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Study of genetic diversity in Mungbean

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ABSTRACT

An experiment was conducted to study heritability in broad sense, association effects, direct and indirect effect of yield attributing traits on yield among 12 green gram genotypes. ISSR markers were also used to study the genetic diversity present in the studied genotypes at molecular level. Analysis of variance for RBD indicated presence of significant amount of genetic diversity among the genotypes for all the traits. Phenotypic coefficient of variation was higher than Genotypic coefficient of variation. Path coefficient revealed that most of the yield attributing traits *viz.*, days to 75 percent flowering, duration of reproductive phase, days to maturity, number of secondary branches per plant, number of clusters per plant, grain per pod, pod density and number of seed per pod, traits had positive direct effect on yield per plant. Two clusters were obtained from Mahalobinis D^2 statistics. Traits *viz.*, number of pods per plant, plant height, 1000-seed weight and yield per plant showed high heritability with high genetic advance.

Key words: Green-gram, Heritability broad sense, Path coefficient, Correlation and cluster analysis

Introduction

Pulses are an important part of Indian food habits as it is being relished in one or other form in daily cuisines in different states of India. Production of pulses in India is insufficient to meet the needs of all pulse consumers, which can be inferred, following the import pattern of pulses in India. The country imported a handsome amount of 24.67 million tones of pulses worth rupees 1.61 billion USD in year 2020-21.

Green gram is an important pulse crop of India which is a rich source of protein. Pulse crop not only provides nutrition but it is also an important source of income to marginal farmers. Apart from food, green-gram being short duration crop is an excellent fodder for animal too. The major factors which contribute to low productivity of green-gram in India are: farmers do not use high yielding improved va-

rieties; erratic climatic changes; and incidence of disease and pests. Mung-bean is cultivated in nearly all parts of India mainly as Kharif crop but sometimes farmers grow early maturing varieties as *Kharif* fallow or *Rabi* crop.

Diversity analysis in biometrical genetics is an effective tool to assess the genetic diversity present in experimental population. The existence of genetic diversity in a plant population not only assures a plant breeder for improvement in such population, but also suggests chance of obtaining hybrids if such populations are subjected to hybridization program. Study of genetic diversity is a common practice done in any breeding program, it can be done either traditional breeding using Mahalanobis D^2 statistics and cluster analysis or by using molecular biology tools. In this paper, 12 green gram genotypes were studied by using the former method, to assess the genetic diversity present in them so that such geno-

types can be used in future hybridization program.

Materials and Methods

The present study was undertaken at Genetics and Plant Breeding Research Farm, Lovely Professional University, Phagwara. The experimental material constituted of 12 green gram genotypes were sown in *Kharif* 2017 in three replications in Randomized Block Design. List of genotypes along with their name, source and special characteristic features are given in Table 1.

Data were collected on randomly selected five plants from each of the 12 lines of three replications. Traits which were studied in this experiment are *viz.*, days to 50 percent flowering (DF50), days to reproductive phase (DRP), days to maturity (DM), plant height (PH), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), number of clusters per plant (NCPP), number of pods per plant (NPPP), length of pods (LP), number of seed per plant (NSPP), pod density (PD), 1000-seed weight (TSW), yield per plant (YPP).

Analysis of variance of Randomized Block Design was done according to Panse and Sukhatme (1967). The path coefficient analysis was done according to Dewey and Lu (1959). Heritability in broad sense (h^2_b) was calculated and classified into low (below 30%), medium (30- 60%) and high (above 60%); and genetic advance as percent over mean (at 5%) were computed and categorized into low (0-10%), moderate (10-20%) and high ($\geq 20\%$). Estimates of PCV and GCV was calculated follow-

ing Burton and De Vane (1953) and categorized into low (<10%), moderate (10-20%) and high (>20%). Collected data were subjected to statistical analysis for genetic diversity analysis using Mahalanobis's D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into clusters as per Ward's method.

Results and Discussion

ANOVA results were significant at 1 and 5 percent level of significance for traits *viz.*, days to 50% flowering, days to reproductive phase, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, clusters per plant, pods per plant, grain per pod, pod density, 1000-seed weight, yield per plant (Table 2). These findings are in congruent with work of Canci *et al.* (2014) and Garg *et al.* (2017). Mean value of different traits of all the 12 genotypes of green gram are mentioned in Table 3.

Coefficients of phenotypic and Genotypic Variation

The assessment of coefficient of phenotypic (PCV) and genotypic variations (GCV) revealed that, magnitude of PCV was higher than GCV in present studies (Table 4). Similar findings have been found in work of by and Jyothsna *et al.*, (2016).

Heritability and Genetic advance

Estimates of heritability in broad sense is used to measure the magnitude of phenotypic variation due to their genotype (additive, dominance and epistatic

Table 1. List of varieties along with their source as well as special characteristics

S. No.	Name of Variety/ Inbred line	Source	Characteristics
1	HUM-1	BHU, Varanasi	Spring and Kharif season, Days to Maturity 60-65, Yield 9.4-16.0 q/ha
2	Gold	IIPR	unknown
3	Moongi	PAU, Punjab	unknown
4	HUM-1L	BHU, Varanasi	Summer season, Days to Maturity 60-62, Yield 11.2 q/ha
5	PUSA-460	IARI, New Delhi	unknown
6	MLA 720	PAU, Ludhiana	unknown
7	Kopergane	BHU, Varanasi	Solid and Green bold seeds, Days to maturity 60-65, Yield 8-10q/ha
8	LM-5	BHU, Varanasi	Unknown
9	PUSA-Vishal	IARI, New Delhi	Summer season, bold seed, Days to Maturity 62, Yield 11.0 q/ha
10	LG-420	BHU, Varanasi	Unknown
11	IPM-2	IARI, New Delhi	Large seed suitable for rainy season, Days to Maturity 62-68, Yield 11-12 q/ha
12	SML-668	PAU, Ludhiana	Spring-Summer season, Tolerance to MYMV, Days to Maturity 60-63, Yield 11.3 q/ha

Table 2. Analysis of variance for different characters in Moong bean (mean square)

Traits	Replication 2	Treatment 11	Error 18
DF50	5.08	15.89**	3.54
DRP	12.11	85.18**	11.38
DM	2.52	51.63**	5.5
PH	4.16	96.39**	11.3
NPBPP	0.01	0.71*	0.24
NSBPP	0.55	0.60*	0.17
NCP	28.21	176.74**	9.51
NPP	0.09	1.46**	0.2
LP	0.01	0.72**	0.15
NSP	0.32	3.10**	0.78
PD	0.003	0.02**	0.004
TSW	0.2	2.13**	0.15
YPP	0.91	3.60**	0.41

Significant at 1% (**) and 5% (*)

effect) in a population Nyquist (1991) and Falconer and Mackay (1995). Heritability can be used to measure a population response to selection (Piepho and Mohring, 2007). According to Hanson (1956), heritability affects the magnitude of gain in selection differential expected to obtain as a result of selection in a particular population. Further, Holland *et al.* (2003), explained that estimates of heritability are meaningful for a particular population under defined response units; and the can vary in same population when different breeding scheme are used. In present study, the results gave high heritability with high genetic advance for traits *viz.*, plant

height, no. of pods per plant, 1000-seed weight and yield per plant (Table 4). High heritability with medium genetic advance as percent of mean was recorded for days to maturity; similarly, medium heritability with high genetic advance as percent of mean for duration of reproductive phase and number of clusters per plant (Fig. 1). Moderate heritability with low genetic advance as per cent of mean pod length, days to 75% flowering, number of grains per pod; however, pod density and no. of primary branches per plant recorded low heritability with medium genetic advance as per cent of mean. Num-

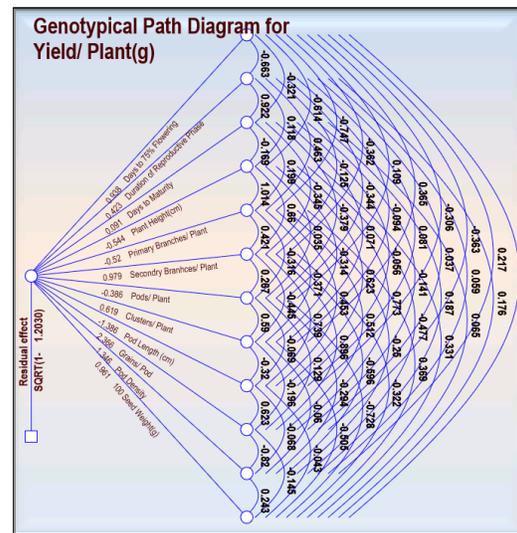


Fig. 1. Graphical representation of ECV, PCV, GCV Genetic advance and Heritability in Broad sense of 13 traits

Table 3. Mean performance of green gram genotypes for 13 different traits

Character	DF50	DRP	DM	PH	NPBPP	NSBPP	NCP	NPP	LP	NSP	PD	TSW	YPP
HUM-1	43.33	18.33	61.66	45.99	3.25	7.35	35.71	2.67	8.04	9.89	0.81	4.33	6.4
Gold	40.66	23.66	64.33	56.88	4.66	7.15	28.28	2.66	7.33	10.46	0.7	5.46	6.77
Moongi	41.66	26.33	68	40.24	2.99	7.14	38.88	3.55	7.26	9.79	0.74	3.56	7.44
HUM-1L	43	24.33	67.33	39.1	3.39	6.71	27.75	2.77	6.63	9.06	0.73	3.47	7.09
PUSA- 460	39	33.33	72.33	44.94	3.65	6.06	33.35	3.49	6.99	7.86	0.89	4.4	5.1
MLA- 720	40.66	30	70.66	45.75	4.25	7.03	25.92	3.35	7.62	8.94	0.86	4.56	5.35
Kopergane	42.66	20.66	63.33	38.1	3.21	6.43	35.03	4.14	6.56	8.27	0.79	4.93	7.24
LM-5	43.66	26	69.66	41.25	3.49	6.49	24.77	3.77	7.81	9.54	0.82	3.96	8.31
PUSA -Vishal	38.33	25.33	63.66	46.61	3.72	7.32	32.9	2.33	7.66	8.91	0.86	3.7	4.92
LG-420	41.33	19.66	61	44.33	3.49	6.44	21.92	2.55	7.31	8.51	0.86	5.43	6.49
IPM-2	44	25.66	69.66	35.11	3.1	6.16	15.84	2.12	6.77	7.03	0.96	5.4	8.05
SML-668	36.66	36.33	73	47.66	3.88	6.99	15.02	1.94	7.77	10.24	0.76	6	7.06
Mean	41.25	25.8	67.05	43.83	3.59	6.77	27.94	2.94	7.31	9.04	0.81	4.6	6.68
S.E±	1.08	1.948	1.35	1.94	0.28	0.23	1.78	0.25	0.22	0.51	0.04	0.22	0.37
C.D. 5%	3.18	5.713	3.97	5.69	0.82	0.69	5.22	0.75	0.64	1.49	0.11	0.65	1.08
C.D. 1%	4.32	7.765	5.36	7.73	1.11	0.94	7.09	1.02	0.87	2.03	0.16	0.89	1.47

ber of secondary branches per plant exhibited low heritability with low genetic advance as per cent of mean. Pyasi (2015) obtained similar findings their results in different types of traits studied by them.

Phenotypic Correlation studies among different traits for yield per plant

The study of character association among traits showed significant positive correlation with yield was days to 75% flowering; while, plant height showed significant negative correlation with yield per plant (Table 5). Pods per plant showed positive significant correlation with secondary branches per plant and negative correlation with duration to reproductive maturity and days to maturity.

Direct and Indirect effects of yield attributing traits on yield

Path coefficient analysis showed (Fig. 2) that, days to 50% flowering, duration of reproductive phase, days to maturity, number of secondary branches per plant, number of clusters per plant, grain per pod, pod density and number of seed per pod, showed positive direct effect on yield per plant (Table 6). While traits which showed negative direct effect on plants were plant height, numbers of primary branches per plant, number of pods per plant and pod length exerted direct negative effect on seed yield per plant. Similar findings have been recorded by Bhanu *et al.*, (2016) and Keerthiga *et al.*, (2018).

Table 4. General Mean, Variance, Coefficient of Variation, Heritability, genetic Advance & Genetic advance as present of mean

Characters	General mean	Range		Variance			Coefficient of variation		Heritability (Broad Sense %)	Genetic advance (5%)	G.A. as percentage of mean
		Mini.	Max.	Geno- typic	Pheno- typic	Enviro- nment	Geno- typic (%)	Pheno- typic (%)			
DF50	41.25	36.66	44	4.11	7.65	3.53	4.91	6.7	54	3.06	7.43
DRP	25.8	18.33	36.33	24.59	35.98	11.38	19.21	23.24	68	8.44	32.73
DM	67.05	61	73	15.37	20.87	5.49	5.84	6.81	74	6.93	10.33
PH	43.83	35.11	56.88	28.36	39.66	11.29	12.15	14.36	72	9.27	21.16
NPBPP	3.59	2.99	4.66	0.15	0.39	0.23	11.02	17.44	40	0.51	14.34
NSBPP	6.77	6.06	7.35	0.14	0.31	0.16	5.6	8.26	46	0.53	7.83
NCPP	27.94	15.02	38.88	55.74	65.25	9.5	26.71	28.9	85	14.2	50.86
NPPP	2.94	1.94	4.14	0.42	0.61	0.19	21.99	26.66	68	1.1	37.38
LP	7.31	6.56	8.04	0.19	0.33	0.14	5.97	7.92	57	0.67	9.23
NSPP	9.04	7.03	10.46	0.77	1.55	0.78	9.71	13.77	50	1.27	14.1
PD	0.81	0.7	0.96	0.004	0.008	0.004	7.78	11.4	47	0.08	10.95
TSW	4.6	3.47	6	0.66	0.8	0.14	17.64	19.54	82	1.51	32.82
YPP	6.68	4.92	8.31	1.06	1.47	0.41	15.41	18.15	72	1.8	26.95

Table 5. Phenotypic correlation coefficient of 13 traits of Green-gram

Character	DF50	DRP	DM	PH	NPBPP	NSBPP	NCPP	NPPP	LP	NSPP	PD	TSW	YPP
DF50	1	-0.68**	-0.29	-0.49**	-0.29	-0.16	0.13	0.29	-0.28	-0.15	-0.01	-0.21	0.41*
DRP		1	0.89**	0.15	0.17	-0.12	-0.3587*	-0.14	0.14	0.03	0.09	0.13	-0.13
DM			1	-0.10	0.05	-0.26	-0.3937*	-0.01	0.01	-0.05	0.10	0.04	0.08
PH				1	0.69**	0.40*	0.05	-0.21	0.3959*	0.49**	-0.33*	0.24	-0.34*
NPBPP					1	0.22	-0.10	0.00	0.17	0.33	-0.27	0.34*	-0.17
NSBPP						1	0.38*	-0.05	0.50**	0.64**	-0.47**	-0.09	-0.07
NCPP							1	0.59**	0.00	0.20	-0.30	-0.53**	-0.23
NPPP								1	-0.13	0.05	-0.20	-0.29	0.13
LP									1	0.61**	-0.08	0.07	-0.05
NSPP										1	-0.82**	0.09	0.23
PD											1	-0.01	-0.30
TSW												1	0.25
YPP													1

Significant at 5% (*) and 1% (**) level of significance

Table 6. Genotypic path coefficient analysis showing direct and indirect effects among different characters.

Character	DF50	DRP	DM	PH	NPBPP	NSBPP	NCPP	NPPP	LP	NSPP	PD	TSW
DF50	0.94	-0.62	-0.30	-0.58	-0.70	-0.34	0.10	0.34	-0.29	-0.34	0.20	-0.29
DRP	-0.28	0.42	0.39	0.05	0.20	-0.05	-0.15	-0.04	0.03	0.02	0.03	0.07
DM	-0.03	0.08	0.09	-0.02	0.02	-0.03	-0.03	0.01	-0.01	-0.01	0.02	0.01
PH	0.33	-0.06	0.09	-0.54	-0.55	-0.36	-0.02	0.17	-0.34	-0.42	0.26	-0.18
NPBPP	0.39	-0.24	-0.10	-0.53	-0.52	-0.22	0.16	0.19	-0.24	-0.27	0.13	-0.19
NSBPP	-0.36	-0.12	-0.34	0.65	0.41	0.98	0.26	-0.44	0.72	0.88	-0.58	-0.32
NCPP	-0.04	0.13	0.15	-0.01	0.12	-0.10	-0.39	-0.23	0.03	-0.05	0.11	0.28
NPPP	0.23	-0.06	0.04	-0.19	-0.23	-0.28	0.37	0.62	-0.20	-0.12	-0.04	-0.31
LP	0.42	-0.11	0.08	-0.86	-0.63	-1.02	0.10	0.44	-1.39	-0.86	0.09	0.06
NSPP	-0.86	0.09	-0.33	1.83	1.21	2.12	0.31	-0.46	1.47	2.37	-1.94	-0.34
PD	0.29	0.08	0.25	-0.64	-0.34	-0.80	-0.40	-0.08	-0.09	-1.10	1.35	0.33
TSW	-0.29	0.17	0.06	0.32	0.36	-0.31	-0.70	-0.49	-0.04	-0.14	0.23	0.96
YPP	0.74	-0.24	0.08	-0.53	-0.65	-0.42	-0.39	0.04	-0.33	-0.06	-0.14	0.08
Partial R ²	0.70	-0.10	0.01	0.29	0.34	-0.41	0.15	0.03	0.45	-0.14	-0.19	0.08

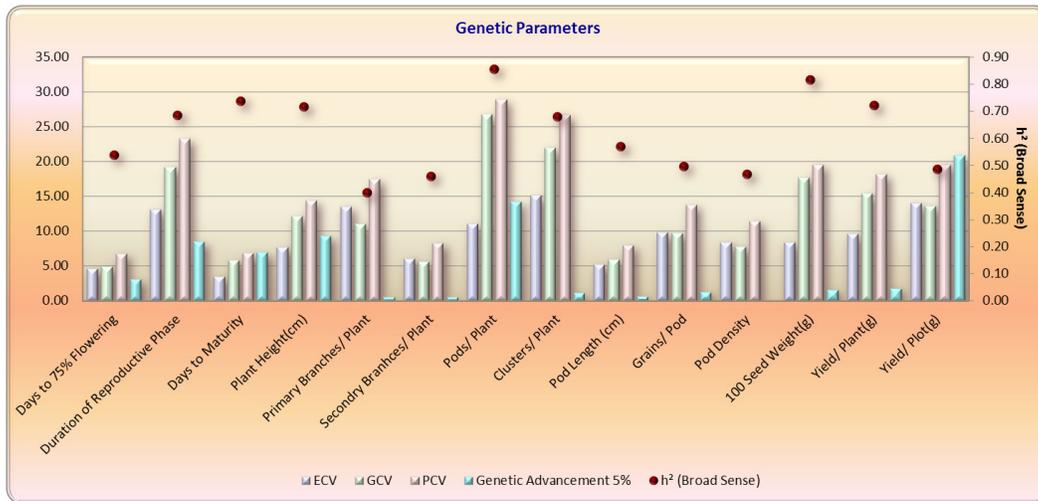


Fig. 2. Genotypical path diagram of 13 traits

R SQUARE = 1.2030
 RESIDUAL EFFECT = SQRT (1- 1.2030)

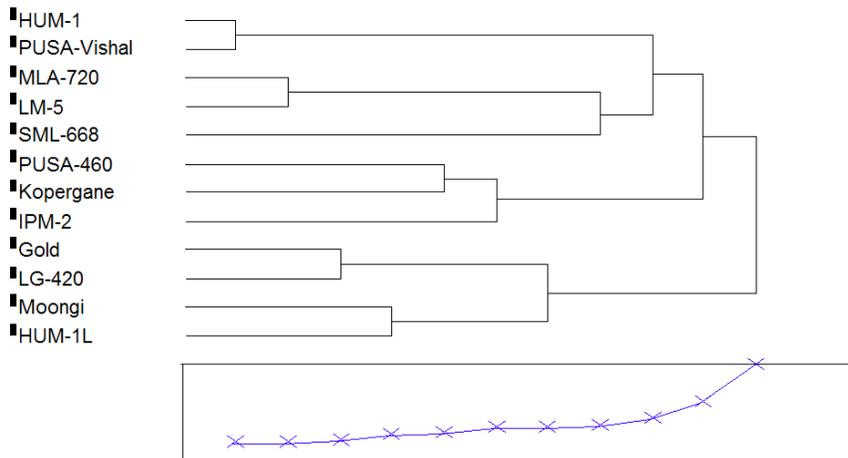


Fig. 3. Dendrogram formed through Hierarchical Clustering by using Ward method

Cluster Analysis

Cluster analysis done according to Mahalobinis D^2 statistics, in 12 mungbean genotypes gave two clusters. Cluster I had eight genotypes and Cluster 2 had four genotypes. Such findings are in congruence of work of Rasal *et al.*, (2017); Ahmad *et al.*, (2013), Gadakh *et al.*, (2013); Abna *et al.*, (2012) and Thippani *et al.*, (2013).

Conclusion

The 12 genotypes used to assess genetic diversity present in them, indicated that, experimental material possessed ample amount of genetic variability for different traits studied. Such material can be used in future hybridization-based breeding program. The estimates of heritability and genetic advance indicated role of non-additive genetic variance in inheritance of traits studied, thus selection practice will be recommended to be delayed if further study is carried out in same breeding material.

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