Characterization and evaluation of mungbean germplasm in Bangladesh

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Abstract

The study aim to establish groups of relatively homogeneous accessions based on morpho-agronomic descriptions, upon which nomination for inclusion in the mungbean core-collection could be based. Three hundred and ten genotypes of mungbean were evaluated to estimate the variation among the genotypes and to find out the short duration line for fitting rice based cropping system in between rice to fighting climate change in Bangladesh. All the genotypes were grouped into fifteen clusters. The composition of various clusters varied from 4 to 32. Cluster XV comprised of 32 genotypes followed by cluster II, V, VII and IX consisting of 31, 28, 29, and 27 genotypes, respectively. There were 24 genotypes in clusters VI and XIV, 22 in cluster XIII, 18 in cluster X and only 4 genotype in cluster III. Cluster III exhibited the lowest mean value for days to flower (36) and days to maturity (59) both in fresh pod and seed harvest followed by cluster XII. The highest pod length (9.1cm) found in cluster II and hundred seed weight (5.54 g) observed in cluster XIII and also the highest yield per plant(4.3 g) in 2nd harvest was recorded in cluster XIII followed by cluster XI (4.2 g). Cluster XI also showed the highest number (5.2) of clusts and pods (15.9) per plant whereas cluster XI had genotypes with the highest plant height (46 cm) and highest number of seeds per pods (10.2) found in cluster IV

Key words : Mungbean, *Vigna radiata*, Characterization, Evaluation, Cluster analysis

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is an important food leguminous crop in Asia, with an annual production of around 3.5 - 4.0 million tons. Over 80% of the mungbean is produced in South Asia. The crop is grown principally for its protein-rich dry seeds (24% protein) which is a major protein source for people in Asian countries as part of a nutritionally balance diet. It is popularly grown as a component in various cropping systems because of its ability to fix nitrogen in association with soil bacteria, early maturity and relatively drought tolerance. The Asian Vegetable Research and Development Center (AVRDC) have accepted responsibility for the global base collection of mungbean (*Vigna radiata* L. Wilczek). This collection has been acquired mainly through personal contact and exchange through different institution and individuals (Tey et al, 1989). The Genetic Resource and Seed Unit (GRSU) of the AVRDC aim to set up a core-collection (Holden and Williams, 1984) or a condensed, yet representative, assembly of accessions from this germplasm collection. Mungbean has been a major pulse crop in Asia since ancient times. Mungbean is a newly introduced pulse crop in several countries such as Australia, Pakistan, Thiland and Egypt. At present mungbean cultivation spreads widely because of its superior digestibility in Africa, South America and in many Asian countries and has been identified as high yielding pulse crop. In Bangladesh, it is cultivated under a wide range of ecological zones in both irrigated and rainfed conditions. During the period of 2010-11, mungbean was cultivated over an area of 163 thousand ha with 150 thousand tones production (Anon., 2011). However, the national average yield (920 kg/ha) is very low as compared to the potential obtained in many other countries. It's grown principally for its protein rich edible seeds that are used as human food, while its herbage is used as a fodder and green manure. It is short growth duration (70-90 days) grain legume crop and high nutritive value. It has ability to fix atmospheric nitrogen in symbiotic association with Rhizobium species. Developing mungbean genotypes with improved determinate growth habit and synchronous maturity is essential. Characterization of germplasm using clustering has got special

attention due to its increased use in crop improvement and the selection of desirable genotypes for breeding crops. Development of cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pests has significantly increased the yield and cultivated area (Ehlers and Hall, 1997). In Bangladesh it is cultivated under a wide range of ecological zones in both irrigated and rain fed conditions. Evaluation of germplasm is useful not only in selection of core collection but also its utilization in breeding programme. The overall effect of plant breeding on genetic diversity has been a long standing concern in the evolutionary biology of crop plants (Simmonds, 1962). In order to develop high yielding cultivars resistant to various stresses, exploitation of the gene pool is of paramount importance. Most of the reports on genetic variability showed a wide range of variability for plant height with moderate to high heritability and high genetic advance, based on studies varying number of genotypes and there were few reports based on the segregating material. A report showed moderate heritability and moderate genetic advance (Patil, 1986). Another report revealed that low heritability and low genetic advance for this trait (Apte et al., 1987) and Rangaiah and Nehru indicated low heritability (5.61%) with 6 % genetic advance. However, Selviet et al. (1994) and Backiyarani and Nadarajan (1996) and Selvam et al. (2000) reported revealed that high heritability (99.89%) with moderate GCV and PCV values.

Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis. The loss of genetic diversity has been dramatic for many cultivated species (Wikes, 1983). Grouping of genotypes by multivariate methods in the study is of practical value to the breeders of mungbean. The objectives of the present study were to investigate the extent of genetic variation and relationships between various mungbean genotypes based on quantitative traits using multivariate analysis and to identify a set of agronomic attributes to be used in future breeding programme.

Materials and Methods

The experiment was conducted during Kharif-I season of 2012 at the Pulses Research Centre, Ishurdi and Pabna. A total of 310 mungbean lines were used to estimate the variation among the genotypes. Each plot consisted of two rows of 4 m long with row to row spacing of 40 cm and plant to plant of 8 cm. Fertilizers used @ 25kg N, 30 Kg P, 25Kg K and 2 Kg Boron per hectare of land and were applied as basal doses during final land preparation. Pesticide (Karate @ 1ml/L water) was sprayed to save the crop from the infestation of pests especially Thrips and Pod borer. Data was recorded on quantitative traits for ten plants randomly sampled. At maturity best individual lines were selected on the basis of earliness, disease reaction, insect susceptibility (against pod borer) and higher yield. The traits were included Days to flower, Days to maturity, plant height, Pods per plant, Pods per cluster, Cluster per plant, Pod length (cm), Seeds per pod, 100 SW (gm) and Grain yield/plant (gm). The genetic diversity was studied following the generalized distance (D^2) of Mahalanobis extended by Rao. The accessions were grouped into clusters using canonical vitiate analysis. The statistical analysis was done using Genstate5 computer software.

Results and Discussion

The quantitative traits of all the genotypes differed from each other with respect to yield and yield contributing characters. The ward's and the average linkage clustering methods are both hierarchical clustering techniques. Starting with each object as a separate cluster, cluster are fused one at a time at each generation based on a defined "distance" as a measure of similarity between clusters until, at the final generation, only one cluster of all the objectives is obtained. Both result in a tree-like presentation of a stage-wise grouping of the objects referred to as a dendrogram (Sneath and Sokal; Clifford and Stephenson; Marriott and Solomon, 1977). Through multivariate analysis, three hundred and ten genotypes were grouped into fifteen clusters based on D^2 values (Table 1). The composition of different clusters varied from 4 to 32 genotypes. Cluster XV comprised of 32 genotypes followed by cluster II, VII, V, IX, XIV, VIII and VI consisting of 31, 29, 28, 27, 24, 24 and 24 genotypes respectively. There were 22 genotypes in clusters XIII, 18 in cluster X, 16 in cluster XII, 14 in cluster I, 11 in cluster IV, 6 in XI while 4 genotypes in cluster III.

Table 1. Distribution of 310 genotypes/ lines of mungbean in different clusters based on quantitative characters

Cluster	No. of genotypes	Name of Genotypes
I	14	$BMXK_1$-00025, 1280001, BMXK-97009-3, 870006-9, BMXK-97001-11, BMXK1-050012-3, BMXK1-03005-4, BMX-95003-7, BMX-99002-7, BMXk1-050012-4, 880091, BMXK2-03011-4, 880013 and 880083
II	31	BMXK-97024-1, $BMXK_1$-06008-6, BMXK1-0020, BM 12016, $BMXK_1$-00003, BM 12003, VC-3960A—88, BMXK-97004-10, BM 12005, BMXK-97008-6, BMX-99002-2, BMX-97001-8, BMXK1-05008-2, BM 12007, BMXK1-01019-2, BM 12008, BMXK1-04005-3, BMXK1-05012-4, BMXK1-05005-6, BMX-99003-3, BM 12011, VC-6144C, BMX-97014-3, BMX-97015-3, BMX1-9902-17, BMX-033311-4, BMXx1-00024, 030005-4, BMX-9007-3, 2764 B and BMXK1-05008-10
III	4	9010-12-5-8, BARIMung-2, Mosk-1 and 880045-1
IV	11	BM 12002, Nilphamary, BMXK1-050012-6, BMXK1-05002-9, BMXK1-05006-8, BMX-96003-3, BMX-94010-11, BMX-99002-12, BM 12012, Local-5 and 880066
V	28	$BMXK_1$-00031, BMXK-94004-2, BMXK1-20027, VC-6173(B-10), BMXK1-03011-6, BMX-94009-12, BMX-94007-12, BMX-94007-11, BMX-94008-3, BMX-94008-6, BMX-95003-1, BINAMung-2, 6170-92, BMXX2-04005-3, BMX-97025-9, BARIMung-6, 3726, BARIMung-3, V-2709, BUMung-2, 30614, BMXK1-0505-6, BMX-95010-10, VC-6144-3, VC-6173(B11), BMX-95001-18, BINAMung-6 and BARIMung-4
VI	24	$BMXK_1$-06002-2, BM 12004, BMXK-92007-3, $BMXK_1$-0109-2, BMX-99003-12, A-47-4, BMXK1-00028, BMXK1-05006-1, BMX-94001-8, BMXK1-00014, VC-5153-(B-19), BMX-99002-5, BM 12010, BMX-94001, BMX-99002-9, BMX-97024-13, BMX1-00016, BMX-95006-4, Vc-6170-92, BMX-94010-10, 88086, BMXk1-00016, 6017 and F-8-1
VII	29	BMXK-97001-1, VC-6170(70-92), BMX-97008-5, BMXK-92011-4, BMXLX-90009-6, BMX-97010-1, BMX-97013-6, BMX-97025-2, BM 12006, BMXK1-05006-3, VC--6144-(B-11), BMXK1-0301-3-1, BMX-94011-2, BMX-97018-5, BMX-03013-10, BMX-94011-10, BMX1-030011-1, BMX-97003-7, Vc-6379(B-11), BM 12014, BMX-03004-1, VC-6184(50-12), BMX-01015-5, 880143, Bmx-95004-43, 880042-8, BMXK1-01015-3, BMX--94001-3 and VC-6153(B-19)
VIII	24	$BMXK_1$-97025-2, BMX-88009-2, BMX-99002-13, BMX-95001-2, BMX-96006-8, BMX-96007-3, BMXx1-03011-5, BMXx1-01019-1, Vc-36143(B-19), VC-6144A, VC-6144-B, BMX-95009-30, 030013-10, BMXX1-05008-6, BMXX1-030013-1, V=cfs-U-1, BMXx1-05001-9, BMXx1-0007, BMXk1-05008-1, BMX-95006-17, 880092, 880099, BUMung-1 and BMX-97004-10
IX	27	BM 12001, $BMXK_1$-00002, $BMXK_1$-00032, BMX-97014-1, VC-6371-93, VC-6148(B-17-26), BM 12009, BMX-95003-9, BM 12013, BARIMung-1, BMX-95001-7, BMX-95004-6, BMX-95004-18, BMXx1-00010, BMXx1-00007, BMX-95004-11, BMX-99009-15, BM 12015, BMX-95006-18, BMXx1-00013, VC-6145(50-12), 880142, BMX-97007-3, 1137-A, 880042-12, 880006-1 and 880013-6
X	18	$BMXK_1$-92007-3, BMX-95003-15, vc-6144c, BMX-95009-13, 050012-3, BMXX1-0001, 3476, BMXX1-05006-1, 805203 A, 88037-3, 880041-6, Baliadanga, 880072, BMX-84-2-24, 880042-7, BMX-95006-19, Nawabganj and BMX-4011-2
XI	6	BMX-96007-2, BMXk1-05002-8, 86197, 880012, 880059 and 86162
XII	16	BMXK1-00229, G-31-9, BMXK1-05001-5, BMX-92007-3, BMX-940011-6, PS-7, BMXk2-03011-1, BMXk1-01019-1, Foridpur local, BMX-9903-12, BMXk1-95006-18, 880018-10, BMX-97024-8, BMX-94011-6, BMXK1-030013-4 and BMXK1-03004-2
XIII	22	$BMXK_2$-0300, $BMXK_1$-06006-4, $BMXK_1$-00009, $BMXK_1$-00023, BMXK-97002-15, VC-6379 (23-11), BMX-95006-22, BMX-95005-10, DL, BMXX1-05008-16, 880001-2, BINAMung-7, BMXk1-030013-8, BMX-95004-12, 2550 A, Thailand, 2523 A, 880038-5, VC-6153(B-20), 40661, BMXK1-050012-8 and 880018-6
XIV	24	$BMXK_1$-01025-2, $BMXK_1$-00026, BMXK-97002-5, BMX--97024-1, BMLX-9010-26, BMX-94004-2, BMX-94011-9, BMX-95006-9, 880020-8, BMXk1-95002-3, BMXk1-05008-3, 880030, 8800104, 4143 A, 880042-5, 9015, BMX-99002-15, 880032-3, BMXK1-0007, 8800115, Gopalgonj, Sona mung, BMX-95002-18 and BMX-95002-8
XV	32	$BMXK_1$-01015-2, $BMXK_1$-00001, BARIMung-5, $BMXK_1$-00011, BMXK-93002-1, BMXK1-03011-1, BMX-96007-1, BMX-95004-24, BMXK1-01015-6, BMX1-03005-3, Vc-6173(B-13), BMX-99001-2, BMX1-030013-5, BMXx1-01015-6, BMX1-01015-3, VC-6151(B-20), BMX-96002-1, IPB-M79-13-29, BMXk1-95001-2, 1168 B, 3890 A, 3300 A, VC-6173-C, VC-6144(B-12), BMXK1-01015-4, 88039-6, BMX-97007, BMXK1-03004-3, 05005-4, BMXK1-020010, BMXK1-05006-9 and BMXK1-01015-5

Table 2.Cluster means for yield and yield contributing characters of 310 mungbean genotypes

Cluster	Days to flower	Days to mature	Plant ht.(cm)	Pods/ plant	Seeds /pod	Clusts /plant	Pods/ cluster	100 SW (g)	Pod-length (cm)	1st Yield/plant (g)	2md Yield/ Plant (g)
I	47	71	39	8.1	10.0	4.0	2.9	4.87	8.4	2.7	3.4
II	43	68	36	8.5	9.7	4.3	2.9	5.47	9.1	2.7	3.8
III	36	59	23	10.5	9.1	4.0	2.9	3.6	6.3	1.5	1.7
IV	47	71	34	14.2	10.2	4.1	3.1	4.39	8.4	2.2	3.1
V	38	61	32	7.7	9.3	3.9	2.6	4.75	7.9	1.8	2.5
VI	42	67	32	7.9	9.5	4.1	2.9	4.69	8	2.1	3.2
VII	38	67	38	8.1	9.7	4.1	2.9	5.46	9	2.8	3.8
VIII	40	70	35	8.3	9.8	4.1	2.6	4.69	7.9	2.1	2.8
IX	38	66	33	8.7	9.3	4.4	2.9	4.01	7.5	2.1	2.9
X	39	67	28	8.3	9.2	3.9	2.4	4.33	6.9	1.6	2.1
XI	46	69	46	15.9	9.9	5.2	3.3	3.97	7.1	2.9	4.2
XII	37	61	37	8.5	10.1	4.0	2.5	4.85	8.5	2.2	3.1
XIII	41	64	43	8.9	10.1	4.8	3.1	5.54	8.6	3.2	4.3
XIV	40	69	42	9.0	10.0	4.4	2.7	4.49	7.7	2.9	4.1
XV	40	64	38	8.7	9.6	4.2	2.8	5.16	8.4	2.7	3.8

N.B.: 1st= First harvest and 2nd= Second harvest

Table 3. Selection of 13 high yielding and 6 long podded mungbean genotypes for next multi-location trial

High yielding Genotypes	Days to flower	Days to Mature	Plant height (cm)	Pods/ plant	Seeds /pod	Cluster /plant	Pods/ cluster	100 SW(g)	Yield/ Plant (g) 1st	Yield /Plant (g) 2nd	Pod-len. (cm)
4143 A	42	69	40	7.4	10.6	4.8	2.0	6.40	5.2	7.7	9.4
BMXk1-05002-8	40	70	43	19.2	12.2	5.0	3.6	6.62	5.5	7.7	9.5
2523 A	40	63	43	10.2	10.6	4.8	2.8	6.15	5.7	7.0	9.5
IPB-M79-13-29	39	64	38	10.0	11.8	4.6	2.2	6.06	4.9	6.7	9.7
BMXk1-95001-2	38	64	38	13.2	9.6	5.4	4.0	3.70	4.6	6.3	7.1
BINAMung-7	39	63	46	11.6	8.6	5.2	3.2	4.94	3.6	6.1	8.2
BMX-94010-10	42	67	33	7.8	10.6	4.0	2.4	3.61	1.9	6.1	7.5
2550 A	40	64	44	9.4	11.6	4.4	2.6	7.33	4.8	6.1	9.5
3890 A	38	63	37	7.2	10.0	5.0	2.2	7.28	4.3	6.1	8.3
BMX-94011-9	43	68	43	7.6	10.8	4.0	3.0	5.09	4.1	6.0	8.6
2764 B	46	69	32	8.4	9.6	5.6	3.4	4.74	4.4	5.8	9.6
VC-6151(B-20)	43	63	39	8.2	9.8	4.6	4.2	6.06	4.0	5.8	10.3
BMX-94011-10	39	67	39	10.6	10.6	4.4	3.4	6.30	4.0	5.5	9.0
Long pod length											
BMX-97014-3	43	66	35	7.6	10.4	5.2	3.2	5.91	3.2	4.2	12.0
BMX-97024-13	40	67	30	7.2	10.0	4.4	2.6	5.50	3.1	5.1	11.6
PS-7	38	62	36	11.4	14.2	3.6	3.0	3.65	2.2	3.4	11.0
BM 12003	43	66	35	6.6	9.4	4.2	2.0	5.44	2.1	2.8	11.0
BMXK1-00229	35	59	35	8.8	12.0	4.2	3.0	3.90	2.1	2.4	10.9
Thailand	40	63	43	6.2	9.8	4.8	1.6	6.48	3.2	4.7	10.7

N.B.: 1st = First harvest and 2nd = Second harvest

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 2). Cluster III exhibited the lowest mean value for days to flower (36) and days to maturity (59) followed by cluster XII. The highest number of pods (15.9) per plant and seeds per pod were observed in cluster XI while the highest hundred seed weight was recorded in cluster XIII (5.54) followed by cluster II. The longest pod length (9.1 cm) was observed in cluster II but the highest yield per plant was recorded in cluster XIII both at first and second harvest followed by cluster XI. Cluster XIII also showed the highest number (4.8) of clusters per plant whereas cluster III had genotypes with the lowest plant height (23 cm).

From the above clusters a total of 13 genotypes were selected from different clusters mainly considering on yield performance (Table 3). The selected lines were 4143 A, BMXk1-05002-8, 2523 A, IPB-M79-13-29, BMXk1-95001-2, BINAMung-7, BMX-94010-10, 2550 A, 3890 A, BMX-94011-9, 2764 B, VC-6151(B-20) and BMX-94011-10 those are high yielding and disease tolerant. The lines may also be used in our breeding programme for the development of high yielding variety. Six long poded lines BMX-97014-3, BMX-97024-13, PS-7, BM 12003, BMXK1-00229 and Thailand local were selected for improvement breeding programme.

Conclusion

There are 13 genotypes 4143 A, BMXk1-05002-8, 2523 A, IPB-M79-13-29, BMXk1-95001-2, BINAMung-7, BMX-94010-10, 2550 A, 3890 A, BMX-94011-9, 2764 B,VC-6151(B-20) and BMX-94011-10 were selected for high yielding and 6 genotypes BMX-97014-3, BMX-97024-13, PS-7, BM 12003, BMXK1-00229 and Thailand were selected for long podded mungbean genotypes for next multiplication trial to find out the desired lines mungbean for crop improvement programm in Bangladesh.

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