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Selecting Superior Mungbean Lines on the Basis of Genetic Diversity and Harvest Index

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Abstract: Three hundred and ten mungbean lines were evaluated in the field for 9 quantitative traits at NARC, Islamabad, Pakistan (33.40° N and 73.07° E). These showed high variance for yield contributing characters except pod length, seeds/pod and seed weight. Germplasm under investigation displayed a wide range of diversity for most of the traits. Pure-lines with unique characters which could help to identify, select and hybridize land races to induce evolution for important traits were identified and for that matter 44 pure-lines were selected and recommended for testing under wide range of agro-ecological condition in pursuit of best mungbean cultivars. Data on harvest index revealed that the genotypes from 25 to 40% harvest index exhibited better performance and thus this range is suggested as one of the criteria for future improvement in mungbean.

Key words: classification, germplasm evaluation, green gram, *Vigna radiata*

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is an important legume crop well suited to tropics and sub-tropics. It is cultivated in many Asian countries including Pakistan, India, Bangladesh, Thailand, Japan and Korea. In Pakistan it is grown under a wide range of agro-ecological zones mainly under irrigated areas. The area under this crop is 1,97,000 ha with production of 92,000 tonnes (Anonymous, 1999). The national average yield of 467 kg ha^{-1} is very low as compared to its potential, and yield obtained in many other countries. One of the reasons for low yield is unavailability of high yielding cultivars with better adaptability. Categorization and evaluation of germplasm for quantitative traits of a plant species and its utilization has received attention from plant breeders because of its increased recognition of germplasm reserves and its importance in proper genotype identification (Virmani *et al*. 1983; Ghafoor *et al*., 1992; Bakhsh *et al.,* 1992; Pezzotti *et al*.,1994; Rabbani *et al*., 1998). Evaluation of germplasm is useful not only in selection of core collection but also in utilization of germplasm in breeding programmes. Results reported by Falcinelli *et al*. (1988) and Veronesi and Falcinelli (1988) showed multivariate analysis to be a valid system for germplasm categorization. Average linkage cluster and Principal Component Analysis (PCA) was conducted for proper identification of genetic diversity to be used in crop improvement. Importance of germplasm in crop improvement has also been reported by many researchers (Anonymous, 1997; Ghafoor *et al.,* 1998).

Germplasm resources are of little value unless they are exploited by the breeders for crop improvement. Unfortunately they have never been utilized to the extent they should have been. A part of negligence is due to lack of information by most of the breeders as to what extent and where the diverse material is available. Availability of useful variation in germplasm collection is essential for systematic breeding. Keeping in view this aspect of germplasm, the study was designed to evaluate mungbean germplasm and subsequent exploitation of desirable genotypes which could prove to be valuable in improvement. This paper reports the diversity in mungbean germplasm for quantitative traits related to yield potential. Correlation coefficient among various traits and investigation for appropriate harvest indices has been discussed. On the basis of performance for specific traits potential genotypes have been identified for future mungbean improvement.

Materials and Methods

Three hundred and ten mungbean accessions, collected from various parts of Pakistan during the past decade were evaluated for various agronomic/quantitative traits in an augmented design under the field condition at National Agricultural Research Centre, Islamabad during summer-1998. One row of 4 meter length for each accession was planted with 75 cm and 10 cm inter and intra-row spacing, respectively. Three varieties viz., NM 121-25, NM 51 and NM 92 were repeated as check after every 20 rows. Data for maturity were recorded on line basis when about 90% pods turned brown/black. Other quantitative traits like branches, pods, grain yield and biological yield were recorded on ten competitive plants selected at random and then averaged to per plant. Pod length and seeds/pod were recorded on ten pods selected at random within genotype. Seed weight was recorded after counting 100 seeds by seed counter and weighed in grams. Harvest index was calculated as economic yield expressed in percentage over total biomass. The data were analyzed for simple statistics and correlation coefficients using computer software MS EXCEL 7.0 for Windows 95. Cluster analysis was conducted using the techniques suggested by Sneath and Sokal (1973) for selected genotypes as listed by using computer software STATISTICA for Windows.

Results and Discussion

The data in Table 1 are about the genetic diversity among 310 genotypes of mungbean for 9 quantitative traits related to yield. The data revealed a wide range of diversity in maturity, branches/plant, pods, pod length, seeds/pod, seed weight, biological yield, grain yield and harvest index in both the sets of analysis indicating a large scope for selection from the material. Variance for pod length, seeds/pod and seed weight was low which indicated that the scope of improvement for these traits by simple selection from this material is limited and hence more germplasm is needed to be acquired from other gene-banks to broaden the genetic base of crop. Breeding techniques like wide hybridization, mutation and other novel techniques can also help in creating genetic variation for particular traits (Ghafoor *et al*. 1998). Correlation results presented in the Table 2 revealed that days to maturity has significant negative correlation with all the characters except with branches where it was insignificant. This means that increase in maturity days was not desirable

Table 1: Basic statistics in total (T) and selected (S) mungbean germplasm

Plant trait		Range	Mean + SE	SD
Days to maturity	T	60-95	72.00±0.44	7.76
	S	60-95	72.00±2.00	13.3
Branches/plant	T	5-80	21.71±0.59	10.38
	S	6-80	26.6±2.42	16.06
Pods/plant	T	2-188	54.05±1.57	27.63
	S	6-188	72.6±5.81	38.54
Pod length (cm)	T	3.4-10.9	6.96±0.05	0.96
	S	4.3-10.9	7.2±0.16	1.07
Seeds/pod	T	2.8-15.0	10.5±0.13	2.25
	S	5.6-15.0	10.7±0.32	2.12
100-seed weight (g)	T	1.21-6.67	3.55±0.04	0.75
	S	2.55-6.67	3.78±0.15	0.97
Biological yield (g)	T	6.27-192.90	77.86±1.83	32.27
	S	6.27-192.90	108.22±10.27	68.14
Grain yield (g)	T	1.02-40.00	14.23±0.49	8.59
	S	2.45-40.00	25.09±2.63	17.47
Harvest index (%)	T	2.54-49.86	18.43±0.49	8.63
	S	6.08-49.86	25.37±1.73	11.49

Table 2: The correlation coefficient among nine quantitative traits in local germplasm of mungbean

Variables	BR	Pods	PL	S/P	SW	BY	GY	HI
DM	0.040	-0.122*	-0.354**	-0.287**	-0.126*	-0.151**	-0.268**	-0.200**
BR		0.592**	0.069	0.088	0.020	0.503**	0.364**	0.040
Pods			0.237**	0.223**	0.109	0.621**	0.614**	0.287**
PL				0.511**	0.364**	0.211**	0.271**	0.177**
S/P					0.050	0.103	0.256**	0.232**
SW						0.036	0.193**	0.239**
BY							0.628**	-0.044
GY								0.679**

DM-days to maturity, BR-branches/plant, Pods-pods/plant, PL-pod length (cm), S/P-seeds/pod, SW-100-seed weight (g), BY-biological yield/plant (g), GY-grain yield/plant (g) and HI-harvest index (%). *-Significant and **-Highly significant

Table 3: Mean values of quantitative traits on the basis of harvest index range

Range	DM	BR	Pods	PL	S/P	SW	BY	GY	HI
0.00-5.00	75	18.3	26.0	5.9	8.0	2.75	73.75	2.71	3.68
5.01-10.00	74	19.9	38.0	6.4	9.4	3.21	71.89	5.59	7.65
10.01-15.00	75	23.7	54.7	7.1	10.6	3.50	87.03	11.27	12.89
15.01-20.00	72	20.9	54.4	7.1	10.6	3.74	76.18	13.28	17.38
20.01-25.00	69	22.6	60.1	7.2	11.5	3.63	79.47	17.81	22.46
25.01-30.00	70	22.1	64.6	7.0	10.8	3.81	77.36	21.03	27.29
30.01-35.00	69	17.7	63.2	7.3	10.4	3.64	78.76	25.47	32.35
35.01-40.00	67	24.0	66.0	7.1	11.5	3.68	67.59	25.80	38.28
40.01-45.00	83	20.1	52.9	5.7	8.3	3.42	45.52	19.49	42.31
45.01-50.00	74	25.0	32.3	7.5	11.6	3.21	56.41	20.13	49.86

DM-days to maturity, BR-branches/plant, Pods-pods/plant, PL-pod length (cm), S/P-seeds/pod, SW-100-seed weight (g), BY-biological yield/plant (g), GY-grain yield/plant (g) and HI-harvest index (%)

Table 4: Selected genotypes from mungbean germplasm on the basis of best performance for specific traits

Traits	Range	Selected accessions
Days to maturity	up to 60 days	Pak 40313, Pak 40578, Pak 40951
Branches/plant	61-80	Pak 41052, Pak 41075
Pods/plant	120-200	Pak 41052, Pak 40304, Pak 40524, Pak 40736
Pod length (cm)	9-11 cm	Pak 40650, Pak 41046, Pak 41051, Pak 41057, Pak 40710, Pak 40716, Pak 41019
Seeds/pod	14-15	Pak 40551, Pak 40061, Pak 40020, Pak 40002
100-seed weight (g)	6-7 g	Pak 41019, Pak 40650, Pak 41065, Pak 41031
Biological yield (g)	151-200	Pak 40346, Pak 40524, Pak 40993, Pak 41075, Pak 40304, Pak 40039, Pak 41052, Pak 40553, Pak 40427, Pak 40044
Grain yield (g)	30-40 g	Pak 40002, Pak 40495, Pak 40553, Pak 40959, Pak 40047, Pak 40018, Pak 40478, Pak 41068, Pak 40490, Pak 40237, Pak 40736, Pak 40039, Pak 40963, Pak 40536, Pak 41046, Pak 40500
Harvest index (%)	39-52%	Pak 40604, Pak 40952, Pak 41094, Pak 41103, Pak 40467, Pak 40959, Pak 40328

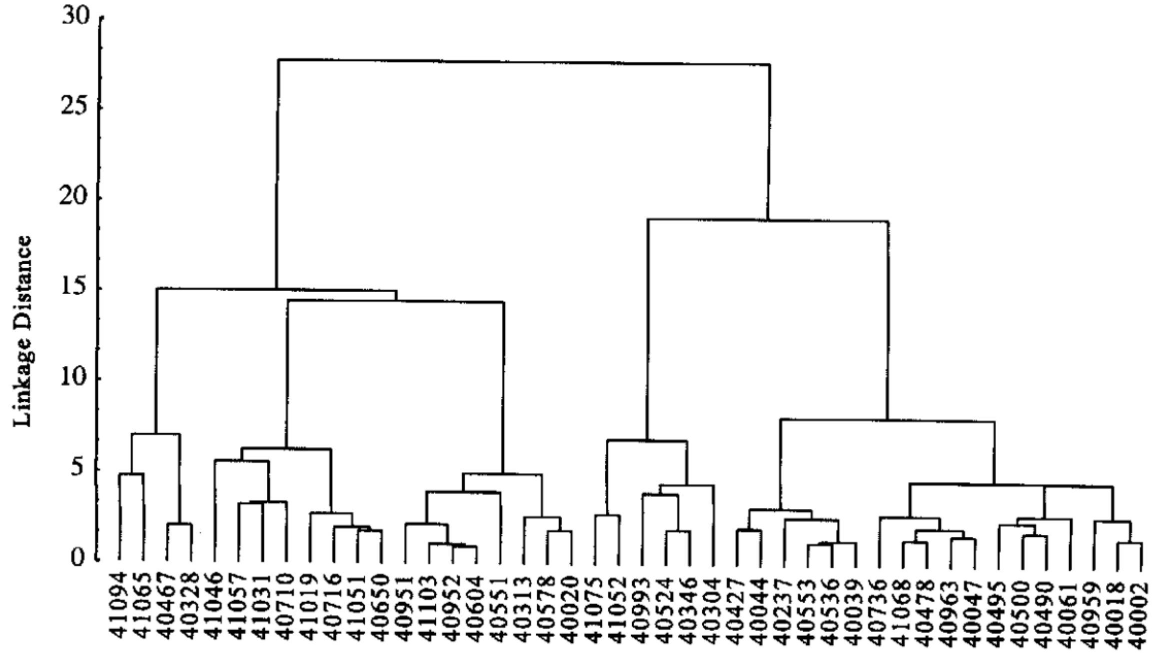

Fig. 1: Phenogtram of 44 selected mungbean genotypes based on quantitative traits

as it has negative effect in most of the economically important traits. Therefore, short to medium maturity mungbean cultivars are suggested to be selected from the germplasm. Branches showed significant positive association with pods, biological yield and grain yield indicating that number of branches could be effective in increasing grain yield in mungbean. Pods/plant has high correlation with pod length, seeds/pod, biological yield, grain yield and harvest index indicating the importance of these traits in mungbean. Pod length is significantly correlated with seeds/pod, seed weight, biological yield, grain yield and harvest index. Grain yield has significantly positive correlation with all the traits except days to maturity, hence, short to medium duration cultivars are suggested to be selected to improve grain yield. Harvest index has also significant positive correlation with pods, pod length, seeds/pod, seed weight and grain yield whereas it has strong negative association with days to maturity. Malik *et al.* (1986) and Ghafoor *et al.* (1993) reported positive association of grain yield with biological yield. Negative association of biological yield with harvest index showed physiological inefficiency for appropriate partitioning of total dry matter towards economic yield. Consequently the varieties with low grain yield attained low harvest index (Table 3). High harvest index is very important for increasing yield potential in crops, but it is very complex character in legumes because it is sensitive to environmental fluctuation and optimum range for legumes needs to be investigated. In order to find the optimum harvest index along with other desirable traits, all the accessions were grouped on the basis of harvest index classes (Table 3). These results gave interesting clue for the selection of high yielding mungbean cultivars from local germplasm. The accessions with harvest index of 35.01-40.1% gave good average values for most of the traits i.e., days to maturity, branches, pods/plant, seeds per pod, and grain yield. The results of this study supported the condition that germplasm with high harvest index is the future potential source for mungbean breeding as the average values for most of the yield contributing traits were high. Similar findings regarding harvest index have already been reported by Malik *et al.* (1986, 1987) in mungbean and Ghafoor *et al.* (1993, 1998) in blackgram. In a previous study conducted by Patel and Shah (1982) and Ghafoor *et al.* (1993), high selection indices were obtained in blackgram where harvest index ranged from 26 to 36%, whereas Ghafoor *et al.* (1998) observed 25-40% harvest index best for selecting high yielding cultivars of blackgram.

On the basis of results, the genotypes falling in harvest index range of 25.01-40.0% along with other specific traits mentioned in the Table 4 were used to construct dendrogram (Fig. 1). In total 44 genotypes with best performance for various characters as listed in the Table 4 were grouped using Ward's method on the basis of nine quantitative traits. As these accessions were best for specific characters and some of these were best for more than one parameter, hence on the basis of genetic diversity, parents are suggested to be included in the breeding programme. The grouping of germplasm by multivariate methods in this study is of practical value to the breeders for selection of desirable parents and transgressive segregates in the proceeding generations. Selected genotypes from diverse groups could be used in breeding programme using selective diallel mating. Tawar *et al.* (1988) conducted genetic divergence in 34 diverse genotypes of mungbean and grouped into five clusters and observed that variability in the parents was related to genetic diversity. Inclusion of diverse genotypes and their implication in breeding programme is suggested. Diverse germplasm plays a vital role in any successive breeding programme preferably if it is collected from the targeted area and/or centre of diversity. The mungbean germplasm under investigation exhibited large variability for most of the traits under study and characterization of germplasm revealed good scope for selection for varietal development. Several potentially important agronomic types have been identified and these may be exploited for genetic potential to transfer the desirable genes and this, along with biochemical analysis will also facilitate in assembling a core collection of accessions from the large genetic resources collection (Tolbert *et al*., 1979; Singh, 1988; Clements and Cowling, 1994; Vierling *et al*., 1994) (Table 4).

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