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Genetic Variability and Association Analyses of Growth and Yield Attributes in *Mucuna Pruriens* (L). Collections from India

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ABSTRACT

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Twenty three collections of *Mucuna pruriens* were evaluated for their genetic variability in ten morphological traits. Analysis of variance for all the 10 characters indicated statistically significant variation among the collections. Collection WBNMP-06 produced highest seed yield (2.47 t/ha) followed by UPMP-06 (2.22 t/ha) and WBNMP-03 (2.00 t/ha) which were statistically at par with each other. Heritability in the broad sense was maximum for 100 seed weight (99%) but its correlation at genotypic level was not significant. It was seen that seed yield (t/ha) had significant positive correlation with pods/cluster (0.67, 0.58) at both genotypic and phenotypic level. Pods/cluster also exhibited highest positive effect on seed yield (2.63) which can be a better trait for selection to enhance yield in *Mucuna pruriens*.

1. Introduction

Mucuna pruriens is an important self-pollinated tropical legume (Duke 1981) with chromosome number 2n=22 (Sastrapradja et al., 1974). It is commonly known as velvet bean or cowhage and belongs to the family papilionaceae. It was also reported to be cultivated extensively as a green manure (Burkill 1966; Duke 1981; Wilmot-Dear 1984). It is locally known as Samuhawai (Manipuri), Uiteme (Mizo), Mesener (Ao Naga) in North Eastern part of India. This legume is used in more than 200 indigenous drug formulations since ancient times in India (Sastry and Kavathekar, 1990) due to which it is considered an important medicinal legume. After the discovery of L-3,4dihydroxyphenyl alanine (L-DOPA), an anti-Parkinson's disease drug, in Mucuna seeds the demand of this legume increased many fold in India as well as in the international drug market (Farooqi, 1999).

Although, it has similar nutritional profile to other food legumes (Bressani et al., 2003), the plant suffers from poor edible attributes due to the presence of high levels of L-DOPA (1-5%). However, after removal of L-DOPA from the seeds it can be used as food since the seeds are rich in protein. Each plant part of Mucuna is reported to possess various medicinal properties. Apart from Parkinson's disease, it is reportedly used for the treatment of various disorders like menstruation disorders, edema, fever, constipation, ulcer, tuberculosis, urinary tract infection and neurological disorders (Katzenschlager et al., 2004). An important key to a reliable and sustainable food crop production is unmasking the genetic diversity of the crop. Genetic divergence is an important tool for an effective selection of parents for hybridization and breeding. To design a successful breeding program, it is important to assess heritability of traits since efficiency of any selection program mainly depends on the magnitude of genetic diversity and heritability of a trait under selection (Falconer and Mackay, 1996).

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effects into direct or indirect effects (Diz et al., 1994). The traits and their usefulness in selection.

2. Materials and Methods

2.1 Plant materials

The magnitude of genetic parameters like analysis of where the alphabets represent the area from where the variance and coefficient of variation estimation at genotypic accessions were collected. For those collections for which (GCV) and phenotypic (PCV) level, heritability and path accession numbers have been obtained from NBPGR, New coefficient analysis of the different traits deciding yield play Delhi are mentioned in the Table 1. The field experiment was key role in deciding the fate of any crop breeding programs. carried out at the research farm of ICAR Research Complex Path coefficient and correlation analysis are important since for NEH Region, Umiam, Meghalaya. The crop was planted it imparts valuable information about the association in Randomized Block Design (RBD) with three replications between two traits and also explains the partitioning of the in a plot size of 5m x 1m. Seeds were pre-soaked with after giving a slight cut on the seed coat to enhance germination. present study was carried out to evaluate the variability in Seeds were sown in the month of June 2013. Standard morphological and quantitative characteristics of *M. pruriens* agronomic practices were carried out for maintenance of the germplasm and study the extent of association among the crop. Ten quantitative agro-morphological traits such as days to flowering, number of clusters per plant, number of flowers per inflorescence, inflorescence length, pod length, pod width, pods per cluster, number of seeds per pod, 100 seed weight and seed yield (t/ha) were evaluated.

2.2 Data analysis

A total of 23 collections of *M. pruriens* were used in the Data analysis was carried out by using SPAR 2 and Microsoft present study which are maintained at the research farm of excel software. Analysis of variance (ANOVA) and ICAR Research complex for NEH Region, Umiam, comparison of means was performed on each trait to check Meghalaya. The collections were given alpha numeric codes whether significant variation among the treatments (accessions) exists.

Table 1. Details of the Mucuna pruriens germplasm evaluated in the present study

SN	C o llectors ID	Accession no*	Place of collection		
1.	ASMMP-18	IC589236	Assam		
2.	ASMMP-30	-	Assam		
3.	MGHMP-25	-	Meghalaya		
4.	MNPMP-02	IC589243	Manipur		
5.	MNPMP-05	-	Manipur		
6.	MNPMP-17	-	Manipur		
7.	MZRMP-04	-	Mizoram		
8.	NGLMP-10	-	Nagaland		
9.	NGLMP-25	IC589247	Nagaland		
10.	NGLMP-41	-	Nagaland		
11.	RJSMP-04	-	Rajasthan		
12.	RJSMP-07	IC589253	Rajasthan		
13.	RJSMP-16	-	Rajasthan		
14.	SKMMP-02	IC589257	Sikkim		
15.	SKMMP-10	IC589254	Sikkim		
16.	UKDMP-05	-	Uttarakhand		
17.	UPMP-02	IC589258	Uttar Pradesh		
18.	UPMP-04	-	Uttar Pradesh		
19.	UPMP-06	-	Uttar Pradesh		
20.	UPMP-13	-	Uttar Pradesh		
21.	WBNMP-03	IC589262	West Bengal		
22.	WBNMP-06	IC589264	West Bengal		
23.	WBNMP-07	IC589265	West Bengal		

* National Gene bank indigenous collection id. The collections without IC number are still under evaluation and characterization.

estimated by using the formula:

GCV (%)=($\sqrt{(\sigma_{a}^{2})}/\mu$)×100;

PCV (%)=($\sqrt{(\sigma^2)}/\mu$)×100

Where, $\sigma_{g}^{2}, \sigma_{p}^{2}$ are genotypic and phenotypic variances and μ is the grand mean.

Heritability in the broad sense (h2bs) was calculated as:

hbs^= $(\sigma_{\sigma}^2)/(\sigma_{p}^2)$

Where, σ_{α}^2 is genotypic variance and σ_{α}^2 is the phenotypic variance.

Genotypic and phenotypic correlation between pairs of traits was estimated by following the methodology given in Singh and Chaudhary (1985). To get better picture of association among the traits, the correlation coefficients were resolved into direct and indirect effects by path analysis.

3. Results and Discussion

3.1 Variation and heritability of growth and yield attributes

In the present study, wide range of variability was observed among all the 10 traits. Genotypic coefficient of variability was maximum in yield followed by clusters per plant (Table-2). Seed yield was the highest in WBNMP-06 (2.47 t/ha) followed by UPMP-06 (2.22 t/ha) and WBNMP-03 (2.00 yield difference among these three t/ha). The collections was not statistically significant at 5% l.s. Lowest yield was observed in UPMP-04 (0.26 t/ha). But UPMP-04 produced very bold seeds having highest 100 seed weight (68.00 g) against the average of 27.21 g for 100 seed weight based on all the collections. As the collections were from wider geographical distribution, significant variation was also observed in days to flowering which varied from 86 to

111 days with an average value of 97.7 (say 98) days. Less variation was observed in pod length, pod width and number of seeds per pod. We could notice much wider range in traits like inflorescence length (5.15 - 49.78 cm) and flowers per inflorescence (6.33 - 50.21), respectively. NGLMP-41 and NGLMP-10 revealed highest inflorescence length (49.78 cm) and flowers per inflorescence (50.21/inflorescence), respectively whereas maximum number of inflorescence or clusters of pod per plant was highest in WBNMP-06 (73.55). This higher number of clusters per plant coupled with higher Number of pods/plant and medium values of flowers/inflorescence and inflorescence length have contributed to result in highest seed yield per ha (2.47/ha) in WBNMP-06. High morphological diversity had also been reported earlier in M. pruriens including leaf, flower, fruit and seed characters (Shetty, 2018).

When F – test was found significant at 5% l.s., the analyses The high range of values of the different morphological traits were proceeded further to determine the critical difference is in close agreement with the earlier results in M. pruriens. (CD) between two means. Genotypic coefficient of variation For example, Shetty (2018) reported values for days to flower (GCV) and phenotypic coefficient of variation (PGV) were initiation ranging from 62 to 137 days, pod length ranging from 7.18 to 10.42 cm and pod width ranging from 1.67 to 2.02 cm. The present study showed a slightly lower GCV values than PCV in all the traits indicating the influence of environment in the expression of these traits. PCV and GCV values above 20% is regarded high, below 10% as low and between 10%-20% as moderate (Deshmukh et al., 1986). Accordingly, high GCV and PCV were observed in characters like clusters/plant, inflorescence length, flowers per inflorescence, pods/clusters, 100 seeds weight and yield. Similar results were reported in cluster bean by Revathi et al., (2017).

> Estimation of GCV, PCV along with heritability is important for a selection to be effective. It is a good index of transmission of characters from parents to their offspring. Heritability was classified as very high if it was greater than 80%, moderately high if it is between 60-79%, medium if thevalue is between 40-59% and low if the value is less than40%. Heritability among the traits studied varied from 36% to 99% as shown in Table 2. Heritability was highest in 100 seed weight (99 %) followed by inflorescence length (96%). This result is supported by similar results in dolichos beans (Borah and Shadeque, 1992; Verma et al., 2015) and in French beans (Mishra et al., 2008). Days to flowering showed moderately high heritability and this was in congruence with earlier reports by Manyasa et al. (2008) in pegion pea. Low heritability was recorded in seeds/pod which was similar to earlier reports by Turk et al. (2007) in grass pea.

3.2 Correlation among the traits and their resolution in to direct and indirect effects

In order to select plants with desirable characteristics, it is important to further analyze the extent of association between yield and its various components. Therefore correlation coefficients at genotypic and phenotypic level were evaluated and the values were tested for significance at 5% level (Table 3). In the present study, the magnitude of the genotypic correlation coefficients was higher than phenotypic correlation coefficients. From the analysis, it was observed that seed yield (t/ha) had significant positive correlation with clusters/plant and pods/cluster (r=0.67, 0.58 respectively) at both genotypic and phenotypic level. Days to flower initiation had significant and positive correlation with inflorescence length, flowers/inflorescence and pods/cluster at genotypic level. Flowers/inflorescence showed significant positive association with pods/cluster at genotypic and phenotypic level.

Genotypes	Days to	Clusters/	Inflorescence	Flowers	Pod Length	pod width	Seeds/Pod	Pod/cluster	100 seed	Yield (t/ha)
Evaluated	flowering	plant	length (cm)	/inflorescence	(mm)	(mm)			weight (g)	
ASMMP-18	107	6.67	33.07	28.9	77.66	14.25	5.23	6.17	22.67	0.31
ASMMP-30	101	26.22	31.57	38.59	70.93	12.41	4.57	7.53	22.71	0.67
MGHMP-25	105	27.22	24.54	31.01	81.36	16.46	5.57	12.53	20.64	1.03
MNP-02	96	46.44	27.79	24.84	72.05	11.46	5.37	9.73	19.64	1.50
MNPMP-05	93	51.66	17.3	18.4	68.32	10.94	4.80	7.27	16.63	0.86
MNPMP-17	96	28.22	22.4	28.56	74.09	11.79	5.23	8.47	22.82	0.75
MZRMP-04	108	36.22	34.69	33.98	69.27	10.24	5.23	11.53	20.71	1.78
NGLMP-10	106	37.78	47.97	50.21	76.57	11.46	5.70	9.60	18.61	1.26
NGLMP-25	106	47.67	45.91	34.28	75.75	12.57	5.00	11.67	20.75	2.42
NGLMP-41	96	17.89	49.78	33.83	68.56	10.88	4.90	8.53	21.24	0.42
RJSMP-04	95	11.33	25.36	31.76	76.70	13.75	4.90	6.30	17.43	0.32
RJSMP-07	90	15.33	29.01	24.21	80.98	13.65	5.13	5.73	26.33	0.33
RJSMP-16	97	41	5.15	6.33	80.53	11.76	4.97	4.17	36.34	0.54
SKMMP-02	89	40	22.28	22.36	54.15	12.09	4.70	12.00	26.70	0.94
SKMMP-10	100	14.56	25.44	28.21	68.09	11.22	4.77	5.53	18.95	0.31
UKDMP-05	88	25.67	9.33	7.74	72.56	13.43	4.63	10.4	25.45	0.80
UPMP-02	111	24.22	11.33	13.18	90.27	16.40	3.83	7.80	50.59	1.56
UPMP-04	86	1.78	7.61	8.99	88.82	15.20	4.80	3.27	68.00	0.26
UPMP-06	86	44.11	10.66	8.53	58.02	14.31	4.63	5.67	51.36	2.22
UPMP-13	89	23.78	12.29	7.63	73.96	13.40	4.93	4.07	23.09	0.32
WBNMP-03	101	44.11	43.43	40.71	71.99	11.96	5.10	12.07	23.83	2.00
WBNMP-06	100	73.55	39.91	36.95	72.96	13.15	4.60	11.20	26.91	2.47
WBNMP-07	102	67.11	30.52	37.37	70.06	12.89	4.57	10.67	24.59	1.97
Mean	97.74	32.72	26.41	25.94	73.64	12.86	4.92	8.34	27.22	1.09
CD(0.05)	7.85	17.47	4.18	7.06	12.63	2.7	0.69	3.60	2.2	0.48
SEd	3.88	8.65	2.07	3.49	6.25	1.34	0.34	1.78	1.09	0.24
PCV (%)	8.71	61.99	51.17	49.61	13.95	16.71	10.56	40.53	46.82	72.14
GCV (%)	7.22	52.65	50.26	46.78	9.3	10.83	6.34	30.97	46.56	67.08
Heritability (bs)	0.69	0.72	0.96	0.89	0.44	0.42	0.36	0.58	0.99	0.86

Table 2. Growth and yield attributes of Mucuna pruriens germplasm evaluated under uniform environment

Pods/cluster showed significant positive correlation with Conclusion vield at genotypic and phenotypic level. Significant negative correlation was observed between pods/cluster. Path coefficient analysis with respect to seed yield was worked out and is presented in Table 4. Pods/cluster exhibited the highest positive effect on seed yield (2.63) followed by 100 seed weight (1.52), pod length (0.87) and flowers/inflorescence (0.56). Therefore these components could be considered as major components for the improvement of seed yield. Pods per plant had been reported to show highest positive direct effect on pod vield (Tikka et al., 2003). Days to flowering had a very less direct effect on seed yield (0.24) but showed high positive indirect effect via pods/cluster. This suggests that selecting genotypes with higher days to flowering should not be recommended for increase in seed yield. In the present study, pods/cluster showed positive association with seed yield and showed direct positive contribution towards seed vield which can be useful for improvement in seed yield in Mucuna pruriens.

From the present study, it can be summarized that there existed wide range of variability in all the traits studied for the selected *M. pruriens* collections. There collections such as WBNMP-06, WBNMP-03 and UPMP-06 had higher productivity (>2 t/ha). But for more consistent results in ranking multi-year and multi-location evaluation is required. Pods/cluster was observed to be a better trait on which the selection should be based on for seed yield improvement and development of varieties with high seed yield.

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Table 3. Genotypic and phenotypic correlation among ten morphological traits in *M. pruriens*

		Clusters/	Inflorescence	Flowers	Pod	Pod	Seeds/	Pod/cluster	100	Yield
		plant	length (cm)	/inflorescence	Length	width	Pod		seed	(t/ha)
		-			(mm)	(mm)			weight	
					. ,				(g)	
Days to	G	0.20	0.55*	0.67*	0.37	0.03	0.19	0.48*	-0.33	0.4
flowering	Р	0.11	0.47*	0.51*	0.24	-0.02	0.03	0.39	-0.25	0.3
Clusters/	G		0.27	0.32	0.53*	-	-0.15	0.63*	-0.23	0.84*
plant						0.43*				
	Р		0.25	0.22	-0.28	-0.15	-0.03	0.52*	-0.19	0.77*
Inflorescence	G			0.93*	-0.18	-	0.5*	0.61*	-0.57*	0.34
length (cm)						0.51*				
	Р			0.86*	-0.13	-0.3	0.3	0.46*	-0.55*	0.32
Flowers	G				-0.16	-	0.51*	0.65*	-0.60*	0.31
/inflorescence						0.43*				
	Р				-0.07	-0.26	0.29	0.46*	-0.56*	0.27
Pod Length	G					0.67*	-0.19	-0.38	0.39	-0.29
(mm)	Р					0.41	0.19	-0.2	0.28	-0.17
pod width	G						-0.49*	-0.17	0.66*	-0.05
(mm)	Р						-0.12	-0.16	0.44*	-0.01
Seeds/Pod	G							0.26	-0.60*	-0.2
	Р							0.11	-0.34	-0.05
Pod/cluster	G								-0.49*	0.67*
	Р								-0.37	0.58*
100 seed	G									0.04
weight(g)	Р									0.04

*- significant at p = 0.05, P=Phenotypic correlation, G=Genotypic correlation

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