



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2021; 10(2): 1443-1445

Received: 10-01-2021

Accepted: 12-02-2021

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Study of genetic variability in velvet bean (*Mucuna pruriens* L.)

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Abstract

A field experiment was conducted at herbal instructional garden of Research Cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh during Kharif 2019-20 to evaluate thirty-one genotypes of velvet bean for genetic variability for 14 characters. The analysis of variance was found to be highly significant for all the 14 characters in velvet bean (*Mucuna pruriens* L.) indicating that enough variability is present in the studied material. Among the desirable characters days to 50 per cent flowering, number of flowers per bunch, inflorescence length, seed index, weight of dry pod, seed yield per plant showed high GCV and PCV. Almost all the characters showed a little variation between PCV and GCV revealing little influence of the environment in the expression of these traits. High heritability accompanied with high genetic advance as per cent of mean was recorded for days to 50 per cent flowering, number of flowers per bunch, inflorescence length, pod length, seed length, seed width, seed index, weight of dry pod, seed yield per plant.

Keywords: velvet bean, GCV, PCV, heritability, seed yield per plant, velvet bean, *Mucuna pruriens*

Introduction

Mucuna pruriens commonly known as velvet bean or itching bean (kawach). *Mucuna pruriens* belong to Fabaceae family 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) [14]. Velvet bean is a self-pollinated crop (Capo-Chichi *et al.* 2001) [6]. It is a climber type crop. They have a yellow and violet colour flower. Pods are two colour green (no pubescence) and brown orange (present pubescence). Brown orange pod have mucunain which cause itching. The centre of origin of velvet bean is not fixed, but it's likely native to tropical Asia (Wulijarni-Soetjijto and Maligalig 1997; Acevedo Rodriguez, 2005) [23, 1] and some scientist possibly said Africa (ILDIS, 2014; USDA-ARS, 2014) [11, 20]. The main differences among cultivated and wild species are present or absent of pubescence. Generally cultivated species does not have pubescence on the pod but wild species generally have pubescence. Hair like structure present on pod called which has mucunain protein that causes 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 brown-orange 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. According to Ayurveda root of velvet bean are bitter, anthelmintic, purgative, aphrodisiac, emollient, thermo genic, diuretic, stimulant, it's considered for to cure constipation, febrifuge and tonic amenorrhoea, elephantiasis, dropsy, neuropathy, consumption, strangury, dysmenorrhoea, ulcers, helminthiasis and fever. (Lindley, 1985). Its leaves use as fodder and pod use for human consumption. (Duke, 1981) [8]. Velvet bean contains toxic compounds like L-dopa and hallucinogenic tryptamines and antinutritional factors such as phenols and tannins. (Awang *et al.*, 1997) [4]. Velvet bean contains a high concentration of L-dopa (4-7%) that's why it is a commercial source of L-dopa, L-dopa is used for the treatment of Parkinson's disease (Lampariello *et al.*, 2012) [14].

Therefore, there is a scope to improve the seed yield of velvet bean by the selection method. Thorough understanding of genetic parameters and the association of plant characters among themselves and with yield is essential for the successful crop improvement programme.

Material and Method

The experiment was conducted during Kharif 2019-20 at herbal instructional garden of Research Cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, with 28 genotypes (collected from various region of Chhattisgarh) with 3 check variety viz. Arka Ashwini, Arka Daksha, Arka Dhanwantri sowed in Randomized Block Design with 3 replication. Observations on 13 different yield contributing characters viz. Days to 50% flowering, Number of flowers per bunch, Inflorescence length, Internode length, Number of pods per bunch, Pod length, Pod width, Number of seeds per pod, Seed length, Seed width, 100 seed weight, Days to maturity, Weight of dry pod, Seed yield per plant were recorded with five randomly selected plants from each genotype of all 3 replication. Analysis of Variance was carried out as per the method suggested by Panse and Sukhatme (1985). Genotypic coefficient of variation and phenotypic coefficient of variation was computed as per Burton (1952) [5], heritability (broad sense) and genetic advance as per cent of mean as per Allard (1960) [3].

Result and Discussion

Analysis of variance for all characters indicated that the mean sum of squares due to genotypes were highly significant for all the characters indicating the presence of a sufficient amount of variability in all genotypes (Table 1). The estimates of genetic parameters (Table 2) revealed that there were close correspondences between GCV and PCV for all the characters. Thus, the results indicated that most of the characters were largely under genetic control. The GCV and PCV estimates were relatively high for days to 50 per cent flowering, number of flowers per bunch, inflorescence length, seed index, weight of dry pod, seed yield per plant. The moderate GCV and PCV values recorded for internode length, number of pods per bunch, pod length, seed length, seed width. The low GCV and PCV value recorded for pod width,

number of seeds per pod, days to maturity. These findings were in accordance with the report of Vadivel *et al.* (2000) [21], Siddhartha *et al.* (2003) [19], Prakash *et al.* (2014) [16], Prakash *et al.* (2015) [17], Shivaprasad *et al.* (2018) [18], Jhanavi *et al.* (2018) [12] and Chinapolaiah *et al.* (2019) [7].

High heritability coupled with genetic advance as per cent of mean has been noticed for days to 50 per cent flowering, number of flowers per bunch, inflorescence length, pod length, seed length, seed width, seed index, weight of dry pod and seed yield per plant indicating lesser influence of environment and prevalence of additive gene action in their expression. Thus selection for improvement of those characters would be more effective. The highest heritability in a broad sense was recorded for seed yield per plant (82.31%), followed by 100 seed weight (92.39%), pod length (84.09%), inflorescence length (83.00%), number of flower per bunch (86.84%), days to % flowering (79.81%), seed length (78.26%), seed width (74.36%), the weight of dry pod (74.12%) (Table 2). The results were in accordance with Siddhartha *et al.* (2003) [19], Lakshmipathaiiah *et al.* (2008) [13], Ahmed (2011) [2], Verma *et al.* (2014) [22], Prakash *et al.* (2014) [16], Prakash *et al.* (2015) [17], Fatema, R. (2015) [9], Shivaprasad *et al.* (2018) [18], Jhanavi *et al.* (2018) [12], Fatema *et al.* (2019) [10] and Chinapolaiah *et al.* (2019) [7]. Moderate heritability coupled with moderate to low genetic advance as per cent of mean recorded by internode length and number of pods per bunch indicated the presence of non-additive gene action and influence of environment on the expression of these characters and thus the selection would be less effective (Table 2). Similar findings were reported by Siddhartha *et al.* (2003) [19], Lakshmipathaiiah *et al.* (2008) [13], Ahmed (2011) [2], Verma *et al.* (2014) [22], Prakash *et al.* (2014) [16], Prakash *et al.* (2015) [17], Fatema, R. (2015) [9], Shivaprasad *et al.* (2018) [18], Jhanavi *et al.* (2018) [12], Fatema *et al.* (2019) [10] and Chinapolaiah *et al.* (2019) [7].

Table 1: Analysis of variance for seed yield and its components in velvet bean (during 2019-20 at IGKV Raipur C.G.)

S.N.	Source of variance	Degree of freedom	Days to 50% flowering	Number of flowers per bunch	Inflorescence length (cm)	Inter-node length (cm)	Number of pods per bunch	Pod length (cm)	Pod width (cm)
1	Replication	2	133.4	2.1	3.6	10.8	0.3	0.7	0.01
2	Genotype	30	1791.21**	36.68**	37.42**	16.21**	2.33**	11.79**	0.11**
3	Error	60	144.31	1.76	2.39	3.63	0.42	0.70	0.04
S.N.	Source of variance	Degree of freedom	Number 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 (g)
1	Replication	2	0.23	0.03	0.01	97.19	61.00	4.01	31.24
2	Genotype	30	0.32**	0.26**	0.12**	2647.14**	351.00**	16.11**	8752.16**
3	Error	60	0.10	0.02	0.01	70.72	100.20	1.68	585.06

** Significant at 1% level, * significant at 5% level.

Table 2: Estimates of genetic parameters for 14 characters in velvet bean

S. No.	Characters	Range		Mean	Coefficient of variation (%)		h ² (bs) (%)	GA	GA as % of mean
		Minimum	maximum		Phenotypic	Genotypic			
1.	Days to 50% flowering	82.0	171.0	115.9	22.7	20.2	79.2	43.0	37.1
2.	Number of flowers per bunch	5.0	16.0	9.4	39.0	36.3	86.8	6.6	69.7
3.	Inflorescence length (cm)	4.9	18.1	10.8	34.8	31.7	83.0	6.4	59.5
4.	Internode length (cm)	14.8	23.9	18.7	15.0	11.0	53.6	3.1	16.6
5.	Number of pods per bunch	2.7	7.3	4.8	21.4	16.6	60.0	1.3	26.4
6.	Pod length (cm)	5.0	13.2	9.9	21.3	19.5	84.1	3.6	36.8
7.	Pod width (cm)	1.3	2.1	1.8	13.8	8.8	40.3	0.2	11.4
8.	Number of seeds per pod	5.0	6.0	5.2	8.0	5.1	41.0	0.4	6.8
9.	Seed length (cm)	1.0	2.3	1.8	17.4	15.4	78.3	0.5	28.1
10.	Seed width (cm)	0.8	1.6	1.3	16.6	14.3	74.4	0.3	25.4
11.	100 seed weight (g)	38.2	176.2	111.4	27.4	26.3	92.4	58.0	52.1
12.	Days to maturity	202.0	251.0	227.1	6.0	4.0	45.5	12.7	5.6

13.	Weight of dry pod (g)	6.0	14.8	10.8	23.5	20.2	74.1	3.9	35.9
14.	Seed yield per plant (g)	25.3	228.9	109.9	52.3	47.5	82.3	97.5	88.7

Conclusion

In the studied genotypes of velvet bean sufficient amount of variability was seen for all characters. High GCV and PCV estimates, high heritability coupled with high genetic advance as per cent of mean was noticed for days to 50 per cent flowering, a number of flowers per bunch, inflorescence length, seed index, weight of dry pod and seed yield per plant. Thus selection for improvement of those characters would be more effective. Moderate heritability coupled with moderate to low genetic advance as per cent of mean recorded by internode length and number of pods per bunch indicated the presence of non-additive gene action and influence of environment on the expression of these characters and thus the selection would be less effective.

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