

GENETIC VARIABILITY STUDIES IN MOTHBEAN [*VIGNA CONITIFOLIA* (JACQ.) MARECHAL] IN AN SEMI-ARID ENVIRONMENT OF NORTH KARNATAKA

A. G. VIJAYA KUMAR, SHRUTI KORADDI*, D. T. KALLESH, S. T. HUNDEKAR AND ISHWAR H. BOODI
AICRP for Dryland agriculture, RARS Vijayapur - 586 101, INDIA
e-mail: shruti.koraddi7@gmail.com

KEYWORDS

Mothbean
Genetic variability
Correlation coefficients
Path analysis

Received on :
16.01.2016

Accepted on :
29.04.2016

*Corresponding
author

ABSTRACT

An experiment was conducted in mothbean genotypes to study the genetic diversity, correlation and path coefficients for yield and its component characters. The estimates of PCV and GCV were high for number of pods per plant (79.35 and 78.74). Higher PCV and moderate GCV values were noticed for number of branches per plant (20.91 and 18.97), plant height (22.57 and 18.90) and seed yield per ha(20.61 and 12.47). Low PCV values were recorded for 100 seed weight (6.31) and pod length (6.71). High heritability coupled with high genetic advance as percent of mean was recorded for number of pods per plant(98.48%,160.94), number of branches per plant(82.29%, 35.45) and plant height(70.08%, 32.59). The genotypes were moderately diverse and were classified into 4 clusters, of which cluster IV was solitary. Seed yield per ha (kg) was found to have positive correlation with number of pods per plant (0.0449), while rest of the traits had negative correlation on seed yield per ha. The path coefficients indicated that the number of pods per plant (0.396), number of seeds per pod (0.1274) and 100 seed weight (0.0465) had direct positive effect on seed yield per ha. Hence, the characters having direct positive influence should be given due importance, while breeding for high yielding types in mothbean

INTRODUCTION

Mothbean [*Vigna aconitifolia*(Jacq.)Marechal] is an important crop of dry and semiarid areas of India. Among kharif pulses, it has the maximum capacity to resist drought conditions and grows well in the area receiving less than 300 mm of rainfall. It is principally grown for its protein rich edible seeds, dry seeds and sprouts. It is an excellent source of easily digestible protein with low flatulence and is consumed as dhal, bean sprouts, noodles, green beans and boiled dry beans. In Karnataka cultivation of moth bean is least among other growing states in India and mainly grown in Northern districts of Karnataka. Besides low productivity, moth bean is also known for plant types of primitive nature, conferring its evolution for survival but not for grain productivity (Yogeesh *et al.*, 2012). The low productivity is attributed to susceptibility of mothbean to biotic and abiotic stresses. (Yogeesh *et al.*, 2012). The efficiency of a crop improvement programme mainly depends on the extent of genetic variability present in the germplasm and heritability of the traits under selection. Yield is regarded as a complex trait, which is influenced by many component traits both in positive and negative directions. Generally, direct selection for yield is not sufficiently effective due to low heritability. (Kumar *et al.*, 2013a;Kumar *et al.*, 2013b). Hence, selection based on its contributing characters could be more efficient and reliable. Therefore, it is desirable to know the mutual relationship between various component traits on which selection can be made for improvement in yield. For any planned breeding program aimed to improve grain yield potential of crops, it is

necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Vast scope lies for genetic improvement of the mothbean through genetic diversity. A neglected and minor pulse crop of Karnataka but nutritionally rich. There is no systematic breeding work done so far in mothbean. Keeping this in view, present study was undertaken to study the diversity in different accessions of mothbean for assessment and creation of diverse lines for further use in the breeding programme and also study the nature and degree of association among the characters and their direct and indirect effects on yield.

MATERIALS AND METHODS

The experiment was conducted with 33 diverse mothbean genotypes evaluated in a randomized complete block design (RCBD) with three replications during the year 2014-15 at the Regional Agricultural Research Station, Vijayapur. The meteorological data of experimentation plot is presented in the table 1. RARS,Vijayapur comes under Northern dry zone (Zone 3) of Karnataka and is situated at 16°49" N latitude, 75°43" E longitude with an altitude of 594 m above mean sea level. The experiment had plot size of 4 meter length of each genotype having 4 rows. Row to row and plant to plant distance were maintained at 45 and 10 cm, respectively. All the recommended agronomic practices to raise a healthy crop were followed. The observations were recorded on five

randomly selected plants per replication for each genotype. The genotypic and phenotypic variances and genetic advance were calculated as suggested by Johnson *et al.* (1955). Genotypic and phenotypic coefficients of variations (Burton, 1952), heritability in broad sense (Lush, 1940), path coefficients for yield and its components traits (Dewey and Lu, (1959) and genetic diversity by Mahalanobis D² technique (Mahalanobis, 1936).

RESULTS AND DISCUSSION

The results of variances for seven characters are presented in the Table 2. The results revealed significant differences among all the genotypes for all the characters under this study, where as replication differences were insignificant indicating proper conduct of the experiment. The mean values for yield and its component traits of mothbean genotypes along with checks are presented in Table 3. Among the 33 genotypes evaluated, none of the genotypes have recorded significant superiority for 100 seed weight, pod width and seed yield per ha however,

five genotypes were identified to be numerically superior. Genotype MBG-09 is found to be significantly superior over check KBMB-1 for the traits *viz.*, number of branches per plant(4), plant height(96.8) and number of pods per plant(207.8), the genotypes BGMB-14, Kavalagi local, BGMB-08 and Pato-line were found to be significantly superior for number of branches per plant and number of pods per plant. Two genotypes CZM-3 and RMB-1005 were found to be significantly superior for number of seeds per pod. The phenotypic coefficients of variation (Table 4.) were higher than genotypic coefficient of variation suggesting the influence of environment on traits under study. Less difference was observed between phenotypic coefficient of variation and genotypic coefficient of variation for the traits number of branches per plants, pod length and number of pods per plant indicating lower influence of environment on these traits. In the present investigation, number of pods per plant(79.35 and 78.74) recorded higher PCV and GCV values indicating substantial variability and scope for improvement. Higher PCV and moderate GCV values were noticed for

Table 1: Meteorological data for the year 2014-15 at Regional Agricultural research Station Vijayapur

Week No.	Air Temperature		Relative Humidity		Wind Speed (KMPH)	Sunshine Duration (h)	Total Rainfall (mm)	Rainy Days	Pan Evaporation (mm/day)
	Max(C)	Min(C)	AM(%)	PM(%)					
23	35	22.4	82.4	43	13.4	7.5	40	2	5.8
24	34.1	22.9	81	44.7	15.8	8.9	0	0	7.3
25	33.1	22.3	82.4	51.7	17.7	6.9	6.8	1	6.7
26	36.3	22.5	78.6	31.3	15.1	8.2	7.6	1	8.8
27	33.8	21.8	84.1	57.4	14	6.1	90.8	2	6.4
28	29.1	21.4	89.7	66.6	15.4	1.6	7	1	3.7
29	28.5	21.9	89.6	65.7	17	1.8	6.6	1	3.6
30	29.1	21.3	90.6	69.4	15.5	3.9	44.6	3	3.9
31	29	21.9	87	67	16.2	3.7	3	0	3.7
32	30.3	21.3	88	60.1	13.8	6.2	1.4	0	4.7
33	31.4	20.8	88	51.6	12.7	6.2	40.2	1	4.9
34	31.9	21.8	90.4	62.1	6.6	7.5	48.7	3	4
35	26.6	20.9	92.6	78.9	11.7	1.3	155.2	4	3.1
36	29.2	21	88.7	60.9	14.1	4.3	19.7	1	3.9
37	31.1	20.8	87.9	52.4	12.3	7.4	0	0	4.8
38	30.4	20.9	90.7	61.7	8.9	4.8	39.5	3	4.1
39	32.9	21.8	83.1	46	5.1	8.3	0	0	4.4
40	34.2	21	80.3	43	5	9.4	10.6	1	5.1
41	32.9	20.8	82.1	48.7	4.9	6.7	13.8	1	4.4
42	33.1	19.9	86.3	43.7	4.3	9.2	0	0	4.5
43	28.7	19	88.9	62.3	5.7	4.6	40.9	2	3.7
44	30.1	14.7	80.6	33.9	4.1	9.5	0	0	3.7
45	31.3	16	76	38.4	4	8.5	0	0	4.2
46	29.3	18.3	92.6	61.1	4.7	5.9	15	3	2.9
47	30.5	15.8	88.6	41.9	3.4	7.7	0	0	3.2
48	30.1	12.3	80.6	29.6	3.9	8.6	0	0	4.2

Table 2: Analysis of variance for different characters in mothbean

Source of variation	df	NB	PH	NPP	NSP	100SW	PL	SY/ha
Replication	2	0.10	32.74	0.98	0.39	0.01	0.03	17142.41
Genotypes	33	1.32**	633.41**	10322.33**	0.90**	0.02**	0.14**	32794.42**
Error	24	0.09	78.90	53.70	0.28	0.01	0.04	12008.64
CD at 5%		0.48	14.49	11.95	0.86	0.16	0.34	178.75
CV %		8.80	12.35	9.86	8.32	5.34	5.11	16.41

*Significant at 5%, **significant at 1%; PH = plant height (cm), NB = No. of branches, NPP = No. of pods per plant, 100SW = 100 seed weight (g), PL = pod length (cm), NSP = No. of seeds per pod, SY/ha = seed yield per ha (kg).

Table 3: Mean values for yield and its component traits in mothbean.

Genotypes	NB	PH	NPP	NSP	100SW	PL	SY/ha
Mannur local-7	3.4	75.8	95.2*	5.9	1.7	3.7	728.8
13RMB-141	3.4	77	109.6*	6.7	1.8	4.3	558.2
RMM-12	3.2	77.6	62	6.7	1.8	4.4	420.0
RMB-00	3.2	40.8	23.47	4.8	1.8	3.6	695.9
BGMB-14	3.6*	73.6	92.8*	5.9	1.8	4.0	747.1
RMB-408	3	69.8	42.2	6.4	1.8	4.2	627.7
BGMBG-6	3.2	53.8	24	6.3	1.9	4.2	701.3
Kavalagi local	3.6*	76.8	102.2*	6.9	1.7	4.2	718.3
BGMB-7	3.6*	74.4	47.2	6.1	1.9	3.9	776.4
GMO-310	3.2	34.2	23.4	6.1	1.9	4.0	606.6
BGMBG-10	2.8	63.6	42.4	6.1	1.7	4.1	686.3
BGMBG-11	2.6	62.8	47.8	7	1.8	4.1	635.5
CZM-3	3.4	91.3	170*	7.2*	1.9	4.3	732.9
RMB-141	3.4	69.2	100.8*	6.3	1.7	4.0	690.8
MB-16	2.8	65	39.4	6.5	1.9	4.4	611.7
BGMB-08	4.6*	89.7	314.6*	5.3	1.7	3.8	768.1
H.M-61	3.8*	80.2	51	6	1.8	4.1	720.6
RMB-101	4*	71	72	6.5	1.8	4.3	751.2
BGMBG-14	3.6*	69.8	67	6.2	1.8	4.1	677.6
Pato-line	4.6*	71	88.2*	6.3	1.7	4.1	621.3
BGMBG-13	4.4*	66.4	51.4	5.9	1.9	3.9	637.8
BGMBG-04	3.4	73	44.2	6.8	1.9	4.3	747.1
GPM-14	3.2	63.6	36.4	6.6	1.8	4.2	523.8
CGM-18	2.6	81.8	51.8	5.1	1.8	3.9	560.0
RMM-102	3.4	97.8*	67.8	6.5	1.9	4.4	615.3
MBG-09	4*	96.8*	207.8*	6.6	1.9	4.1	403.1
RMB-1005	2.8	42.4	24.6	7.3*	1.8	4.6	699.5
RMB-108	2.4	89.6	54.6	6.8	1.7	4.2	535.7
BGMB-11	2.6	62	49.4	6.3	1.7	4.2	870.2
GPM-11	3.0	75.4	39.6	5.8	1.8	3.9	793.3
BGMBG-16	5.2*	81.2	54.8	6.7	1.9	4.0	619.0
MNL-1	2.2	79.6	80.8	6.3	1.7	4.1	757.6
KBMB-1(C)	3	77.2	73.6	6.3	1.9	4.6	791.9
CD at 5%	0.48	14.49	11.95	0.86	0.16	0.34	178.75

*Significantly superior to best checks C - check; PH=plant height (cm), NB=No. of branches, NPP= No. of pods per pod, 100SW = 100 seed weight (g), PL = pod length (cm), NSP = No. of seeds per pod, SYP=seed yield per ha (kg).

Table 4: Estimates of variability parameters for different quantitative traits

Characters	Mean	Range	GCV	PCV	h^2 bs(%)	GA	GAM
Number of branches	3.37	2.2-5.2	18.97	20.91	82.29	1.20	35.45
Plant height(cm)	71.94	34.2-97.8	18.90	22.57	70.08	23.45	32.59
Number of pods per plant	74.31	23.4-314.6	78.74	79.35	98.46	119.59	160.94
Number of seeds/pod	6.31	4.8-7.3	7.22	11.02	42.95	0.62	9.75
100 seed weight(g)	1.81	1.7-1.9	3.37	6.31	28.45	0.07	3.70
Pod length(cm)	4.13	3.6-4.6	4.35	6.71	42.02	0.24	5.81
Seed yield/ha(kg)	667.6	403.1-870.2	12.47	20.61	36.59	103.72	15.54

number of branches per plant, plant height and seed yield per ha. Low PCV and GCV values were recorded for 100 seed weight(6.31 and 3.37) and pod length(6.71 and 4.35). Genetic contribution to phenotypic expression of traits is better reflected by the estimates of heritability. A high estimate of heritability indicates the presence of more fixable variability. In this study, high heritability coupled with high genetic advance as percent of mean was recorded number of pods per plant(98.48%, 160.94), number of branches per plant(82.29%, 35.45) and plant height(70.08%, 32.59), indicates the predominance of additive gene action. While rest of the traits viz., number of

seeds per pod(42.95%, 9.75), pod length (42.02%, 5.81) and 100 seed weight(28.45%, 3.70) exhibited low heritability coupled with low genetic advance percent of mean. The current conclusions are supported by Muhammed *et al.* (2006) and Muhammed *et al.* (2007) in soybean.

The D^2 analysis of 33 genotypes revealed that genotypes were moderately diverse and were classified into 4 clusters. (Table 5). Cluster I had the largest number of genotypes (22 genotypes) followed by cluster II (6 genotypes) and cluster III (4 genotypes), while cluster IV was solitary. Cluster I alone with 22 genotypes indicated that majority of genotypes under

Table 5: Distribution of 33 mothbean genotypes in different clusters based on D² statistics

Clusters	No of genotypes	Genotypes
Cluster. I	22	RMB-141, GPM-14, BGMB-14, RMB-101, BGMBG-10, MNL-1, RMM-102, BGMBG-04, Kavalagi local, RMB-1005, BGMBG-6, BGMB-7, BGMBG-13, GPM-11, BGMB-08, CZM-3, RMB-00, GMO-310, 13RMB-141, Mannur local-7, BGMBG-16, H.M-61.
Cluster. II	6	KBMB-1,CGM-18,BGMBG-14,Pato line, RMB-108,MBG-09
Cluster. III	4	RMM-12,RMB-408,BGMB-11,BGMBG-11
Cluster. IV	1	MB-16

Table 6: Cluster means and per cent contribution for various yield and yield attributing characters in mothbean

Character	Cluster. I	Cluster. II	Cluster. III	Cluster. IV	% Contribution
PH	70.34	80.53	65.05	89	2.27
NB	3.32	3.53	3.1	4.6	0
NPP	61.58	85.97	66.3	314.6	18.18
SY/ha	617.97	419.43	760.29	752.44	79.55
100 SW	1.81	1.81	1.84	1.73	0
PL	4.16	4.1	4.06	3.84	0
NSP	6.4	6.23	6.15	5.3	0

PH = plant height (cm), NB = No. of branches, NPP = No. of pods per plant, 100SW = 100 seed weight (g), PL = pod length (cm), NSP = No. of seeds per pod, SYP = seed yield per ha (kg).

Table 7: Average intra (diagonal) and inter-cluster D² values in mothbean

Clusters	Cluster. I	Cluster. II	Cluster. III	Cluster. IV
Cluster. I	101.54	223.33	172.47	295.59
Cluster. II		107.75	355.21	409.97
Cluster. III			109.78	258.48
Cluster. IV				0

study had narrow genetic diversity among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity. However, the unidirectional selection potential for one particular trait or a group of linked traits in several places may produce similar phenotypes which can be aggregated into one cluster irrespective of their geographic origin (Jethava, 1996).

The maximum cluster mean for number of pods per plant was recorded in cluster IV (314.6) and the maximum value for plant height was recorded in Cluster IV (89) and for No of seeds per pod in cluster I (6.4). Seed yield per ha in clusters III (760.29) and cluster IV (752.29) recorded higher values (Table 6). The results on the contribution of individual traits towards total divergence suggested that the Seed Yield per ha (79.55 %) contributed highest for divergence followed by Number of pods per plant (18.18%) and Plant height (2.27%) contributed the maximum divergence. The characters contributing maximum diversity can be given more emphasis for the purpose of fixing priority of parents in hybridization programme. The highest inter cluster distance was observed between genotypes of cluster II and cluster IV (409.97) followed by cluster II and III (355.21) (Table 7). These clusters are quite divergent from each other and the genotypes belonging to these clusters can be used as parents for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give better recombinants (Bhatt, 1970). Gohil and Pandya (2006) suggested that for creating

variability and developing the best selection criteria, a large number of divergent lines, instead of few, should be used in the hybridization. Gohil and Pandya (2006) have pointed out in *Salicornia brachiata* Roxb (a nontraditional oilseed) that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability. Minimum distance between clusters I and III indicated close genetic relation between these two clusters and selection of parents from these two clusters should be avoided.

The study of genotypic correlation coefficient indicated the extent of relationship between different variables. The relationship among yield contributing characters as well as their influence on yield provides information for exercising selection pressure for genetic improvement in seed yield. The results of genotypic correlation coefficient analysis are presented in Table 8. Seed yield per ha was found to be non significant and positively correlated with number of pods per plant (0.0449). Characters *viz.*, number of branches per plant and number of pods per plant were also positively and significantly correlated with each other. This implies that improvement in one character would simultaneously improve the other related traits and finally increase the seed yield. The results, thus, revealed that number of pods per plant, number of branches per plant were the important attributes, which contributed towards higher yield. Therefore, more emphasis should be given to these components during selection for higher yield.

Seed yield in mothbean is the sum total of several components characters which directly or indirectly contributes to it. The information derived from correlation studies indicated only mutual association among the characters. Whereas, path coefficient analysis helped in understanding the magnitude of direct and indirect contribution of each character on the dependant characters like seed yield. Partitioning of correlation

Table 8: Genotypic correlation coefficients among various traits in mothbean

Characters	PH	NB	NPP	100 SW	PL	NSP	SY/ha
PH	1.00	0.2343	0.5918**	0.0221	0.1089	0.1627	-0.256
NB		1.00	0.4208*	0.1967	-0.242	-0.0899	-0.1659
NPP			1.00	-0.1119	-0.1381	-0.0644	0.0449
100 SW				1.00	0.2251	0.1727	-0.0931
PL					1.00	0.7537**	-0.1532
NSP						1.00	-0.1051
							1.00

Table 9: Estimates of direct and indirect effects of various traits on seed yield per ha in mothbean

Traits	PH	NB	NPP	100 SW	PL	NSP	r
PH	-0.4199	-0.0984	-0.2485	-0.0093	-0.0457	-0.0683	-0.256
NB	-0.0673	-0.2872	-0.1209	-0.0565	0.0695	0.0258	-0.1659
NPP	0.2344	0.1667	0.396	-0.0443	-0.0547	-0.0255	0.0449
100 SW	0.001	0.0091	-0.0052	0.0465	0.0105	0.008	-0.0931
PL	-0.0249	0.0554	0.0316	-0.0515	-0.2288	-0.1725	-0.1532
NSP	0.0207	-0.0115	-0.0082	0.022	0.096	0.1274	-0.1051

*Significant at 5%; **significant at 1%; PH= plant height (cm), NB= No. of branches, NPP= No. of pods per plant, 100SW = 100 seed weight (g), PL = pod length (cm), NSP= No. of seeds per pod; Residual value=0.8999; r= genotypic correlation

coefficient into direct and indirect effects provided the information about the nature and magnitude of effects of other characters on seed yield. The results of the present investigation on path analysis (Table 9.) revealed that the number of pods per plant(0.396) had maximum and positive direct effect on seed yield per ha followed by number of seeds per pod(0.1274) and 100 seed weight (0.0465). While plant height(-0.4199), number of branches per plant(-0.2872) and pod length(-0.2288) had negative direct effect on seed yield per ha. The path analysis also indicated that maximum indirect effect was exhibited by seed yield through number of pods per plant(0.2344) and number of branches(0.1667). These results concur with those reported by Muhammad *et al.*, (2007) and Hamdi *et al.*, (2008) in soybean. Plant height exhibited negative indirect effect through most of the characters. High Residual value (0.8999) indicated that other factors influencing the yield were not considered in the model and requires further study. The results were also confirmed by Ball *et al.*,(2001) in soybean. Hence, the characters having direct positive influence *viz.*, number of pods per plant, number of seeds per pod and 100 seed weight should be given due importance, while breeding for high yielding types in mothbean.

REFERENCES

- Ball, R. A., McNew, R. W., Vories, E. D., Keisling, J. C. and Purcell, L. C. 2001. Path analysis of population density effects on short-season soybean yield. *Agron. J.* **93**: 187-195.
- Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Australian J. Agri. Res.* **21**: 1-7.
- Burton, G. W. 1952. Quantitative inheritance in grass. *Proceedings of 6th international grassland congress.* **01**: 24-83.
- Dewey, D. R. and LU, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy J.* **51**: 515-518.
- Gohil, R. H. and Pandya, J. B. 2006. Genetic divergence in *Salicornia* (*Salicornia brachiata*) *Indian J. Genet.* **66**: 75-76.
- Hamdi, A. Abd-Elmohsen, M. El-Emam, A. A. M. and Mersal, I. F. 2008. Evaluation of some promising soybean genotypes for agronomic and seed technology characteristics in North Egypt. *Proceeding of the 2nd Field Crops Conference, FCRI, Giza, Egypt.* October. pp. 14-16.
- Jethava, A. S., Yusufzi, A. S., Poshiya, V. K. and Yaddoria, M. A. 1996. *Gujarat Agri. Uni. Res. J.* **22**(1): 25.
- Johnson, H. W. Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environment variability in soybean. *Agronomy J.* **47**: 314-318.
- Kumar, N., Joshi, V. N. and Dagla, M. C. 2013a. Multivariate analysis for yield and its component traits in maize (*Zea mays* L.) under high and low N levels. *The Bioscan.* **8**(3): 959-964.
- Kumar, N., Tikka, S. B. S., Dagla, M. C., Ram, B. and Meena H. P. 2013b. Genotypic adaptability for seed yield and physiological traits in sesame (*Sesamum indicum* L.). *The Bioscan. (Supplement on Genetics and Plant Breeding).* **8**(4): 1503-1509.
- Lush, J. L. 1940. Intra-sire correlations and regression of offspring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production.* **33**: 293-301.
- Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proceedings of National Academy of Science India.* **2**: 49-55.
- Muhammad, A., Ali, N. and Ghafoor, A. 2006. Character correlation and path coefficient in soybean [*Glycine max* (L.) Merrill.], *Pak. J. Bot.* **38**(1): 121-136.
- Muhammad, F. A. M., Ashraf, M., Qureshi, A. S. and Ghafoor, A. 2007. Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. *Pak. J. Bot.* **39**(2): 405-413.
- Yogeesh, L. N., Viswanatha, K. P., Ravi, B. A. and Gangaprasad S. 2012. Genetic variability studies in Mothbean germplasm for seed yield and its attributing characters. *Electronic J. Plant Breeding.* **3**(1): 671-675.

