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Genetic variability and divergence studies in mungbean (*Vigna radiata*) under rainfed conditions

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ABSTRACT

Twenty three genotypes of moongbean were evaluated in two different environments for variability stability performance. The present investigation was conducted to provide information on the nature and magnitude of genetic variability and divergence among 23 genotypes of mungbean under different environments. It was measured by seed yield/plant under rainfed conditions during *kharif* 2016 and 2017. Seed yield/plant showed significant correlation with number of seeds/pod and negative correlation with days to maturity. These genotypes were divided into five clusters on the basis of D^2 statistics. Maximum inter cluster distance was exhibited by cluster IV and intra-cluster distance by cluster I. Hence, the genotypes of cluster III & IV shall be utilized for the hybridization programme for the development of high yielding varieties (HYVs) of mungbean.

Key words: Correlation, Divergence, Path analyses, *Vigna radiata*

Mungbean (*Vigna radiata* (L.) Hepper), popularly known as greengram in India. It is an important short duration pulse crop and self-pollinating diploid (2n=2x=22) with a small genome size estimated to be 0.56 pg/1C (574 Mbp) (Gupta *et al*. 2008). Genetic improvement mainly depends upon the amount of genetic variability present in the base population and serves as a valuable source of base population for providing wide variability. Genetic diversity is an important factor and also a pre-requisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombination.

The study of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is helpful for framing the effective breeding programme (Pushpa *et al*. 2013). A throughout knowledge of existing genetic variation and degree of association between seed yield and yield contributing traits are essential for developing high yielding genotypes of mungbean. Identification of important yield components and information about the nature and magnitude of their direct and indirect contributions towards the manifestation of seed yield is very essential for devising successful crop breeding strategy in any crop. The correlation analysis provides information about the relative importance of various yield components in the expression of yield and thus, helps in formation of appropriate selection strategy.

Assessment of divergence or similarity among the genotypes would help in an identification of genotypes that may be used in cross breeding programme for producing transgressive segregants. Limited systematic breeding programmes for breeding superior genotypes have been taken up for developments of high yielding genotypes in mungbean have been initiated. Vast scope lies for genetic improvement of mungbean through genetic diversity study to understand the diversity in different genotypes for assessment and creation of diverse line for further breeding. Hence, study on "genetic variability and divergence studies in mungbean genotypes under rainfed conditions" was taken up with the view of selecting parents for hybridization programme.

MATERIALS AND METHODS

The experimental materials comprised 23 diverse genotypes of mungbean, viz. V-1133, K-851, IPM2-3-2, IPM-99-152, PDM -139, IPM 2057 , PM-2-14 , IPM 2-3, Ganga 8, BM63, ML-2056, MH-9-8-1, MH-521, Pusa 0672, Pusa Vishal, EC-520016, MG-331, IPR-57, SML-668, ML-818, LG-460, PM-5, and IPM 95-31 received from ICAR- Indian Institute of Pulses Research, Kanpur during *kharif* 2016. The experiments were conducted in randomized block design with 3 replications. Each entry was represented by 5 rows of 3.0 m row length with a spacing of 30 × l0 cm^2. A fertilizer dose of 20:40:20 kg NPK/ha was applied and need based plant protection measures

*Corresponding author e-mail: ssalgotra@gmail.com were followed at experimental farm of Advanced Centre for Rainfed Agriculture (ACRA) Dhiansar of SKUAST-Jammu during *kharif* 2016 and 2017. The pooled mean data of three replications of both the years were used for statistical analysis. The observations were recorded on eight quantitative traits, viz. days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of seeds/pod, pod length, 1000 seed weight and seed yield/plant.

Statistical analyses

Correlation coefficients were calculated for all character combinations at phenotypic and genotypic levels by the formula given by Miller *et al*. (1958). Assessment of genetic divergence was done by using Mahalanobis D^2 (Mahalanobis 1936) statistic and the genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977). Broad sense heritability was estimated (Falconer *et al*. 1996) and pooled broad sense heritability was calculated (Hill *et al.* 2012).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) showed highly significant ($P<0.001$) differences among the genotypes for the pooled analysis with respect to all the characters under study indicated high genetic variability and is an indication of the fact that in spite of highly interactive with environments, the genotypic differences among the genotypes were highly significant across the environments.

Genotypic and phenotypic coefficient of variation

Estimation of PCV and GCV components helps to access the magnitude of genetic variation present in the genotypes for trait per se. Phenotypic coefficient of variation was higher than genotypic coefficient of variation (GCV) for all the characters, however, minor difference was observed between PCV% and GCV% for characters, viz. plant height, days to 50% flowering, pod length, days to maturity, 1000 seed weight and seed yield/plant whereas higher estimates for number of primary branches/plant in pooled over years. High GCV was shown by number of primary branches/plant and seed yield/plant. Improvement could be possible through selection in these traits. Characters like days to 50% flowering, seeds/pod and days to maturity recorded low GCV. These results are in agreement with findings of Singh *et al.* (2009).

Heritability and genetic advance

The quantitative characters are governed by many genes and are more influenced by environment. The phenotype observed is not transmitted entirely to next generation. Therefore, it is necessary to know the proportion of observed variability that is heritable. High magnitude of heritability was obtained for most of the characters except for number of pods/plant (Table 1). High heritability estimate was recorded by characters, viz. plant height (98 %), number of pods/plant (84.14%), 1000 seed weight (99.0 %), seed yield/plant (98.0 %), days to fifty % flowering (80.0 %), number of primary branches/plant (77.0%), number of seeds/pod (92.0%) except days to maturity (68.0%) indicated that these traits were stable across environments with relatively less G × E interactions and phenotypic selection will be more effective. The consistent values of GCV and PCV for all the traits except primary branches/plant and seed yield/plant showed that these traits were less affected by environment. The presence of high heritability values for yield and yield attributing traits in pooled analyses indicated selection would be more effective under rainfed conditions.

Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in an improving the traits because its estimates value is derived by

Table 1 Analysis of variance and estimates of mean, PCV, GCV, ECV, heritability $(h^2)_{bs}$ and genetic advance (GA) for different morphological traits

Source of variation	df	DFL	PH (cm)	PBR/P	PL (cm)	S/P	Days to maturity	1000 seed weight (g)	GY/P
Environments	1.00	2.62	0.77	1.81 *	0.28 *	0.18	8.47 **	0.35	0.15*
Genotype	22.00	34.92***	494.91***	6.08 ***	3.71 ***	3.82 ***	13.69***	443.82 ***	16.92***
Error	115.00	1.38	1.01	0.28	0.04	0.05	0.98	0.17	0.03
CD (0.05)	-	1.34	1.15	0.61	0.24	0.26	1.13	0.47	0.21
CV	-	2.38	1.92	15.45	2.73	1.97	1.25	0.81	2.70
PCV (%)	-	5.35	17.46	32.54	10.49	7.20	2.22	17.06	24.94
GCV (%)	-	4.79	17.36	28.64	10.13	6.93	1.83	17.04	24.79
ECV (%)	-	2.38	1.92	15.45	2.73	1.96	1.25	0.81	2.69
H $(h^2)_{bs}$	-	0.80	0.98	0.77	0.93	0.92	0.68	99.00	0.98
GA (% mean)	-	8.84	35.53	51.93	20.14	13.73	3.12	35.06	50.78

*, **&*** significant at 0.05%, 0.01% and 0.001% level, respectively, DF (days to 50% flowering), PH (plant height), PBR/P (Primary branches per plant), DTM (days to maturity), PL-Pod length, S/P- (Seeds per pod), 1000 SW (1000- seed weight), GY/P (grain yield per plant), DFL-Days to 50% flowering.

Table 2 Genotypic and phenotypic correlations coefficient analysis for seed yield and yield attributing traits

Trait	Correl.	PH	PBR/P	PL	S/P	DTM	1000 SW
DF	G	-0.17	0.54	-0.31	-0.09	0.02	0.27
	P	-0.15	0.41 ***	-0.28 **	-0.06	-0.02	0.24 **
PH	G		0.19	-0.02	-0.05	0.33	-0.09
	P		0.17 *	-0.02	-0.04	0.25 **	-0.09
PBRP^{-1}	G			-0.05	-0.12	0.52	0.21
	P			-0.06	-0.06	0.42 ***	0.19 *
PL	G				0.30	-0.11	0.25
	P				0.29 ***	-0.09	0.24 **
SP^{-1}	G					0.11	0.11
	P					0.08	0.11
DTM	G						0.20
	P						0.16
GY	G						-0.12
	P						0.12

G-Genotype and P-Phenotype.*, **&*** Significant at .05%, 0.01% and 0.001% level, respectively

involvement of heritability, phenotypic standard deviation and intensity of selection (Sinha and Wagh, 2013). High heritability (98.3%) coupled with high genetic advance as per cent of mean was recorded by number of primary branches/plant (32.54%) and seed yield/plant (24.94%) indicated the influence of additive genes affecting these traits. High heritability along with moderate genetic advance was observed for plant height, pod length and 1000 seed weight revealed additive gene action influencing these traits.

Correlation coefficients

The genotypic and phenotypic correlations among different seed yield attributing characters in mungbean genotypes were presented in Table 2. The correlation coefficient estimates, the degree and direction of association between a pair of characters and help simultaneously were proved useful for simultaneous improvement of the correlated traits through selection. Seed yield/plant showed highly significant association with number of seeds/pod revealed an importance of this character in determining the seed yield/plant under rainfed conditions of varying environments during *kharif* 2016 and 2017. Seed yield/plant showed negative significant association with plant height, number of primary branches/plant and days to maturity indicated the importance of these traits in decreasing the seed yield/plant.

Correlation study showed negatively significant association with number of primary branches/plant. It appears that bushy plants escape the adverse effect of drought conditions on seed yield/plant. Thus, it can be assumed that seed yield/plant is the outcome of number of seeds/pod rather than seed weight. Negative and non-significant correlated with days to 50% flowering, whereas positive

Table 3 Average inter and intra-cluster distance (Tocher Method) and distribution of genotypes

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	No. of genotypes K method	Name of genotypes	Clusters by Tocher Method	Name of genotypes
Cluster 1	2.47	3.7	5.25	5.08	6.13	3	(03) Pusa vishal, IPM99-125, IPM-2057	Cluster 1 (22)	SML-668, ML-2056, IPM-9531, Pusa-0672, IPR-57, IPM-99-125, MG-331, IPM-2-3, EC-520016, ML-818, IPM-2-3-2, MH-521, MH-9-8-1, IPM-2057, K-851, BM-63, PM-5, LG-460, Ganga-8, V-1133, Pusa Vishal, PM-2-14
Cluster 2	-	0.00	8.16	6.47	2.89	1	PDM-139 (1)	Cluster 2 (1)	PDM-139
Cluster 3	-	-	0.00	12.27	8.58	7	IPM-2-3, SML-668, PM-2-14, IPM-95-31, Ganga-8, LG-460, MG-331		-
Cluster 4	-	-	-	0.00	8.20	5	PM-5, MH-521, IPM-2-3-2, BM-63, EC-520016		-
Cluster 5	-	-	-	-	0.00	7	ML-818, Pusa-0672, IPR-57, ML-2056, MH-9-8-1, V-1133, K-851		-

and non-significant correlated with pod length and 1000 seed weight. This situation indicated that in order to select high yielding genotypes of greengram, it is an essential to consider the number of seeds/pods with the increasing magnitude and simultaneous improvement of positively correlated character. These results are in close agreement with the findings of Imrie and Butler (2005).

Genetic diversity

For a successful breeding programme, the diversity of parents is of an utmost importance, since the crosses made between the parents with maximum genetic divergence are more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents based on information about the genetic variability and genetic diversity present in the available germplasm. Mahalonobis D^2 values have grouped the 23 genotypes of mungbean into five distinct clusters on the basis of clustering by K method and two clusters as per Tocher's method shown in Table 3. The estimates of average intra and inter-cluster distances for five clusters revealed that the genotypes present within a cluster have good genetic divergence from each other with respect to aggregate effect of eight characters under study, while greater genetic diversity was observed between the genotypes belonging to different clusters. The maximum inter cluster distance was between cluster III and IV (12.27) followed by cluster III and V (8.58) suggesting that the crosses involving varieties from these two clusters would give desirable recombination. While the minimum inter cluster distance was recorded 3.7 between cluster I and II indicating that genotypes of these clusters had maximum number of gene complexes and genotypes of these clusters were genetically close. Such genotypes can also be used in breeding programmes for developing biparental crosses between the most diverse and closest groups to break the undesirable linkages between yield and its associated traits (Haddad *et al.* 2004). High or optimum genetic divergence is desired between the parents for hybridization since the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster is very low.

In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. Genotypes in cluster III and IV are highly divergent followed by those in cluster III and V and cluster II and III. Hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties.

From the present study, it was concluded that 23 genotypes of mungbean were evaluated in different environments for variability and genetic divergence. Seed yield/plant showed significant positive correlation with number of seeds/pod and negatively with days to maturity. Twenty-three genotypes were divided into five clusters on the basis of D^2 statistics. Maximum inter cluster distance was exhibited by cluster IV and intra cluster distance by cluster I. Hence, the genotypes of cluster III & IV shall be utilized for the hybridization programme.

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