Original Research Article

Principal Component Assessment of Sweet Potato [*Ipomoea batatas* (L.) lam] Genotypes for Yield and Quality Traits

S.S. Solankey[1,2]* and P.K. Singh[2]

[1]Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural University, Sabour, Bhagalpur- 813 210 (Bihar), India
[2]Department of Vegetable Science, N.D.U.A. & T., Kumarganj, Faizabad- 224 229 (U.P.), India
Corresponding author

A B S T R A C T

Keywords

Eigen value, Euclidean distance, Genetic diversity, Principal components

An experiment was conducted to assess principal component and genetic diversity in 20 sweet potato genotypes procured from diverse sources *viz.,* CIP (Peru), NDUA&T (Faizabad, India). Out of seventeen studied traits, eleven quantitative characters and six qualitative traits were studied. Each pair of genotypes *viz.*, CIP-4 and CIP-2; NDSP-4 and CIP-4; as well as NDSP-4 and CIP-9 exhibited greatest dissimilarity with Euclidean distances of 9.8 so the genotypes should be preferred for sound selection programmes. The first five principal components (PCs) with Eigen values greater than one were accounted for 76.0% of the total variance and proportionate contributed of each PC was 26.0, 20.3, 13.7, 9.2 and6.9, respectively. The first principal component (PC_1) exhibited positive association with length of vine, length of vine internodes, petiole length, number of leaves per plant, number of branches (main), number of days required for maturity, number of tubers per plant, yield per plot, fresh weight of tubers per plant, dry matter content, starch content and whereas negative association with moisture content, total soluble solids, length of tuber and sugar content. The second PC (PC_2) have positive association with number of days required for maturity, girth of tuber, length of tuber, dry matter content and starch content. The given technique of analysis could be fruitful to select diverse parents and widen indigenous gene-pool of sweet potato.

Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam] is a member of the Convolvulaceae, the morning-glory family and belongs to the genus Ipomoea. Sweet potato is an important secondary staple in the tribal regions of India and consumed as vegetable, boiled or often fermented into food and beverages. The cultivated sweet potato (*Ipomoea batatas* L. Lam.) is an autohexaploid originated from Northern South America and Southern part of Central America, has grown in all over word (Afuape *et al*., 2011). Sweet potato is an important crop which ranks sixth of the world after wheat, rice, corn, potatoes and barley. Sweet potato germplasm is estimated at more than 1,000 species in the world but only 142 species are identified by researchers. Although the potential is quite large, but genetic studies as a basis for the development of cultivars is still limited. Asia is the world's largest sweet potato

producing region out of which 90% of total world production contributed by China alone. However, India ranked on seventh position with total area of 0.12 million hectares and production 1.12 million tones edible tubers, whereas productivity of the crop is 9.0 tonnes per ha (FAOSTAT, 2009). Sweet potato is grown as rainfed crop during *Kharif* (June-August) as well as irrigated crop during *Rabi* (October - December) in several states of India mainly in Assam, Bihar, Karnataka, Kerala, Madhaya Pradesh, Maharashtra, Orissa and Uttar Pradesh. As one of the oldest vegetables known to mankind, have been in cultivation since about 10,000 years ago (Veasey *et al.*, 2008), the crop has evolved into many morphotypes creating broad genetic diversity for most of the desirable agronomic traits. Sweet potato is a highly heterozygous and cross pollinated groups in which several traits show continues variability there is extensive variability within the species which could be exploited by the plant breeders (Afuape *et al.*, 2011). Genetic diversity could be boost by germplasm collections and assembly of new clones. Genetic diversity assessment within a population could provide information relevant to genetic relationship of concerned genotypes. This genetic relationship between two individuals could be measured based on the similarity and dissimilarity coefficient of studied characters (Soegianto *et al.*, 2011). Understanding the nature and magnitude of variability existing among sweet potato genetic materials for important traits is vital for the effective utilization of such materials for breeding purposes. Objective of this study was to assess principal components and genetic relationship among various genotypes of sweet potato using quantitative and qualitative traits. Data will be useful for the sake of effective selection and differentiation of various genotypes. It

would also be helpful for plant breeders to select readily diverse parents which would add new germplasm base for sweet potato breeding program.

Materials and Methods

Twenty sweet potato genotypes of diverse origin were procured from from International Potato Centre (CIP), Peru and NDUA&T, (Faizabad, India). The experiment was arranged in a randomized complete block design (RCBD) with four replications. This experiment was carried out at Vegetable Research Field of NDUA&T, Faizabad, India, during planting season of October. Each genotype was planted on 3m long and 2.4 m wide plot holding four rows. Each row accommodated ten plants and thus forty plants adjusted on per plot. Vine cutting from the top portion of 3-4 months old mother plants were taken for planting. All the agronomical practices were applied to raise good and healthy crops. The maturity of sweet potato crop was identified as a symptom of slightly turn yellow colour and slat to shed after 100-135 days to planting. During harvesting of mature tuber were digged carefully with the help of spade avoiding any mechanical injury. Under present experiment, seventeen studied traits were partitioned in two major groups of 11 quantitative and 6 qualitative traits evaluated for each genotype. Quantitative traits including all morphological characters was namely six aerial parts *viz.*, length of vine (LV), length of vine internodes (LVI), length of petiole (LP), number of leaves/plant (NLPP), number of branches per/plant (NBPP), days required to maturity (DRM) and five storage root characters were recorded *viz.*, number of tuber/plant (NTPP), fresh weight of tubers/plant (FWTPP), size of tuber width (SRW), size of tuber length (STL) and tuber yield/plot (TYPP). While six qualitative traits were

namely dry matter content (DMC), moisture content (MC), total soluble solids (TSS), starch content (SC), total sugar content (TSC) measured in mg/ 100g and total carotene content (TCC) measured in IU/ 100g estimated by the standardized protocol of Dubois *et al.* (1956). For each trait under present study, data were recorded on five randomly taken plants from the middle two row of each plot and expressed on per plant basis.

All studied characters were also analyzed by numerical taxonomic techniques using principal component analysis (PCA) and cluster analysis (Sneath and Sokal, 1993). Euclidean dissimilarity coefficients were calculated for all the genotypes of sweet potato from their morphological data. Estimates of Euclidean distance coefficients were made for all pairs of genotypes. The resulting Euclidean dissimilarity coefficients were used to evaluate the relationship among the entries using complete linkage method NTSYSpc version 2.01 (Roulf, 2002). PCA was also performed with the same data matrix. Scattered plots of first three principal components were produced to provide a graphical representation of the pattern of variation among all the genotypes of sweet potato (Statistica, version 10.0).

Results and Discussion

Dissimilarity coefficient of 20 genotypes ranged from 1.0 to 9.8 (Table 1). 'NDSP-65 and CIP-1' , 'CIP-440038 and CIP-8' and 'NDSP-9 and CIP SWA-1' were the closest genotypes with the lowest dissimilarity index of 1.0 followed by pairs of genotypes 'CIP-6 and CIP-1', 'CIP-4434 and CIP-4', 'NDSP-10 and CIP-4', 'CIP SWA-2 and CIP-5', 'CIP-4434 and CIP-9', and 'NDSP-10 and CIP-9' having Euclidean distance of 1.1. The genotypes 'CIP-4 and CIP-2', 'NDSP-4 and CIP-4', 'NDSP-4 and CIP-9

exhibited the greatest dissimilarity with Euclidean distances of 9.8 Genotypes CIP-2, CIP-4, CIP-9, CIP-3 and CIP SWA-2 exhibited the maximum Euclidean distances of all the other sweet potato genotypes used (Table 1). Pipan et al. (2017) suggested that selection and breeding can also improve genetic potential and increase genetic uniformity in sweet potato. In sweet potato similar pattern of Euclidean dissimilarity index was reported by Ahmadizadeh and Felenji (2011).

The first five principal components (PCs) with eigen values greater than one accounted for 76.0% of the variability amongst 20 sweet potato genotypes (Table 2). The first principal component (PC_1) accounted for 26.0% of total variation. The quantitative traits that contributed more positively to PC_1 was length of vine, length of vine internodes, petiole length, number of leaves per plant, number of branches (main), number of days required for maturity, number of tubers per plant, yield per plot, fresh weight of tubers per plant, girth of tuber, dry matter content, starch content, and carotene content whereas moisture content, total soluble solids, length of tuber and sugar content were negatively associated with PC_1. Principal component 2 (PC_2) had 20.3 % of the total variability. Number of days required for maturity, girth of tuber, length of tuber, dry matter content and starch content have positive contribution to PC_2, whereas rest of traits were negatively associated with PC_2 (Table 2). Principal component 3 (PC_3) exhibited 13.7% of the total variation in studied traits and having positive association with length of vine, number of leaves per plant, number of branches (main), number of days required for maturity, moisture content and carotene content while remain traits were negatively associated with PC_3.

Table.1 Euclidean distances based on 17 quantitative and qualitative traits for 20 sweet potato genotypes

Genotype	CIP-1	CIP-2	CIP-3	CIP-4	CIP-5	CIP-6	CIP-7	CIP-8	CIP-9	CIP SWA-1	CIP SWA-2	CIP-4027	CIP-4434	CIP-420027	CIP-440038	CIP-442074	NDSP-4	NDSP-9	NDSP-10	NDSP-65
CIP-1	0.0																			
CIP-2	3.2	0.0																		
CIP-3	6.2	3.8	0.0																	
CIP-4	2.2	9.8	2.8	0.0																
CIP-5	4.5	1.4	5.1	2.4	0.0															
CIP-6	1.1	2.3	1.7	1.4	3.5	0.0														
CIP-7	6.2	3.0	6.8	4.0	1.8	5.2	0.0													
CIP-8	3.9	7.2	4.5	1.7	7.5	2.9	2.3	0.0												
CIP-9	2.2	9.7	2.8	5.8	2.4	1.4	4.0	1.7	0.0											
CIP SWA-1	1.6	1.7	2.2	7.3	3.0	6.7	4.6	2.3	7.1	0.0										
CIP SWA-2	5.5	2.4	6.1	3.3	1.1	4.6	6.7	1.7	3.3	4.0	0.0									
CIP-4027	5.8	2.6	6.4	3.6	1.4	4.8	3.9	1.9	3.6	4.2	3.0	0.0								
CIP-4434	1.7	1.8	2.3	1.1	2.9	6.5	4.7	2.4	1.1	5.7	4.0	4.3	0.0							
CIP-420027	1.2	4.3	8.9	3.4	5.6	2.1	7.3	5.0	3.4	2.7	6.6	6.9	2.7	0.0						
CIP-440038	6.4	3.2	7.0	4.2	2.0	5.4	2.2	2.5	4.2	4.8	8.8	5.9	4.9	7.5	0.0					
CIP-442074	3.9	7.5	4.5	1.7	7.0	2.9	2.3	1.0	1.7	2.3	1.7	1.9	2.4	5.0	2.5	0.0				
NDSP-4	3.2	1.2	3.8	9.8	1.4	2.3	3.0	7.0	9.8	1.7	2.4	2.6	1.8	4.3	3.2	7.3	0.0			
NDSP-9	2.6	6.2	3.2	4.2	2.0	1.7	3.6	1.3	4.0	1.0	3.0	3.2	1.2	3.7	3.8	1.3	6.3	0.0		
NDSP-10	3.2	3.8	3.8	1.1	1.3	2.2	3.0	7.0	1.1	1.6	2.3	2.6	1.7	4.3	3.2	6.9	3.3	6.5	0.0	
NDSP-65	1.0	2.3	1.6	1.3	3.5	3.1	5.2	2.9	1.3	6.2	4.6	4.8	7.2	2.1	5.4	2.9	2.2	1.6	2.2	0

Table.2 Variation among sweet potato genotypes accounted for first five principal components

Traits	PC1	PC2	PC3	PC4	PC5
Eigenvalues	4.4	3.4	2.3	1.6	1.2
Cumulative eigenvalues	4.4	7.9	10.2	11.8	12.9
Variance (%)	26.0	20.3	13.7	9.2	6.9
Cumulative variance (%)	26.0	46.2	60.0	69.2	76.0
Traits	**Eigenvectors**				
Length of vine (cm)	0.363	-0.198	0.317	0.024	-0.015
Length of vine internodes (cm)	0.342	-0.111	-0.025	0.303	0.322
Petiole length (cm)	0.284	-0.024	-0.076	-0.006	0.408
Number of leaves per plant	0.298	-0.265	0.195	0.094	-0.215
Number of branches (main)	0.164	-0.110	0.309	-0.229	-0.409
Number of days required for maturity	0.385	0.023	0.021	0.226	0.014
Number of tubers per plant	0.063	-0.298	-0.399	-0.012	0.032
Yield per plot (kg)	0.324	-0.135	-0.368	-0.173	-0.100
Fresh weight of tubers per plant (g)	0.309	-0.145	-0.368	-0.257	-0.072
Girth of tuber (cm)	0.120	0.176	-0.138	-0.452	-0.202
Length of tuber (cm)	-0.122	0.062	-0.190	-0.300	-0.124
Dry matter content (%)	0.228	0.447	-0.037	0.117	-0.121
Moisture content (%)	-0.194	-0.466	0.062	-0.099	0.181
Total soluble solids (%)	-0.175	-0.106	-0.198	0.527	-0.387
Starch content (%)	0.210	0.455	-0.038	0.141	-0.128
Sugar content (%)	-0.005	-0.243	-0.164	0.230	-0.458
Carotene content (IU / 100g)	0.095	-0.091	0.448	-0.175	-0.141

Fig.1 Scattered diagram of first two principal components based on mean values of 17 quantitative traits in 20 genotypes of sweet potato
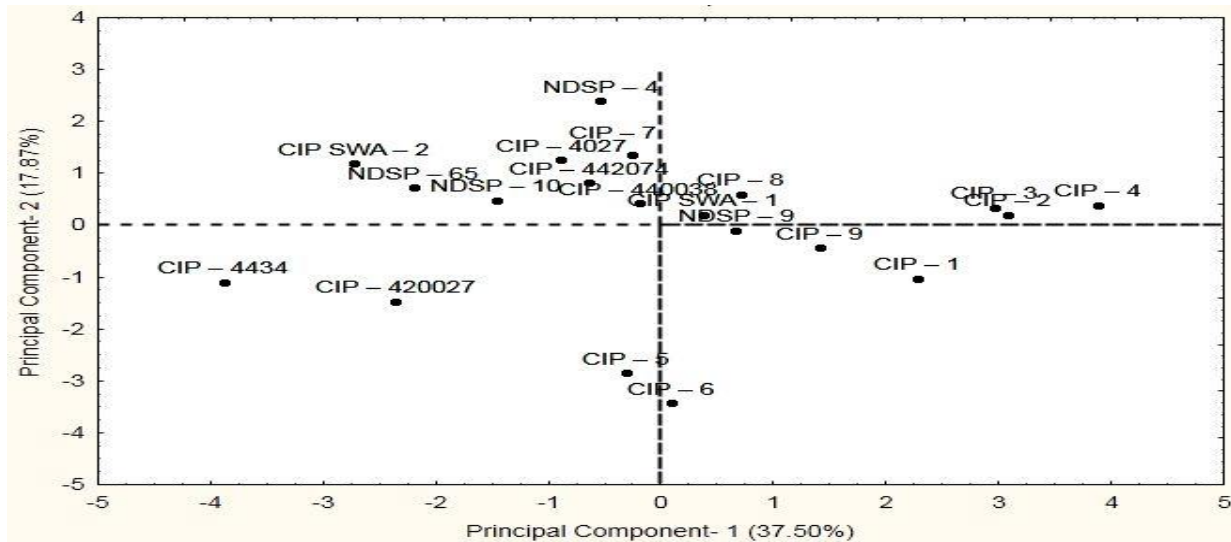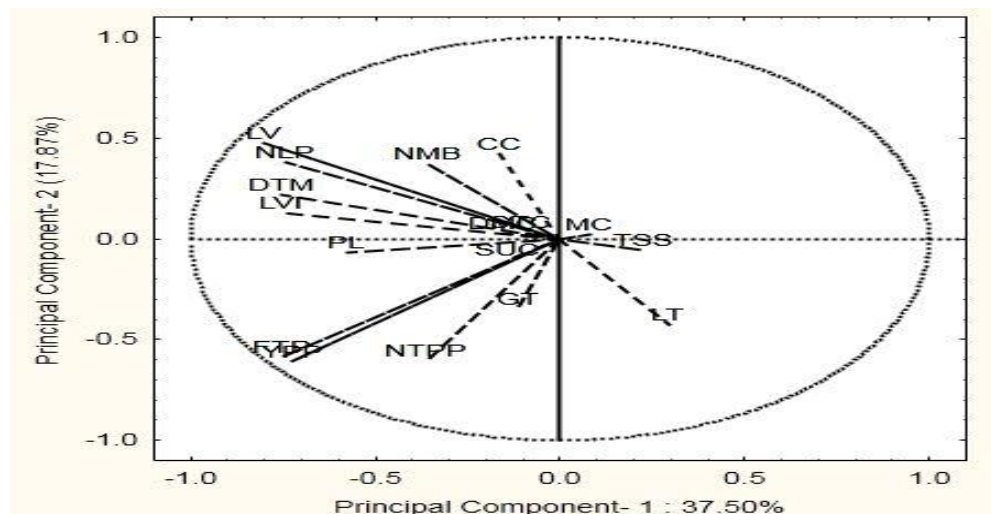
Fig.2 Principal component biplot for yield and quality component in sweet potato

The first two PCs were plotted to observe the relationship between 20 genotypes of sweet potato (Fig. 1) as similar reported by Tairo *et al*. (2008); Afuape *et al*. (2011) and Ravishanker *et al.,* (2013). The projection of component traits on PC_1 and PC_2 revealed that the number of tubers per plant, fresh weight of tubers per plant (g) and girth of tuber (cm) are positively associated with yield per plot (Kg) (Fig.2).

On the basis of above facts and figures the evaluated genotypes of sweet potato genotypes have narrow genetic base due to undergone high level of genetic erosion and selection pressure by the farming communities. It may be due to utilization of same ancestors and seed source by the farmers for the cultivation of crop. This preliminary investigation provided useful information regarding their yield and quality traits. The given technique of analysis could be helpful to select diverse parents and widen indigenous gene-pool of sweet potato for future breeding programs.

References

Afuape S O, Okocha P I and Njoku D (2011). Multivariate assessment of the agromorphological variability and yield components among sweet potato (*Ipomoea batatas* (L.) Lam) landraces. *African Journal of Plant Science*, 5 (2): 123-132.

Ahmadizadeh M and Felenji M (2011). Evaluating diversity among potato cultivars using agro-morphological and yield components in fall cultivation of Jiroft Area. *American-Eurasian Journal of Agriculture and Environmental Sciences,* 11 (5): 655-662.

Dubois M, Gilles R A, Hamilton J K, Rabers P A and Smith F (1956). Use of phenol reagent for the determination of total sugar. *Annals of Chemistry*, 28: 350.

FAOSTAT. (2009). Production Year Book for 2008. Rome, Italy.

Pipan B, Znidarcic D, Kunstelj N and Meglic V (2017). Genetic evaluation of sweet potato accessions introduced to the central european area. *Journal of Agricultural Science and Technology (JAST),* 19 (4): 1139-1150.

Ravishanker, Kumar, S, Baranwal D K, Chatterjee A and Solankey S S (2013). Genetic diversity based on cluster and

principal component analyses for yield and quality attributes in Ginger (*Zingiber officinale* Roscoe). *Intern Journal of Plant Breeding and Genetics*, DOI: 10.3923.

Roulf F J (2002). *NTSYS–pc: Numerical Taxonomy and Multivariate Analysis System*. Version 2.01. Exter Publishing Ltd., Setauket, NY.

Sneath P H A and Sokal R P (1993). *Numerical Taxonomy: The Principles and Practices of Numerical Classification.* W.H. Freeman & Co., San Francisco, USA. 573p.

Soegianto Andy, Ardiarini Noer Rahmi and Sugiharto Arifin Noor (2011). Genetic Diversity of Sweet Potato (*Ipomoea batatas* L.) in East Java, Indonesia.

Journal of Agricultural Science and Food Technology, 1 (9):179-183.

Tairo F, Mneney E and Kullaya A (2008). Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasm collection from Tanzania. *African Journal of Plant Science*, 2 (8): 77-85.

Veasey E A, Borges A, Rosa M S, Queiroz Silva J R, Bressan E de A and Peroni N (2008). Genetic diversity in Brazilian sweet potato (*Ipomoea batatas* (L.) Lam., *Solanales Convolvulaceae*) landraces assessed with microsatellite markers. *Genetics and Molecular Biology*, 31 (3): 725-733.