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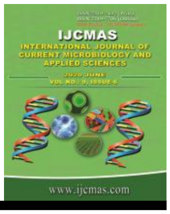

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Genetic, Character Association and Multivariate Studies of Seed Yield with Different Traits in Mungbean (*Vigna radiata* (L.) Wilkzek)

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ABSTRACT

Keywords

character association , eigen value, Mungbean, PCA, Tochers method

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The present study was conducted during *kharif*, 2018 to evaluate 38 genotypes of mungbean [*Vigna radiata* (L.) Wilczek]with 12 different traits using general statistics, character association, principal component analysis and cluster analysis. The basic descriptive statistics had showed considerable variance for all the traits. The results of character association studies revealed that Days to first flowering, Days to 50% maturity, Days to pod initiation, Number of primary branches per plant, Number of clusters per plant, Number of pods per plant and seed yield per plant exhibited highly significant positive correlation at both genotypic and phenotypic levels. Through Principal component analysis (PCA), a total cumulative variance of about 73.59% was revealed within four principal components with eigenvalues >1 among the twelve. PC1 with high values contributed more towards the phenology and vegetative growth whereas the PC2 with high values contributed more towards the reproductive growth. All the 38 genotypes were grouped into 6 clusters by Tochers method which will help us in selecting promising genotypes which can be used as parents in future breeding programmes.

Introduction

Pulses have been considered as an important constituent of Indian diet, because of their high protein content (22-25%). Out of all pulses Mungbean [*Vigna radiata* (L.) Wilczek] also known as greengram, is an important pulse crop cultivated round the year in almost all parts of India. It is a self-pollinated, diploid (2n=22) legume grown mainly as a kharif season crop. It is the native of IndoBurma region of Hindustan center (Vavilov, 1926). It spread, in early times, to other Asian countries and later to Africa, Australia, America, and West Indies. India is the largest producer, followed by China. It is also grown in many tropical African countries.

India's pulses imports are increasing drastically with a growth rate of 6.06% per annum. To cut down this and move towards exports there should be an increase in production in the country. The favourable weather conditions and change in economic environment are found to be the important factors in increasing the production to meet the domestic as well as external demand (Gamanagatti, *et al.*, 2013).

In India, mungbean occupies an area of about 40.70 lakh hectares with an output of around 19.01 lakh tonnes with a productivity of 467 kg/ha (Source: DES, Ministry of Agri. And FW (DAC&FW), Govt. of India; 2017-18). The projected pulses productivity required for growing population by 2020 is 1200 kg/ha and Hence, for increasing the production and productivity to meet the increasing demand, there is a need to replace the low yielding, long duration, local mungbean varieties with the high yielding, bold seeded, early varieties tolerant to both biotic and abiotic stresses which can be made possible by selecting the diverse parents with the help of principal component analysis, cluster analysis and other descriptive statistics. Thus the selected parents can be used in our future breeding programmes in order to develop a highly yielding and resistant genotype which can help in doubling the farmers income in future generations.

Materials and Methods

The Mungbean germplasm used for the present study consists of 38 genotypes, which were obtained from different sources in India (Table 1) from AICRP MULLaRP**.** Among these 38 genotypes there were 2 checks (‘Pant M4 and IPM 2-3’) and 4 mutants taken from advanced lines of mutation of Pusa Vishal and SML 668. The experiment was conducted during *kharif* , 2018 in Randomized Block Design with three replications in Pulse Research Farm of Birsa Agricultural University, Ranchi, Jharkhand. Each genotype was sown in 4 rows of 4 m length with a spacing of 30 x 10 cm between and within rows. A basal dose of fertilizer was applied at the rate of 20:40:20 NPK kg per hectare. All the other recommended package of practices were followed during the crop growth to raise a good crop. The genotypes were harvested as and when pods matured.

The data had been collected from ten random plants from each genotype and in each replication and observations were recorded on Days to first flowering, Days to 50% maturity, Days to pod initiation, Plant height (cm), Number of Primary branches per plant, Number of Clusters per plant, Number of Pods per plant, Number of Seeds per pod , 100-seed weight, Seed yield per plant (g), Disease incidence (%) (Anthracnose and Powdery Mildew),Total Protein Content (%).

The data thus recorded was subjected to various statistical techniques which includes the descriptive statistics, correlation (analyzed by using OPSTAT), Heritability, PCV (Phenotypic Coefficient of variation) (analysed by using Window STAT), principal component analysis (analysed by using SPSS) and wards minimum variance (analysed by using R software) inorder to analyze the genotypes and identify the best performing ones among the genotypes selected.

Results and Discussion

All the 38 genotypes of mungbean for all the twelve traits were analysed by using the basic descriptive statistics like mean, SE, range, PCV, heritability and the results thus obtained were represented in the Table 2.

Correlation coefficient analysis

Information on the association of yield components with yield and the relative contribution of component characters towards yield will be very helpful for developing of elite genotypes and in formulating a breeding strategy. Selection solely on yield is not much effective, as seed yield is a complex character and is influenced by number of traits.

Hence, selection of genotypes with desirable characters could be greatly enhanced if significant correlation between yield and its component characters are established.

In the present study, correlation estimates were obtained for 12 characters in 38 genotypes of mungbean at both phenotypic and genotypic levels (Table 3) and the results are discussed below. In general, phenotypic correlation coefficients were higher than genotypic correlation coefficients which indicates that the environmental influence is also there in the expression of characters (Jyothsna and Anuradha, 2013).

The association analysis revealed that seed yield per plant had showed positive significant association with primary branches per plant and clusters per plant with has been reported by Raje and Rao (2000), Chandra *et al.,* (2016), Sai *et al.,* (2015) and negative significant association with days to 50% maturity.

The trait days to first flowering recorded positive and significant relationship with days to 50% maturity and days to pod initiation which were an important component in identifying the duration of the crop (Shweta (2011), (Srivastava and Singh (2012), Begum *et al.,* (2013). The trait 50% flowering had showed a negative relationship with seed yield. The reason for this can be because of the exposure of the crop to a large amount of time which can subject it to huge amount of stresses. Hence the result states us to go for a short duration crops and develop them accordingly by selecting that trait. Number of primary branches per plant recorded highly significant and positive association with Clusters per plant and pods per plant, seeds per plant and seed yield per plant (Patel *et al.,* (2012), Reddy *et al.,* (2011a), Lalinia and Khameneh (2014), Sai *et al.,* (2015), Chandra *et al.,* (2016) , which states that with an increase in number of primary branches per plant we can improve the remaining traits related to increase in production of our crop like clusters per plant, seeds per plant, pods per plant and seed yield per plant. Plant height, Number of Primary branches per plant, clusters per plant and pods per plant had showed a negative relationship with anthracnose which depicts that with an increase in any of these traits along with some good management practices there is a chance of reducing this disease incidence which will indirectly helps us in reducing the crop loss and increasing the production.

Principal component analysis (PCA)

Multivariate analysis especially principal component analysis is generally used for compression, reduction and transformation of data which helps in analysing the genetic diversity of the genotypes thus considered. In the present study, a total of four principal components which contributed to a variance of about 73.59% out of all the twelve components of 38 genotypes (Table 4. and Fig 1). Populations with high PC1 values were with an eigen value of about 3.39 and a variane of about 28.41% had been explained by them. They mainly contributed towards the phenology and vegetative growth traits like days to first flowering , days to 50% maturity , days to pod initiation and plant height whereas the populations with high PC2 contributed were with an eigen value of about 2.67, variance explained was around 22.38% and they contributed more towards the reproductive growth traits like primary branches , clusters , pods and seed yield. The remaining two components viz., PC3, PC4 were with an eigen value of 1.49 and 1.25 respectively and the variation revealed by them was less when compared with the first two components (which was around 50.69% , PC 1 and PC 2 combinedly)which was around 12.4% (PC 3) and 10.4% (PC 4).

Table.1 List of thirty eight genotypes of mungbean and their source of origin

S.No.	ENTRY	SOURCE	PEDIGREE
1	SKNM 1504	SDAU , S.K. Nagar	GM 9923 x GM 3
2	Pusa M 1771	IARI, New Delhi	MH318 x Pusa 9531
3	Pusa M 1772	IARI, New Delhi	IPM02-14 x Pusa Vishal
4	RMG 1097	RARI , Durgapura	RMG 492 x MUM 2
5	COGG 13-39	TNAU , Coimbatore	CO 6 x SML 668
6	MH 1323	CCS HAU , Hisar	MH 318 x AKM 99-4
7	SML 1808	PAU , Ludhiana	ML 1349 x Mash 1-1
8	IPM 512-1	IIPR , Kanpur	IPM 99-125 x Co 5
9	VGG 16-055	NPRC , Vamban	VBN (Gg)2 x SM47
10	NVL 855	Nirmal Seeds Pvt Ltd., PACHORA	NVS-242(1)x NVS-321s1
11	MDGVV-18	Mahodaya Hybrid Seeds Pvt.Ltd.,Jalna	Local sel. X BPMR-145
12	OBGG-56	OUAT ,Berhampur	OBGG 52 x Kendrapara Local
13	VGG-16-036	NPRC , Vamban	IPM 03-01 x SPS 5
14	AKM 12-28	PDKV, Akola	AKM 9911 x BM 2003-2
15	TMV 126	BARC , Mumbai	Samrat x Kopergaon
16	NMK 15-08	NAU , Navsari	Meha x GM 4
17	SVM-6133	SVHS , Hissar	SML-668 x Pusa-9531
18	BM 2012-9	ARS , Badnapur	Mutant of BPMR 145
19	KM 2355	CSUA&T , Kanpur	KM 2241 x KM 2273
20	PM 14-3	GBPUA&T, Pantnagar	PM 6 x PusaRatna
21	AKM 12-24	PDKV, Akola	AKM 9911 x AKM 9904
22	IPM 410-9	IIPR , Kanpur	IPM 03-1 x NM 1
23	DGG 7	ARS , Dharwad	Mutant of sel. 4
24	IGKM 2016-1	IGKV , Raipur	(Pairymung x Pushavishal)
25	SKNM 1502	SDAU , S.K. Nagar	GM 9912 x GM 4
26	RMB 12-07	BAU , Ranchi	PusaVaishal x DGG-1
27	JAUM 0936	SKUAST , Samba	MH 96-1 x SML 668
28	OBGG 58	OUAT ,Berhampur	VC 1560 A x VA 6370-92
29	PM 14-11	GBPUA&T, Pantnagar	COGG 912 x PM 5
30	MGG-387	ARS , Madhira	Madhiarmung xAsha-1-7
31	ML 2479	PAU , Ludhiana	Pusa 105 x ML 1354
32	KM 17-130	BAU , Ranchi	Pusa Vishal x DGG-1
33	PRMB –15-70	BAU , Ranchi	M_4 Generations of SML 668 (70 KR)
34	SRMB -15-20	BAU , Ranchi	M_4 Generations of SML 668 (20 KR)
35	PRMB -15-40	BAU , Ranchi	M_4 Generations of Pusa Vishal (40 KR)
36	SRMB -15-60	BAU , Ranchi	M_4 Generations of Pusa Vishal (60 KR)
37	Pant M4 (C)	GBPUA&T,Pantnagar	T 44 x UPU 2
38	IPM 2-3 (C)	IIPR , Kanpur	IPM99-125 x Pusa Bold 2

Table.2 Basic statistics for 14 quantitative traits in mungbean genotypes

Character	RANGE		PCV (%)	Heritability (Broad sense) (%)	Mean ± S.E.
	Min.	Max.			
Days to first flowering	29.33	46.33	13.08	97.00	35.85±**0.96**
Days to 50% maturity	31.00	66.01	6.00	95.40	58.17±**1.51**
Days to pod initiation	38.00	54.02	10.15	96.90	44.43±**1.19**
Plant Height (cm)	34.33	74.82	20.29	96.20	53.13±**2.10**
Number of primary branches per plant	1.53	4.53	35.27	98.00	2.21±**0.11**
Number of clusters per plant	5.27	14.77	22.55	89.61	6.68±**0.49**
Number of pods per plant	8.67	20.30	27.27	92.72	14.59±**1.07**
Number of seeds per pod	8.07	14.07	14.24	73.10	11.23±**0.83**
100-seed weight (g)	1.80	5.01	15.69	82.90	2.99±**0.19**
Seed yield per plant (g)	4.16	8.41	20.09	83.30	5.69±**0.47**
Total protein content (%)	16.69	28.14	13.73	98.90	21.11±**0.30**

Table.3 Estimates of Phenotypic and Genotypic correlation coefficients between yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]

Character		**Days to 50% maturity**	**Days to pod initiation**	**Plant height (cm)**	**Number of primary branches per plant**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**100-seed weight (g)**	**Seed yield per plant (g)**	**Disease incidence (%)**		**Total protein content (%)**
											Anthracnose	**Powdery Mildew**	
Days to first flowering	G	0.515**	0.942**	0.160	0.164	0.213	0.296	0.133	0.054	-0.069	-0.221	-0.122	0.082
	P	0.522**	0.938**	0.148	0.160	0.194	0.277	0.130	0.056	-0.057	-0.132	-0.121	0.081
Days to 50% maturity	G		0.554**	0.115	-0.296	-0.065	0.202	0.012	-0.245	-0.425*	-0.263	-0.091	0.221
	P		0.559**	0.102	-0.289	-0.064	0.186	0.016	-0.208	-0.370*	-0.242	-0.062	0.213
Days to pod initiation	G			0.228	0.148	0.203	0.226	0.154	0.049	-0.057	-0.162	-0.123	0.094
	P			0.213	0.145	0.176	0.207	0.135	0.051	-0.048	-0.141	-0.102	0.092
Plant height (cm)	G				-0.167	-0.025	0.023	-0.235	0.254	-0.075	-0.331*	0.152	0.173
	P				-0.165	-0.008	0.021	-0.214	0.225	-0.067	-0.302	0.132	0.159
Number of primary branches per plant	G					0.818**	0.408*	0.379*	0.121	0.463**	-0.332*	-0.234	-0.174
	P					0.771**	0.394*	0.336*	0.114	0.422**	-0.303	-0.213	-0.167
Number of clusters per plant	G						0.714**	0.177	0.088	0.472**	-0.391*	-0.081	-0.083
	P						0.682**	0.133	0.077	0.418**	-0.362*	-0.062	-0.081
Number of pods per plant	G							0.045	-0.144	0.100	-0.372*	-0.142	-0.161
	P							0.039	-0.138	0.095	-0.351*	-0.122	-0.157
Number of seeds per pod	G								-0.052	0.130	0.163	-0.091	-0.271
	P								-0.030	0.097	0.143	-0.073	-0.186
100-seed weight (g)	G									0.375*	0.062	0.152	0.273
	P									0.369*	0.043	0.132	0.270
Seed yield per plant (g)	G										0.031	-0.022	-0.094
	P										0.022	-0.013	-0.091
Disease incidence (%) Anthracnose	G											-0.023	-0.234
	P											-0.021	-0.198
Disease incidence (%) Powdery Mildew	G												-0.352*
	P												-0.323*

P and G are phenotypic and genotypic correlation coefficients, respectively
Significant at 5% level - * Significant at 1% level - **

Table.4 The eigen values, per cent variability, cumulative per cent variability for four principal components in mungbean [*Vigna radiata* (L.) Wilczek]

Character	**PC 1**	**PC 2**	**PC 3**	**PC 4**
Eigen value	3.39	2.67	1.49	1.25
% of variance explained	28.41	22.38	12.4	10.4
Cumulative variance explained	0.28	0.50	0.63	0.74

Table.5 Character loading of four principal components for twelve characters of thirty eight genotypes of mungbean [*Vigna radiata* (L.) Wilczek]

Character	PC 1	PC 2	PC 3	PC 4
Days to first flowering	0.48	0.01	-0.01	0.29
Days to 50% maturity	0.37	-0.21	-0.12	-0.19
Days to pod initiation	0.49	-0.02	0.01	0.28
Plant height(cm)	0.49	-0.15	0.06	0.06
Number of primary branches per plant	0.11	0.53	0.01	0.01
Number of clusters per plant	0.19	0.49	0.05	-0.34
Number of pods per plant	0.23	0.32	-0.22	-0.39
Number of seeds per pod	0.02	0.25	-0.21	0.51
100 seed –weight (g)	0.004	0.11	0.66	0.26
Seed yield per plant (g)	-0.02	0.36	0.42	-0.07
Disease incidence (%) Anthracnose	-0.12	0.11	-0.09	0.23
Disease incidence (%) Powdery Mildew	-0.09	0.14	-0.07	0.18
Total protein content (%)	0.07	-0.21	0.49	-0.13

Table.6 Clustering pattern of thirty eight genotypes of mungbean based on Tocher's method of classification

Cluster	No.of genotypes	Name of genotypes
1	31	SKNM 1504, Pusa M 1771, Pusa M 1772, RMG 1097, COGG 13-39, MH 1323, SML 1808,IPM 512-1,VGG 16-055, NVL 855, MDGVV-18, OBGG-56, AKM 12-28, TMV 126, NMK 15-08, SVM-6133, KM 2355, PM 14-3, AKM 12-24, IPM 410-9, DGG 7, IGKM 2016-1, SKNM 1502, RMB 12-07,JAUM 0936,OBGG 58, MGG-387, KM 17-130, IPM 2-3, PRMB-17-70 , Pant M4
2	3	BM 2012-9, PM 14-11, ML 2479
3	1	VGG-16-036
4	1	PRMB-15-40
5	1	SRMB-15-60
6	1	SRMB-15-20

Table.7 Mean intra (bold) and inter-cluster distances among the clusters in mungbean [*Vigna radiata* (L.) Wilczek]

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**11.42**	17.14	17.49	16.79	19.11	23.03
Cluster II		**13.11**	20.82	25.67	19.42	26.87
Cluster III			**0**	16.05	19.61	18.71
Cluster IV				**0**	18.74	19.11
Cluster V					**0**	15.83
Cluster VI						**0**

Table.8 Cluster means for twelve different characters in thirty eight genotypes of mungbean [*Vigna radiata* (L.)Wilczek]

	Days to first flowering	Days to 50% maturity	Days to pod initiation	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Seed yield per plant (g)	Total protein content (%)
Cluster I	35.29	60.78	43.94	52.15	1.99	6.38	14.29	11.15	2.90	5.51	20.82
Cluster II	41.78	64.78	50.89	65.77	2.02	6.44	13.93	10.73	3.68	5.29	26.47
Cluster III	47.00	62.00	53.00	70.62	2.97	7.73	19.40	9.47	2.92	6.51	18.20
Cluster IV	31.33	48.67	40.00	49.14	3.08	6.31	11.55	12.00	3.12	7.81	16.69
Cluster V	41.00	57.33	48.00	34.33	4.53	7.80	12.87	14.07	3.12	6.94	24.07
Cluster VI	38.67	58.00	47.67	50.93	5.53	14.77	25.60	13.47	3.35	8.41	18.46

Table.9 Diverse mungbean promising genotypes for twelve different characters in Tocher's and Principal component analysis method

	Character		**Cluster (Tocher's)**	**Cluster (PCA)**	**Suitable Genotypes**
1	Days to first flowering	Early	I	I	SKNM 1504
		Late	III	IV	VGG-16-036
2	Days to 50% maturity	Early	I	I	AKM 12-24
		Late	I	I	IPM 2-3
3	Days to pod initiation	Early	I	I	SKNM 1504
		Late	I	I	JAUM 0936
4	Plant height(cm)	Dwarf	V	IV	SRMB-15-60
		Tall	I	I	MGG-387
5	Number of primary branches per plant	More	V	IV	SRMB-15-20
		Less			RMG-1097
6	Number of clusters per plant	More	VI	III	SRMB-15-20
		Less			VGG 16-055 IGKM 2016-1
7	Number of pods per plant	More	I	I	MH 1323
		Less			SVM-6133
8	Number of seeds per pod	More	V	IV	SRMB-15-60
		Less			PM 14-11
9	100 seed –weight (g)	Bold	II	V	BM 2012-9
		Small			IGKM 2016-1
10	Seed yield per plant (g)	High	VI	III	SRMB-15-20
		Low			COGG 13-39 KM 2355
11	Disease incidence (%) Anthracnose	High			IGKM 2016-1
		Low	V	IV	SRMB-15-60
	Disease incidence (%) Powdery Mildew	High			MDGVV-18
		Low	I	I	SML 1808
12	Total protein content (%)	High	II	V	PM 14-11
		Low			PRMB 15-40

Fig.1 Scree plot showing eigen value variation for twelve quantitative traits in mungbean

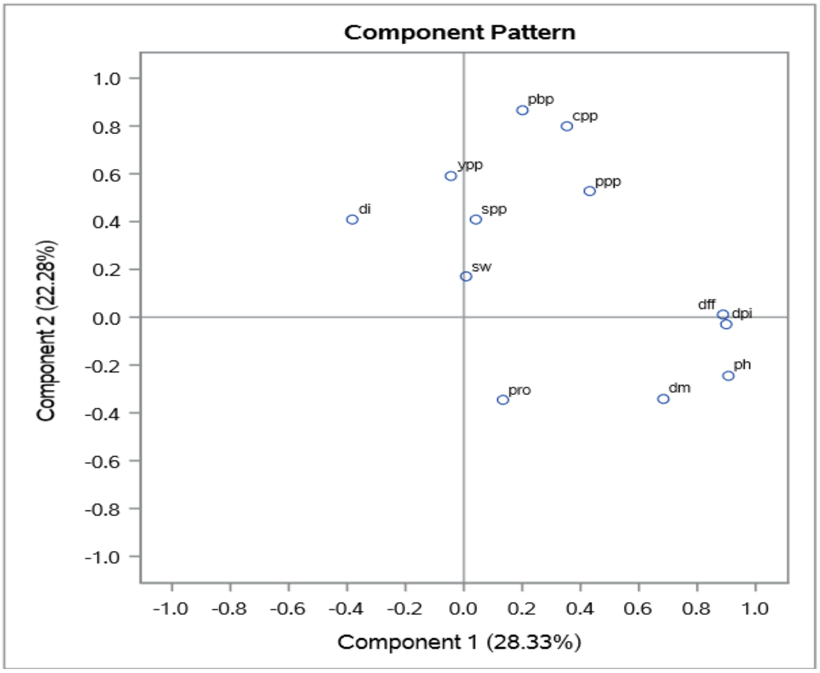

Fig.2 Distribution of greengram genotypes across two components

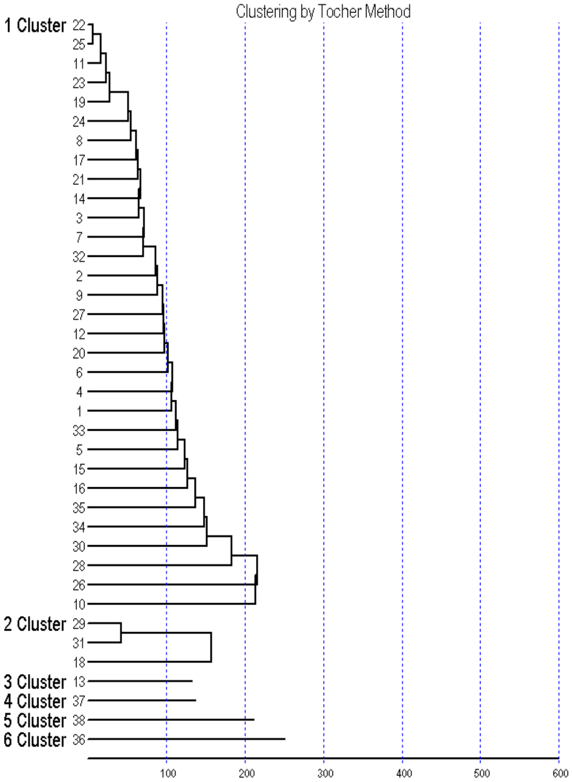

Fig.3 Diagram illustrating the clustering pattern of thirty eight genotypes of mungbean by Tocher's method of classification

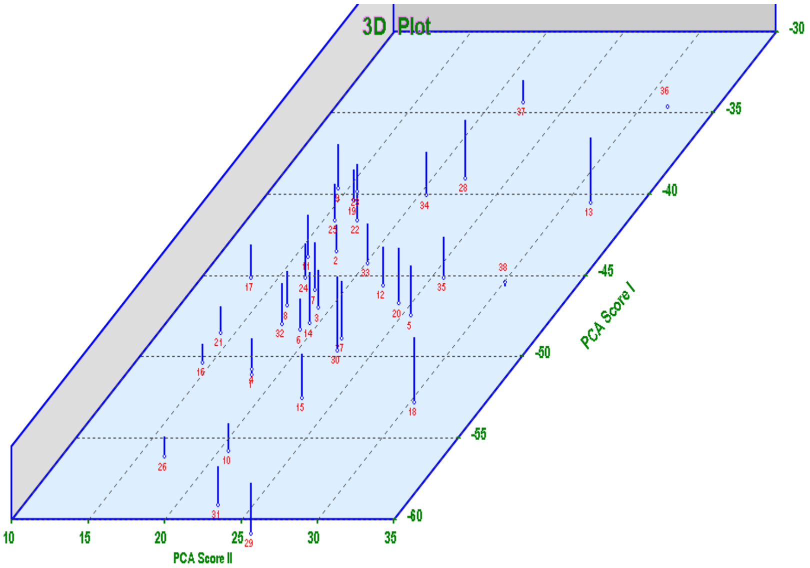

Fig.4 Three dimensional view showing relative position of genotypes of green gram [Vignaradiata (L.) Wilczek] based on PCA scores

The distribution pattern of the genotypes was depicted in a 3D plot which states how diverse the genotypes were (Fig 4). Mehandi *et al.*, (2015) studied twenty one greengram genotypes and reported that PC1 was positively contributed by less number of seeds per pod, major contribution of PC 2 through number of pods per plant, seeds per pod, number of clusters per plant.

Cluster analysis

To determine the genetic relationship between the genotypes and make them get utilized in our future breeding programmes we can opt for an analysis technique like Cluster analysis. This technique had grouped these 38 genotypes into 6 clusters among which cluster I was the largest with 31 genotypes followed by cluster II (with 3 genotypes) (Table 6 and Fig 3). It is noted that genotypes collected from different geographical origins were grouped in same cluster which indicates the absence of relationship between geographical diversity and genetic diversity. The mean value of the clusters for 12 different morphological traits also depicts the presence of variability (Table 8). Cluster VI comprising of only one genotype had showed its highest value towards number of primary branches(5.53), clusters (14.77), pods per plant (25.60) and seed yield per plant (8.41g) which depicts its representation towards more reproductive growth. Cluster V had represented its highest mean value towards the trait number of seeds per pod (14.07) whereas cluster II had showed its highest value towards the total protein content (26.47%) and 100 seed weight (3.68g).

Hence the genotype in this cluster can be used for developing of bold sized seeds there by the quality of the produce can be increased. Selecting the diverse genotypes basing on these component characters leads to better adaptation of the crop. Researchers like Singh *et al.*, (2014) , Katiyar *et al.*, (2009) and many others, gave emphasis on presence and need of high or very high genetic diversity to create the high genetic variation and genetic gain under selection. In the present study the only one genotype in cluster II, with more number of primary branches, clusters, pods and seed yield per plant can be considered as a potential donor in our future breeding programmes for improving the yield which was the ultimate motto of a plant breeder.

Comparing both Tocher's and principal component analysis and other descriptive statistical techniques, the diverse mungbean promising genotypes for twelve different characters were represented in the table 9. The genotypes 'SKNM 1504' had showed earliness in flowering and pod initiation, 'SRMB 15-60' had showed had showed dwarf stature with more number of seeds per pod and with low disease incidence , 'SRMB 15-20' had showed more number of primary branches per plant, cluster per plant and high seed yield.

Along with these the genotype 'BM 2012-9', had bold sized seeds. Hence we can consider these genotypes in our future breeding programmes and can be utilized in developing of new a new variety or hybrid through which ultimate motive of the plant breeders ie yield can be achieved.

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