Biological Forum – An International Journal 13(4): 1257-1261(2021)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Divergence Studies in Yardlong Bean (*Vigna ungiculata* subsp *sesquipedalis* L.) Genotypes

***Mithun Kumar*[1], *M. Anjanappa*[2], *R.K. Ramachandra*[3*] *and Meenakshi Sood*[4]**
[1]*Department of Vegetable Science, College of Horticulture, Bengaluru, (Karnataka), India.*
[2]*College of Horticulture (UHS, Bagalkot), Kolar, (Karnataka), India.*
[3]*Horticutural Research & Extension Centre, Hogalagere, Kolar, (Karnataka), India.*
[4]*College of Horticulture (UHS, Bagalkot), Bengaluru, (Karnataka), India.*

(Corresponding author: R.K. Ramachandra)*

(Received 01 October 2021, Accepted 27 November, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Characterization of germplasm is crucial for using and enhancing plant genetic resources in diverse breeding programmes, hence the field experiments were conducted at the Department of Vegetable Science, College of Horticulture, Kolar, Karnataka, India during 2020–21 with 45 genotypes of yardlong bean (*Vigna ungiculata* subsp. *sesquipedalis* L.). Genetic diversity among the genotypes was worked out using Mahalanobis D^2 statistics. On the basis of genetic distance, these genotypes were broadly grouped into six clusters. Cluster I was the largest, consisting of 34 genotypes, while cluster III contained 6 genotypes, followed by cluster II, consisting of 2 genotypes, and clusters IV, V and VI, consisting of one genotype each. Among the different characters studied, pod yield per plant (27.98 %) contributed the most to the total genetic diversity among the genotypes, followed by 100 seed weight (14.60%), number of primary branches (10.91%), number of pods per plant (10.51%) and pod girth (8.69%). The maximum inter-cluster distance was recorded to be 596.22 between cluster II and cluster III. Cluster III showed the maximum intra-cluster distance (238.07). The genotypes belonging to the clusters with the maximum inter-cluster distance are genetically more divergent and these genotypes could be used in hybridization programmes to obtain promising segregants.

Keywords: Yardlong bean, genetic diversity, clusters, hybridization.

INTRODUCTION

Yardlong bean is a common leguminous vegetable crop in Asia's tropics and subtropics regions of the world. *Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdc. is thought to have been selected and grown in South-East Asia for its long, tender pods by vegetable varieties of *Vigna unguiculata* introduced from India (Steele and Mehra, 1980). Yardlong beans are a lesser-known and under-utilized vegetable in India, primarily in Kerala, Tamil Nadu, coastal Andhra Pradesh, coastal Karnataka and Odisha. It is also grown in West Bengal, Assam and the North Eastern Hill (NEH) area to some degree. It's a nutrient-dense legume vegetable that's also known as "poor man's meat" because it's a cheap and plentiful source of digestible protein (23.5-26.3%) (Ano and Ubochi, 2008). It also contains a lot of Vitamin A (865 IU) and Vitamin C (18.8 mg/100 g), iron (0.47 mg/100 g), phosphorus (59 mg/100 g), magnesium (44 mg/100 g), sodium (4 mg/100 g), calcium (50 mg/100 g), zinc (0.37 mg/100 g), copper (0.05 mg/100 g) and selenium (5 g/100 g) (Benchasri *et al*., 2011). A cosmopolitan vegetable crop and a key tropical Indian pulse (Vavilapalli *et al*., 2014). The maximum pod length (0.5–1m) and climbing growth habit are the major characteristics that distinguish this species from species like *Unguiculata* (Xu *et al*., 2010) and other varieties.

Genetic diversity is the most important requirement for any successful crop improvement programme because it offers a wide range of variants for effective selection, which can be accomplished through hybridization, recombination, mutation, and selection. Natural selection has depleted genetic variability in legumes, making traditional breeding methods ineffective (Reena and Mehta 2014). Yardlong beans are primarily a warm-season crop that can withstand high humidity. Furthermore, crop acclimatisation to warm weather (Hall 2004), poor soil properties (Hamidou *et al*., 2007). Despite the fact that the yardlong bean is regarded as a high-nutrition crop with adaptability to a wide range of environments, as a result, a study was undertaken with the broad goal of evaluating the divergence in the 45 yardlong bean genotypes.

A better understanding of genetic diversity or genetic similarity could aid in long-term selection (Chowdhury *et al.*, 2002) benefits in plants. Genetic diversity assessment is necessary to determine the source of genes for a specific character within the available germplasm. The genetic basis of crop diversity, with the ultimate goal of identifying useful allele genes and genomic region variation that can aid in the modification of a crop's desired characteristics, Assessment of genetic diversity among different genotypes is an important part of the breeding process for selecting better genotypes (Pidigam *et al.*, 2019).

The objectives of this study are to assess the degree of genetic divergence among 45 yardlong bean genotypes.

MATERIAL AND METHODS

The present study was carried out to assess the diversity among 45 diverse genotypes of yardlong bean. The 45 genotypes were grown with a simple RCBD with two replications at the College of Horticulture, Kolar, India. Kolar is located in the drought-prone district of Karnataka and is part of the maidan (plains) region. It spans an area of 3969 km^2 and is located between the north latitudes of 12°45′54″ and 13″ 35′47″ and the east longitudes of 77°50′29″ and 78°35′18. The experimental plot was thoroughly ploughed twice, the stubbles were removed, and the clods were crushed. The soil was harrowed twice to bring into a fine tilth. The recommended dosage of FYM and fertilizers were applied as per the UHSB package of practice. From the total fertilizer quantity 50 per cent of nitrogen and full dose of phosphorous and potassium nutrient were applied at time of sowing and remaining 50 per cent of nitrogen was applied at 30 days after sowings as a top dressing. Observations on vine length, internodal length, number of nodes on main vine, primary branches, days to 50 per cent flowering, number of cluster per plant, number of pods per clusters, number of pods per plant, pod length, pod girth, average pod weight, number of seed per pod,100 seed weight, TSS, ascorbic acid (mg/100g), protein content in pod (%) and pod yield per plant were recorded on the five plants chosen at random in each genotype in each replication and the mean of five plants were taken for analysis. The genetic divergence was estimated using the D^2 statistic of Mahalanobis (1936) and the population was grouped into cluster by following methods suggested by Tocher (Rao, 1952). The intra and inter- cluster distances were calculated formula described by Singh (1985).

RESULTS AND DISCUSSION

The analysis of variance for different quantitative traits for forty five genotypes of yardlong bean revealed highly significant (P=0.001) differences among the genotypes for all 17 characters studied. Based on the relative magnitude of D^2 estimates (Table 1), 45 genotypes were broadly grouped into six clusters with a variable number of genotypes, revealing the presence of a considerable amount of genetic diversity in the materials. Among the six clusters, cluster I contained 34 genotypes, followed by cluster III, which contained six genotypes, cluster II contained two genotypes, and cluster IV, V, and VI contained one genotype each. The pattern of the group revealed that significant variability existed among the genotypes. The mean intra and inter cluster D^2 values are given in Table 2. The intra cluster D^2 values varied from 0.00 (cluster IV, V, VI) to 238.07 (cluster III). Cluster III had the maximum D^2 value (238.07), followed by cluster I (118.78) and cluster II (21.34), and no intra cluster distance was observed in cluster IV, V and VI. The inter cluster D^2 values of the six clusters revealed that the highest inter cluster distance (596.22) was between cluster II and cluster III, while the lowest (92.03) was observed between cluster IV and V. The inter cluster distance was minimum between cluster IV and V, indicating the narrow genetic diversity and maximum between cluster II and cluster III, followed by cluster II and cluster VI, indicating wider genetic diversity among the genotypes included in these cluster groups, which could be used in the yield improvement of yardlong bean. A wide range of variability was observed in the cluster means for all the characters studied (Table 3).

Table 1: Clustering pattern of 45 genotypes of yardlong bean using Tocher's method.

Cluster	No. of genotypes	Genotypes
I	**34**	COHBYBCO1,COHBYBCO2,COHBYBCO3,COHBYBCO4,COHBYBCO5,COHBYBCO8,COHBYBCO9,COHBYBCO10,COHBYBCO11,COHBYBCO12,COHBYBCO15,COHBYBCO16,COHBYBCO17, COHBYBCO18,COHBYBCO19,COHBYBCO20,COHBYBCO21,COHBYBCO22,COHBYBCO23, COHBYBCO24,COHBYBCO25,COHBYBCO26,COHBYBCO27,COHBYBCO28,COHBYBCO30, COHBYBCO34,COHBYBCO35,COHBYBCO37,COHBYBCO38, Vyjayanthi, Vellayani Jyothika, Sarika and Malika
II	**02**	COHBYBCO36 and COHBYBCO40
III	**06**	Arka Mangala, COHBYBCO6, COHBYBCO7, COHBYBCO13, COHBYBCO14 and COHBYBCO32
IV	**01**	COHBYBCO31
V	**01**	COHBYBCO33
VI	**01**	COHBYBCO29

Table 2: Average intra and inter cluster distance D^2 for different parameter of yardlong bean genotypes.

	Cluster Distances					
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster 1	**118.78**	220.09	263.48	217.33	242.22	370.59
Cluster 2		**21.34**	596.22	305.32	286.27	497.52
Cluster 3			**238.07**	408.60	448.65	406.51
Cluster 4				**0.00**	92.03	463.44
Cluster 5					**0.00**	400.85
Cluster 6						**0.00**

Note: diagonal values indicates intra cluster distance

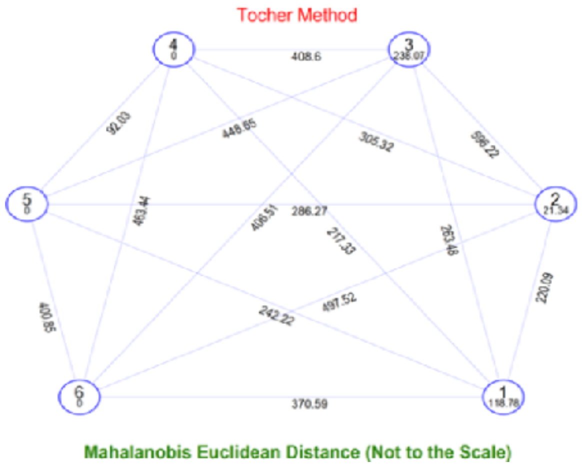

Fig. 1. Distance between inter and intra cluster distances in yardlong bean genotypes.

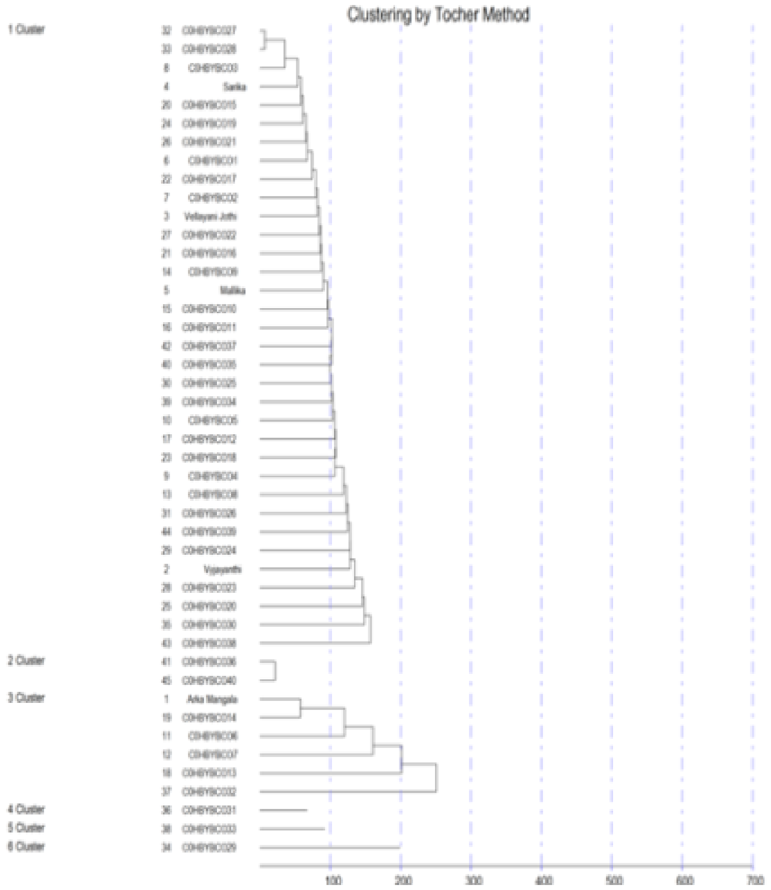

Fig. 2. Dendogram showing the genetic diversity among 45 genotypes of yardlong bean using Tocher's method.

Characters like vine length (301.59), number of clusters per plant (27.96), number of pods per cluster (2.48), number of pods per plant (51.25), pod length (51.28), average pod weight (21.93), number of seeds per pod (17.08), protein content in pod (17.52), TSS (4.08), and pod yield per plant (764.78) were observed with genotypes in cluster III. While in cluster VI, recorded higher cluster means for primary branches (7.50), days to 50 per cent flowering (50.48), pod girth (9.12) and 100 seed weight (16.62). The genotypes in cluster V recorded maximum mean values for characteristics like number of nodes on the main vine (21.20) and ascorbic acid content (27.12). The genotypes in cluster IV recorded a higher cluster mean value for internodal length (15.58). The genotypes with maximum mean values are used as parents in future breeding and, based on the genetic distance and clustering pattern, the most divergent genotypes were from clusters III, VI, and V, which could be used as best parents in a crop improvement programme. There is a lot of research being done on several elements of the yardlong bean, including genetic diversity (Sarutayophat *et al.*, 2007; Benchasri and Bairaman, 2010; Ullah *et al.*, 2011; Mahmudul Huque *et al.*, 2012).

The diversity of parents is of the utmost importance for a successful breeding programme, as the crossing made between parents y to produce desired recombinant in progeny. It is, however, preferable, depending upon information about the genetic diversity found in accessible germplasm, to select appropriate genetically different parents. The choice of the parents mainly depends on the contribution of characters towards divergence (Table 4).

Table 3: Mean values of different characters in six clusters of yardlong bean.

Characters	Clusters					
	I	II	III	IV	V	VI
Vine length (cm)	296.93	268.15	301.59	266.88	261.70	90.42
Internodal length (cm)	14.97	13.04	15.46	15.58	13.46	8.60
Number of nodes on main vine	19.47	17.00	20.58	18.20	21.20	11.60
Primary branches	3.65	2.88	5.01	3.50	4.90	7.50
Days to 50 per cent flowering	68.07	67.23	64.57	67.48	71.49	50.48
Number of cluster per plant	24.79	22.93	27.96	17.08	20.14	23.69
Number of pods per cluster	2.27	1.83	2.48	2.32	1.73	2.21
No. of pods per plant	39.25	29.41	51.25	42.82	26.06	40.15
Pod length (cm)	38.68	25.76	51.28	42.82	26.06	40.15
Pod girth (mm)	7.73	6.84	7.80	8.26	5.75	9.12
Average pod weight (g)	15.01	10.19	21.93	8.89	10.07	13.25
Number of seeds per pod	15.74	15.14	17.08	12.49	12.60	16.40
100 seed weight (g)	15.50	12.67	15.06	12.98	14.28	16.62
TSS (°Brix)	3.64	3.62	4.08	2.77	3.73	3.24
Ascorbic acid (mg/100g)	15.63	11.11	17.41	26.50	27.12	13.21
Protein content in pod (%)	15.40	10.48	17.52	12.58	14.27	8.67
Pod yield per plant (g)	554.26	333.02	764.78	256.44	233.76	516.42

Table 4: Per cent contribution from different characters to the total divergence in yardlong bean genotypes.

Sr. No.	Source	Contribution %	Times ranked
1.	Vine length (cm)	2.00	20.00
2.	Internodal length (cm)	0.10	1.00
3.	Number of nodes on main vine	0.61	6.00
4.	Primary branches	10.91	109.00
5.	Days to 50 per cent flowering	4.00	40.00
6.	Number of cluster per plant	0.10	1.00
7.	Number of pods per cluster	2.00	20.00
8.	No. of pods per plant	10.51	105.00
9.	Pod length (cm)	4.44	44.00
10.	Pod girth (mm)	8.69	87.00
11.	Average pod weight (g)	3.54	35.00
12.	Number of seeds per pods	1.82	18.00
13.	100 seed weight (g)	14.6	146.00
14.	TSS (˚Brix)	4.50	45.00
15.	Ascorbic acid (mg/100g)	0.20	2.00
16.	Protein content in pod (%)	4.04	40.00
17.	Pod yield per plant (g)	27.98	280.00

The character pod yield per plant ranked first (280 times) with maximum contribution of 27.98 per cent followed by 100 seed weight (14.60 %), primary branches (10.91 %), number of pods per plant (10.51%), pod girth (8.69 %), pod length (4.44%), TSS (4.50%), protein content in pod (4.04%), days to 50 per cent flowering (4.00%), vine length (2.00%), number of pods per plant (2.00%), number of seeds per pod

(1.82%), number of nodes on main vine (0.61%), ascorbic acid (0.20%), internodal length (0.10%) and number of pods per plant (0.10%). Hence, the pod yield per plant, 100 seed weight, primary branches, number of pods per plant, pod girth and pod length were considered to be important traits contributing towards genetic divergence. Similar divergence studies were carried by Das and Mishra (2008) in yardlong bean, Nagalakshmi *et al.*, (2010) in cowpea, Costa *et al*., (2013) in cowpea, Rambabu *et al*., (2016) in yardlong bean.

CONCLUSION

Yardlong bean, which belongs to the leguminous family, is an equally valuable vegetable crop in Karnataka. The productivity of the yardlong bean is higher than that of other cowpea species, and it is in high demand as a vegetable, particularly in South India and some parts of North India. In addition to picking a genotype from the hybridization clusters, the selection of parents based on the level of genetic difference with regard to particular characteristics of interest can be considered. This means, that if we want to improve the pod yield, the breeder can choose parents who diverge greatly with respect to the characters. Among the 45 genotypes evaluated, better performing genotypes can be selected and breeding can be done to develop high yielding yardlong bean varieties suited to the eastern dry zone of Karnataka.

Acknowledgements. The authors are gratefully thankful to College of Horticulture, Bengaluru, University of Horticultural Sciences, Bagalkot for encouragement and facilitation for undertaking the experiment.
Conflict of Interest. None.

REFERENCES

Ano, A. O., & Ubochi, C. I. (2008). Nutrient composition of climbing and prostrate vegetable cowpea accessions. *African Journal of Biotechnology*, *7*(20).

Benchasri, S., & Bairaman, C. (2010). Evaluation of yield, yield components and consumers' satisfaction towards yardlong bean and cowpea in agricultural organic system. *Bulgarian Journal of Agricultural Science*, *16*(6): 705-712.

Benchasri, S., Bairaman, C., & Nualsri, C. (2012). Evaluation of yardlong bean and cowpea for resistance to *Aphis craccivora* Koch in Southern Part of Thailand. *Journal of Animal and Plant Sciences*, *22*(4): 1024-1029.

Chowdhury, M. A., Vandenberg, B., & Warkentin, T. (2002). Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). *Euphytica*, *127*(3): 317-325.

Costa, E. M. R., Silva, K., Rocha, M. D. M., Medeiros, A. M., & Anunciação Filho, C. J. (2013). Genetic divergence among African cowpea lines based on morphoagronomic traits. *Embrapa Meio-Norte-Artigo em periódico indexado (ALICE)*.

Das, S. R. & Mishra, H. N. (2008). Genetic divergence in Yardlong bean. *Orissa J. of Horti*., *36*(2): 103-107.

Hall, A. E. (2004). Breeding for adaptation to drought and heat in cowpea. *European Journal of Agronomy*, *21*(4): 447-454.

Hamidou, F., Zombre, G., & Braconnier, S. (2007). Physiological and biochemical responses of cowpea genotypes to water stress under glasshouse and field conditions. *Journal of agronomy and crop science*, *193*(4): 229-237.

Huque, A. M., Hossain, M. K., Alam, N., Hasanuzzaman, M., & Biswas, B. K. (2012). Genetic divergence in yardlong bean (*Vigna unguiculata* (L.) Walp. ssp. *sesquipedalis* Verdc.). *Bangladesh Journal of Botany*, *41*(1): 61-69.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. National Institute of Science of India.

Nagalakshmi, R. M., Kumari, R. U., & Boranayaka, M. B. (2010). Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electronic Journal of Plant Breeding*, *1*(4): 453-461.

Pidigam, S., Munnam, S. B., Nimmarajula, S., Gonela, N., Adimulam, S. S., Yadla, H., & Amarapalli, G. (2019). Assessment of genetic diversity in yardlong bean (*Vigna unguiculata* (L.) Walp subsp. *sesquipedalis* Verdc.) germplasm from India using RAPD markers. *Genetic Resources and Crop Evolution*, *66*(6): 1231-1242.

Rambabu, E., Reddy, K. R., Kamala, V., Saidaiah, P., & Pandravada, S. R. (2016). Genetic variability and heritability for quality, yield and yield components in yardlong bean (*Vigna unguiculata* (L.) Walp. ssp. *sesquipedalis* Verdc.). *Green Farming*, *7*: 63-67.

Rao, C. R. (1952). Advanced statistical methods in biometric research.

Reena, N., & Mehta, A. K. (2014). Induced genetic variability in cowpea [Vigna *unguiculata* (L.) Walp] var. Pusa Komal. *The Bioscan.*, *9*(2 Supplement): 829-833.

Sarutayophat, T., Nualsri, C., Santipracha, Q., & Saereeprasert, V. (2007). Characterization and genetic relatedness among 37 yardlong bean and cowpea accessions based on morphological characters and RAPD analysis. *Warasan Songkhla Nakharin (Sakha Witthayasat lae Technology)*.

Singh, R. K. (1985). Biometrical methods in Quantitative Genetic Analysis. Kalyani Pub. Ludhiana. *New Delhi, Revised Ed.*, *318*.

Steele, W. M., & Mehra, K. L. (1980). Structure, evolution, and adaptation to farming systems and environments in Vigna. *Structure, evolution, and adaptation to farming systems and environments in Vigna.*, 393-404.

Ullah, M. Z., Hasan, M. J., Rahman, A. H. M. A., & Saki, A. I. (2011). Genetic variability, character association and path analysis in yard long bean. *SAARC J. Agri*, *9*(2): 9-16.

Vavilapalli, S. K., Celine, V. A., & Vahab, A. M. (2014). Assessment of genetic divergence in among yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* [L.]) genotypes. *Legume genomics and genetics*, *5*(5).

Xu, P., Wu, X., Wang, B., Liu, Y., Qin, D., Ehlers, J. D., & Li, G. (2010). Development and polymorphism of Vigna unguiculata ssp. unguiculata microsatellite markers used for phylogenetic analysis in asparagus bean (*Vigna unguiculata* ssp. *sesquipedialis* (L.) Verdc.). *Molecular breeding*, *25*(4): 675-684.

How to cite this article: Kumar, M.; Anjanappa, M.; Ramachandra, R. K. and Sood, M. (2021). Genetic Divergence Studies in Yardlong Bean (*Vigna ungiculata* subsp *sesquipedalis* L.) Genotypes. *Biological Forum – An International Journal, 13*(4): 1257-1261.