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Research Paper

# Study on Genetic Divergence in Yardlong Bean (*Vigna unguiculata* spp. *sesquipedalis*)

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## ABSTRACT

An experiment was carried out on genetic divergence for yield attributing characters in thirty-three genotypes of yardlong bean collected from different sources and the experimental field was laid out at farmer's field in Pudukurapettai village, Virudhachalam, Tamil Nadu, India. The Mahalanobis D<sup>2</sup> statistics was used to estimate the divergence among the thirty-three genotypes and results revealed that the genotypes were grouped into four clusters. The intra cluster distance was maximum (280.51) in cluster IV and the cluster II (48.39) showed minimum intra cluster distance. The maximum inter cluster distance was found between cluster II and IV (408.23) and minimum inter cluster distance was observed between cluster I and II (135.61). The three top contributors for genetic diversity were pod yield per plant (50.37%), pod length (29.16%) and number of pods per plant (7.57%).

Key words: Yardlong bean, D<sup>2</sup>, Cluster mean, Genetic contribution

Yard long bean belonging to family leguminaceae is cultivated mainly for its crisp and tender green pods which are consumed in both fresh as well as in cooked form. Yardlong bean is also known as Snake bean, Chinese long bean and Asparagus bean due to its long slender pods. All cultivated Vigna unguiculata are found within the universally accepted V. unguiculata subspecies unguiculata classification, which is then commonly divided into 4 cultivar groups: unguiculata, biflora, sesquipedalis, and textilis [1]. Yard long bean is considered to be originated in Central Africa and widely distributed in India, Indonesia, Phillippines and Sri-Lanka. The crop is mainly cultivated for its green pods that are used as a vegetable. It is a highly nutritive vegetable containing a good amount of digestible protein both in pods (23.5-26.3%) and in leaves, also contains, calcium, iron, riboflavin, phosphorus, potassium, vitamin A, vitamin C, folate, magnesium, and manganese [2-3]. Since it is a warm-season crop, it tolerates heat and dry conditions better than common field or lima beans [4]. Knowledge on genetic diversity or genetic similarity could help to get long term selection gain in plants. Evaluation of genetic diversity is important to know the source of genes for a particular character within the available germplasms. The objective of this study was to analyse the genetic divergence of yardlong bean for better crop improvement.

### **MATERIALS AND METHODS**

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The present investigation was carried at farmer's field in Pudukurapettai village, Virudhachalam, Tamil Nadu during the January 2019 to April 2019. 33 Yardlong bean genotypes were collected from different sources such as twenty-nine genotypes from NBPGR Thrissur, Kerala, two varieties from Kerala Agricultural University (Vyjayanthi and Lola). One from IIHR (Arka Mangala) and one from East West Seed International Pvt Ltd (Reenu) were evaluated in randomized block design with three replications with spacing of 1.50  $\times$ 0.45 m. The size of each experimental plot is 8.75 m. Observations were recorded on randomly selected five plants in each experimental plot. The observations were recorded on days to first flowering, vine length (cm), days to first picking, pod length (cm), pod width (cm), fresh pod weight (g), number of pods per plant, number of pickings and pod yield per plant (g). Mahalanobis D<sup>2</sup> statistics was used for estimating the genotypic divergence among the thirty-three genotypes. The  $D^2$  statistics between the populations as estimated from the sample on the basis of P character. Accordingly, error variance – covariance matrix was obtained. The correlated variables were transformed into uncorrelated variables by pivotal condensation method as given by [5]. For determining the group constellations, a relatively simple criterion as suggested by [5] was followed. After establishing the group constellations or clusters, the average inter and intra cluster divergence (distance) were worked out taking into consideration of all the component D<sup>2</sup> values possible among the members of the two clusters. The square root of D<sup>2</sup> values gives the distance (D) between the clusters. Ranking individual  $D^2$  values, contributed by each character was done as the highest contributor taking rank one and the lowest, rank nine. The character with the least rank total was taken to contribute the maximum genetic divergence and the one with the highest rank total, the least of genetic divergence.

#### **RESULTS AND DISCUSSION**

The thirty-three genotypes were grouped into four clusters by the application of clustering technique. The composition of different clusters and their origin are presented in (Table 1). The cluster I comprised of twenty-one genotypes of diverse origin; thus, the maximum numbers of genotypes were included in this cluster. It was followed by cluster II with two genotypes, cluster II with seven genotypes and cluster IV with three genotypes.

Table 1 Composition of D <sup>2</sup> clusters for yardlong bean genotypes						
Clusters	Number of genotypes	Name of genotypes				
Ι	21	IC- 622569, IC- 622579, IC-622590, IC -622597, IC- 622598, IC- 622599, IC- 622600, IC - 622601, IC- 622602, IC- 626137, IC- 626138, IC- 626139, IC- 626140, IC- 626142, IC - 626143, IC -626145, IC- 626146, IC -626147, IC- 626148, IC- 626149 and IC -626152				
II	2	IC 630380 & IC 630381				
III	7	IC- 626153, IC- 626154, IC- 630377, IC -630378, IC- 630379, IC -630383 and Lola				
IV	3	Arka Mangala, Reenu and Vyjayanthi				

The intra and inter cluster distance among four clusters where computed and furnished in (Table 2). The intra cluster distance ranged from 48.39 (cluster II) to 280.51 (cluster IV). The intra cluster distance was maximum (280.51) in cluster IV followed by cluster III (272.62). The cluster II (48.39) showed

minimum intra cluster distance. The maximum inter cluster distance was found between cluster II and IV (408.23) followed by clusters I and IV (394.27). The minimum inter cluster distance was observed between cluster I and II (135.61).

Table 2 Average intra (Bold) and inter-cluster D<sup>2</sup> and D values in yardlong bean

Clusters	Ι	II	III	IV
T	31027.77	18390.28	60509.02	155448.71
1	(176.14)	(135.61)	(245.98)	(394.27)
II		2342.38	59102.22	166651.81
11		(48.39)	(243.10)	(408.23)
III			74324.46	112020.23
111			(272.62)	(334.69)
IV				78687.57
1 V				(280.51)

The cluster mean values for nine characters were studied and furnished in (Table 3). Regarding days to first flowering, cluster IV recorded minimum number of days to first flowering (50.96 days) followed by cluster III (51.92 days) and maximum mean value for days to first flowering was recorded in cluster I (53.00 days). The maximum mean value for vine length was recorded in cluster II (325.50 cm) followed by cluster IV (318.08 cm) and minimum mean value

for days to first picking was recorded in cluster III (61.59 days) followed by cluster II (63.80 days) and maximum mean was recorded in cluster I (64.71 cm). Cluster IV (51.30 cm) recorded maximum cluster mean value for pod length followed by cluster III (32.10 cm) and minimum cluster mean value was (23.93 cm) cluster II. The maximum mean value for pod width was recorded cluster IV (3.02 cm) followed by cluster III (2.86 cm) and minimum cluster mean value (2.29 cm) was observed in cluster I.

Table 3 Cluster means for various ch	aracters of yardlong bean
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Cluster	DFF	VL	DFP	PL	PW	FPW	NPP	NP	PYP
Ι	53.00	285.08	64.71	25.36	2.29	10.41	36.52	11.60	381.51
II	52.38	325.50	63.80	23.93	2.76	7.58	36.26	11.90	273.54
III	51.92	299.76	64.21	32.10	2.86	15.00	37.47	11.97	574.63
IV	50.96	318.08	61.59	51.30	3.02	19.40	36.71	11.93	693.61
General mean	52.07	307.10	63.58	33.17	2.73	13.10	36.74	11.85	480.82

DFF: Days to first flowering, VL: Vine length (cm), DFP: Days to first picking, PL: Pod length (cm), PW: Pod width (cm), FPW: Fresh pod weight (g), NPP: Number of pod per plant, NP: Number of pickings & PYP: Pod yield per plant (g)

The maximum mean value for fresh pod weight was observed in cluster IV (19.40 g) followed by cluster III (15.00 g) and minimum cluster mean value (7.58 g) was recorded in cluster II. Number of pod per plant recorded maximum cluster mean value of (37.47) cluster III followed by cluster IV (36.71 g) and minimum cluster mean value of (36.26) was recorded in cluster II. Number of picking recorded maximum cluster mean value of 11.97 (cluster III) and minimum cluster mean value of (11.60) in cluster I. Pod yield per plant recorded maximum cluster mean value of 693.61 g (cluster IV) followed by cluster III (574.63 g) and minimum cluster mean value of (273.54 g) was observed in cluster II. These findings corroborates with the report of [6] in Cowpea; [7] in Cluster bean; [8] in French bean.

The contribution of the character towards the total genetic divergence is important in deciding the characters for selection. The relative contribution of each character towards the expression of genetic diversity estimated over character wise  $D^2$  value is presented in (Table 4). The three top contributors for genetic diversity are pod yield per plant (50.37%), pod length (29.16%) and number of pods per plant (7.57%).

Understanding the magnitude of genetic diversity for yield components is one of the important steps involved in any successful crop improvement programme. In the study,  $D^2$  analysis was used to assess the genetic divergence among the thirty-three genotypes to plan efficient breeding programme. Genetic drift and selection may also be important attributes,

which contribute towards genetic divergence among genotypes of a geographical distribution [9]. In this regard, genotypes belonging to more diverse groups irrespective of different region should be selected for an effective breeding programme. These observations are in accordance with the results of [10-11].

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Table 4 Contribution	of various	cnaracters	towards	poa yiela	per	plant in	yardlong bean

S. No.	Characters	Number of first rank	Contribution (%)
1.	Days to 1st flowering	1	0.18
2.	Vine length cm)	27	5.11
3.	Days to 1st picking	0	0.00
4.	Pod length (cm)	154	29.16
5.	Pod width (cm)	2	0.37
6.	Pod weight (g)	18	3.40
7.	Number of pods / plant	40	7.57
8.	Number of picking	20	3.78
9.	Pod yield / plant (g)	266	50.37
	Total	528	100



FIG 1 Yardlong Bean (Vigna unguiculata spp. sesquipedalis)

#### **CONCLUSIONS**

Based on the above results, Cluster II and IV showed high genetic divergence between them and crossing between the types of these two clusters may result in high heterosis for good characters. The cluster IV showed highest desirable mean value for days to first flowering, days to first picking, pod length, pod width, fresh pod weight, pod yield per plant, whereas the cluster III showed highest desirable mean value for number of pods per plant and cluster II recorded maximum mean value for vine length. Desirable types can be selected from the clusters based on the objective of the breeding programmes. Absence of relationship between the genetic diversity and geographical distance was thus brought to focus by the present study. Genetically diverse types having useful characters from the same region can be effectively used for the breeding programmes.

#### LITERATURE CITED

- 1. Perrino P, Laghetti G, Spagnoletti Zeuli PL, Monti LM. 1993. Diversification of cowpea in the Mediterranean and other centres of cultivation. *Genetic Resources and Crop Evolution* 40: 121-132.
- 2. Asian Vegetable Research Development Center. 2015. *How to Grow Yard Long Bean*. Retrieved from http://203.64.245.61/web\_crops/ indigenous /SI-yard\_ long\_ bean.pdf
- 3. Ano AO, Ubochi CI. 2008. Nutrient composition of climbing and prostrate vegetable cowpea accessions. *African Journal of Biotechnology* 7(20): 3795-3798.
- 4. Rubatzky VE, Yamaguchi M. 1997. World Vegetables: Principles, Production and Nutritive Values. Second Edition, XXIV. pp 844.
- 5. Rao CR. 1952. Advanced Statistical Methods in Biometric Research. John Wiley and Sons Inc. pp 390.
- 6. Gupta RK, Parmila, Arya M, Kumar A, Kumari P. 2019. Study on genetic variability in cowpea [*Vigna unguiculata* (L.) Walp]. *Curr. Jr. Appl. Sci. Technology* 33(2): 1-8.
- Kumar V, Ram RB, Yadav RK. 2014. Genetic diversity in cluster bean [Cyamopsis tetragonoloba (L) Taub.] for morphological characters. Indian Jr. of Sci. Technology 7(8): 1144-1148.
- 8. Vidyakar V, Lal GM, Singh MK, Kumar A. 2017. Study on genetic diversity in French bean (*Phaseolus vulgaris* L.). Jr. *Pharmacogn. Phytochemistry* SP1: 184-187.
- 9. Murthy BR, Arunachalam V. 1966. The nature of divergence in relation to breeding system in crop plants. *Indian Journal of Genetics* 26: 188-198.
- Rambabu E, Reddy KR, Kamala V, Saidaiah P, Pandravada SR. 2016. Genetic divergence for quality, yield and yield components in Yardlong bean [*Vigna unguiculata* (L.) Walp. ssp.sesquipedalis Verdc.]. *Legume Research* 39(6): 900-904.
- 11. Sivakumar V, Celine VA, Vahab AM. 2014. Assessment of genetic divergence in among yardlong bean (*Vigna unguiculata* subsp. sequipedalis [L.]) genotypes. *Legume Genom. Genetics* 5(1): 1-3.