



GENETIC DIVERGENCE IN SWEET POTATO [*IPOMOEA BATATAS* (L.) LAM]

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Abstract

The present investigation was undertaken to study the mean performance of sweet potato genotypes to assess the cluster analysis in sweet potato for tuber yield and its components at Research and Instructional Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), India; during the *rabi* season of 2013-2014. A set of 12 genotypes of sweet potatoes were subjected to D² analysis for 14 characters and based on D² values four cluster were formed. No relationship was found between genetic divergence and geographic distribution. TSS and dry matter per cent of tuber contributed high towards total divergence which offered due attention to these characters while selecting for increased tuber yield. The maximum inter cluster distance was observed in between cluster I and IV. The maximum intra cluster distance was observed in cluster III. Hence, genotypes belonging to this cluster *viz.*, Indira Naveen, Sree Rethna, Indira Nandini, Gouri, IGSP-21, IGSP-25, IGSP-39 may be utilized as parent in future breeding programmes with the genotype belonging to cluster IV *i.e.*, IGSP-20 as maximum inter cluster distance.

Key words : Sweet potato, selection, genetic divergence, cluster analysis, tuber yield.

Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam.] locally known as *Shakarkand* belongs to the family Convolvulaceae and is one of the most popular tuber crops in India and abroad because of its yield potential and high calorific value. Sweet potato is the world's seventh most important food crop other than wheat, rice, maize, barley, potato and cassava. Sweet potato is a highly heterozygous and cross-pollinated crop in which many of the traits show continuous variation. Since, it is highly heterozygous, there is extensive variability within the species, which is available for exploitation by plant breeders (Jones *et al.*, 1986). Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctness among genotypes (Ali *et al.*, 2008). 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. The D² analysis classifies the genotype into relatively homogeneous groups in such

a way that within cluster diversity is minimized and between clusters diversity is maximized. Looking to the above, we classify the genotypic set based on multivariate analysis for generating more heterotic cross combinations and finally superior useful hybrids.

Materials and Methods

The investigation was carried out at Research and Instructional Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), India; during the *rabi* season of 2013-2014. Twelve genotypes of sweet potatoes (Indira Madhur, Indira Naveen, Indira Nandini, Sree Rethna, Gauri, IGSP.C-15, IGSP-20, IGSP-21, IGSP-24, IGSP-25, IGSP-36 and IGSP-39) taken and the experiment was arranged in a Randomized Complete Block Design, with three replications. Each genotype was planted on 2 m long and 1.8 m wide plot consisting four rows which accommodated nine plants per row and twenty seven plants per plot. A distance of 60 cm maintained between the plots. Vine cutting of 20 cm upper portions from sweet potato nursery were taken and vertically planted on 1st November 2013 in the well-

Table 1 : Composition of clusters.

Cluster number	Number of genotypes included	Names of genotypes
I	3	Indira Madhur, IGSP-C-15, IGSP-24
II	1	IGSP-36
III	7	Indira Naveen, Sree Rethna, Indira Nandini, Gouri, IGSP-21, IGSP-25, IGSP-39,
IV	1	IGSP-20

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

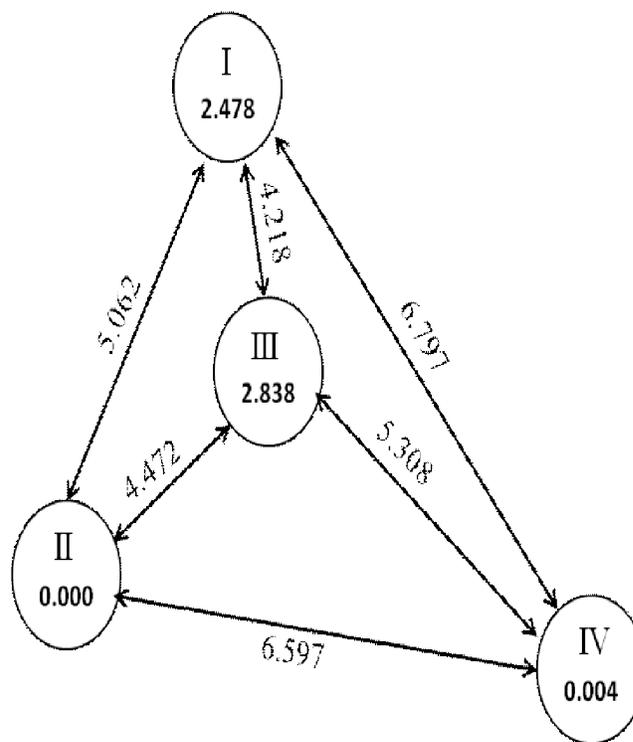
Cluster	I	II	III	IV
I	2.478	5.062	4.218	6.797
II		0.000	4.472	6.597
III			2.838	5.038
IV				0.004

prepared field at 60 cm × 20 cm spacing on the ridges. Hoeing and earthing up operations were done twice at 30 and 60 days after planting. During the courses of this experiment, no serious disease or insect pest infestations were noticed and thus crop protection measures were not employed. For each character under study, data were recorded on five randomly taken plants from each plot and expressed on plant basis. The mean of five plants used for statistical analyses. Observation on important characters *viz.*, vine length (cm), inter node length (cm), vine diameter (cm), vine weight (g), number of tubers per plant, neck length (cm), tuber length (cm), tuber diameter (cm), tuber yield per plant (g), biological yield per plant (g), harvest index (%), dry matter percentage of vine (%), dry matter percentage of tuber (%) and total soluble solids (TSS) were recorded. The data obtained on above 14 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) D^2 statistics.

The genotypes were grouped into different clusters by Tocher's method (Rao, 1952). The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude.

Results and Discussion

On the basis of D^2 analysis 12 genotypes of sweet potatoes were grouped into four clusters (table 1). Maximum number of genotypes were grouped into

**Fig. 1** : Diagram showing intra and inter cluster distances of 12 genotypes in sweet potato.

cluster III, which consisted of 7 genotypes (Indira Naveen, Sree Rethna, Indira Nandini, Gouri, IGSP-21, IGSP-25 and IGSP-39) followed by cluster I consisted 3 genotypes (Indira Madhur, IGSP-C-15 and IGSP-24), cluster II (IGSP-36) and IV (IGSP-20) (1 and 1 genotype, respectively). From the clustering pattern, it was found that the genotypes from different region were independent of their genetic origin. Hence, the genotypes studied were reliable enough for hybridization and selection. Similar opinions were also exhibited by Sattar *et al.* (2011) in potato, Islam (2004), Singh *et al.* (2007) and Bhardwaj *et al.* (2013) in bottle gourd.

The intra and inter-cluster D^2 values have been presented in table 2. The maximum inter cluster distance was observed in between cluster I and IV (6.797) followed by cluster II and IV (6.597), cluster I and II (5.062) and

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

Clusters/ Characters	Vine length (cm)	Inter node length (cm)	Vine diameter (cm)	Vine weight (g)	Nos. of tuber	Neck length (cm)	Tuber length (cm)	Tuber diameter (cm)	Yield (t/ha)	Biological yield (g)	Harvest index (%)	Dry matter % of vine	Dry matter % of tuber	TSS (%)
I	52.19	2.13	0.41	160.53	3.41	4.19	14.57	2.57	15.06	361.34	55.46	22.4	28.29	12.4
II	91.13	2.70	0.45	446.1	4.0	1.84	16.21	3.0	10.11	580.3	23.3	19.27	21.53	7.27
III	102.17	3.74	0.41	471.36	4.38	5.19	16.23	2.73	20.37	741.25	36.78	23.76	32.44	9.50
IV	104.93	3.40	0.46	532.43	3.37	7.39	18.51	4.15	37.33	1030.2	48.3	20.1	27.13	11.10

Table 4 : Contribution of each character to divergence.

Characters	Vine length (cm)	Inter node length (cm)	Vine diameter (cm)	Vine weight (g)	No. of tubers	Neck length (cm)	Tuber length (cm)	Tuber diameter (cm)	Yield (t/ha)	Biological yield (g)	Harvest index (%)	Dry matter % of vine	Dry matter % of tuber	TSS (%)	Total
Number times appearing first time	8	0	0	1	0	0	4	0	8	3	4	2	17	19	66
Per cent contribution	12.12	0	0	1.51	0	0	6.06	0	12.12	4.54	6.06	3.06	25.75	28.78	100

cluster III and IV (5.038). This suggested that in the hybridization programmed involving parents from clusters I and IV are expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties. The minimum inter cluster distance was observed in between I and III (4.218) followed by cluster II and III (4.472) indicating minimum diversity (differences) for the genes under study.

The maximum intra cluster distance was observed in cluster III (2.838) followed by cluster I (2.478), cluster IV (0.004) and cluster II (0.000), which indicate distance within the cluster. With the help of D2 values within and between clusters an arbitrary cluster diagram was constructed, which shows the relationship between different genotypes (fig. 1). However, the diagram was not drawn following the exact scale.

Genotypes belonging to the clusters with maximum inter cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregant (Seetharaman *et al.*, 1988). The present study revealed that in terms of inter cluster distance and characters with high D² values, there is a scope for varietal improvement through hybridization program involving the selected genotypes under cluster I and IV. These results are in general agreement with the findings of Islam (2004), Singh *et al.* (2007) and Bhardwaj *et al.* (2013).

Mean performance of clusters

Vine length showed the highest mean performance for cluster IV (104.93 cm), followed by cluster III (102.17 cm), cluster II (91.13 cm) and cluster I (52.19 cm). Inter node length exhibited the highest mean performance for cluster III (3.74 cm) followed by cluster IV (3.40 cm), cluster II (2.70 cm) and cluster I (2.13 cm). Vine girth showed the highest mean performance for cluster IV (0.46 cm) followed by cluster II (0.45), cluster III and cluster I had same (0.41). Vine weight exhibited the highest mean performance for cluster IV (532.43 g) followed by cluster III (471.36 g), cluster II (446.1 g) and cluster I (160.53 g).

As regards to number of tuber per plant, the highest average performance (4.38) was recorded in cluster III (4.38), which was followed by cluster II (4.0), cluster I (3.41) and cluster IV (3.37). Neck length showed maximum cluster mean performance in cluster IV (7.39 cm) which was followed by cluster III (5.19 cm), cluster I (4.19 cm) and cluster II (1.84 cm). Tuber length exhibited the highest mean performance for cluster IV (18.51 cm) followed by cluster III (16.23 cm), cluster II

Table 5 : Diserable genotypes based on cluster.

Characters/Cluster	I	II	III	IV
Vine length (cm)	Indira Madhur	IGSP-36	Sree Rethna	IGSP-20
Inter node length	Indira Madhur	IGSP-36	Sree Rethna	IGSP-20
Vine diameter (cm)	IGSP-C-15	IGSP-36	IGSP-25	IGSP-20
Vine weight	Indira Madhur	IGSP-36	Indira Naveen	IGSP-20
Number of tubers	Indira Madhur	IGSP-36	Gouri	IGSP-20
Neck length (cm)	Indira Madhur	IGSP-36	IGSP-25	IGSP-20
Tuber length (cm)	Indira Madhur	IGSP-36	IGSP-25	IGSP-20
Tuber diameter (cm)	Indira Madhur	IGSP-36	IGSP-39	IGSP-20
Tuber yield (t/ha)	IGSP-C-15	IGSP-36	Indira Naveen	IGSP-20
Biological yield (g/plant)	IGSP-C-15	IGSP-36	Indira Naveen	IGSP-20
Harvest index (%)	IGSP-C-15	IGSP-36	IGSP-39	IGSP-20
Dry matter % of foliage	Indira Madhur	IGSP-36	IGSP-25	IGSP-20
Dry matter % of tuber	IGSP-24	IGSP-36	IGSP-39	IGSP-20
TSS (%)	IGSP-C-15	IGSP-36	IGSP-25	IGSP-20

(16.21 cm) and cluster I (14.57 cm). Tuber diameter showed maximum cluster mean performance in cluster IV (4.15 cm), which was followed by cluster II (3.0 cm), cluster III (2.73 cm) and cluster I (2.57 cm).

Tuber yield per hectare showed maximum cluster mean performance in cluster IV (37.33 t/ha) followed by cluster III (20.37 t/ha), cluster I (15.06 t/ha) and cluster II (10.11 t/ha). As regards to biological yield per plant, the highest average performance was recorded in cluster I (1030.2 g) followed by cluster III (741.2 g), cluster II (580.13 g) and cluster I (361.34 g). Harvest index exhibited the highest mean performance for cluster I (55.46%) followed by cluster IV (48.3%), cluster III (36.78%) and cluster II (23.3%).

Dry matter per cent of foliage showed maximum cluster mean performance in cluster III (23.76) followed by cluster I (22.4), cluster IV (20.1) and cluster II (19.27). Dry matter per cent of tuber showed maximum cluster mean performance in cluster III (32.44) followed by cluster I (28.29), cluster IV (27.13) and cluster II (21.53). Total soluble solids exhibited the highest mean performance for cluster I (12.4%) followed by cluster IV (11.10%), cluster III (9.50%), and cluster II (7.27%).

Results of analysis revealed that cluster I was found to be better for harvest index and TSS whereas, cluster III exhibited the highest inter node length, numbers of tubers, dry matter per cent of vine and dry matter per cent of tuber. Similarly, cluster IV has better genotype for highest vine length, vine diameter, vine weight, neck length, tuber length, tuber diameter, tuber yield t/ha and biological yield. These findings were closely associated

with the reports of Mannan *et al.* (1993) in colocassia, Naskar (1996) and Ahmed *et al.* (1998) in sweet potato, Sattar *et al.* (2011) in potato.

In the contribution of each character to divergence presented in table 4, which showed TSS contributes highest (28.78%) to divergence followed by dry matter per cent of tuber (25.75%), tuber yield t/ha (12.10%), vine length (12.1%), harvest index (6.06) and tuber length (6.06). Whereas, biological yield (4.54%), dry matter % of vine (3.06%) and vine weight (1.51%) contributes lowest to divergence.

The better genotypes can be selected for most of characters on the basis of mean performance in the cluster. The best genotypes which had chosen for different characters are presented in table 5.

Conclusion

The present study revealed that in terms of inter cluster distance and characters with high D^2 values, there is a scope for varietal improvement through hybridization programme involving the selected genotypes under cluster I and IV. Thus, while planning hybridization programme for the development of heterotic hybrids and better transgressive segregants one should select genotypes IGSP-20 (cluster IV) for highest vine length, vine diameter, vine weight, neck length, tuber length, tuber diameter, tuber yield t/ha and biological yield. Similarly, Indira Madhur, IGSP-C-15, IGSP-24 from cluster I was found to be better for harvest index and TSS which diserable for processing characters.

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