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Divergence studies in sweet potato (*Ipomoea batatas* L)

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ABSTRACT

Sixteen genotypes of sweet potato (*Ipomoea batatas* L) from diverse geographical regions were evaluated to understand the extent of genetic diversity through 16 characters. Mahalanobis's D^2 analysis established the presence of wide genetic diversity among these genotypes by formation of 5 clusters. Clusters I and III comprised maximum number of genotypes followed by cluster II whereas cluster V was monogenotypic. The maximum intra-cluster distance was found in cluster III (D^2= 4,828.64) followed by cluster I (D^2= 2,597.26). However the maximum inter-cluster distance was observed between clusters IV cluster V (D^2= 34,082.51). The genotypes Kamala Sundari, SV-98, Ozarde Local and S-56-2 recorded maximum tuber yield than rest of the genotypes. Hence it is essential to evaluate these high yielding genotypes over the location to understand stable performance for their commercial utilization. Selection of genotypes is recommended from the clusters showing higher inter-cluster distance ie clusters IV and V as parents in recombination breeding programmes for obtaining desirable segregants.

Keywords: Sweet potato; genetic diversity; cluster; genotypes; characters

INTRODUCTION

Sweet potato is a dicotyledonous plant belonging to family Convolvulaceae. The genus *Ipomoea* includes more than 40 species out of which *Ipomoea batatas* is of economic importance. Sweet potato (*Ipomoea batatas* L) ranks fifth in importance for its calorific contribution in developing countries after rice, wheat, maize and cassava. It is one of the world's highest yielding crops and is widely grown as an important staple food crop in many parts of the tropics and sub-tropics over a wide range of environmental conditions. It is hexaploid species with 96 chromosomes (2n= 6X= 96).

Collection and evaluation of genotypes of any crop is a pre-requisite for any breeding programme which provides a greater scope for exploiting genetic diversity. A quantitative assessment of the genetic divergence among the collection of germplasms and relative contribution of different traits towards the genetic divergence provide essential and effective information to a breeder in hybridization programme and thereby genetic improvement of yield.

MATERIAL and METHODS

The present investigations were conducted to study the genetic divergence in sweet potato (*Ipomoea batatas* L) cultivars at instructional cum research farm of Section of Horticulture, RCSM College of Agriculture, Kolhapur, Maharashtra during kharif season. Sixteen genotypes of sweet potato were evaluated in randomized block design with two replications. Each plot measuring 3.00 m x 2.40 m comprising 60 vines of individual genotype was planted in six rows with one vine per hill plot at a spacing of 60 cm × 20 cm. All agronomical operations and plant protection measures were carried out regularly to ensure satisfactory crop growth.

The experimental material consisted of 16 genotypes viz X-108-2, H-85/70, IB-90-15-9, IB-90-11-1, DR-64, Shree Vardhini, CIPSWA-2, S-56-2, 365/2, SV-98, Konkan Ashwini, Shree Bhadra, Ozarde Local, 1870-1, DR-17 and Kamala Sundari. Observations on length of vine, number of primary branches per vine, intermodal length, volume of tuber, length of tuber, number of tubers per vine, girth of tubers, weight of peel, weight of flesh, flesh to peel ratio, average weight of tuber, tuber yield per vine, marketable yield, days required for maturity of tubers, per cent incidence of root weevil and total yield of tubers were recorded. Genetic diversity was studied using Mahalanobis's D^2 analysis (Mahalanobis 1936).

RESULTS and DISCUSSION

The D^2 values corresponding to all the possible combinations among the sixteen genotypes were computed. These 16 genotypes were grouped into 5 clusters; the clusters I and III comprised 5 genotypes, cluster II comprised 3, cluster IV comprised 2 whereas cluster V was monogenic having single genotype X-108-2 (Table 1). The formation of solitary clusters might be due to total isolation preventing the gene flow or intensive human selection for diverse adaptive complexes.

The present investigations confirm the earlier findings of Karuri et al (2010) in sweet potato, Ahmadizadeh and Felenji (2011) in potato and Kabeya et al (2012), Turyagyenda et al (2012) and Malualem et al (2013) in cassava.

The intra- and inter-cluster D^2 values among seven clusters are presented in Table 2. The intra-cluster distance varied from 0.00 in cluster V to the maximum distance in cluster III (4,828.64). This reveals the presence of divergence in cluster III. The maximum inter-cluster distance for D^2 value (34,082.51) was recorded between clusters IV and V.

The data on means of all the sixteen characters are presented in Table 3. A wide range of variation was observed among different clusters or all the cluster means. Cluster II recorded the maximum mean values for vine length (1.78 m) and internodal length (2.59 cm); cluster III had the maximum value for tuber length (17.08 cm); cluster IV had maximum mean value for tuber volume (166.35 ml), number of tubers per vine (2.55), tuber girth (17.66 cm), peel weight (19.10 g), flesh weight (204.63 g), flesh to peel ratio (11.04), average tuber weight (223.70 g), tuber yield per vine (0.54 kg) and marketable yield (43.30 tonnes/ha) while cluster V recorded the maximum mean for number of primary branches per vine (4.80). In the present study, the possibility of choice of highly divergent and desirable types based on D^2 cluster means and inter-cluster distances was also examined.

Selection of genotypes is recommended from the clusters showing higher inter-cluster distance

Table 1. Distribution of genotypes into different clusters

Cluster	Genotypes
I	H-85/70, KonkanAshwini, DR-64, Shree Vardhini, 1870-1
II	IB-90-15-9, Shree Bhadra, IB-90-11-1
III	CIPSWA-2, Ozarde Local, S-56-2, 365/2, DR-17
IV	SV-98, Kamala Sundari
V	X-108-2

Table 2. Average intra- and inter-cluster D^2 and D values

Cluster	I	II	III	IV	V
I	2,597.26 (50.96)	6,676.82 (81.71)	16,860.07 (129.84)	26,519.42 (162.84)	7,801.97 (88.32)
II		1,963.99 (44.31)	10,639.15 (103.14)	20,147.47 (141.94)	14,044.42 (118.50)
III			4,828.64 (69.48)	10,518.03 (102.55)	24,319.20 (155.94)
IV				3,510.73 (59.25)	34,082.51 (184.61)
V					0.00 (0.00)

Figures in parentheses denote D values

Table 3. Mean performance of 5 clusters of sweet potato for various characters

Cluster	Character							
	Vine length (m)	Number of primary branches/vine	Internodal length (cm)	Tuber volume (ml)	Tuber length (cm)	Number of tubers/vine	Tuber girth (cm)	Peel weight (g)
I	1.66	3.80	2.54	76.17	14.08	1.54	10.70	10.38
II	1.78	3.77	2.59	110.10	15.85	1.40	14.05	15.17
III	1.69	3.82	2.18	150.42	17.08	2.36	13.90	16.34
IV	1.34	3.70	2.15	166.35	16.69	2.55	17.66	19.10
V	1.64	4.80	2.25	20.10	11.84	1.20	7.18	5.00

Table 3. Contd…..

Cluster	Character							
	Flesh weight (g)	Flesh to peel ratio	Average tuber weight (g)	Tuber yield/vine (kg)	Marketable yield (tonnes/ha)	Days taken to tuber maturity	Per cent root weevil incidence	Total tuber yield (tonnes/ha)
I	63.76	6.45	75.25	0.11	8.97	113.10	24.0	9.38
II	109.75	7.89	124.88	0.17	13.87	116.00	35.0	14.25
III	141.32	8.98	157.02	0.35	28.17	115.90	35.2	29.11
IV	204.63	11.04	223.70	0.54	43.30	118.00	44.5	43.97
V	24.70	5.28	29.15	0.03	2.42	109.00	10.0	2.76

(clusters IV and V) also with total yield of tubers as parents in recombination breeding programmes for obtaining desirable seggregants.

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