects is a function of the F_1 mean value in relation to mid parent heterosis contributing to dominance gene effects (Cukadar-Olmedo and Miller, 1997). It is possible that the epistasis significantly contributed to genetic variance. Beside the additive and dominance genetic effects, epistasis components have also contributed to genetic variation with different magnitude for most of the yield and yield component traits. In such situation, the appropriate breeding method can effectively exploit the three types of gene effects. Confounding the epistatic interaction effects in the models suggested complexity of the inheritance of these yield and yield component traits were polygenic (Khattak *et al.*, 2004a, Khan *et al.*, 2007). The traits *viz.*, days to first flower open, days to maturity, plant height and pod length showed negative and significant [i] effect in Sona/ DMS 03-17-2 and pod length and seed index in Sona/ DMS 01-34-2, whereas number of primary branches per plant, number of pods per plant, number of seeds per pod, seed index, biological yield per plant, harvest index and seed yield per plant showed positive and significant [i] effect in Sona/ DMS 03-17-2 and for days to maturity, plant height, number of pods per plant, biological yield per plant, harvest index and seed yield per plant in Sona/ DMS 01-34-2. Additive x dominance [j] gene effect was found positive and significant only for seed index in Sona/ DMS 03-17-2 and for days to first flower open in Sona/ DMS 01-34-2, whereas negative and significant for days to maturity, number of nodes on main stem, pod length, number of seeds per pod and harvest index in Sona/ DMS 03-17-2 and for pod length in Sona/ DMS 01-34-2. Dominance x dominance [l] was found positive and significant for days to first flower open, DM and number of nodes on main stem in Sona/ DMS 03-17-2 and for days to maturity, number of primary branches per plant, number of secondary branches per plant, average inter-nodal length, number of pods per plant, biological yield per plant, harvest index and seed yield per plant in Sona/ DMS 01-34-2, whereas negative and significant for plant height, number of primary branches per plant, number of pods per plant, seed index, biological yield per plant and seed yield per plant in Sona/ DMS 03-17-2 and for days to first flower open and seed index in Sona/ DMS 01-34-2. The model with conceding gene interactions showed that although [d] and/ or [h] with at least one interaction ([i], [j], [l]) were found significant for all the agro-morphological traits in both crosses baring some exceptions, revealed their complex inheritance nature. The similar results were also obtained by Patil and Kajjidoni (2005) for days to first flowering, pod length and harvest index; Singh *et al.* (2007) for days to first flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and seed yield per plant; Patel *et al.* (2012) for days to flowering, plant height and seed yield per plant.

Further, the [h] and [l] sign was found opposite for days to first flower open, days to maturity, number of pods per plant, seed index, biological yield per plant and seed yield per plant in both crosses; whereas for number of primary branches per plant in Sona/ DMS 03-17-2 and for number of secondary branches per plant and harvest index in Sona/ DMS 01-34-2, indicated the duplicate type of digenic epistatic interaction in respective crosses. These findings were agreed with the similar reports of Singh *et al.* (2006), Aliyu *et al.* (2007) and Khodambashi *et al.* (2012), Singh *et al.* (2015) for most of the traits. This kind of digenic epistasis generally hinders the improvement by practicing the selection. Hence, higher magnitude of dominance [h] and [l] type of interaction effect would not be desirable. It may give promising lines for respective traits, selection should be delayed after several generations of selection through single seed decent (SSD) till fixation for accumulating the favourable genes. The selection of elite lines from delayed selection and subsequent inter mating is also more important under this situation to recover/ develop the high yielding mungbean lines by improving some important yield and yield component traits with some unique features in later generations. The elite lines recovered from

Sona/ DMS 03-17-2 and Sona/ DMS 01-34-2 may be superior in terms of early maturity with more number of branches, pods high seed index, biomass and yield. However, the small and bold seeded parents with contrasting qualitative traits *viz.*, seed coat colour (yellow and green) and seed luster (dull and shiny) were involved in crossing, therefore high yielding bold seeded with shiny seed coat genotypes may be developed in later generations by fixing the favourable genes for these traits. In later generations, these traits may also be incorporated into a single line after recovering the elite lines from same population and genes may be easily incorporated due to sister line. The Biparental mating might be performed among transgressive segregants and/ or RILs may throw good frequency of desirable recombinants by converting the repulsion phase linkage into coupling phase due to forced recombination and thereby release greater amount of concealed genetic variations mostly, which governs by additive genes.

The inheritance pattern of seed colour and seed luster are presented in Table 4 and Table 5, respectively. Green seed was found dominant over yellow; and dull seed luster was found dominant over shiny in both crosses. F_2 and back cross population score also fit the expected 3: 1 and 1:1 for seed colour and seed luster, indicating that these traits are under the monogenic control and could be easily exploited in mungbean improvement programme. Similar findings were also observed earlier by Sriphadet *et al.* (2010). Lambrides *et al.* (2004) reported the dominant and recessive epistatsis for genetic control of seed lustre. The monogenic control of these traits may be used in breeding programme to develop the varieties with bold, yellow and shiny seeded mungbean.

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Table 4: Segregation ratio for seed colour in two mungbean crosses

Population	Total	Green	Yellow	Observed	Expected	χ^2
Sona	61	0	61	—	—	—
DMS 03-17-2	66	66	0	—	—	—
F_1	58	58	0	—	—	—
F_2	883	680	203	3.35:1	3:1	1.91
$B_{1:1}$	57	25	32	0.78:1	1:1	0.86
$B_{1:2}$	50	50	0	—	—	—
Sona	60	0	66	—	—	—
DMS 01-34-2	58	58	0	—	—	—
F_1	47	47	0	—	—	—
F_2	724	557	167	3.34:1	3:1	0.44
$B_{1:1}$	48	26	24	1.08:1	1:1	0.33
$B_{1:2}$	40	40	0	—	—	—

Table 5: Segregation ratio for seed coat luster in four mungbean crosses

Population	Total	Dull	Shiny	Observed	Expected	χ^2
Sona	66	66	0	—	—	—
DMS 03-17-2	60	0	60	—	—	—
F_1	63	63	0	—	—	—
F_2	1135	844	291	2.90:1	3:1	0.25
$B_{1:1}$	57	27	30	0.90:1	1:1	0.16
$B_{1:2}$	50	50	0	—	—	—
Sona	61	61	0	—	—	—
DMS 01-34-2	64	0	64	—	—	—
F_1	58	58	0	—	—	—
F_2	724	560	164	3.41:1	3:1	2.13
$B_{1:1}$	48	23	25	0.92:1	1:1	0.08
$B_{1:2}$	40	40	0	—	—	

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