Diversity, Genetic Analysis and Character Association in Sweet Potato

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ABSTRACT. *Experiments on evaluation of germplasms, compatibility and fruit set, genetic diversity and correlation coefficient of traits, and combining ability analysis were conducted on sweet potato. Wide variations were observed in plant and root characters among 428 accessions. The storage root yield ranged from 5.28 to 48.61 t/ha. The dry matter content was found to vary from 18.60 to 35.84 percent. Multivariate analysis of divergence among the accessions for 12 characters led to their grouping into six clusters. The intercluster D^2 values varied from 6.40 (between clusters III and VI) to 830.60 (between cluster II and VI). The highest and lowest intra-cluster distances were observed in cluster VI (3.60) and IV (1.78), respectively.*

Higher broad sense heritability and high genetic advance were observed for length of vine and individual root weight. Number of storage roots per plant and root dry matter content had a high degree of positive correlations with the root yield. Out of 182 cross combinations, 134 combinations were cross compatible. Thirteen cross combinations were incompatible in reciprocal crosses while 22 crosses were incompatible unilaterally but the reciprocal crosses were successful. Fruit set percentage ranged from 4 - 68 percent.

The variances due to GCA were highly significant for all the characters studied indicating the importance of additive gene effects. The parent SP-495 was found to be the best combiner followed by SP-527, SP-484, and SP-217 for yield and SP-108 for number of roots per plant and dry matter content which could be used in simple recurrent selection. The higher SCA

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values for root yield in a number of cross combinations indicated non-additive gene action and offered possibilities of improving the crop by selective mating.

INTRODUCTION

Among the food crops of Bangladesh, Sweet potato (*Ipomoea batatas* (L.) Lam.) is the ninth largest in area and the fourth in production. In 1990-91, it covered 50,046 ha and production was 482,635 metric tons. The average yield of the crop is only 9.64 t/ha (Ministry of Planning, 1992). Primitive production methods and low yield potential of the local cultivars have been identified as the major reasons for the low yield. In 1980, a research programme for the improvement of the crop was started at Tuber Crops Research Centre (TCRC) of BARI, Joydebpur. Since then, three new improved cultivars namely, Kamala Sundari, Tripti and Daulatpuri have been developed. But, none of them possesses all the qualities that are desired by the consumers. All the cultivars are of the late maturing type and thus are not suitable for the existing cropping systems. Early bulking clones with high yield, insect resistance and high carotene with good taste and storage quality are needed to make sweet potato a more attractive crop for the farmers and consumers.

It is important to investigate the genetic variability and the correlations of yield and yield components of diverse genetic material following a biometrical model that allows to quantify the magnitude of different gene action. Therefore, the present study was conducted to achieve the following objectives:

i)   to evaluate the germplasm for yield and different physio-morphological characters and to assess the cross-compatibility relationship among some selected parents;

ii) to study the genetic diversity of yield and its components and to examine the inter-relationships among the yield components and;

iii) to analyse the combining ability of parents and crosses, and the mode of gene action for some important traits.

MATERIALS AND METHODS

Five experiments were conducted on sweet potato at TCRC, BARI, Joydebpur, Bangladesh during 1992-93 to 1994-95 winter seasons.

Evaluation of germplasm

An experiment was conducted in randomized complete block design (RCBD) with three replications. Each plot consisted of a single row of 3 m. Spacings between and within row were 60 cm and 30 cm, respectively. The top and second cuttings of 25-30 cm of 428 accessions were planted in the field on November 29, 1992. Manures and fertilizers were applied at the rate of 5 tons cowdung, 135 kg urea, 95 kg TSP and 135 kg MP. Recommended crop management practices were followed. Harvesting of storage roots was done at 140 days after planting. Observations were recorded on different characters *viz*; plant type, vine growth rate, vine internodal length and pigmentation, leaf size and colour, storage root flesh colour, yield and dry matter content by adopting the descriptors for sweet potato developed by CIP, AVRDC and IBPGR (1991).

Based on divergence analysis, fourteen lines were selected and grafted on morning glory (*Ipomoea setosa*) to induce flowering. The grafted plants were transplanted in the field on November 28, 1993 in rows of 1.5 m apart. The cultivars were self pollinated (50 flowers in each cultivar) as well as crossed in all possible combinations. Altogether 700 self pollinations and 4550 cross pollinations covering 182 different combinations were made by hand. Compatibility of crosses was estimated on the basis of percent fruit set.

Diversity analysis, genetic parameters and correlation of traits

The data on different characters *viz*., plant type, petiole length, vine growth rate, vine- pigmentation, mature leaf shape, foliage colour, total vine length, storage root skin and flesh colour, yield and dry matter content of ninety accessions were subjected to statistical analysis. Multivariate analyses were performed using GENSTAT 5 program.

The data on length of vine, length of petiole, number of storage roots, individual root weight, root yield per plant and dry matter content of ninety accessions were used for correlation coefficients. The analyses of variance (Panse and Shukhatme, 1957) and co-variance were carried out (Goulden, 1959). Genotypic and phenotypic co-efficients of variation were computed

(Burton, 1952). Heritability in broad sense and genetic advance were calculated (Allard, 1960). Correlation co-efficients (Hayes *et al.*, 1955; Singh and Chowdhury, 1985) were computed.

Combining ability and gene action

Based on cross compatibility seven diverse genotypes were selected as parents and those were crossed in all possible combinations following 7x7 half diallel mating design excluding reciprocals during winter season of 1993-94. Twenty one F_1 were produced. Hybrid seeds were scarified in H_2SO_4 for germination and seedlings were raised. The vine cuttings of progeny lines along with their parents were planted on 3rd December, 1994. The experiment was conducted in a randomized complete block design with three replications. Each cross consisted of twenty genotypes and each genotype in turn had 18 clones. Each experimental entry was placed in a 1.80 m single row plot with 60 cm inter and 30 cm intra row spacings, respectively, making a unit plot size of 1.8 x 0.6 m.. Recommended fertilizer and crop management practices were followed. Harvesting was done at 140 days after planting and data on vine and petiole length, number of roots per plant, root length, diameter, yield and dry matter content were recorded. The analysis for combining ability was done following model 1 and method 2 of Griffing (1956). For variance of half diallel method of Jones (1965) and for genetic components of variation method of Hayman (1954), Jones (1965) and Mather and Jinks (1971) were adopted.

RESULTS AND DISCUSSION

Evaluation of genetic resources

a) Morphological variability

Plant type

The accessions showed wide range of differences in plant types. About 48.36% of the accessions were found to be semi-compact types followed by compact types (29.20%) and only 1.88% of extremely spreading types. Rajendran and Vimala (1989) in a preliminary evaluation with 894 accessions of sweet potato found that majority of the genetic stocks were twining and trailing types.

Vine growth rate, vine internodal length and pigmentation

The vine growth rate among the accessions exhibited wide variation. Of them, 68.92% showed slow, 22.43% intermediate and only 8.60% fast vine growth. Most of the accessions (74.06%) produced short internodal length followed by 17.76% very short length and 8.18% intermediate length. With respect to vine pigmentation, 60.98% accessions produced green vine, 17.99% green vine with pigmented nodes and rest pigmentation of different colours.

Leaf size and colour

The accessions exhibited wide variations in mature leaf size, and colour. Among the accessions 65.89% had small leaves while 34.11% were found with medium size leaves. This striking variation in leaf sizes might be due to inherent size effect. Among the accessions evaluated, 62.62% produced green leaves, 34.58% green with pigmented edge while the rest the different colour.

b) Storage root characters

The results indicated that 57.47% accessions produced root yield in the range of 10-20.0 tons/ha. The high yielding accessions were SP-495 (48.61 t/ha) SP-527 (45.36 t/ha), SP-292 (45.35 t/ha), SP-477 (45.12 t/ha), SP-484 (45.00 t/ha), SP-294 (44.47 t/ha), SP-480 (44.23 t/ha) and SP-293 (41.58 t/ha).

Storage root flesh colour and dry matter

Wide variation was observed in storage root flesh colour and dry matter content. Among the accessions, 86.68% exhibited roots of white flesh and rest of the produced cream, dark cream, dark yellow and pale yellow flesh colour of the roots. In respect to dry matter content, 84.35% of the accessions produced roots of moderate dry matter (25-30%), while 15.18% showed high dry matter of >30% at 140 days harvest.

c) Selection of promising accessions

On the basis of high yield, high dry matter, number of roots, compactness and weight of vines per plant 90 promising lines were selected as valuable accessions. Results of the present study indicated that the variations

observed in different traits promise better selection scope for genetic improvement of sweet potato.

d) Compatibility and fruit set

All the cultivars were found to be self incompatible. Out of 182 cross combinations, 134 combinations were found cross compatible and 13 as incompatible in reciprocal crosses while 22 crosses were incompatible unilaterally, but the reciprocal crosses were highly successful. This corroborates the findings of Srinivasan and Vimala (1981). Fruit set percentage ranged from 4-68% and maximum was obtained in the cross of SP-217 x SP-108 (68.00%). In the present study, 48 cross combinations did not produce fruits. The results revealed that the accessions SP-161, SP-217, SP-527, SP-108, SP-236 and SP-296 showed comparatively higher level of cross compatibility as compared to other compatible clones.

Diversity analysis, genetic parameters and correlation of traits

The 90 promising selected accessions were grouped into six clusters (Table 1) according to D^2 analysis. Clusters VI and II were the largest with 27 and 21 accessions, respectively. Cluster III comprised of 16 accessions while clusters I, V and IV comprised 10, 9 and 7 accessions, respectively. Naskar and Srinivasan (1985) grouped 22 accessions of sweet potato into nine clusters and observed clustering pattern was not consistent over the years. They found that two cultivars 'V$_2$' and 'Kalmegh' were highly divergent from others. No relationship was found between genetic divergence and geographic distribution of the accessions which indicates that the geographic diversity is not an adequate index of the genetic diversity. Similar opinions were also suggested by Mannan *et al.* (1994) in *Colocasia esculenta*. The inter-cluster D^2 values varied from 6.40 (between clusters III and V) to 830.60 (between clusters II and VI); the intra-cluster D^2 values varied from 1.78 (cluster IV) to 3.60 (cluster VI). Accessions belonging to the clusters separated by high estimated statistical distance could be used in hybridization programme for obtaining a wide spectrum of variations among the segregants (Seetharaman *et al.*, 1988).

The mean, co-efficients of phenotypic and genotypic variation, broad sense heritability estimates and expected genetic advance for six characters of sweet potato are presented in Table 2. For all the characters studied, genotypic coefficient of variation was lower than the phenotypic one, indicating the larger influence of environment. Length of vine and individual root weight had high

Table 1.   **Clustering pattern of 90 sweet potato accessions based on Mahalanobi's D² statistic.**

Cluster No.	Accessions in each cluster with their places of collection in parentheses
I	SP-016 (AVRDC), SP-019 (AVRDC), SP-186 (Feni,) SP-193 (Norshingdi), SP-434 (Chittagong), SP-465 (Jamalpur), SP-484 (Natore), SP-499 (Shirajgong),SP-527 (Bagerhat), SP-536 (Shatkhira).
II	SP-070 (Dinajpur), SP-079 (Barishal), SP-084 (Jessore), SP-097 (Comilla), SP-099 (Comilla), SP-108 (Comilla),SP-138 (Barishal), SP-155 (Puerto Rico), SP-161 (AVRDC), SP-172 (AVRDC), SP-223 (Mymensingh), SP-227 (Mymensingh), SP-236 (Kishoreganj), SP-238 (Kishoreganj), SP-251 (Borguna), SP-331 (Brahmanbaria), SP-349 (Chittagong), SP-386 (Rajbari), SP-392 (BARI-hybrid), SP-394 (BARI-hybrid), SP-483 (Rajshahi).
III	SP-023 (AVRDC), SP-100 (Comilla), SP-145 (AVRDC), SP-190 (Norshingdhi), SP-217 (Mymensingh), SP-218 (Mymensingh), SP-220 (Mymensingh), SP-231 (Manikgong), SP-262 (Borguna), SP-277 (Pirojpur), SP-306 (Borguna), SP-309 (Borguna), SP-397 (BARI Hybrid), SP-407 (Moulovibazar), SP-418 (Bhoda), SP-513 (Nilphamari).
IV	SP-142 (AVRDC), SP-203 (Mymensingh), SP-281 (Patuakhali), SP-296 (Patuakhali), SP-379 (Gopalgong), SP-393 (BARI-hybrid), SP-396 (BARI-hybrid).
V.	SP-025 (AVRDC), SP-029 (AVRDC), SP-436 (Rangamati), SP-469 (Tangail), SP-471 (Tangail), SP-473 (Noagaon), SP-494 (Sirajgonj), SP-495 (Sirajgonj), SP-502 (Panchagarh).
VI	SP-013 (AVRDC), SP-017 (AVRDC), SP-022 (AVRDC), SP-026 (AVRDC), SP-027 (AVRDC), SP-028 (AVRDC), SP-030 (AVRDC), SP-038 (TARI), SP-039 (TARI), SP-058 (USA), SP-062 (USA), SP-083 (Jessore), SP-149 (AVRDC), SP-162 (AVRDC), SP-176 (Chandpur), SP-210 (Mymensingh), SP-287 (Patuakhali), SP-289 (Patuakhali), SP-292 (Patuakhali), SP-294 (Patuakhali), SP-298 (Borguna), SP-351 (Gazipur), SP-364 (Tangail), SP-388 (BARI-hybrid), SP-395 (BARI-hybrid), SP-422 (Bhola), SP-477 (Rajshahi).

Table 2. Estimates of genetic parameters for six characters in Sweet potato.

Characters	Mean	Phenotypic co-efficient of variation	Genotypic co-efficient of variation	Broad sense heritability (%)	Genetic advance as percentage of mean
Storage root yield/plant (g)	475.44	40.01	38.63	93.21	76.83
Length of vine (cm) at 60 DAP	46.92	47.18	45.94	94.83	92.16
Length of petiole (cm)	11.63	30.12	27.62	84.05	52.16
No. of storage roots/plant	4.31	26.34	23.31	78.30	42.49
Individual storage root wt (g)	122.88	42.98	41.73	94.27	83.46
Dry matter content (%) of storage root	28.50	14.57	13.49	85.65	25.71

heritability estimates associated with high genetic gain in the present study. Kamalam *et al.* (1977) obtained such heritability with high genetic advance for length of vine and number of tubers which indicates the presence of additive gene effects and hence they suggested individual plant selection for these traits would be effective in sweet potato.

Number of storage roots per plant and root dry matter content had a significant positive correlation with yield (Table 3). Similar results in sweet potato have also been reported by Thamburaj and Muthukrishnan, 1976.

Combining ability and gene action

In the analysis of variance, mean squares for genotypes was highly significant for all the characters (Table 4). The variances due to GCA and SCA were highly significant for all seven characters indicating the importance of both additive and non-additive gene effects. This may be attributed to high ploidy level in sweet potato where there are better chances for intergenomic interaction and enhancement of genetic variability. In all the cases the variance ratio of SCA/GCA is lower than unity suggesting the importance of additive gene action in sweet potato. This is in agreement with the findings of Vimala

Table 3.   Phenotypic (P) and genotypic (G) correlation co- efficiénts among six characters of sweet potato.

Character		Petiole length	No. Of storage roots per plant	Individual root wt.	Storage root dry matter content	Storage root wt. per plant
Vine length	P - 0.073		-0.123	-0.067	0.124	0.091
	G - 0.069		-0.148	-0.063	0.134	0.101
Petiole length	P		-0.050	-0.030	0.122	0.161
	G		-0.058	-0.010	0.134	-0.167
No. of storage roots per plant	P			-0.120	-0.207*	0.243*
	G			-0.138	-0.252*	0.292**
Individual storage root weight	P				-0.202*	-0.233*
	G				-0.217*	-0.262**
Storage root dry matter content	P					0.317**
	G					0.331**

*   = $p < 0.05$
** = $p < 0.01$

and Lakshmi, (1991) who reported greater importance of additive genetic variance than non-additive variance for root yield. But Pillai and Amma (1989) found equal importance of additive and non-additive genetic effects for root yield in sweet potato.

The analysis of genetic components indicated that the additive effects (a) and the dominance effects (b) were highly significant for all seven characters under study indicating the importance of both additive and dominance components (Table 5). The significant values of D, H_1 and H_2 showed the importance of both additive and dominance gene effects in the

Table 4. Analysis of variance for combining ability for some characteristics in sweet potato.

Source of variance	d.f.	Mean squares						
		Vine length	Petiole length	Roots per plant	Root length	Root diameter	Root weight/plant	Dry matter content
Block	2	14.65	0.92	0.99	2.54	0.25	1794.94	0.75
Genotype	27	2475.64*	5.95*	10.19*	29.99*	4.55*	37793.17*	14.65*
Error	54	55.19	0.44	1.29	1.56	0.35	1434.14	1.42
GCA	6	3534.80*	5.72*	3.72*	37.03*	5.72*	37277.56*	16.36*
SCA	21	51.05*	0.92*	3.30*	2.27*	0.32*	5546.34*	1.60*
Error	54	18.40	0.15	0.43	0.52	0.12	478.05	0.47
SCA/GCA	-	0.01	0.16	0.89	0.06	0.06	0.15	0.10

* = $P < 0.01$

Table 5. Jones analysis for half diallel table for genetic components of variation for different characters in sweet potato.

Source of variance	d.f.	Mean sum of squares						
		Vine length	Petiole length	Roots per plant	Root length	Root diameter	Root weight/plant	Dry matter content
a (GCA)	6	14.65	5.72*	3.72*	37.03*	5.72*	37277.56*	16.36*
b 1	1	111.63*	7.07*	7.44*	3.05*	2.30*	25958.86*	4.84*
b 2	6	48.44*	0.56	3.68*	3.45*	0.23	3197.26*	1.02*
B 3	14	47.84*	0.63*	2.85*	1.71*	0.21*	5095.05*	1.62*
E	56	17.91	0.15	0.43	0.53	0.11**	428.34	0.46

* = $P > 0.01$

Table 6.   Estimates of genetic components of variation and ratios for different characters in sweet potato.

Component of variation/ratio	Character						
	Vine length	Petiole length	Roots per plant	Root length	Root diameter	Root weight/plant	Dry matter content
D	1397.00**	3.00**	1.00	27.00**	3.00**	19203.00**	8.00**
	± 46.27	± 0.20	± 1.48	± 0.88	± 0.12	± 2956.94	± 0.70
H_1	171.16	2.96**	13.32**	9.15**	0.89	20388.31**	5.27**
	± 111.40	± 0.48	± 3.57	± 2.11	± 0.30	± 7118.76	± 1.80
H_2	139.48	2.55**	10.25**	6.36**	0.76**	17796.59**	4.67**
	± 98.16	± 0.43	± 3.14	± 2.11	± 0.30	± 7118.76	± 1.58
F	- 191.84	1.13**	1.88	16.09**	0.84**	5602.59	1.97
	± 111.01	± 0.48	± 3.56	± 1.86	± 0.13	± 7093.65	± 1.79
h_2	53.71	3.88**	3.96	1.43	1.23**	14294.66**	2.48*
	± 65.93	± 0.29	± 2.11	± 1.25	± 0.18	± 4212.98	± 1.06
Ey	17.91	0.15**	0.43	0.53	0.11**	482.34	0.47
	±16.36	± 0.07	± 0.52	± 0.31	± 0.04	± 1045.44	± 0.26
$(H_1/D)^{\lambda}$	0.35	0.99	3.65	0.58	0.54	1.03	0.81
$(H_2/4H_1)$	0.20	0.22	0.19	0.17	0.21	0.22	0.22
$\dfrac{(4DH_1)1/2 + F}{(4DH_1)1/2 - F}$	0.67	1.47	1.80	3.09	1.69	1.33	1.36
h^2/H_2	0.38	1.52	0.39	0.23	1.62	0.80	0.53
$H^2(bs)$	0.93	0.80	0.69	0.85	0.80	0.89	0.75

** = $P > 0.01$

inheritance of petiole length, root length, root weight per plant and dry matter content (Table 6). The highly significant values of H_1 and H_2 for petiole length, number of roots per plant, root length, root weight per plant and dry matter

content suggested the association of non-additive type of gene action for these traits. Jong (1974) concluded that additive genetic variance is more important than non-additive genetic variance in determining storage root weight, average size of roots, percent dry matter content, dry weight of roots and top weight. But in the present study for number of roots per plant, the main component of genetic variance was found to be of the non-additive type. Similar findings were also reported by Vimala and Lakshmi (1991) for vine characters in sweet potato.

The results on GCA effects indicated that the parent SP-495 was found to be a good general combiner for all the characters, SP-161 for petiole length, SP-527 for root length, SP-484 for storage root weight per plant, SP-217 for root yield and SP-108 for number of roots per plant and dry matter content. Pillai and Amma (1989) have also reported high GCA for vine length, petiole length, mean root weight and yield in sweet potato.

The results on SCA effects showed that out of 21 crosses only six, *viz.*, SP-495 x SP-527, SP-495 x SP-217, SP-495 x SP-161, SP-527 x SP-217, SP-527 x SP-161 and SP-484 x SP-217 seem to be promising for the exploitation of yield in sweet potato. However, among the parents, SP-495, SP-527, SP-484 and SP-217 which were found to be good general combiners could be used in simple recurrent selection as suggested by Pillai and Amma (1989).

CONCLUSION

The results of the study showed a marked variation in different plant and root characters which promises better selection scope for genetic improvement of sweet potato. The results of crossing behaviour of 14 selected parents indicated that the parents SP-161, SP-217, SP-108, SP-216, SP-296 and SP-527 were highly cross compatible and these could be used in hybridization programme of sweet potato. The parents, SP-495, SP-484, SP-217 and SP-108 are good combiners and can be used in simple recurrent selection. Some crosses seem to be promising for exploiting the yield potential. Divergence analysis indicated that 90 accessions were included in six different clusters.

There is a scope for varietal improvement through hybridization programme involving the selective genotypes possessing desirable characters from diverse clusters. The study of genetic parameters and correlation of traits suggests the importance of the length of vine and individual root weight as the major components of root yield in sweet potato. The prevalence of both additive and non-additive gene effects indicate the possibility of improving the

crop by recurrent selection as well as by selective mating. Initially, breeding for improving the number of roots per plant, high yield and dry matter content, should first be undertaken through accumulation of favorable additive genes either through mass selection or full-sib family selection. The selected individuals or full-sib families should be inter-crossed to take the advantage of the non-additive gene actions for the characters. In the present study, partial, complete and over-dominance as well as additive components were observed to be pre-dominant for yield.

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REFERENCES

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley Sons, Inc. New York.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Int. Grassld. Cong. 1: 277-283.

CIP, AVRDC and IBPGR. (1991). Descriptors for sweetpotato. *In*: Human, Z. (Ed). International Board for Plant Genetic Resources, Rome, Italy.

Goulden, C.H. (1959). Methods of Statistical Analysis. Wiley and Sons, Inc., New York.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci. 9: 463-493.

Hayes, H.K., Immer, F.R. and Smith, D.C. (1955). Methods of Plant Breeding, 2nd Ed., New York. McGraw Hill Book Co., Inc.

Hayman, B.I. (1954). The analysis of variance of diallel table. Biometrics. 10: 235-244.

Jones, R.M. (1965). Analysis of variance of the half diallel table. Heredity. 20: 117-121.

Jong, S.K. (1974). General and specific combining ability in a diallel cross among six sweet potato *Ipomoea batatas* (Lam) clones. Korean J. Breeding. 6: 116-122

Kamalam, P., Biradar, R.S., Hrishi, N. and Rajendram, P.G. (1977). Path analysis and correlation studies in sweet potato (*Ipomoea batatas* Lam.). J. Root Crops. 3(1): 5-11.

Mannan, M.A., Ahmed, M.S., Bhuiyan, M.K.R., Haque, M.A. and Rashid, M.M. (1994). Divergence analysis of Panikachu (*Colocasia esculenta* (L.) Schott) - an aquatic edible aroid in Bangladesh. J. Root Crops. 20(1): 26-30.

Mather, K. and Jinks, J.L. (1971). Biometrical Genetics (2nd Edn.), Chapman and Hall Ltd., London.

Ministry of Planning. (1992). Year Book of Agricultural statistics of Bangladesh. Ministry of Planning. Govt. of Bangladesh.

Naskar, S.K and Srinivasan, G. (1985). Genetic divergence in sweet potato. J. Root Crops. 11(1): 57-59.

Panse, V.G. and Shukhatme, P.V. (1957). Statistical methods for Agricultural Workers. I.C.A.R., New Delhi.

Pillai, P.K.T and Amma, C.S.E. (1989). Combining ability in sweet potato. J. Root Crops. 15(1): 39-43.

Singh, R.K. and Chowdhury, B.D. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

Rajendran, P.G. and Vimala, B. (1989). Genetic resources of tuber crops, CTCRI, Trivandrum. Silver Jubilee, Commemoration. Vol. 1963-88. 4-11.

Seetharaman, R.N. De. R., Sinha, M.K. and Banerje, S. P. (1988). Genetic divergence in rice. Indian J. Genet. 48: 189-194.

Srinivasan, G. and Vimala, B. (1981). Studies on compatibility and fruitset in different cultivars of sweet potato. J. Root Crops. 7(1): 21-24.

Thamburaj, S. and Muthukrishanan, C.R. (1976). Association of metric traits and path analysis in sweet potato (*Ipomoea batatas* Lam.). Madras Agric. J. 63: 1-8.

Vimala, B. and Lakshmi, K.R. (1991). Heritability estimates in sweet potato. J. Root Crops. 17 (Special issue): 35-38.