

EVALUATION OF SWEET POTATO GENOTYPES FOR HIGH YIELD AND RICH IN β -CAROTENE CONTENT

M. R. Ahmed¹, M. M. Hossain², M. K. R. Bhuiyan³
M. M. Rahman⁴ And M. A. Karim⁵

¹Bangladesh Public Administration Training Centre, ²Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), ³Bangladesh Agricultural Research Institute, ⁴Department of Horticulture, BSMRAU and ⁵Department of Agronomy, BSMRAU.

Abstract

The research was under taken to screen out suitable genotypes of sweet potato (*Ipomoea batatas* L.) for developing β -carotene rich bakery processed products. The experiment evaluated and clustered the twenty eight genotypes on the basis of four yield contributing characters (total fresh tuber yield, β -carotene content, dry matter and dry yield). It was found a strong relation between flesh color and β -carotene content. Deep orange flesh color of sweet potato had the highest β -carotene but it was not present in white flesh sweet potato. Hierarchical cluster analysis showed an over riding importance of total fresh tuber yield and β -carotene among the four characters. The 28 genotypes were clustered into four groups. Among the four clusters, the mean yield of cluster 2 is the highest (58.95 t/ha) followed by the mean yield of cluster 4 but the average value of β -carotene in cluster 2 was not satisfactory (0.43mg/100g), whereas cluster 4 contained the highest average value of β -carotene (1.75 mg/100g). So among the four clusters, cluster 4 was consistent with the objectives of study. All the members of the cluster (group 4) provided the satisfactory total fresh, tuber yield but the CIP-440074-2 genotype and Kamala Sundari variety had the highest β -carotene.

Keywords: Sweet potato, yield and β -Carotene.

Introduction

Vitamin A deficiency is a major problem in Bangladesh. Dietary vitamin A deficiency causes debilitating health problems such as xerophthalmia, corneal lesions, keratomalace and in many instances death. These problems affecting young children from Africa to Asia countries (WHO, 1995).

Sweet potato has been received increasing attention to agriculturalists and ecologists interested in developing sustainable food production systems in the tropics, because it has remarkable pro-vitamin A quantities (Woolfe, 1992). It can grow well in soils with limited fertility; it is relatively drought tolerant, provides good ground cover

and is usually cultivated without fertilizer or pesticide (Ewell, 1990).

Widely consumed varieties, however, are white or pale yellow in flesh color and contain very little β -carotene. Orange-fleshed and deep yellow fleshed sweet potato storage roots are high in β -carotene, are less eaten. Consumption of orange-fleshed and deep yellow fleshed sweet potato roots and sweet potato-based processed foods would provide sustainable, cost-effective and necessary vitamin A (Ameny and Wilson, 1997). Therefore, the use of colored-fleshed sweet potatoes as a food source of pro-vitamin A merits further attention. But most of the cultivated sweet potato in Bangladesh are mostly white or pale yellow which having little or no vitamin A (Woolfe, 1992).

The genetic variability in sweet potato lines is one of the most important factors for widely varies nutrient composition on sweet potato root (Woolfe, 1992). This was a reflection of the wide spectrum of the root flesh color of sweet potato. White fleshed roots of some CIP (International Potato Centre) genotypes had the lowest total carotenoid, whereas orange- fleshed some genotypes had the highest. Carotenoids especially β -carotene are largely responsible for flesh color (Almeida-Muradian *et al.*, 1992;

Takahata *et al.*, 1993). Therefore, 27 CIP genotypes and one released variety Kamala Sundari were put in to evaluation trail with the following to objectives.

1. Evaluation of yield contributing characters and β -carotene content of the selected 28 genotypes of sweet potato including Kamala Sundari and
2. screening out suitable genotypes of sweet potato for developing processed products.

Materials and Methods

Twenty eight sweet potato genotypes of diverse growth habits and yield potentials were selected for the study. Table 1 shows the list of the genotypes along with their some phenotypical characters. Among the genotypes 27 were CIP genotypes and one (Kamala Sundari) was high yielding varieties developed by the Bangladesh Agricultural Research Institute (BARI). The experiment was conducted at Tuber Crops Research Centre (TCRC), BARI, Joydebpur, during November 2008 to May 2009 and the field evaluation pictorial view has been shown in Fig. 1. The vines were planted on 14 November 2008 in the field having plot size of 3.0 m \times 3.0 m with 60 cm \times 30 cm space. Each genotype replicated thrice following RCBD. The crop was

fertilized with recommended doses. Crop was harvested on 23 April 2009. Data were recorded from 10 randomly selected plants. The following data were recorded: length of main vine (cm), number of tubers per plant, fresh weight of tuber/plant (g), length of tuber (cm), diameter of tuber (cm), marketable fresh tuber yield (t/ha), non marketable fresh tuber yield (t/ha), total fresh tuber yield (t/ha), dry matter (%), dry yield (t/ha) and β -carotene (mg/100g).

Table 1. List of selected 28 sweet potato genotypes including Kamala Sundari with phenotypic characters

Germplasms		Skin color of tuber	Flesh color of tuber
CIP-441553		Dark cream	Orange
CIP190083. 5		Dark cream	Purple
CIP-400541		Dark cream	Medium orange
CIP-194513. 15		Dark cream	Dark orange
CIP-441132		Cream	Medium orange
CIP-440027		Dark cream	Dark orange
CIP-187016. 2		Dark cream	Pale orange
CIP-440031		Cream	Medium orange
CIP-440034	White		White
CIP-194515. 15		Dark yellow	Medium orange
CIP-440021		Dark cream	Dark orange
CIP-440267. 2		Dark cream	Medium orange
CIP-420014		Dark yellow	Dark orange
CIP-440074-2		Cream	Yellow
CIP-440020	Cream		Orange
CIP-440513		Dark cream	Light orange
CIP-440281		Dark cream	White
CIP-440112		Cream	Dark cream
CIP-194541. 45		Dark cream	Orange
CIP-401430		Pale yellow	Purple
CIP-440139		Dark yellow	Dark orange
CIP-441357	Dark	yellow	White
CIP-194573. 9		Medium orange	Light orange
CIP-194549. 6		Dark yellow	White
CIP-440047		Cream	Dark orange
CIP-440280	Cream		White
Kamala Sundari		Light red	Deep orange

Source: Alam *et al.* , 2008

The cluster and discriminate function analyses were performed in the data of four yield contributing characters like total fresh tuber yield (t/ha), β -carotene content (mg/100g), dry matter (%) and dry yield (t/ha) for classification of characters genotypes into a number of groups. The statistical package SPSS version 10.0, 1999 was used in conducting these analyses. The cluster analysis indicates the grouping of a number of genotypes into several clusters having similar characteristics on the basis of variables considered in the analysis.

Two types of cluster analysis such as k-means (non-hierarchical or quick) and hierarchical cluster analysis were employed. k-means cluster analysis is mostly suitable for variables having similar units such as length of main vine (cm), length of tuber (cm), diameter of tuber (cm) etc. While the hierarchical cluster analysis is mostly used for the variables of dissimilar units such as growth duration (day), plant height (cm), dry matter (%), yield (t/ha).

Discriminant Function Analysis (DFA) was employed for conformity of the results on grouping the genotypes. In addition, the precession level of the clustering was also accessed through DFA. The discriminatory functions (e. g. , the principal components in the

analysis) played the vital role in identifying the set of variables contributed more in clustering a large number of genotypes into homogenous groups. Through step wise procedures of DFA, structure matrix of variables, test of equality of group means and Mahalanobis distance (D^2) analysis were done.

Result and discussion

Twenty eight sweet potato genotypes including Kamala Sundari formed the treatments variables. Details of the genotypes are presented in Table 2 From the table 1 and table 2, it was found that a strong relation between flesh color and β -carotene content. The orange flesh color leads to more β -carotene, while white flesh was almost absence of it. The deep orange flesh Kamala Sundari contain highest β -carotene (4.25 mg/100g) and CIP-187016.2 genotype produced the highest yield (62.27 t/ha). The yellow flesh genotype CIP-440074-2 produced considerable yield (44.25 t/ha) and also having second highest β -carotene (2.53mg/100g) content. This is supported with the findings of Ameny and Wilson (1997) who stated that white or pale yellow flesh contain but very little β -carotene and orange-fleshed sweet potato roots high in carotenoids.

Table 2. Yield contributing characters of the selected 28 genotypes of sweet potato including Kamala Sundari

Germplasms	Total fresh tuber yield(t/ha)	Dry yield (t/ha)	Dry matter (%)	β -carotene (mg/100g)
CIP-441553	17.85	7.35	24.93	1.05
CIP190083.5	61.58	14.28	22.83	.06
CIP-400541	26.21	6.86	26.17	.56
CIP-194513.15	37.30	11.40	30.33	1.03
CIP-441132	54.88	12.66	23.17	.74
CIP-440027	42.39	8.50	20.17	1.03
CIP-187016.2	62.27	13.80	22.33	1.15
CIP-440031	33.60	7.55	22.17	1.25
CIP-440034	26.23	8.48	32.33	.00
CIP-194515.15	61.92	11.13	17.67	.37
CIP-440021	47.32	7.66	16.17	.95
CIP-440267.2	54.89	11.60	21.17	.23
CIP-420014	32.72	8.63	26.50	1.05
CIP-440074-2	44.25	12.09	27.33	2.53
CIP-440020	29.21	7.30	25.00	.22
CIP-440513	27.09	7.18	26.33	.33
CIP-440281	35.53	9.38	26.33	.00
CIP-440112	46.79	13.32	28.17	1.25
CIP-194541.45	38.00	9.09	24.00	.97
CIP-401430	25.15	6.50	26.03	.13
CIP-4401.39	48.20	11.69	24.00	.95
CIP-441357	58.05	11.94	20.67	.00
CIP-194573.9	59.11	15.31	25.50	.00
CIP-189151.3	25.69	4.58	17.83	.00
CIP-194549.6	37.29	10.65	28.33	.01
CIP-440047	45.03	10.42	23.00	1.32
CIP-440280	18.64	4.66	24.83	.00
Kamala Sundari	42.33	9.84	23.25	4.25

Cluster analysis was performed using the four parameters; total fresh tuber yield (t/ha), β -carotene (mg/ 100g), dry matter (%) and dry yield (t/ha). Hierarchical cluster analysis was done at first to find out the most important characters for clustering (Table 3).

The correlations of total fresh tuber yield (t/ha) and β -carotene (mg/100g) with standardized canonical discriminate functions were 0.872 with function 1 and 0.993 with function 2

respectively. The other values for dry matter (%) and dry yield (t/ha) were 0.988 and 0.862 respectively but these correlation values against function 3. So the analysis showed an overriding importance of total fresh tuber yield (t/ha) and β -carotene (mg/ 100g). In addition, test of equality of group means indicated that total fresh tuber yield (t/ha) and β -carotene (mg/100g) were significant at 0% and 3% level of significant respectively (Table 4).

Table 3. Structure Matrix of 4 variables measuring correlation with discriminate function by hierarchical cluster and discriminate function analyses

Yield Characters	Function		
	1	2	3
Total fresh tuber yield (t/ha)	0.872	-0.323	0.179
β -carotene (mg/100g)	0.045	0.993	0.078
Dry matter (%)	-0.092	0.003	0.988
Dry yield (t/ha)	0.308	-0.093	0.862

Table 4. Tests of Equality of 4 Group Means for four variables (yield contributing characters) evaluated in 28 sweet potato genotypes including Kamala Sundari by hierarchical cluster and discriminate function analyses

Yield Characters	Wilks' Lambda	F	df1	df2	Sig.
Total fresh tuber yield (t/ha)	.047	162.288	3	24	.000
Dry matter (%)	.777	2.296	3	24	.103
Dry yield (t/ha)	.283	20.298	3	24	.000
β -carotene (mg/100g)	.564	6.179	3	24	.003

The three canonical discriminant functions were also used in the analysis. The function 1 (total fresh tuber yield) and function 2 (β -carotene) explained 97.1% and 2.7% of variance along with

canonical correlation coefficient of 0.981 and 0.649 respectively (Table 5.5). So both the two functions contributed 99.8% variance.

Table 5. Percent contributed by discriminant function in explaining the variance on the basis of three canonical discriminant functions of 28 sweet potato genotypes including Kamala Sundari by DFA

Function	Eigen value	% of Variance	Cumulative %	Canonical correlation
1	26.221	97.1	97.1	0.981
2	0.729	2.7	99.8	0.649
3	0.064	2.0	100.0	0.246

Finally, hierarchical clustering was employed and a dendrogram was developed with the four parameters; total fresh tuber yield (t/ha), (mg/100g), dry matter (%) and dry yield (t/ha) and grouped the 28 genotypes into four (Table 6).
-carotene

Table 6. Grouping of 28 sweet potato genotypes including Kamala Sundari by hierarchical clustering based on four yield contributing characters

Cluster	No of genotypes in each cluster	Genotype
1	8	CIP-441553, CIP-440280, CIP-440034, CIP-401430, CIP-189151.3, CIP-440020, CIP-440513, CIP-400541
2	7	CIP-441132, CIP-440267.2, CIP-441357, CIP-194573.9, CIP190083.5, CIP-194515.15, CIP-187016.2
3	6	CIP-440031, CIP-420014, CIP-194513.15, CIP-194541.45, CIP-440281, CIP-194549.6
4	7	Kamala Sundari, CIP-440074-2, CIP-440027, CIP-440047, CIP-4401.39, CIP-440112, CIP-440021

Pair-wise Mahalanobis distances (D^2) analysis among 4 clusters was done by step-wise DFA (Table 7) and it was found that among 4 clusters, cluster 2 showed the highest distant unit of 35.205 with cluster 1 followed by the distance between clusters 2 and 4 (23.887). Several workers did similar

D^2 analysis to identify the distinct clusters in different studies (Wilfredo *et al.*, 2000).

In the figure (Fig. 2) function 1 and function 2 represent total fresh tuber yield and β -carotene respectively and it was revealed that the average linkage and distribution of the 28 sweet potato

genotypes in the four clusters where lowest yield and two genotypes of group showed group 2 leads to highest yield 4 represented highest β -carotene content with less β -carotene and group 1 having with considerable yield.

Table 7. Pair wise Mahalanobis distance (D^2) between 4 clusters of 28 sweet potato genotypes including Kamala Sundari

Cluster	1	2	3	4
1		35.205	21.215	11.623
2	35.205		14.112	23.887
3	21.215	14.112		10.059
4	11.623	23.887	10.059	

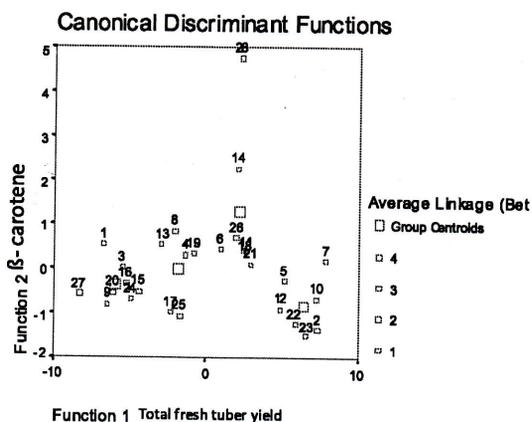


Fig. 1. The average linkage and distribution of the genotypes in the four clusters.

Moreover, the comparative descriptive statistical parameters were shown in Table 8. It was found that 28%, 25%, 21% and 25% of 28 genotypes were oriented respectively in cluster 1, 2, 3 and 4. Among the four clusters, the mean yield of cluster 2 is the highest (58.9 t/ha) followed by the mean yield

of cluster 4 but the average value of β -carotene in cluster 2 was not satisfactory (0.36 mg/100g), whereas cluster 4 (45.18 t/ha) contained the highest average value of β -carotene (1.75 mg/100g). So among the four clusters, cluster 4 was consistent with the objectives of study.

Table 8. Descriptive statistics of initial and selected genotypes under each cluster and the percentage of genotypes out of their respective total number

Cluster No.	No. of genotype under each	Percent of Total	Yield			Total yield (t/ha)%			Dry matter%			Dry yield			β -Carotene(g/100g)		
			Min	Max	Mean \pm SE	Min	Max	Mean \pm SE	Min	Max	Mean \pm SE	Min	Max	Mean \pm SE	Min	Max	Mean \pm SE
1	8	17.85	29.21	24.5 \pm 4.05	17.83	32.33	25.43 \pm 3.92	4.58	8.48	6.61 \pm 1.35	0	1.05	0.28 \pm 0.36				
2	7	54.88	62.27	58.9 \pm 3.17	17.67	25.5	21.90 \pm 2.43	11.13	15.31	12.96 \pm 1.54	0	1.15	0.36 \pm 0.43				
3	6	32.72	38	35.74 \pm 2.17	22.17	30.33	26.27 \pm 2.92	7.55	11.4	9.45 \pm 1.38	0	1.25	0.17 \pm 0.56				
4	7	42.33	48.2	45.18 \pm 2.34	16.17	28.17	23.15 \pm 4.10	7.66	13.32	10.50 \pm 2.01	0.95	4.25	1.75 \pm 1.23				
Initial total																	
Selected																	
1 0																	
2 0																	
3 0																	
4	2	7	42.33	44.25	43.29	1.33	23.25	27.33	25.29	2.88	9.84	12.09	10.96	1.59	2.53	4.25	3.39
28 genotype																	

Canonical Discriminant Functions

Average Linkage (Between Groups) = 4

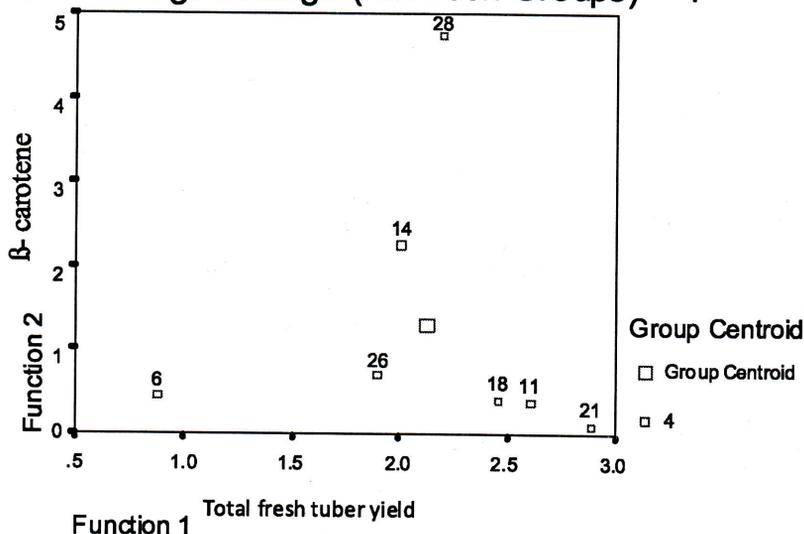


Fig. 2. The average linkage and distribution of the genotypes in cluster 4.

In the above figure (Fig. 2) function 1 and function 2 represent total fresh tuber yield and β -carotene respectively. All the members of the cluster (group 4) provided the satisfactory total fresh tuber yield but the 14 (CIP-440074-2 genotype) and 28 (Kamala Sundari) had the highest β -carotene. Considering the overall results, total fresh tuber yield and β -carotene was treated as an important tool for selecting genotypes.

Conclusion

The deep orange flesh Kamala Sundari contain highest β -carotene (4.25 mg/100g) and CIP-187016.2 genotype produced highest yield (62.27 t/ha). The yellow flesh genotype CIP-440074-2 produced considerable yield (44.25 t/ha) and also having second highest β -carotene (2.53 mg/100g) content. The genotypes CIP-440074-2 and Kamala Sundari were selected for sweet potato processed products which having highest β -carotene and satisfactory yield among the twenty eight genotypes of sweet potato.

Reference

- Alam, M. S., M. K. R. Bhuiyan, H. C. Mohanta and S. Attaluri. 2008. Annual report, 2008-09, Tuber Crops Research Centre, Bangladesh Agricultural Research Institute. P. 67.
- Almeida-Muradian, L. B. M. V. C. de Penteadó and V. L. P. de Ferreira. 1992. Relationship between carotenoid content and Hunter colour parameters of Brazilian sweet potato. *Revista Espanola de Ciencia Y Tecnologia de Alimentos*. 36:611-619.
- Ameny, M. A. and P. W. Wilson. 1997. Relationship between Hunter color and β -carotene content in white-fleshed African sweet potato. *J. Sci. Food Agric*. 73:301-306.
- Ewell, P. I. 1990. Sweet potato in Eastern and Southern Africa. Paper presented in the workshop on sweet potatoes in the food system of Eastern and Southern Africa held in 1990 in Nairobi, Kenya.
- Takahata, Y., T. Noda and T. Nagata. 1993. HPLC determination of β -carotene content of sweet potato cultivars and its relationship with colour values. *Japanese Journal of Breeding*. 43: 421-427.
- WHO. 1995. World Health Organisation Micronutrient Deficiency. MDIS working paper. WHO/NUT/95. 3, Geneva, Switzerland.
- Wilfredo, R. P. Barriga and H. Figueroa. 2000. Multivariate analysis of the genetic diversity of Bolivia quinoa germplasm. *Plant Genetic Resources News letter*. 122: 16-23.
- Woolfe J. A. 1992. SWEET POTATO: an untapped food resource. Cambridge University press. New York, USA. pp. 1-363.