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Study of the genetic diversity in velvet bean (Mucuna pruriens L.) using D² analysis

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Abstract

The present experiment carried out during *Kharif* 2019-20 at the Herbal Instructional Garden of Research Cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh using 28 genotypes of velvet bean including cultivated and wild species with three check variety *viz*. Arka Dhanwantari, Arka Ashwini, Arka Daksha. In D² analysis, four clusters are formed. In the first cluster, nine genotypes appeared. Highest inter-cluster distance recorded among cluster-I and cluster-IV. Intercluster distance is higher than intra-cluster distance means high genetic diversity present among clusters. The crossing of genotypes from various clusters will, therefore, help to obtain better recombinants with higher genetic variability for the different traits taken under study.

Keywords: Velvet bean, D² statistics and cluster analysis

Introduction

Mucuna pruriens commonly known as velvet bean, devil bean, cowhage, kewanch, cowitch and atmagupta (Anonymous, 1985)^[1]. Mucuna pruriens (L.) is an important underutilized tribal pulse with diploid chromosome number (2n=22) which belonging to the family Fabaceae and subfamily Papilionaceae. Mucuna has annual and perennial approx 150 species. Genus Mucuna is underutilized wild legume crop. Velvet bean (Mucuna pruriens) found in the tropical and subtropical area of the world. Its good source of dietary proteins, it has high protein concentration around 25% to 35%. Digestibility of velvet bean protein is high as compared to rice, soybean, lima bean (Lampariello 2012)^[7]. Velvet bean is a self-pollinated crop (Capo-Chichi et. al., 2001)^[2]. Its is a climber type crop. They have a yellow and violet colour flower. Pods are two colour green (no pubescence) and browny orange (present pubescence). Browny orange pod have mucunain which cause itching. Velvet bean is an annual climber crop. The leaves have pubescence, three foliate leaves present, white or violet flower length is ranging from 2.5 to 3.7 cm long, it has s shape curved pod, green or brownorange colour pod found, pod length ranging from 10 to 20 cm long covered with pubescence, seed length ranging from 5 to 6 mm, seed colour is white or black in colour and number of seeds present in per pod is four to six. Its seeds are widely used in Ayurvedic system of medicine to the treatment of male fertility, nervous disorders and as an aphrodisiac. Mucuna seed is a constituent of more than 200 indigenous drug formulations. Velvet bean contains toxic compounds like L-dopa and hallucinogenic tryptamines and antinutritional factors such as phenols and tannins. The seeds are rich source of L-Dopa; L-Dopa is a non-protein amino acid extracted from the seed of mucuna and used in the treatment of Parkinson's disease (Lampariello et al., 2012)^[7]. L-Dopa extracted from seeds of mucuna is more effective than the synthetic drug to the treatment of Parkinson's disease. Unprocessed velvet bean contains a toxic chemical that's why exhibited tolerance level to insect pest (Duke, 1981)^[3]. Mucuna is a hardy crop it can tolerate adverse environmental conditions such as drought, low soil fertility and high soil acidity. Mucuna is effective in lowering the nematode population (Queneherve et al. 1998)^[9]. Velvet bean has a nematicidal allelopathic activity which is important for crop improvement. (Gliessman et al., 1981)^[5]. Velvet bean used for reclamation of degraded land, in India 187 mha waste land present which is approx 56.83% of total geographical area. The D² statistic is useful tool to assess the genetic divergence among population. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1928)^[8]. Analysis and utilization of available genetic diversity is a short-term strategy for developing improved cultivars for meeting immediate requirement of the farmers and the end users.

Materials and Methods

The present investigation "Study the genetic diversity in velvet (Mucuna pruriens L.) using D² analysis" was carried out during Kharif 2019-20 at the Herbal Instructional Garden of Research Cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh. The material under study constituted 28 genotypes of velvet bean including cultivated and wild species which are collected from various regions of Chhattisgarh with three check variety viz. Arka Dhanwantari, Arka Ashwini, Arka Daksha. All the 28 genotypes with three check varieties were planted in Randomized Block Design (RBD) with three replication during the Kharif 2019. Each entry was planted in 2 rows of 4 meter length having plant to plant spacing within rows at 1 meter distance, 1.5 meter between rows, and 2 meter between replication. Doses of N:P:K was 20:60:60 Kg per hectare was provided to acquire the normal growth of the crop. The experimental materials was subjected to, quantitative traits. The quantitative traits such as days to 50% flowering, inflorescence length, number of flowers per bunch, days to maturity, internode length, number of pods per bunch, pod length, pod width, weight of dry pod, number of seed per pod, seed length, seed width, 100 seed weight, seed yield per plant were recorded.

The D2 statistic was originally developed by P.C. Mahalanobis in 1928^[8], Rao (1952)^[10] suggested the application of this technique for the assessment of genetic divergence between the populations. It measures the forces of differentiation at intra and inter-cluster levels and determines the relative contribution of each component trait to the total divergence. The genotypes were grouped into a number of clusters as per the standard procedure.

Result and Discussion

The existence of genetic divergence among thirty-one velvet bean genotype was examined using Mahalanobis D2 statistics. The clustering pattern of 31 velvet bean genotype on the basis of D2 analysis is presented in table 1 the genotype were grouped into 4 distinct non overlapping clusters. The highest number of genotype 9 appeared in cluster- I, followed by 8 genotype in cluster- IV, 7 cluster in each cluster- II and cluster- III.

The genotypes constituting, cluster- I are MP-3, MP-10, MP-20, MP-24, MP-26, MP-30, MP-32, MP-34, Arka Dhanwantari (check-3), cluster- II constituting MP-5, MP-6, MP-7, MP-14, MP-18, MP-19, MP-31, cluster- III constituting MP-1, MP-9, MP-12, MP-13, MP-15, MP-33, Arka Daksha (check-2) and cluster- IV constituting MP-2, MP-4, MP-8, MP-11, MP-17, MP-23, MP-29, Arka Ashwini (check-1).

The average intra and inter-cluster distance are presented in table number 2 Cluster- IV showed the highest intra-cluster distance, followed by cluster-III, cluster-I, and cluster-II. The highest inter-cluster distance in velvet bean 31 genotype found between cluster-I and cluster- IV, which is followed by cluster- III and cluster- IV, cluster- I and cluster- II, cluster- I and cluster- II, cluster- I and cluster- IV, cluster- II and cluster- II.

Mean cluster value for seed yield and its component in velvet bean genotype given in table number 3 cluster-I showed high cluster mean for days to maturity and days to 50% flowering. Cluster-II showed high cluster mean values for days to maturity and day to 50% flowering. Cluster –III showed high cluster mean for days to maturity and seed yield per plant. Cluster-IV showed a high mean value for days to maturity and seed yield per plant. The highest cluster mean for days to 50 percent flowering was observed for cluster-I (123.25 days) and lowest mean recorded in cluster-IV (106.85).

Similar results found Verma *et al.*, $(2014)^{[11]}$ for the number of pod per bunch show maximum percentage contribution in genetic diversity of french bean (Phaseolus vulgaris L.), Gangadhara *et al.*, $(2014)^{[4]}$ for days to 50% flowering contributed the maximum to the total genetic diversity among the genotypes than a hundred seed weight, pod weight, and pod length and Kumar *et al.*, $(2014)^{[6]}$ for Hundred seed weight contributed 33.83% towards total divergence followed by pod weight.

S.no.	Genotypes	Location	S.no.	Genotypes	Location
1	MP 1	Bilaspurilaspur	17	MP 18	Balrampur
2	MP 2	Bilaspur	18	MP 19	Raipur
3	MP 3	Bilaspur	19	MP 20	Raipur
4	MP 4	Bilaspur	20	MP 23	Ambikapur
5	MP 5	Bilaspur	21	MP 24	Baloda Bazar
6	MP 6	Bilaspur	22	MP 26	Baloda Bazar
7	MP 7	Bilaspur	23	MP 29	Raipur r
8	MP 8	Bilaspur	24	MP 30	Baloda Bazar
9	MP 9	Dhamtari	25	MP 31	Baloda Bazar
10	MP 10	Dhamtari	26	MP 32	Raipur
11	MP 11	Dhamtari	27	MP 33	Rajnandgaon
12	MP 12	Dhamtarimtari	28	MP 34	Bilaspur
13	MP 13	Dhamtari	29	Arka Dhanwantari (check-1)	IIHR Bangalore
14	MP 14	Balrampur	30	Arka Ashwini (check-2)	IIHR Bangalore
15	MP 15	Balrampur	31	Arka Daksha (check-3)	IIHR Bangalore
16	MP 17	Balrampur			

Table 1: Details of the genotypes used under study

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S.No. Genotypes 50% per bunch length (cm) length (cm) 1. MP 1 82.0 5.0 7.2 23.9 2. MP 2 91.0 15.3 14.0 23.6 3. MP 3 104.0 13.3 18.1 20.5 4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.7 7 MP 7 127.3 13.7 12.7 17.7	per bunch 5.3 5.7 6.0 6.0 5.3 4.7 4.7 4.7	length (cm) 12.0 11.4 11.1 10.6 8.5 8.7 9.7 10.2	width (cm) 1.9 2.0 2.0 1.8 1.9 1.6 1.8	per pod 5.3 5.7 5.7 5.7 5.7 5.7 5.0 5.0	length (cm) 2.3 2.0 2.0 2.0 1.8 1.6	width (cm) 1.6 1.5 1.6 1.4 1.4	weight (g) 148.4 108.0 110.3 115.8 103.8	maturity 202.0 206.7 206.0 229.3	pod (g) 11.6 10.9 13.9 10.4	per plant 95.2 152.9 76.2
Inoversity bunch (cm) 1. MP 1 82.0 5.0 7.2 23.9 2. MP 2 91.0 15.3 14.0 23.6 3. MP 3 104.0 13.3 18.1 20.5 4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.7 7 MP 7 127.3 13.7 12.7 17.7	bunch 5.3 5.7 6.0 6.0 5.3 4.7 4.7 4.7	(cm) 12.0 11.4 11.1 10.6 8.5 8.7 9.7 10.2	1.9 2.0 2.0 1.8 1.9 1.6 1.8	pod 5.3 5.7 5.7 5.7 5.7 5.0 5.0	2.3 2.0 2.0 1.8 1.6	(\mathbf{chi}) 1.6 1.5 1.6 1.4 1.4 1.4	(g) 148.4 108.0 110.3 115.8 103.8	202.0 206.7 206.0 229.3	(g) 11.6 10.9 13.9 10.4	plant 95.2 152.9 76.2
1. MP 1 82.0 5.0 7.2 23.9 2. MP 2 91.0 15.3 14.0 23.6 3. MP 3 104.0 13.3 18.1 20.5 4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	5.3 5.7 6.0 6.0 5.3 5.3 4.7 4.7 4.7	12.0 11.4 11.1 10.6 8.5 8.7 9.7 10.2	1.9 2.0 2.0 1.8 1.9 1.6 1.8	5.3 5.7 5.7 5.0 5.0 5.0	$ \begin{array}{r} 2.3 \\ 2.0 \\ 2.0 \\ 1.8 \\ 1.6 \\ \end{array} $	1.6 1.5 1.6 1.4 1.4	148.4 108.0 110.3 115.8 103.8	202.0 206.7 206.0 229.3	11.6 10.9 13.9 10.4	95.2 152.9 76.2
2. MP 2 91.0 15.3 14.0 23.6 3. MP 3 104.0 13.3 18.1 20.5 4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	5.7 6.0 5.0 5.3 4.7 4.7 4.7	11.4 11.1 10.6 8.5 8.7 9.7 10.2	2.0 2.0 1.8 1.9 1.6 1.8	5.7 5.7 5.0 5.0	2.0 2.0 2.0 1.8 1.6	1.5 1.6 1.4 1.4	108.0 110.3 115.8 103.8	206.7 206.0 229.3	10.9 13.9 10.4	152.9 76.2
3. MP 3 104.0 13.3 18.1 20.5 4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	6.0 6.0 5.0 5.3 4.7 4.7 4.7	11.1 10.6 8.5 8.7 9.7 10.2	2.0 1.8 1.9 1.6 1.8	5.7 5.7 5.0 5.0	2.0 2.0 1.8 1.6	1.6 1.4 1.4	110.3 115.8 103.8	206.0 229.3	13.9 10.4	76.2
4. MP 4 110.7 8.3 7.5 19.4 5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	6.0 5.0 5.3 4.7 4.7 4.7	10.6 8.5 8.7 9.7 10.2	1.8 1.9 1.6 1.8	5.7 5.0 5.0	2.0 1.8 1.6	1.4 1.4	115.8	229.3	10.4	101 0
5. MP 5 145.0 6.0 10.4 14.8 6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	5.0 5.3 4.7 4.7 4.7	8.5 8.7 9.7 10.2	1.9 1.6 1.8	5.0 5.0	1.8 1.6	1.4	103.8			181.9
6. MP 6 142.3 9.0 9.7 18.6 7 MP 7 127.3 13.7 12.7 17.7	5.3 4.7 4.7 4.7	8.7 9.7 10.2	1.6 1.8	5.0	1.6	1.0	105.0	251.0	8.4	81.9
7 MP7 1273 137 127 177	4.7 4.7 4.7	9.7 10.2	1.8	50		1.3	104.1	234.3	10.5	113.8
7. IVII / 127.5 15.7 12.7 17.7	4.7	10.2		5.0	1.7	1.3	101.5	230.0	9.2	106.6
8. MP 8 107.0 5.7 9.5 19.0	4.7		1.7	5.3	1.8	1.3	117.0	227.7	11.7	147.2
9. MP 9 96.0 12.7 7.6 18.9		10.6	1.9	5.0	1.9	1.3	128.2	225.3	12.0	83.9
10. MP 10 109.7 10.0 11.9 21.9	5.7	11.7	1.9	6.0	1.9	1.5	116.0	220.0	14.0	73.8
11. MP 11 131.3 12.0 10.5 17.5	5.0	9.8	1.8	5.0	1.7	1.3	119.0	230.0	10.7	228.9
12. MP 12 82.0 7.7 4.9 18.5	3.7	12.1	2.0	5.3	2.2	1.5	157.7	225.0	13.8	53.2
13. MP 13 82.0 5.3 6.1 19.4	4.3	11.1	2.1	5.0	2.3	1.6	176.2	209.7	14.8	88.5
14. MP 14 157.0 8.7 16.5 21.1	4.7	8.8	1.6	5.0	1.7	1.3	129.4	230.3	10.3	116.9
15. MP 15 113.3 13.7 11.6 18.6	4.7	12.3	2.1	6.0	2.0	1.5	137.2	220.7	13.9	114.6
16. MP 17 106.7 6.0 6.5 18.4	4.3	10.5	1.9	5.0	1.9	1.4	111.5	227.7	8.6	175.3
17. MP 18 171.0 14.0 13.8 15.8	5.0	8.7	1.3	5.0	1.6	1.3	103.7	246.7	11.5	121.5
18. MP 19 160.7 12.7 10.1 15.7	5.0	7.8	1.4	5.3	1.5	1.1	81.9	240.3	7.9	115.9
19. MP 20 123.7 16.0 16.2 18.4	4.7	10.5	1.8	5.3	1.7	1.3	119.4	231.7	13.7	70.5
20. MP 23 119.0 7.7 12.9 15.9	4.3	9.8	1.8	5.0	1.7	1.2	108.8	234.0	9.9	205.3
21. MP 24 123.3 11.3 13.6 15.7	3.0	5.0	1.7	5.0	1.0	0.8	38.2	234.0	6.3	25.3
22. MP 26 102.3 6.3 14.3 18.2	4.0	5.3	1.6	5.0	1.1	0.9	47.1	234.0	6.4	42.2
23. MP 29 97.0 5.0 7.1 17.2	2.7	10.1	1.8	5.0	2.0	1.4	112.0	226.7	11.9	163.0
24. MP 30 130.0 5.7 7.3 16.4	4.3	5.5	1.8	5.0	1.6	0.8	52.6	234.0	6.0	29.0
25. MP 31 150.0 8.3 7.9 19.3	4.3	9.3	1.7	5.0	1.6	1.3	104.3	234.0	10.2	146.2
26. MP 32 101.3 7.0 13.2 15.4	5.3	9.1	1.7	5.0	1.8	1.3	97.1	232.7	10.7	82.5
27. MP 33 110.3 5.3 8.5 17.6	4.3	11.0	2.0	5.0	1.9	1.5	117.3	225.7	12.3	103.9
28. MP 34 91.7 13.3 13.2 21.8	5.0	10.5	1.7	5.0	1.9	1.4	120.1	219.7	11.0	52.4

Table 2: Mean performance of	genotype for seed	yield per plant and	its component in Velvet bean
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	Genotypes	Days to 50% flowering	No. of flowers per bunch	Inflorescence length (cm)	Inter- node length (cm)	No. of pods per bunch	Pod length (cm)	Pod width (cm)	No. of seeds per pod	Seed length (cm)	Seed width (cm)	100 seed weight (g)	Days to maturity	Weight of dry pod (g)	Seed yield per plant
29	Arka Dhanwantari (check-1)	135.3	9.7	15.3	18.1	5.3	9.0	2.0	5.0	1.9	1.4	93.2	220.3	9.2	47.3
30	Arka Ashwini (check-2)	82.7	5.3	5.8	21.8	5.0	13.2	2.0	5.7	2.0	1.5	161.3	225.0	12.3	216.3
31	Arka Daksha (check-3)	106.7	11.3	10.5	18.9	7.3	11.9	2.0	5.7	2.0	1.6	113.5	225.7	11.9	95.2

Table 3: Clustering pattern of velvet bean genotype based on D² statistics

Cluster no.	No. of genotypes	Name of genotypes
Ι	9	MP-3, MP-10, MP-20, MP-24, MP-26, MP-30, MP-32, MP-34, Arka Dhanwantari (check-3)
II	7	MP-5, MP-6, MP-7, MP-14, MP-18, MP-19, MP-31,
III	7	MP-1, MP-9, MP-12, MP-13, MP-15, MP-33, Arka Daksha (check-2)
IV	8	MP-2, MP-4, MP-8, MP-11, MP-17, MP-23, MP-29, Arka Ashwini (check-1)

Table 4: Average intra (diagonal and bold) and inter-cluster distance Values in velvet bean genotype

Cluster no.	Ι	Ш	III	IV
Ι	1,958.4	10,628.0	9,676.4	28,108.8
II	10,628.0	1,681.0	6,293.3	9,272.4
III	9,676.4	6,293.3	2,374.5	12,877.4
IV	28,108.8	9,272.4	12,877.4	3,110.6

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(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)
Cluster no.	Days to 50% flowering	No. of flowers per bunch	Inflorescence length (cm)	Inter- node length (cm)	No. of pods per bunch	Pod length (cm)	Pod width (cm)	No. of seeds per pod	Seed length (cm)	Seed width (cm)	100 seed weight (gram)	Days to maturity	Weight of dry pod (gram)	seed yield per plant (gram)
Ι	123.3	9.0	10.2	18.2	4.5	9.3	1.8	5.0	1.8	1.3	112.0	228.1	10.5	86.2
II	118.8	9.3	11.9	19.5	5.1	9.5	1.7	5.4	1.7	1.3	105.6	228.2	10.4	114.3
III	114.6	11.1	11.9	18.3	5.0	10.8	1.9	5.4	1.9	1.4	116.3	224.8	12.2	119.9
IV	106.9	7.9	8.8	18.5	4.6	9.9	1.8	5.1	1.9	1.3	111.9	228.4	10.2	120.6

Table 5: Mean cluster value for seed yield and it's component in velvet bean genotype



Fig 1: Statistical distance (D2 analysis among) among 31 genotype of velvet bean

Conclusion

Maximum and minimum seed yield per plant observed in MP-11 (228.9 g) and MP-24 (25.33 g) respectively. Based on the in D2 analysis 31 genotype of velvet bean were grouped into 4 distinct non overlapping clusters. The highest number of genotype 9 appeared in cluster- I, followed by 8 genotype in cluster- IV, 7 genotype in each cluster- II and cluster- III. D2 analysis inter-cluster distance was higher than the intra-cluster distance in all cases means wider diversity present among the genotype of a distinct group.

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