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Estimation of genetic divergence in sweet potato [*Ipomea batatas* (L.)] for tuber yield and its attributing traits

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Abstract

The genetic divergence among 28 genotypes of sweet potato [*Ipomea batatas* (L.)] was determined through Cluster analysis and Mohalanobis's D^2 analysis. The cluster analysis grouped all 28 sweet potato genotypes into 8 major clusters based on D^2 value. Extreme genetic divergence was estimated among clusters. Maximum number of genotypes were grouped into cluster I included 10 genotypes. Which would be fruitful for developing heterotic cross combination. The maximum intra-cluster distance was shown by cluster I (149.06) followed by cluster II (128.68) indicating maximum diversity within these clusters. Cluster V showed highest mean value for no. of tubers per plant (4.29), which was followed by cluster III (4.25), cluster VII (3.57), cluster VI (3.52) and cluster I (3.37). Tuber weight per plant showed maximum cluster mean performance in cluster VI (381.26 g), which was followed by cluster V (378.96 g), cluster III (360.28 g), cluster VI (293.80 g) and cluster I (258.959 g).

Keywords: Sweet potato, cluster, divergence, genotypes and tuber yield

Introduction

Sweet potato [*Ipomea batatas* (L.)] is one of the most popular and extensively consumed tubers vegetable crops grown worldwide due to its acclimatization to a wide variety of environments, as well as its high nutritive value. Sweet potato commonly known as "Shakarkand". In Chhattisgarh it is locally known as "Kalmal Kanda", 'Maati Kanda' and 'Kevat Kanda' is one of the most popular and important tubers crops in India and abroad because of its yield potential and high calorific value. It is a globally important root crop, ranked second most important tropical and subtropical staple root crop in area and production after cassava (FAOSTAT, 2014). Sweet potato ranks fifth after rice, wheat, maize and cassava, sweet potato (CIP, 2018). In India sweet potato occupied 1.16 lakh thousand ha area with 12.07 lakh thousand mt production and having productivity of 10.2 thousand mt/ha (Anon., 2019), whereas in Chhattisgarh it covers 4.47 thousand ha area with 48.15 thousand mt production and having productivity of 10.75 thousand mt/ha (Anon., 2020) ^[1]. For productive breeding programme information about extends of genetic variability, correlation is basic requirement. In any crop improvement programme, evaluation of germplasm to assess the existing variability is a preliminary step. Genotypes exhibiting high variability for desirable characters that contribute to the yield are to be selected in such a programme of evaluation in the breeding programme, selection of parents for hybridization is largely based on high yield potentials, wide adoption and genetic diversity. In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-requisite for hybridization programme for obtained progenies with important desirable characters like disease resistance, earliness, quality or even performance of a particular character for the yield improvement and future utilization of local germplasm. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme. Being cross pollinated crop, due to monoecy there is an ample scope for exploitation of heterosis in it. Genetically diverse parents are likely to segregate and produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1 's and broad spectrum of variability in segregating generations (Arunachalam, 1981) ^[3]. Keeping this in view, the present study was focused to assess the genetic diversity of 28 promising bottle gourd genotypes using Mahalanobis D^2 statistics.

Materials and Methods

The experiment was carried out during the year 2020-2021 in *Kharif* season at Instructional cum Research Farm of S.G. Collage of Agriculture and Research Station, Jagdalpur, Bastar (C.G.). The experimental material comprised of twenty-eight genotypes along with two checks Indira Nandini as local check and Sree Bhadhara as national check. The experiment was laid out in a randomized block design with three replications at the spacing of 60 cm between rows and 20 cm between plants to plant. A net plot size of 2 x 1.8 m was kept for each genotype. All the recommended cultural practices were taken to grow a healthy crop. Data were recorded on five randomly selected plants for thirteen characters *viz.* vine length (cm), vine internode length (cm), vine weight per plant (fw) g., length of tubers (cm), diameter of tubers (cm), TSS of tubers (%), starch (%), dry matter of tubers (%), dry matter of foliage (%), no. of tubers per plant, tubers weight per plant (g), harvest index (%), were recorded on five competitive random plants from each replication. Three important characters *viz.* tubers yield (t/ha), marketable tubers yield (t/ha) and weevil infested tubers yield (t/ha) were calculated on the basis of observed data.

Result and Discussion

The analysis of variance revealed significant differences

among sweet potato genotypes for all characters suggesting considerable genetic variability in the population. Using the estimated D^2 values as squares of generalized distance, 28 genotypes were grouped into 8 clusters (Table 1). Maximum number of genotypes were grouped into cluster I (TSP-16-2, SGCARS-38, Bhu Sona, IGSP-34, SGCARS-5, SGCARS-1, Gouri, Bhu Krishana, C.G. Shakarkand Narangi, IGSP-KSKL-13-26) included ten genotypes followed by cluster III (Indira Nandini, C.G. Shakarkand Priya, Bhu Kanti, Sree Rethana, Sree Bhadhara, Indira Naveen) included six genotypes, cluster II (TSP-16-7, IGSP-26, TSP-16-1, SGCARS-17, TSP-16-4) included five genotypes and cluster IV (TSP-16-5, TSP-16-6, IGSP-30) included three genotypes. Which is followed by cluster V (Indira Madhur), cluster VI (TSP-16-8), cluster VII (TSP-16-10) and cluster VIII (TSP-16-3) had only one genotypes in each cluster.

The intra-cluster distance varied from 0.00 to 149.06 (Table 2). The maximum intra-cluster distance was shown by cluster I (149.06) followed by cluster II (128.68), cluster III (114.44), cluster IV (85.89), which is followed by cluster V, VI, VII and VIII had only (0.00) each intra cluster distance. These results are in general agreement with the findings of Anon (2000), Anshebo *et al.* (2003) [5], Teshome *et al.* (2003) [9], Martins *et al.* (2012) [7], Dash *et al.* (2015) [6] and Tripathi *et al.* (2017) [8].

Table 1: Composition of cluster

Cluster number	Number of genotypes included	Name of genotypes
I	10	TSP-16-2, SGCARS-38, Bhu Sona, IGSP-34, SGCARS-5, SGCARS-1, Gouri, Bhu Krishana, C.G. Shakarkand Narangi, IGSP-KSKL-13-26.
II	5	TSP-16-7, IGSP-26, TSP-16-1, SGCARS-17, TSP-16-4
III	6	Indira Nandini, C.G. Shakarkand Priya, Bhu Kanti, Sree Rethana, Sree Bhadhara, Indira Naveen
IV	3	TSP-16-5, TSP-16-6, IGSP-30
V	1	Indira Madhur
VI	1	TSP-16-8
VII	1	TSP-16-10
VIII	1	TSP-16-3

Table 2: Intra (bold) and Inter cluster distance values in sweet potato

Cluster	I	II	III	IV	V	VI	VII	VIII
I	149.06	422.54	229.10	396.04	190.34	250.23	274.51	516.07
II		128.69	552.96	225.52	584.93	215.04	704.67	217.79
III			114.45	702.03	198.34	237.31	573.31	607.05
IV				85.90	489.73	382.84	352.20	302.12
V					0.00	304.61	239.42	660.55
VI						0.00	588.41	287.63
VII							0.00	828.91
VIII								0.00

Mean Performance of Clusters

The mean performance for different clusters of genotypes for tuber and its components are presented in table 3. The data of cluster means for all the characters showed appreciable differences. Vine length (cm) showed maximum cluster mean performance in cluster III (189.79 cm), which was followed by cluster II (167.60 cm), cluster III (154.44 cm), cluster VI (150.33 cm) and cluster I (141.94 cm). Vine internode length showed maximum cluster mean performance in cluster VIII (9.40 cm), which was followed by cluster II (4.76 cm), cluster III (4.50 cm), cluster IV (4.42 cm) and cluster VI (4.05 cm). Vine weight per plant (fw) (g) showed maximum cluster mean performance in cluster VI (350.55 g), which was followed by cluster III (302.86 g), cluster II (271.24 g) and

cluster I (269.07 g) and cluster VIII (231.00 g). Length of tuber per plant (cm) showed maximum cluster mean performance in cluster V (17.50 cm), which was followed by cluster VI (16.55 cm) and cluster III (15.40 cm). Diameter of tuber (cm) showed maximum cluster mean performance in cluster VI (4.80 cm), which was followed by cluster V (4.47 cm), cluster III (3.90 cm) and cluster VIII (3.24 cm). TSS of tuber (%) showed maximum cluster mean performance in cluster VII (12.01 %), which was followed by cluster IV (11.65 %), cluster VI (11.35 %) and cluster VIII (11.20 %). Starch (%) showed maximum cluster mean performance in cluster V (21.48 %), which was followed by III (19.889 %), cluster I (12.78 %) and cluster VIII (10.96 %). Dry matter of tuber (%) showed maximum cluster mean performance in cluster VII (27.81 %), which was followed by cluster V (24.20 %), cluster I (24.17 %) and cluster III (23.61 %). Dry matter of foliage (%) showed maximum cluster mean performance in cluster VI (58.77 %), which was followed by cluster III (53.68 %), cluster II (45.46 %), cluster V (43.55 %) and cluster I (41.04 %). Number of tubers per plant showed maximum cluster mean performance in cluster V (4.29), which was followed by cluster III (4.25), cluster VII (3.57), cluster VI (3.52) and cluster I (3.37). Tuber weight per plant showed maximum cluster mean performance in cluster VI

(381.26 g), which was followed by cluster V (378.96 g), cluster III (360.28 g), cluster VI (293.80 g) and cluster I (258.959 g). Harvest index (%) showed maximum cluster mean performance in cluster V (72.99 %), which was followed by cluster VII (70.25 %), cluster IV (56.68 %), cluster III (55.00 %), cluster VI (52.84 %) and cluster I (49.17

%). Tuber yield (t/ha) showed maximum cluster mean performance in cluster VI (25.41 t/ha), which was followed by cluster V (25.26 t/ha), cluster III (24.01 t/ha), cluster VII (19.58 t/ha), cluster I (17.26 t/ha), cluster II (15.23 t/ha) and cluster IV (13.371 t/ha).

Table 3: Mean performance of genotypes in individual cluster for tuber yield and its components

Character / Cluster	VL	VIL	VWPP	LOT	DOT	TSS	S	DMT	DMF	NTPP	TWPP	HI	TY
I	141.94	3.94	269.08	12.70	2.52	10.80	12.78	24.18	41.04	3.38	258.96	49.18	17.26
II	167.60	4.77	271.24	9.84	2.50	9.80	9.50	9.74	45.47	2.33	226.52	45.72	15.23
III	189.80	4.51	302.87	15.41	3.90	9.64	19.88	23.62	53.69	4.25	360.28	55.01	24.02
IV	100.29	4.43	152.67	9.19	1.68	11.65	10.30	13.21	26.11	1.81	200.60	56.68	13.37
V	94.22	3.08	140.33	17.50	4.47	9.67	21.48	24.20	43.56	4.30	378.96	73.00	25.26
VI	150.33	4.06	350.56	16.56	4.80	11.36	10.26	13.27	58.78	3.52	381.26	52.84	25.42
VII	67.22	2.78	124.33	12.08	1.83	12.01	10.94	27.82	16.01	3.58	293.81	70.25	19.59
VIII	154.44	9.40	231.00	9.11	3.24	11.20	10.97	11.39	39.33	1.89	198.31	46.17	13.22

VL- Vine length (cm), VIL- Vine internode length (cm), VWPP- Vine weight per plant (fw) (g), LOT- Length of tuber (cm), DOT- Diameter of tuber (cm), TSS- TSS of tuber (%), S- Starch (%), DMT- Dry matter of tuber (%), DMF- Dry matter of foliage (%), NTPP- No. of tubers per plant, TWPP- Tuber weight per plant (g), HI- Harvest Index (%), TY- Tuber yield (t/ha)

1.2 Contribution of characters towards divergence

In the contribution of each character to divergence presented in table 4 which showed dry matter of tuber percent contributes highest (41.80 %) to divergence followed by vine length (16.14%), harvest index (14.81%), TSS of tuber (7.14

%), vine internode length (6.35 %), starch (3.97 %), tuber weight per plant (3.44 %), vine weight per plant (2.91 %), dry matter of foliage (1.06 %), number of tubers per plant (1.06 %), length of tuber per plant (0.79 %), diameter of tuber (0.53 %).

Table 4: Desirable genotypes based on cluster

Cluster Characters	I	II	III	IV	V	VI	VII	VIII
1.	Bhu Krishana, Bhu Sona	TSP-16-4, SGCARS-1	Bhu Kanti, Sree Rethana	TSP-16-5, TSP-16-6	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
2.	IGSP-KSKL-13-26, Bhu Sona	SGCARS-1, TSP-16-4	Sree Rethana, Indira Naveen	TSP-16-5, IGSP-30	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
3.	IGSP-34, TSP-16-2	TSP-16-7, SGCARS-1	Bhu Kanti, Sree Bhadhara	IGSP-30, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
4.	IGSP-KSKL-13-26, C.G.Shakarkand Narangi	SGCARS-1, IGSP-26	Indira Naveen, Bhu Kanti	IGSP-30, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
5.	Gouri, SGCARS-38	IGSP-26, SGCARS-1	C.G. Shakarkand Priya,	IGSP-30, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
6.	TSP-16-2, Bhu Sona	TSP-16-4, TSP-16-7	Bhu Kanti, C.G. Shakarkand Priya	IGSP-30, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
7.	Bhu Sona, C.G. Shakarkand Narangi	TSP-16-7, TSP-16-1	Sree Rethana, Indira Naveen	TSP-16-6, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
8.	SGCARS-5, IGSP-34	TSP-16-1, SGCARS-1	Indira Naveen, Sree Bhadhara	TSP-16-5, IGSP-30	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
9.	IGSP-34, SGCARS-1	SGCARS-1, TSP-16-7	Indira Nandini, Indira Naveen	IGSP-30, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
10.	Gouri, C.G. Shakarkand Narangi	SGCARS-1, IGSP-26	C.G.Shakarkand Priya, Indira Nandini	TSP-16-6, TSP-16-5	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
11.	C.G.Shakarkand Narangi, Gouri	TSP-16-1, TSP-16-4	Indira Naveen, Sree Bhadhara	TSP-16-5, TSP-16-6	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
12.	IGSP-KSKL-13-26, Bhu Krishana	TSP-16-1, TSP-16-4	Sree Bhadhara, Indira Naveen	TSP-16-5, TSP-16-6	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3
13.	C.G.Shakarkand Narangi, Gouri	TSP-16-1, TSP-16-4	Indira Naveen, Sree Bhadhara	TSP-16-5, TSP-16-6	Indira Madhur	TSP-16-6	TSP-16-10	TSP-16-3

1. Vine length, 2. Vine internode length (cm), 3. Vine weight per plant (fw) g, 4. Length of tuber (cm), 5. Diameter of tuber (cm), 6. TSS of tuber (%), 7. Starch (%), 8. Dry matter of tuber (%), 9. Dry matter of foliage (%), 10. No. of tubers per plant, 11. Tuber weight per plant (g), 12. Harvest Index (%), 13. Tuber yield (t/ha)

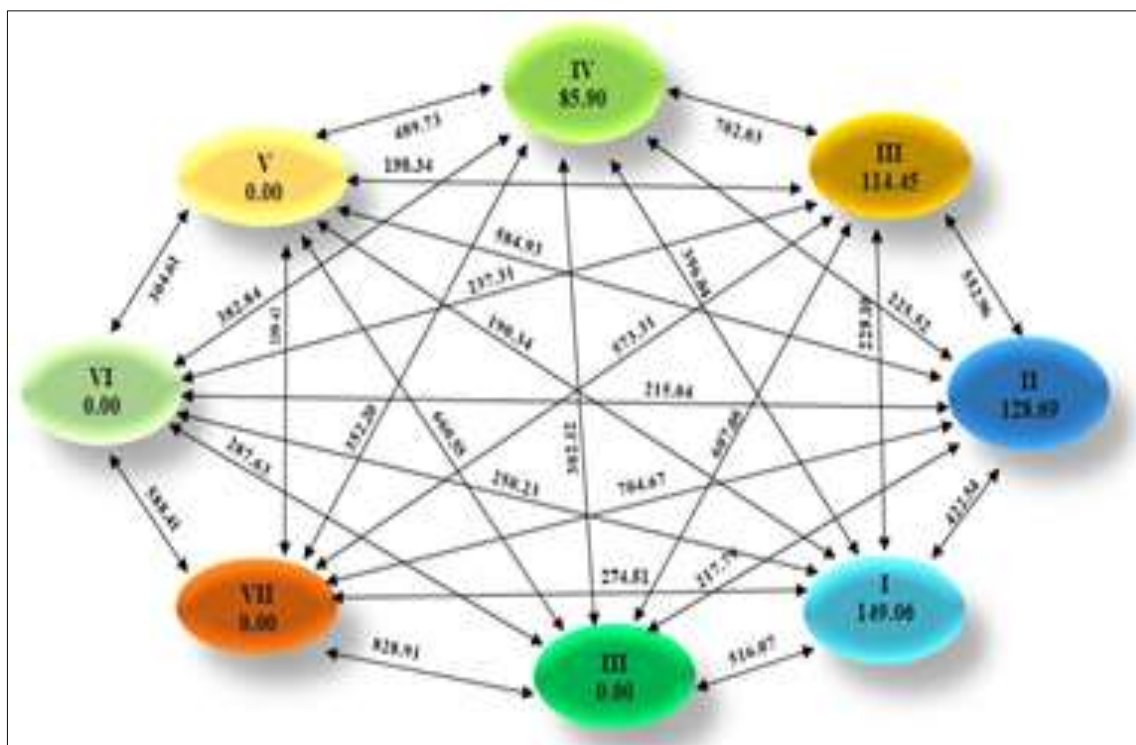


Fig. 4.1: Diagrammatic representation of different intra and inter cluster distance of sweet potato (values inside circle is intra cluster distance)

Table 5: Contribution of each character to divergence

Character Cluster	VL	VIL	VWPP	LOT	DOT	TSS	S	DMT	DMF	NTPP	TWPP	HI	TY	Total
Number times appearing first time	61	24	11	3	2	27	15	158	4	4	13	56	0	378
Percent contribution (%)	16.14	6.35	2.91	0.79	0.53	7.14	3.97	41.80	1.06	1.06	3.44	14.81	0	100

VL - Vine length (cm), VIL - Vine internode length (cm), VWPP - Vine weight per plant (fw) (g), LOT - Length of tuber (cm), DOT - Diameter of tuber (cm), TSS - TSS of tuber (%), S- Starch (%), DMT- Dry matter of tuber (%), DMF - Dry matter of foliage (%), NTPP - No. of tubers per plant, TWPP - Tuber weight per plant (g), HI - Harvest Index (%), TY - Tuber yield (t/ha)

Conclusion

The inter-cluster distances in present investigation were higher than the intra-cluster distance reflecting the wider diversity among the breeding lines of the distant group. Hence, it is suggested that inter crossing of genotypes from diverse clusters showing high mean performance will be helpful in obtaining better recombinants with higher genetic variability. Genetic divergence is one of the useful tools for selection and efficient use of parents for hybridization to develop high yielding potential cultivars/hybrids. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining stronger heterosis and gives broad spectrum of variability in segregating generation.

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