Electronic Journal of Plant Breeding, 8(4): 1148-1158 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00167.3

Research Article

Genetic Divergence in Moth Bean (*Vigna aconitifolia* (Jacq) Marechal)

S.N.Kohakade, V.V. Bhavsar and V. Y. Pawar

Department of Agricultural Botany, College of Agriculture Dhule-424 004 (MPKV), (M.S.), India.
E- mail: vypawar2gene@gmail.com

(Received: 26 July 2017; Revised: 6 Dec 2017; Accepted: 28 Dec 2017)

Abstract

An experiment was undertaken by utilizing forty four moth bean genotypes for eleven yield and yield contributing characters to assess genetic divergence. The analysis of variance has shown that there was significant variation among the genotypes in all the traits. The multivariate analysis carried out using Mahalanobis D^{2-}statistics, indicated wider genetic diversity in the genotypes of moth bean. Out of seven cluster formed, cluster I was largest with eighteen genotypes, followed by cluster IV with twelve genotypes, cluster III with seven genotypes, cluster II with four and V, VI, VII were mono-genotypic. The clustering pattern indicated absence of relationship between genetic diversity and geographical origin of the genotypes. The maximum inter cluster distance was observed between cluster IV and V (D^2=29.12) while, lowest divergence was noticed between cluster V and VI (D^2=4.46). Maximum intra cluster distance observed within cluster IV (D^2=5.12) while lowest intra cluster distance was observed within cluster I (D^2=3.85). The variance for cluster means were high for days to 50% flowering (32.56%), 100- seed weight (13.95%), length of main axis (13.21%) and number of seeds per pod (10.57%) and was low for number of primary branches and pod length. Based on inter-cluster distances, cluster mean and *per se* performance, and divergence class the genotypes *viz.,* DHMB-32, DHMB-26, DHMB-31, DHMB-30 and DHMB-16 were distinct and diverse and can be classified as promising genotypes. These four genotypes can be used for inter-crossing to obtain heterosis and also wider variability in moth bean. Hybridization between the genotypes of cluster IV with the genotypes of cluster V may result in exploiting more heterosis with maximum genetic divergence and are likely to produce desirable transgressive segregants in segregating generations for further crop improvement.

Key words
Genetic diversity, D^2 value, cluster, genotype.

Introduction

Pulses occupy a unique position in Indian agriculture because of their nutritive value and ability to improve the fertility of soil. In India, the total area under pulses was 25.26 million ha with production of 19.25 million ton 2015-2016. Out of total pulses area in India, under Maharashtra is 34.08 lakh ha and the production is 24.04 lakh tons and area under moth bean was 0.278 lakh ha and the production is 0.096 lakh ton Tiwari and Shivhare (2016). Moth bean {*Vigna aconitifolia* (Jacq) Marechal} belongs to family Leguminosae /Fabaceae sub family papilionaceae. Chromosomal constitution of a species is 2n= 22. Popularly, it is also known as ‘Mat’, ‘Matki’ and ‘Moth bean’ in different regions. It is an important crop of dry and semi-arid areas of India and some countries of Asia. Among kharif pulses, it has maximum capacity to resist drought condition. It is an excellent source of high quality protein (23.6%) in the diet of low income group in developing countries.

Genetic diversity which is pre-requisite for any successful breeding programme is of paramount importance. Genetic divergence among the parents play a vital role in cultivar improvement because a cross involving genetically diverse parents is likely to generate more variability in segregating generations, and also which can be used for the desired improvement. Generally, plant breeders select the parents on the basis of phenotypic diversity. Hence the knowledge of genetic diversity among the parents with respect to characters which are to be improved is essential. Keeping these things in the view, an effort has been made in the present study to evaluate a set of moth bean genotypes with the objective to study the nature and magnitude of divergence among the genotypes of moth bean.

Materials and methods

The experimental material comprising forty four genotypes of moth bean were grown in Randomized Block Design with three replications at the research farm of Department of Genetics and plant breeding, College of Agriculture, Dhule, during *Kharif* season of 2016. The seeds were sown by dibbling. Each entry was represented by single row of 3m length with spacing of 10 cm between rows. Data were recorded on five randomly and competitive plants of each genotype from each replication for eleven quantitative characters *viz*., days to 50% flowering, days to maturity, length of main axis (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). Effective method suggested by Mahalanobis (1936) known as "Mahalanobis D^2 statistics" or "D^2 technique" is widely used to know genetic diversity in the germplasm. It was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters and a logical grouping of genotypes following Tocher's method (Rao, 1952).

Results and discussion

Analysis of variance for eleven characters indicated that the genotypes used in the present studies were significantly different (Table 1). The mean performances of 44 genotypes of moth bean for eleven characters studied are presented in Table 2. The genotype DHMB-16 (43.67 days) was the earliest for flowering (46 days) and days to maturity (90.33days). The genotypes DHMB-31 (20.64g) recorded the highest seed yield per plant, maximum number of cluster per plant (56.73), maximum pods per cluster (2.53) and maximum number of pods per plant (143.53). While the genotype DHMB-24 produced maximum pods per cluster (2.59) and highest seed yield per plant (20.15g).

On the basis of D^2 values, the forty four genotypes evaluated for eleven characters were grouped into seven clusters by using the Tocher's method as described by Rao (1952). Cluster I was largest with 18 genotypes followed by cluster IV (12 genotypes), cluster III (7 genotypes) and cluster II (4 genotypes), while clusters V, VI and VII were monogenotypic. In the present investigation grouping of genotypes into 7 clusters suggested the presence of substantial amount of genetic diversity in the material under investigation. The clustering pattern and the eco-geographical regions of origin of each line are given in Table 1 and 3. Cluster I was the largest including 18 lines indicates that there was no association between clustering pattern and eco-geographical distribution of the cultures. Murty and Arunachalam (1966) and Somayajulu *et al.* (1970) while working with different crops, reported that geographical distribution does not necessary reflect genetic divergence. Cluster II which include 4 lines, cluster III include 7 lines and cluster IV include 12 lines under study had varieties from different eco-geographical regions, thus supporting the view that geographic distribution and genetic divergence do not follow the same trend. This confirms the results reported by Bhavsar and Birari (1991) and Deokar *et al.* (1991) in moth bean. Wide range of diversity was reported by many workers while evaluating moth bean genotypes (Henry and Krishna (1986); Natrajan *et al.* (1988); Jindal (1990) ;Deokar *et al.* (1991); Kakani *et al.* (2003); Patil *et al.* (2008); Bangar *et al.* (2009); Das *et al.* (2010); Babbar *et al.* (2012); Yogeesh *et al.* (2012).

The maximum intra cluster distance was observed for cluster IV (D^2 =5.12) followed by cluster III (D^2=4.90) suggesting that genotypes present in these clusters might have different genetical architecture (Fig.1, Fig.2 and Table 4). However, lowest intra cluster distance was observed in cluster I (D^2=3.85) indicating that genotypes present in these cluster might have genetical similarities with one another and appeared to have evolved from common gene pool. Cluster V, VI and VII showed no intra cluster distance due to its monogenotypic nature.

Maximum inter cluster distance was observed between cluster IV and cluster V (D^2=29.12) followed by distance between cluster II and cluster IV (D^2=28.95), cluster IV and cluster VI (D^2=27.80), cluster III and cluster IV (D^2=26.43) ; cluster IV and VII (D^2=24.67) indicating, wide divergence among these clusters and suggest that genotype present in one cluster differ entirely from those present in other clusters. The minimum inter cluster distance was found between cluster V and cluster VI (D^2=4.46) followed by cluster I and cluster III (D^2=5.72), cluster II and cluster V (D^2=5.96), cluster III and cluster V (D^2=5.99); cluster I and cluster VII (D^2=6.04). The low inter cluster distance between these clusters revealed that genetic constitution of genotypes had close proximity.

Based on mean performance of clusters for 11 characters (Table 5) it was observed that cluster II exhibited the highest seed yield per plant and was characterized by highest number of primary branches, number of pods per cluster and number of pods per plant. All these characters appeared to have played important role in determining seed yield of these cluster. Cluster VI and cluster VII showed nearly comparable seed yield. Cluster VI was characterized by length of main axis, number of pods per cluster and number of pods per plant whereas, cluster VII possessed more number of primary branches, number of cluster per plant, pod length, number of seeds per pod and 100 seed weight. Cluster IV was low seed yield but has highest pod length and imparting earliest. On the basis of mean performance of different clusters, it was observed that cluster II, V, VI and VII were performing well for most of the characteristics.

The variance of cluster mean provides information on relative importance of different characters towards seed yield. Relative percent contribution of different characters towards total genetic divergence is given in table 6. In the present study the variance for cluster means were high for days to 50% flowering (32.56%), 100 seed weight (13.95%), length of main axis (13.21%) and number of seeds per pod (10.57%). These results were agreement with Natarajan *et al.* (1988) for days to 50% flowering and Henry and Krishna (1986) for days to maturity, and Gopalkrishna, *et* *al.* (2012) for number of seeds per pod and 100 seed weight in mung bean (*Vigna radiate* L.).

The magnitude of contribution by number of primary branches and pod length was low. These results were contradictory with the findings of Henry and Krishna (1986) for seed yield per plant.

The mean of seven clusters and four intra-clusters (as monogenotypic cluster V, VI and VII had no intra-cluster distance) was 11.69 and standard deviation 8.95. The minimum (X) and maximum (Y) values among these distances were 3.85 and 29.12, respectively.

Grouping of cluster pairs into the divergence class (DC) is presented in Fig 3. On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC2 and DC3. While crossing among the genotypes of a cluster, the per se performance of the genotypes for different traits such as earliness (days to 50% flowering and days to maturity), length of main axis, number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, yield per plant etc. should be taken into account so, that desirable transgressivie segregants would be obtained following after hybridization.

The present study revealed no parallelism between genetic divergence and geographical distribution of genotypes which was demonstrated by grouping of genotypes from same origin into different clusters separated by high genetic distance. This suggested, that genetic drift and selection in different environments may cause geographical distances.

Considering inter-cluster distances, cluster mean and *per se* performance, and divergence class the genotypes *viz.*, DHMB-32, DHMB-26, DHMB-31, DHMB-30 and DHMB-16 were distinct and diverse and can be classified as promising genotypes. These genotypes can be used for inter-crossing to obtain heterosis and also wider variability in moth bean. Hybridization between the genotypes of cluster IV with the genotypes of cluster V may result in exploiting more heterosis with maximum genetic divergence and are likely to produce desirable transgressive segregants in segregating generations for further crop improvement.

.

References

Babbar, A., V. Prakash, P. Tiwari and M. A. Iquebal. 2012. Genetic variability for chickpea under late sown season. *Legume Res.,* 35 (1):1-7.

Bangar, N. D., Amita Lakra and B. H. Chavan, 2009. Genetic Divergence in moth bean. J. Maharashtra agric. Univ., 34(1): 010-013.

Bhavsar, V. V. and S. P. Birari. 1991. Genetic Divergence in moth bean, [*Vigna aconitifolia* (Jacq) marechal.] Biovigyanam, 17 (2): 118-120.

Das, A. M., K. Biswas and K. G. Dastidar. 2010. Genetic divergenece in green gram (*Vigna radiata*). Scialert.net/abstract/doi : Ja.2010 .pp.126-130

Deokar, A. T., S. P. Birari and V. V. Bhavsar. 1991 Genetic Diversity in respect of grain yield and its components in moth bean *Vigna aconitifolia.* (Jacq) Marechal] Annals Agril. Res., 12(1):83-87.

Gopalkrishna, J., B. Sunilkumar, and M. Prakash. 2012 Studies on genetic diversity in mung bean (*Vigna radiate* L.). Legume Res., 35 (1) : 50-52.

Henry, A. and S. R. Krishna. 1986. Genetic divergence in moth bean. Indian J. Agric. Sci. 56 (4): 298-299.

Jindal, S. K. 1990. Interspecific divergence in moth bean for grain yield and its components. Annals Arid Zone, 27 (3-4): 267-270.

Kakani, R. K., R. C. Sharma and D. K. Garg. 2003. Genetic Divergence, variability and character association in moth bean. Advances Arid Legumes Res., pp. 98-103.

Mahalanobis, P. C. 1936. On the generalized distance in statistics. Proc. Nat. Ins. Sci., India, 2 (1): 49-55.

Murty, B. R. and V. Arunachalam. 1966. The nature of divergence in relation to breeding system in some crop plants. Indian J. Genet.Pl. Breed., 26; 188-198

Natarajan, C., K. Thiyagarajan and R. Rathnaswamy. 1988. Association and genetic diversity studies in green gram. Madras Agric. J. 75 (7-8) :238-245.

Patil, S .C., H. E. Patil and V. M .Jambhale. 2008. Genetic divergence studies in moth bean (Vigna aconitifolia). J.Maharashtra agric. Univ., 33(2):161-164

Rao, C. R. 1952. Advanced statistical methods in Biometrical Research. John Willey and Sons Inc., New York.

Somayajulu, P. L., A. B. Joshi, and B. R. Murty. 1970. Genetic divergence in wheat. Indian J. Genet. Pl. Breed., 30; 47-48.

Tiwari, A. K. and A. K. Shivhare 2016. PULSES IN

India: retrospect and Prospects Director, . Govt. of India, Ministry of Agri. & Farmers Welfare (DAC&FW), Directorate of Pulses Development, Vindhyachal Bhavan, Bhopal, M.P.- 462004,(Website: http://dpd.dacnet.nic.in, email : dpd.mp@nic.in, Printed Year-Nov., 2016) : 112-113.

Yogeesh, L. N., K. P. Viswanatha and B. A. Ganagaprasad. 2012. Genetic variability studies in moth bean germplasm for seed yield and its attributing characters. Electronic Journal Plant Breeding,3(1):671-675

Table.1. Analysis of variance for different characters in moth bean.

SI. No.	Characters	Mean sum of square		
		Replication	Genotype	Error
1	Days to 50% flowering	1.96	1464.9**	2.82
2	Days to maturity	2.550	1273.26**	6.67
3	Length of main axis (cm)	9.490	9951.60**	35.49
4	Number of primary branches	0.12	7.67**	0.19
5	Number of cluster per plant	0.034	419.32**	11.29
6	Number of pods per cluster	0.037	0.52**	0.02
7	Number of pods per plant	1.330	3303.82**	45.99
8	Pod length (cm)	0.011	0.108**	0.032
9	Number of seeds per pod	0.062	2.988**	0.139
10	100 seed weight (g)	0.011	0.290**	0.010
11	Grain yield per plant (g)	0.016	65.177**	0.957

*, ** Indicates significance at 5% and 1% level, respectively.

Table 2. Mean performance of moth bean genotype.

SI. No.	Genotypes	Source	Days to 50% flowering	Days to maturity	Length of main axis (cm)	No. of primary branches	No of clusters /plant		No of pods/ plant	Pod length (cm)	No of seeds / pod	100 seed weight (g)	Seed yield /plant (g)
1	MBS-0835	Solapur	99.33	148.67	130.78	6.73	58.88	1.62	95.39	3.58	6.67	2.25	10.06
2	MBS-0845	Solapur	93.33	143.00	148.71	4.37	41.35	1.53	63.73	3.24	6.08	2.04	6.04
3	MBS-0803	Solapur	91.67	141.67	153.13	3.89	29.70	1.65	49.61	3.26	5.95	2.40	4.76
4	MBS-0847	Solapur	99.66	149.33	146.27	4.71	25.42	2.41	61.67	3.23	6.21	2.43	6.55
5	MBS-0828	Solapur	95.33	143.67	152.03	3.97	37.68	1.38	52.53	3.19	6.03	2.15	4.89

6	MBS-0855	Solapur	94.33	146.67	143.47	5.32	36.96	1.84	68.31	3.18	6.05	2.14	6.35
7	MBS-0853-2	Solapur	93.00	145.00	145.56	4.77	34.40	1.69	59.97	3.49	6.72	2.14	6.15
8	MBS-0853-1	Solapur	93.00	143.00	149.15	5.01	38.85	1.75	68.12	2.99	6.13	2.07	6.02
9	MBS-0814	Solapur	93.67	143.33	149.75	4.37	36.24	1.49	54.21	3.14	6.56	2.29	5.85
10	MBS-0605	Solapur	98.67	146.67	141.15	5.63	37.32	2.17	81.53	3.56	6.53	2.35	8.39
11	MBS-0851	Solapur	99.33	144.33	143.06	6.00	38.90	2.23	85.60	3.33	6.29	2.20	8.44
12	MBS-27(C)	Solapur	98.67	148.67	140.93	5.68	38.23	2.03	76.53	3.25	6.08	2.03	6.80
13	DHMB-1	Rahuri	50.67	104.67	16.15	2.99	15.71	1.32	20.75	3.64	4.67	1.58	1.88
14	DHMB-2	Kada	92.33	143.67	144.97	5.81	31.46	1.78	56.73	3.21	5.88	2.13	5.21
15	DHMB-3	Nandurbar	98.67	145.33	136.45	5.95	41.13	1.94	78.15	3.44	6.31	2.84	8.71
16	DHMB-4	Akole	95.33	148.67	150.27	4.32	31.03	1.57	47.12	3.43	6.59	2.21	4.79
17	DHMB-5	Man	104.67	154.00	137.29	8.10	57.52	1.88	108.17	3.83	6.90	2.56	12.98
18	DHMB-6	Sindakheda	50.33	102.67	14.47	2.5	17.65	1.21	21.36	3.38	3.19	2.44	1.83

Table 2 Continued…….

SI. No.	Genotypes	Source	Days to 50% flowering	Days to maturity	Length of main axis (cm)	No. of primary branches	No of clusters /plant	No. of pods / cluster	No of pods/ plant	Pod length (cm)	No of seeds / pod	100 seed weight (g)	Seed yield /plant (g)
	DHMB-7	Nandurbar	95.67	145.67	151.03	4.6	35.97	1.39	50.97	3.08	6.20	2.13	4.18
	DHMB-8	Sindakheda	46.00	103.67	16.18	3.39	18.68	1.43	26.72	3.51	3.70	1.55	2.12
	DHMB-9	Rohane,	97.33	147.33	145.12	5.57	39.72	1.95	77.59	3.00	5.84	2.35	7.05
	DHMB-10	Wambori,	47.33	105.33	14.67	2.87	20.37	1.25	24.47	3.36	3.31	2.03	1.94
	DHMB-11	Dhule	54.33	102.00	16.54	2.56	14.78	1.53	22.62	3.45	4.70	2.66	2.17
	DHMB-12	Baragaonnandur	97.67	148.00	138.66	5.07	33.78	2.25	76.56	3.11	6.19	2.14	7.32
	DHMB-13	Baragaonnandur	59.67	110.33	14.48	2.71	16.10	1.62	26.38	3.55	4.68	2.52	2.38
	DHMB-14	Dahiwade,	96.33	143.67	136.94	5.00	34.59	1.78	65.14	3.24	6.36	2.37	6.86
	DHMB-15	Shevgaon,	90.33	139.33	149.80	4.53	33.57	1.43	49.73	3.18	6.45	2.13	4.82
	DHMB-16	Shirur,	43.67	90.33	11.63	2.49	16.59	1.33	22.06	3.51	4.45	1.98	2.25
	DHMB-17	Karjat,	98.67	146.33	143.25	5.75	35.89	1.87	67.12	3.30	6.21	2.85	7.63
	DHMB-18	Shrigonda,	95.33	144.00	147.03	4.83	25.23	2.14	54.67	3.38	6.09	2.95	5.53
	DHMB-19	Pathardi	46.67	100.67	14.64	4.50	28.21	1.34	38.87	3.66	4.20	2.29	2.60
	DHMB-20	Akole,	97.33	141.67	146.05	5.12	34.00	2.10	67.87	3.38	6.09	2.08	6.63
	DHMB-21	Pathardi	47.33	103.33	15.09	2.31	24.61	1.23	30.28	3.39	4.24	2.58	6.45
	DHMB-22	Man	98.00	142.67	143.97	6.05	41.89	1.84	77.58	3.26	5.60	2.23	7.84
	DHMB-23	Baramati,	51.33	109.33	16.46	4.57	31.30	1.36	42.61	3.75	4.66	2.24	3.04
	DHMB-24	Karjat,	106.67	155.67	129.56	7.75	54.16	2.59	140.29	3.41	6.63	2.65	20.15
	DHMB-25	Parner,	100.67	152.33	137.69	6.37	49.15	2.15	98.31	3.58	6.46	2.34	10.77
	DHMB-26	Dhule	102.67	149.33	139.33	6.69	47.41	2.33	110.68	3.28	5.55	2.15	10.95
	DHMB-27	Dhule	51.67	103.33	15.16	3.68	23.94	1.36	32.57	3.51	4.31	2.27	3.13

Table 2 Continued…….

SI. No	Genotypes	Source	Days to 50% flowering	Days to maturity	Length of main axis (cm)	No. of primary branches	No of clusters /plant	No. of pods / cluster	No of pods/ plant	Pod length (cm)	No of seeds / pod	100 seed weight (g)	Seed yield /plant (g)
40	DHMB-28	Dhule	50.67	97.33	15.36	3.09	30.17	1.39	41.85	3.44	4.21	2.19	3.11
41	DHMB-29	Shrigonda,	106.33	153.67	135.37	7.85	45.16	2.39	108.27	3.48	6.37	2.79	13.82
42	DHMB-30	Shewgaon,	104.67	158.67	122.67	6.50	56.11	2.62	145.23	3.21	6.19	2.76	18.08
43	DHMB-31	Karjat,	105.67	156.33	124.26	8.78	56.73	2.53	143.53	3.51	6.61	2.71	20.64
44	DHMB-32	Ambegaon	103.33	150.66	143.21	6.67	47.75	2.42	113.24	3.25	5.38	2.84	12.51
	G. Mean		**84.93**	**135.09**	**107.44**	**5.01**	**35.08**	**1.79**	**66.05**	**3.37**	**5.67**	**2.32**	**6.94**
	S.E. ±		**0.97**	**1.49**	**3.43**	**0.53**	**1.94**	**0.086**	**3.91**	**0.10**	**0.22**	**0.058**	**0.565**
	C.D. at 5 %		**2.72**	**4.19**	**9.67**	**0.57**	**5.46**	**0.24**	**11.01**	**0.29**	**0.61**	**0.16**	**1.59**
	C.V. (%)		**1.98**	**1.91**	**5.55**	**7.01**	**9.27**	**8.28**	**10.27**	**5.29**	**6.59**	**4.34**	**14.08**

Table 3. Grouping of forty four moth bean genotypes into different clusters.

SI. No.	Cluster	No. of genotypes	Name of genotypes
1	I	18	MBS-0828, DHMB-7, MBS- 0845, MBS-0814, DHMB-15, MBS-0853-2, MBS-0853-1, DHMB-4, MBS-0855, DHMB-2, MBS-0803, DHMB-14, DHMB-9, MBS-27(C), DHMB-12, DHMB-22, DHMB-2O, MBS-0605
2	II	4	DHMB-24, DHMB-31, DHMB-30, DHMB-29
3	III	7	DHMB-3, DHMB-17, DHMB-18, MBS-0847, MBS-0851, DHMB-25, DHMB-5
4	IV	12	DHMB-19, DHMB-23, DHMB-27, DHMB-21, DHMB-10, DHMB-6, DHMB-28, DHMB-16, DHMB-1, DHMB-8, DHMB-11, DHMB-13
5	V	1	DHMB-32
6	VI	1	DHMB-26
7	VII	1	MBS-0835

Table 4. Average intra and inter cluster distance (D^2 values) for eleven characters in moth bean.

Clusters	I	II	III	IV	V	VI	VII
I	3.85	10.52	5.72	24.31	8.80	7.41	6.04
II		4.17	8.29	28.95	5.96	7.37	10.44
III			4.90	26.43	5.99	6.27	7.39
IV				5.12	29.12	27.80	24.67
V					0.00	4.46	9.78
VI						0.00	8.43
VII							0.00

(Underlined figures indicate intra-cluster D^2 values.)

Table 5. Cluster means for eleven characters in seven clusters of forty four moth bean genotypes

SI. No.	Characters	Cluster average							Cluster mean
		I	II	III	IV	V	VI	VII	
1	Days to 50% Flowering	95.11	103.83	99.57	49.97	103.33	102.67	99.33	93.41
2	Days to maturity	144.57	156.08	147.95	102.75	150.67	149.33	148.67	142.86
3	Length of main axis(cm)	146.15	127.89	141.58	15.07	143.21	139.33	130.78	120.57
4	No. of primary branches	4.95	7.72	5.96	3.14	6.67	6.69	6.73	5.98
5	No. of clusters / plant	35.93	53.04	39.03	21.51	47.75	47.41	58.88	43.6
6	No. of pods / cluster	1.76	2.53	2.09	1.36	2.42	2.33	1.62	2.02
7	No. of pods /plant	63.56	134.33	79.10	29.29	113.24	110.68	95.39	89.37
8	Pod length (cm)	3.23	3.40	3.44	3.51	3.25	3.28	3.58	3.38
9	No. of seeds /pod	6.18	6.45	6.35	4.19	5.38	5.55	6.67	5.82
10	100 seed weight (g)	2.19	2.73	2.60	2.19	2.84	2.15	2.25	2.42
11	Seed yield / plant (g)	6.11	18.17	8.66	2.41	12.51	10.95	10.06	9.84

Table 6. Relative percent contribution of different characters towards tota genetic divergence in moth bean.

SI. No.	Characters	No. of times ranked 1^{St}	Percent contribution
1	Days to 50% flowering	308	32.56
2	Days to maturit	33	3.49
3	Length of main axis (cm)	125	13.21
4	Number of primary branches	1	0.11
5	Number of cluster per plant	60	6.34
6	Number of pods per cluster	51	5.39
7	Number of pods per plant	77	8.14
8	Pod length (cm)	10	1.06
9	No of seeds per pod	100	10.57
10	100 seed weight (g)	132	13.95
11	Grain yield per plant (g)	49	5.18

Fig 1. Clustering by Tocher method. (10, 20, 30, 40, 50 on X axis are genetic dissimilarity)

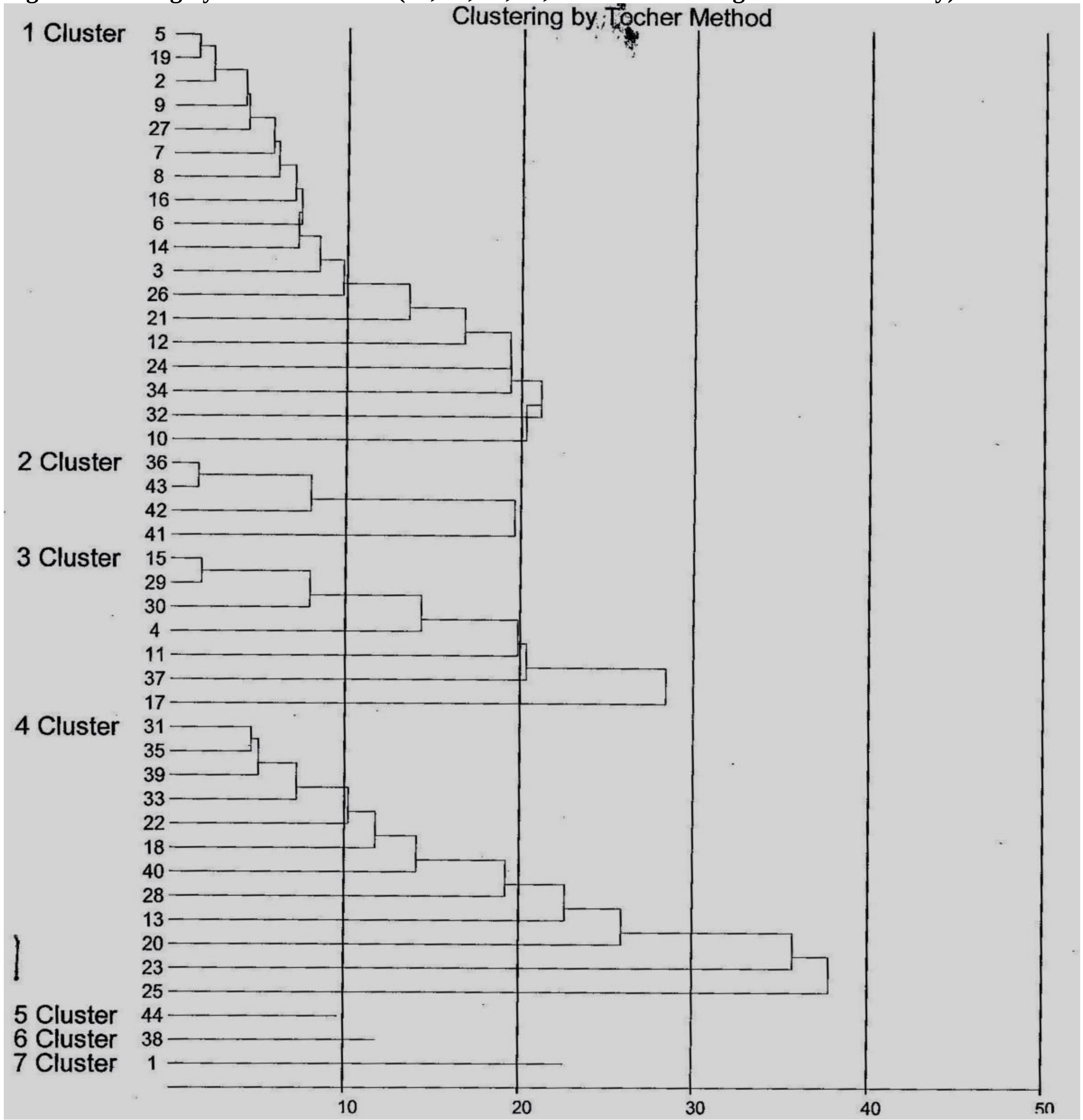

Fig 2. Cluster diagram of forty four germplasm in moth bean.

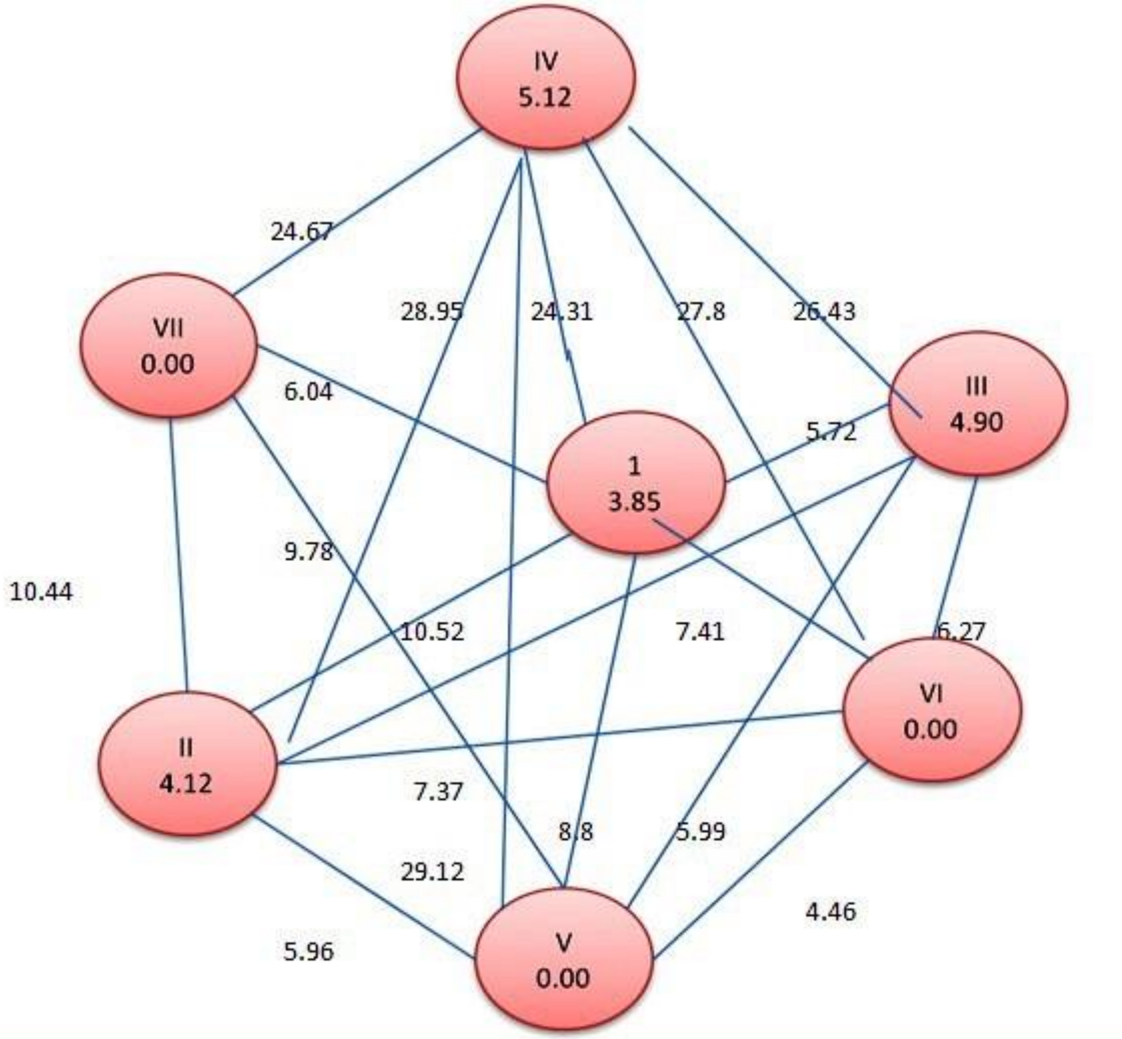

Fig 3. **Divergence Classes (DC) of moth bean genotypes.**

		DC 4	DC 3	DC 2		DC 1
↓		↓	↓		↓	↓
X		m-s	M		m+s	Y
(3.85)		(2.75)	(11.69)		(20.64)	(29.12)

M= The mean of seven clusters and four intra-clusters (as monogenotypic cluster V, VI and VII had no intra-cluster distance) was 11.69.

X= Minimum value of distance 3.85.

Y=Maximum valie of distance 29.12.

S=Standard deviation 8.95.

m-s= Mean - Standard deviation.

m+s= Mean + Standard deviation.