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Study on Multivariate Analysis in Sweet potato [*Ipomoea batatas* (L.) Lam]

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ABSTRACT
Thirty accessions of Sweet potato were assessed for genetic diversity by adopting Mahalanobis (D^2) statistics considering of eighteen characters were grouped into 6 clusters. Cluster II had the maximum number of genotypes (8) followed by cluster I (7), cluster IV (5), cluster VI (4) and cluster V and III (3). Maximum inter cluster distance was observed between cluster-II and cluster-VI. Maximum intra cluster distance was recorded in cluster- VI. Hence, genotypes belonging to cluster- VI viz., ST-14, SWA-2, Sree Kanaka, Kamala Sundhari may be utilized as parent in future breeding programmes with the genotype belonging to cluster II viz., A-14, Pusa Safed, 82/ 16, Sree Nandini, 90-10-17, S-30/ 17, Pol4-9, OP-219 as maximum inter cluster distance. Multivariate analyses revealed maximum divergence among the clusters signifying their role in exploitation of heterosis.
Key words: *Sweet potato (Ipomoea batatas (L.) Lam.), genetic divergence, cluster analysis.*

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INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam.) is an important starchy food crop grown throughout the tropical and sub-tropical parts of the world belongs to family Convolvulaceae. Since, it is highly heterozygous, there is extensive variability within the species, which is available for exploitation by plant breeders [1]. Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctness among genotypes [2]. Assessment of genetic diversity in germplasm collections imposes the categorization of accessions and useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. For crop improvement in sweet potato, knowledge on genetic diversity helps the breeder in choosing desirable parents for use in the breeding program. The diverse genotypes or accessions can be

crossed to produce superior high yielding hybrids possessing resistance to various abiotic and biotic stresses. In the present scenario, there is an urgent need to evaluate the available sweet potato accessions for the extent of genetic diversity. D^2 analysis permits precise comparison among all possible pairs of populations before effecting actual crossing programme of the cultivars in a desired genetic architecture. Hence an attempt has been made in the present investigation with the objective: set the based on multivariate analysis for generating more heterotic cross combinations and finally superior useful hybrids.

MATERIALS AND METHODS

The field experiment was conducted with 30 genotypes in a Randomized Block Design with 3 replications in *kharif* season, 2013 at the experimental farm of the Dept. of Vegetable Science, Horticultural College & Research Institute of Dr. Y.S.R. Horticultural University, Andhra Pradesh, India. This location at 16.830 N latitude and 81.5°E longitude with an average rainfall of 900 mm at an altitude of 34 m above mean sea level. Well matured healthy and disease free cuttings of previous season of each 30 genotypes were used as planting material for the experiment. The cuttings of 20-30 cm in length were planted in primary nursery at a distance of 30 cm between rows and 20 cm in the row. Ultimately when the nursery vines reach a sufficient length, the cuttings were made and planted in the secondary nursery. After one month, healthy cuttings of 20-30 cm in length with 3-4 nodes were planted in the main field. The cuttings obtained from apical and middle portion of vine have been found to produce larger number of sprouts and higher yield of tubers than basal cuttings [3]. Manures and fertilizers were applied as per the recommendations of CTCRI indicated that 10t /ha of farmyard manure and synthetic fertilizer rate of N–P2O5–K2O at 70:60:100 kg /ha was applied to soils. The field was brought to a fine tilth and 10t/ha of well-decomposed cow dung manure mixed in the soil at field preparation. The experiment was arranged in a randomized complete block design with three replications in 3.0 × 2.4 m plots. Seven week old cuttings of at least 20-30 cm length with 3 to 4 nodes were transplanted manually at a spacing of 60 × 20 cm between and within rows and 5-7cm depth. Plots were kept free from weeds.

The mean of five plants used for statistical analyses. Observation on eighteen important characters *viz.*, Vine length (cm), Vine inter nodal length(cm), Petiole length (cm), No. of branches per plant, No. of leaves per plant, Total leaf area (cm^2), No. of roots per plant, Root length (cm), Root girth (cm), Root yield/plant (g), β-carotene (mg/100g f.w.), β-carotene (mg/100g f.w.), Starch (%),Total sugar (%),Reducing sugar (%),Non reducing sugar (%),Plant dry matter (%),Root dry matter (%) and Root yield (t/ha) were recorded. The data obtained on above 18 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis [4] D^2 statistics.

RESULTS AND DISCUSSION

Percent contribution of different characters

Based on these D^2 values, per cent contribution of different characters towards genetic divergence was computed. The results on per cent contribution of each character towards genetic divergence are presented in (Table 1) and Fig.1.

The character, β-carotene (mg/100g f.w.) ranked first for 242 times with a maximum contribution of 55.63 per cent followed by starch (19.08 %), total sugars (11.03%), total leaf area (6.44%), root dry matter content (3.68%), number of leaves per plant (2.07%), root yield per plant (0.69%), petiole length (0.46%), root girth (0.46 %), vine length (0.23%) and reducing sugar (0.23%).

Vine internodal length (cm), number of branches per plant, number of roots per plant, root length (cm), plant dry matter content (%), non reducing sugar (%) and total root yield (t/ha) did not contributed anything towards the genetic diversity.

Table 1: Percent contribution of different characters towards diversity in Sweet potato genotypes

Sl. No.	Character	No. of times ranked 1st	Percent contribution (%)
1	Vine length (cm)	1	0.23
2	Vine inter nodal length(cm)	0	0.00
3	Petiole length (cm)	2	0.46
4	No. of branches per plant	0	0.00
5	No. of leaves per plant	9	2.07
6	Total leaf area (cm^2)	28	6.44
7	No. of roots per plant	0	0.00
8	Root length (cm)	0	0.00
9	Root girth (cm)	2	0.46
10	Root yield/plant (g)	3	0.69
11	β-carotene (mg/100g f.w.)	242	55.63
12	Starch (%)	83	19.08
13	Total sugar (%)	48	11.03
14	Reducing sugar (%)	1	0.23
15	Non reducing sugar (%)	0	0.00
16	Plant dry matter (%)	0	0.00
17	Root dry matter (%)	16	3.68
18	Root yield (t/ha)	0	0.00

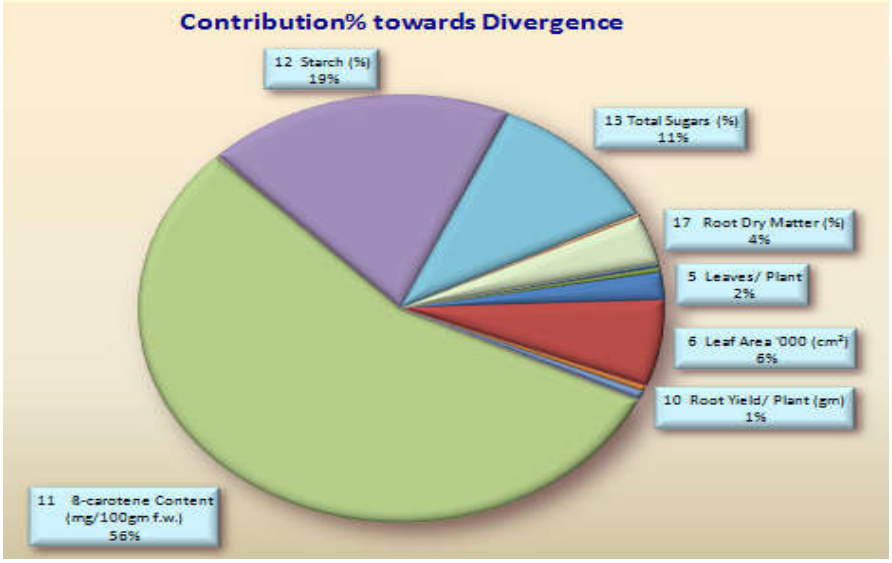

Fig. 1: Relative contribution of different characters to genetic divergence in sweet potato

Clustering pattern of genotypes

Procedure suggested by Ward [5] was used to group 30 sweet potato genotypes into six clusters by treating estimated D^2 values as the square of the generalized distance. The pattern of distribution of 30 genotypes into various clusters is indicated in (Table 2).

Cluster I consisting of seven genotypes *viz.,* Pol.13-4, Pol.21-1, Accession-5, Sree bhadra, S-30, S-30/25, S-30/11. Cluster II having eight genotypes *viz.,* A-14, Pusa safed, 82/16, Sree nandini, 90-10-17, S-30/17, Pol.4-9, OP-219. Cluster III having three genotypes *viz.,*CO-1, 362-9,90/704. Cluster IV consisting of five genotypes *viz.,* RNSP-5, 85-15, Accession-11, Accession-22, 440127. Cluster V comprising three genotypes *viz.,* Sree rethna, Kiran and 90-10-11. Cluster VI having four genotypes *viz.,* ST-14, SWA-2, Sree kanaka, Kamala sundari.

3. Mean intra and inter cluster distances

The mean intra and inter cluster D^2 values among the six clusters are given in the (Table 3) and Fig 2. The intra cluster distance ranged from 324.43 (cluster II) to 586.89 (cluster VI).

The inter cluster D^2 values varied from 569.13 to 4705.38 and maximum genetic divergence existed between clusters II and VI (4705.38) followed by cluster III and VI (3973.33) indicating wider genetic diversity among the genotypes included in these groups. Cluster I exhibited a close relation with cluster III followed by cluster II, while it was distant from cluster VI. Cluster II showed close relation with cluster III, while it was distant from cluster VI. Cluster III showed a close relation with cluster II and I, while it was distant from cluster VI. Cluster IV showed close relation with cluster V, while it was distant from cluster VI. Cluster V showed close relation with cluster IV and II and it was distant from cluster VI. Cluster VI exhibited close relation with cluster IV and it was distant from cluster II.
The present findings are in agreement with earlier investigations of Naskar [6], Ahmed *et al.* [7], Oliveira *et al.* [8], Nandi *et al.* [9], Badade *et al.* [10], Teshome *et al.* [11], Mondal [12], Teshome *et al.* [13], Rao *et al.* [14], Haydar *et al.* [15], Silva *et al.* [16].

Table 2: Clustering pattern of sweet potato genotypes (Ward's method)

Cluster	No. of genotypes	Genotypes
I	**Seven**	Pol.13-4, Pol.21-1, Accession-5, Sree Bhadra, S-30, S-30/25, S-30/11
II	**Eight**	A-14, Pusa Safed, 82/16, Sree Nandini, 90-10-17, S-30/17, Pol4-9, OP-219
III	**Three**	CO-1, 362-9, 90/704
IV	**Five**	RNSP-5, 85-15, Accession-11, Accession-22, 440127
V	**Three**	Sree rethna, Kiran, 90-10-11
VI	**Four**	ST-14, SWA-2, Sree Kanaka, Kamala Sundhari

Table 3: Average intra (bold) and inter-cluster D^2 values for six clusters in sweet potato genotypes. (Ward's method)

Clusters	I	II	III	IV	V	VI
I	**405.927**	744.011	616.273	1139.512	1579.596	3260.132
II		**324.43**	569.139	1503.537	1045.427	4705.384
III			**429.745**	1385.456	1360.789	3973.332
IV				**551.448**	906.944	1582.484
V					**415.699**	3200.696
VI						**586.892**

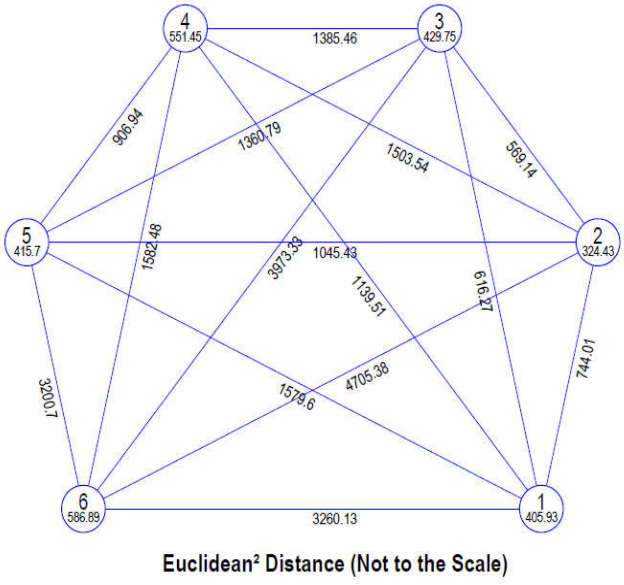

Fig. 2: Mean inter and intra cluster distances of 30 sweet potato genotypes

Cluster mean analysis

The mean values of six clusters for 18 characters are presented in (Table 4). The genotypes of cluster V recorded the highest mean value for vine length (247.79 cm) followed by cluster II (164.61 cm) while the genotypes of cluster VI recorded the lowest mean value for Vine length (124.97 cm).

The genotypes of cluster V recorded the highest mean value for vine intermodal length per plant (9.52) followed by cluster I (6.08) while the lowest mean value was registered by the genotypes of cluster VI (5.22).The genotypes of cluster VI recorded the highest mean value for petiole length (29.94 cm) followed by cluster II (26.88 cm) while the genotypes of cluster IV recorded the lowest mean value for petiole length (24.36 cm).

The genotypes of both cluster III and V recorded the highest mean value for number of branches per plant (7.67) followed by cluster II (7.17) while the genotypes of cluster VI recorded the lowest mean value for number of branches per plant (4.42).The genotypes of cluster V recorded the highest mean value for number of leaves per plant (336.00) followed by cluster III (265.56) while the lowest mean value was registered by the genotypes of cluster VI (140.83).

The genotypes of cluster V recorded the highest mean value for total leaf area (343.55 □000cm²) followed by cluster III (281.81 □000cm²) while the lowest mean value was registered by the genotypes of cluster VI (49.40 □000cm²).

The maximum mean value for number of roots per plant was recorded by the genotypes of cluster IV (3.40) followed by cluster VI (3.25) whereas the minimum mean value was recorded in cluster I (2.43). Root length recorded its maximum mean value in the genotypes of cluster VI (15.67 cm) followed by cluster III (15.26 cm).The lowest mean value was recorded in the genotypes of cluster II (13.03 cm).

The genotypes of cluster II recorded highest mean value for root girth (18.17 cm) followed by cluster VI (17.90 cm), while the genotypes of cluster III recorded lowest mean value for root girth (14.97 cm). Root yield per plant recorded its highest mean value in the genotypes of cluster IV (405.32 g) followed by cluster VI (350.07 g), while the genotypes of cluster III (253.51 g) recorded the lowest mean value.

The maximum mean value for β-carotene was recorded by the genotypes of cluster VI (7.41 mg/100g f.w.) followed by cluster IV (4.39 mg/100g f.w.) whereas the minimum mean value was recorded in cluster II (1.34 mg/100g f.w.). The genotypes of cluster III recorded highest mean value for starch content (22.67 %) followed by cluster I (20.43 %), while the genotypes of cluster V recorded lowest mean value for starch content (12.62 %).

The genotypes of cluster III recorded highest mean value for total sugar (7.20 %) followed by cluster VI (5.70 %), whereas the genotypes of cluster V recorded lowest mean value for total sugar content (3.26 %).The maximum mean value for reducing sugar was recorded by the genotypes of cluster III (5.80 %) followed by cluster VI (4.95 %) whereas the minimum mean value was recorded in cluster V (2.59 %).

The genotypes of cluster III recorded highest mean value for non reducing sugar (1.40 %) followed by cluster IV (1.03 %), whereas the genotypes of cluster V recorded lowest mean value for non reducing sugar content (0.66 %).

The genotypes of cluster I recorded maximum mean value for plant dry matter content (28.28%) followed by cluster VI (24.83%), while the genotypes of cluster III recorded minimum mean value for plant dry matter content (18.93%).

The maximum root dry matter content was recorded in the genotypes of cluster III (26.99 %) followed by Cluster V (26.44 %) whereas; minimum value was recorded in the genotypes of cluster IV (23.16 %). The genotypes of cluster IV recorded highest mean value for total root yield (21.01 t/ha) followed by cluster VI (17.27 t/ha). The lowest mean value was recorded in cluster V (13.78 t/ha).

Table 4: Clusters means for eighteen characters in 30 sweet potato genotypes (Ward's method)

Cluster	Vine length (cm)	Vine internodal length(cm)	Petiole length (cm)	No. of Branches /plant	No. of leaves per plant	Total Leaf area (cm^2)	No. of roots per plant	Root length (cm)	Root girth (cm)	Root Yield (g)	β-carotene (mg/100g f.w.)	Starch(%)	Total sugar(%)	Reducing sugar(%)	Non reducingSugar (%	Plant dry matter (%)	Tuber dry matter (%)	Root yield(t/ha)
I	134.02	6.08	26.79	4.10	212.52	66.35	2.43	14.77	16.58	262.17	2.00	20.43	5.65	4.76	0.89	25.28	23.36	15.69
II	164.61	6.07	26.88	7.17	246.29	221.24	3.13	13.03	18.17	280.44	1.34	18.10	4.25	3.50	0.75	23.55	24.27	16.19
III	128.96	5.63	25.80	7.67	265.56	281.81	3.00	15.26	14.97	253.51	2.08	22.67	7.20	5.80	1.40	18.93	26.99	15.58
IV	129.29	5.98	24.36	6.53	192.40	141.64	3.40	15.07	16.62	405.32	4.39	13.18	4.79	3.77	1.03	22.53	23.16	21.01
V	247.79	9.52	25.44	7.67	336.00	343.55	2.67	14.53	16.22	264.12	3.83	12.62	3.26	2.59	0.66	24.80	26.44	13.78
VI	124.97	5.22	29.94	4.42	140.83	49.40	3.25	15.67	17.90	350.07	7.41	16.24	5.70	4.95	0.75	24.83	23.40	17.27

CONCLUSION

Based on the intra and inter-cluster distances among the groups, suggestions were made to attempt crosses to obtain new desirable recombinants in sweet potato between the genotypes of clusters II and VI followed by cluster III and VI. Based on the findings of the present investigation the conclusion drawn for further improvement of sweet potato genotypes for cultivation in Coastal districts of Andhra Pradesh is that the genotypes *viz.*, A-14, Pusa safed, 82/16, Sree nandini, 90-10-17, S-30/17, Pol.4-9, OP-219 (Cluster II) and ST-14, SWA-2, Sree kanaka, Kamala sundari (Cluster VI) and CO-1, 362-9, 90/704 (Cluster III) show a lot of genetic diversity. Hence crosses between these genotypes are likely to produce new recombinants with desired traits. Based on the mean performance and genetic parameters, the genotypes Accession-22, 440127, SWA-2 and ST-14 can be selected for further evaluation for their suitability for cultivation.

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