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Studies on genetic divergence in yardlong bean (*Vigna ungiculata* (L.) walp. ssp. *sesquipedalis* verdc.)

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Abstract
Genetic divergence among 24 genotypes of yardlong bean (*Vigna ungiculata* (L.) walp. ssp. *sesquipedalis* verdc.) was investigated to select the parents for hybridization using Mahalanobis D^2 statistics. Cluster analysis was used for grouping 24 yardlong bean genotypes. The genotypes fall into five clusters. Cluster II had the maximum (8) and cluster I had the minimum (3) number of genotypes. Cluster I (382.16) had highest intra-cluster distance and the lowest in cluster IV (140.69). The inter cluster D^2 values of the five clusters revealed that highest inter cluster generalized distance (1986.11) was between cluster I and cluster IV, while the lowest (373.36) was between cluster III and cluster IV. The characters *i.e.,* pod yield, ascorbic acid content, 100 seed weight, protein percentage, pod length, yield per hectare, TSS, vine length, yield per plot, number of pods per cluster and titrable acidity contributed maximum towards divergence among yardlong bean genotypes.

Keywords: Yardlong bean, genetic divergence, d^2 analysis, cluster means

1. Introduction
Yardlong bean (*Vigna ungiculata* (L.) walp. ssp. *Sesquipedalis* verdc. 2n=22) belonging to family leguminaceae is cultivated mainly for its crisp and tender green pods which are consumed both fresh as well as in cooked form. It is also called as asparagus bean, Chinese long bean, pea bean, string bean, snake bean, snake pea, snap pea, bodi and borboti. Yardlong beans, as the name suggests, differ from cowpeas in their very slender long green beans, which have a beautiful delicate flavour. This legume is also known as poor man's meat as it is a rich and inexpensive source of vegetable protein along with vitamin A, thiamin, riboflavin, calcium, phosphorus, sodium, potassium, magnesium, vitamin C and micronutrients like iron, zinc, manganese and cobalt (Ano and Ubochi, 2008) [1].

The success of phenotypic selection depends upon the range of genetic diversity available in the population. More diverse the parents within a reasonable range, better are the chances of improving economic characters in the resulting offsprings. The genetic divergence among parents influence the expression of heterosis and in the development of transgressive seggregants. Heterosis was exploited in yardlong bean for many characters like earliness, dwarfness and high yield. Under local agro climatic conditions, it is desirable to study the nature and degree of divergence in a population of different groups. Cluster analysis can be used in the estimation of genetic divergence and group them into clusters according to the magnitude of genetic distance.

The knowledge of genetic divergence provides us a sound scientific basis for the selection of genotypes to be used in hybridization programme for further improvement. The multivariate D^2 analysis using Mahalanobis D^2 statistics provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936) [2].

Material and methods
The present investigation entitled "studies on genetic variability in yardlong bean (*Vigna ungiculata* (L.) walp. ssp. *sesquipedalis* verdc.) was conducted during *kharif,* 2017-18 at College of Horticulture, Venkataramannagudem. Twenty four genotypes (Table 1) of yardlong

bean collected from various places were sown in Randomized Block Design with 3 replications. Each genotype of a replication consists of eight plants, sown in two rows with a spacing of 2m between the rows and 1m between the plants. All the package of practices were followed as per the recommendation. Data pertaining to the characters such as vine length (cm), number of primary branches per plant, number of nodes per plant, terminal leaf breadth (cm), terminal leaf length (cm), days to first flowering, days to 50% flowering, days to first harvest, length of harvesting period, pod length (cm), pod girth (mm), number of clusters per plant, length of cluster stalk, number of pods per cluster, number of pods per plant, seed number per pod, ascorbic acid content (mg/100g), TSS (°Brix), protein content (mg/100g), titrable acidity (%), 100 seed weight, pod yield per plant (kg), pod yield per plot (kg) and pod yield per hectare (tonnes) were collected from 5 randomly selected plants from each plot in each replication and subjected to statistical analysis.

The grouping of genotypes into different clusters was done using the Euclidean's method. The criterion was that the two genotypes belonging to the same cluster should at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977) [3].

Table 1: List of 24 genotypes of yardlong bean used in the study and their sources

S. No.	Genotype	Source
1.	Arka mangala	IIHR, Bangalore
2.	Vizianagaram Local	Vizianagaram, Andhra Pradesh
3.	Lola	Kerala Agricultural University (KAU)
4.	Vijayanthi	Kerala Agricultural University (KAU)
5.	Bhagyalakshmi	Kerala Agricultural University (KAU)
6.	Geethika	Kerala Agricultural University (KAU)
7.	Anashwarya	Kerala Agricultural University (KAU)
8.	Narsipatnam Local	Visakhapatnam, Andhra Pradesh
9.	Bobbili Local	Vizianagaram, Andhra Pradesh
10.	Ankur	Vizianagaram, Andhra Pradesh
11.	Indus	Vizianagaram, Andhra Pradesh
12.	Hazaribagh Local	Hazaribagh, Jarkhand
13.	Ramgarh Local	Ramgarh, Jarkhand
14.	Sabbavaram Local	Visakhapatnam, Andhra Pradesh
15.	Khunti Local	Khunti, Jarkhand
16.	Gumla Local	Gumla, Jarkhand
17.	Anakapalli Local	Visakhapatnam, Andhra Pradesh
18.	Rayagada Local	Rayagada, Odisha
19.	Trivendrum Local	Trivendrum, Kerala
20.	Koraput Local	Koraput, Odisha
21.	East west	Visakhapatnam, Andhra Pradesh
22.	Srikakulam Local	Srikakulam, Andhra Pradesh
23.	Eesa	Visakhapatnam, Andhra Pradesh
24.	Bhubaneswar Local	Bhubaneswar, Odisha

Results and Discussion

The D^2 value between any two genotypes was calculated as the sum of squares of the differences between the mean values of all the 24 characters and was used for the final grouping of the genotypes. Based on D^2 values, the 24 genotypes were grouped into five highly distinct clusters (Table 2). Among five clusters, cluster II was the largest consisting of 8 (*viz.*, Vijayanthi, Rayagada Local, Gumla Local, Trivendrum Local, Geethika, Ramgarh, Srikakulam Local, Lola) genotypes followed by cluster V, IV, III and I with 5 (*viz.*, Hazaribagh Local, Khunti Local, Vizianagaram Local, Sabbavaram local, Koraput Local), 4 (*viz.*, Ankur, Eesa, East West, Narsipatnam Local), 4 (*viz.*, Anaswarya, Indus, Anakapalli Local, Bhagya Lakshmi) and 3 (Arka Mangala, Bhubaneswar Local, Bobbili Local) genotypes respectively.

Table 2: Clustering pattern of 24 genotypes of yardlong bean (Euclidean's method)

Cluster	No. of genotypes	Genotypes
I	3	Arka Mangala, Bhubaneswar Local, Bobbili Local
II	8	Vijayanthi, Rayagada Local, Gumla Local, Trivendrum Local, Geethika, Ramgarh Local, Srikakulam Local, Lola
III	4	Anaswarya, Indus, Anakapalli Local, Bhagya Lakshmi
IV	4	Ankur, Eesa, East West, Narsipatnam Local
V	5	Hazaribagh Local, Khunti Local, Vizianagaram Local, Sabbavaram Local, Koraput Local

Mean values of five clusters (Table 3) are Cluster I genotypes recorded highest mean values for the parameters i.e., number of primary branches per plant (6.96), Number of nodes per plant (18.48), days to first harvest (52.10), length of harvesting period (48.54), pod girth (24.1mm), number of clusters per plant (50.19), Length of cluster stalk (19.71), number of pods per cluster (3.51), number of pods per plant (176.16), titrable acidity (0.80), 100 seed weight (21.08), pod yield per plant (2.64), pod yield per plot (19.67) and pod yield per hectare (12.28). Cluster III genotypes recorded highest mean values for the parameters i.e., number of days to first flowering (43.97), days to 50 per cent flowering (45.60) and TSS (3.37). Cluster IV genotypes recorded highest mean values for the parameters i.e., terminal leaf breadth (7.71), terminal leaf length (16.51) and seed number per pod (15.91). Cluster V genotypes recorded highest mean values for the parameters i.e., vine length (293.03), pod length (58.87), pod ascorbic acid content (19.61) and protein content (27.74).

Table 3: Mean values of clusters for twenty four characters in 24 genotypes of yardlong bean (Euclidean's method)

S. No.	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1	Vine length (cm)	287.12	291.92	213.66	265.84	293.03
2	Number of primary branches	6.96	5.73	4.04	3.98	4.54
3	Terminal leaf breadth (cm)	7.37	7.16	7.08	7.71	7.39
4	Terminal leaf length (cm)	15.86	16.18	15.06	16.51	15.98
5	Number of nodes per plant	18.48	17.20	13.76	17.65	17.62
6	Days to first flowering	45.01	45.07	43.97	44.16	45.04
7	Days to 50% flowering	46.40	45.92	45.60	45.74	46.14
8	Days to first harvest	52.10	52.67	53.31	52.48	53.38
9	Length of harvesting Period	48.54	44.74	41.94	39.39	41.99
10	Pod length (cm)	58.87	44.76	31.36	29.34	46.82
11	Pod girth (mm)	24.16	22.47	18.47	18.74	21.22
12	Number of clusters per plant	50.19	42.39	31.10	31.42	38.02
13	Length of cluster stalk (cm)	19.71	17.63	15.27	15.42	16.80
14	Number of pods per cluster	3.51	3.40	2.83	2.80	3.13
15	Number of pods per plant	176.16	144.03	88.28	87.69	119.00
16	Seed number per pod	15.71	15.73	14.81	15.91	14.59
17	Ascorbic acid (mg/100g)	18.24	12.99	10.13	16.95	19.61
18	TSS (°Brix)	3.23	3.24	3.37	3.04	3.05
19	Protein content (mg/100g)	26.35	27.48	25.69	27.50	27.74
20	Titrable acidity (%)	0.80	0.79	0.80	0.80	0.79
21	100 Seed weight (g)	21.08	17.29	13.52	13.97	18.88
22	Pod yield per plant (kg)	2.64	2.16	1.32	1.32	1.79
23	Yield per plot (kg)	19.67	16.13	10.13	9.90	13.45
24	Yield per hectare (tonnes)	12.28	10.10	6.33	6.18	8.40

The mean intra and inter cluster D^2 values are given in the Table 4. The intra cluster D^2 value ranged from 140.69 (Cluster IV) to 382.16 (Cluster I). The cluster I had the maximum D^2 value (382.16) followed by cluster III (367.80), cluster II (249.39), cluster V (181.34) and cluster IV (140.69). The inter cluster D^2 values of the five clusters revealed that highest inter cluster generalized distance (1986.11) was between cluster I and cluster IV, while the lowest (373.36) was between cluster III and cluster IV. The inter cluster distance was minimum between cluster III and IV indicating narrow genetic diversity and maximum between clusters I and IV followed by I and III indicating wider genetic diversity among the genotypes included in these groups.

Table 4: Average intra and inter-cluster D^2 values for five clusters in 24 genotypes of yardlong bean (Euclidean's method)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	382.16	588.75	1899.75	1986.11	952.75
Cluster II		248.39	813.73	1013.59	537.09
Cluster III			367.80	373.36	657.80
Cluster IV				140.69	423.15
Cluster V					181.34

The per cent contribution of each character towards divergence is presented in Table 5. The character, pod yield exhibited maximum contribution (38.77%) followed by ascorbic acid content (28.26%), 100 seed weight (11.59%), protein content (11.23%), pod length (4.35%), yield per hectare (2.17%), TSS (1.45%), vine length (1.09%), yield per plot (0.36%), number of pods per cluster (0.36%) and titrable acidity (0.36%). The characters number of primary branches per plant, terminal leaf breadth, terminal leaf length, number of nodes per plant, days to 1st flowering, days to 50% flowering, days to 1st harvest, length of harvesting period, pod girth, number of clusters per plant, length of cluster stalk, number of pods per plant and seed number per pod contributed nothing towards diversity. These findings are in line with Kumar *et al.* (2014) [4] in French bean, Siva Kumar *et al.* (2014) [5] in cowpea, Girish *et al.* (2012) [6] in Cluster bean and Praveen *et al.* (2017) [7] in Cluster bean.

Table 5: Per cent contribution of different characters towards diversity in yardlong bean genotypes

S. No	Source	% Contribution	Times ranked first
1	Vine length (cm)	1.09%	3
2	Number of primary branches per plant	0.00%	0
3	Terminal leaf breadth (cm)	0.00%	0
4	Terminal leaf length (cm)	0.00%	0
5	Number of nodes per plant	0.00%	0
6	Days to first flowering	0.00%	0
7	Days to 50% flowering	0.00%	0
8	Days to first harvest	0.00%	0
9	Length of harvesting Period	0.00%	0
10	Pod length (cm)	4.35%	12
11	Pod girth (mm)	0.00%	0
12	Number of clusters per plant	0.00%	0
13	Length of cluster stalk (cm)	0.00%	0
14	Number of pods per cluster	0.36%	1
15	Number of pods per plant	0.00%	0
16	Seed number per pod	0.00%	0
17	Ascorbic acid content (mg/100g)	28.26%	78
18	TSS (°Brix)	1.45%	4
19	Protein content (mg/100g)	11.23%	31
20	Titrable acidity (%)	0.36%	1
21	100 Seed weight (g)	11.59%	32
22	Pod yield per plant (kg)	38.77%	107
23	Yield per plot (kg)	0.36%	1
24	Yield per hectare (tonnes)	2.17%	6

Conclusion
Genetic divergence assessed using Mahalanobis' D^2 statistics revealed that the 24 genotypes of yardlong bean were grouped into five clusters. Among the 24 characters studied, pod yield per plant contributed maximum towards divergence followed by ascorbic acid content, protein percentage, 100 seed weight, pod length, pod yield per hectare, vine length, pod yield per plot, titrable acidity and number of pods per cluster. Cluster I exhibited highest intra cluster distance followed by cluster III. High inter cluster distance was observed between cluster I and cluster IV followed by cluster I and cluster III. Highest cluster mean values were recorded for most of the traits with the genotypes present in cluster V.

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