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## Genetic Variability for Yield and Other Agronomic Traits in Sweet Potato

<sup>1</sup>Engida Tsegaye, <sup>2</sup>Nigussie Dechassa and <sup>2</sup>E.V. Devakara Sastry

<sup>1</sup>Awassa Agricultural Research Center, P.O. Box 6 Awassa, Ethiopia

<sup>2</sup>Department of Plant Sciences, Alemaya University, P.O. Box 138 Dire Dawa, Ethiopia

**Abstract:** Understanding the nature and magnitude of variability among sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes for traits of economic importance is vital to plan effective breeding programs. A replicated field experiment was carried out using thirty sweet potato genotypes selected at random from the germplasm collection of diverse sources. The specific purpose was to estimate the nature and magnitude of variability among yield and yield related traits in the crop plant. Observations were recorded on sixteen characters. The analysis of variance revealed that there were highly significant ( $p < 0.01$ ) differences among the genotypes for all the characters. Wide ranges of genotypic variability were observed among the genotypes for most of the characters. In vine traits, 32.4 to 82.5% of the observable variability was due to the genetic variation while in root traits this value ranged from 43.04 to 76.81% indicating the existence of immense inherent variability among the genotypes. The contributions of genetic variance to phenotypic variance were only 32.4 and 43.04%, for above ground dry matter content and storage root dry yield per plant, respectively suggesting the important role of environment in the expression of these traits. High genotypic coefficients of variation along with high heritability and expected genetic advances were recorded for vine length, vine internode length, leaf area, above ground fresh and dry weights, number of storage root per plant, individual storage root weight, storage root fresh yield per plant. Thus, future improvement of the crop plant should exploit the genetic variability available in the germplasm collection.

**Key words:** Components of variance, Ethiopia, genetic advance, heritability, sweet potato genotypes

### INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a dicotyledonous plant belonging to the family Convolvulaceae. This family includes about 55 genera and more than 1000 species (Watson and Dallwitz, 2000). However, only *Ipomoea batatas* is of economic importance as a source of food (Onwueme and Charles, 1994).

The amount of variability that exists in the germplasm collections of any crop is of utmost importance towards breeding for better varieties. Particularly, genetic variability for a given character is a basic prerequisite for its improvement by systematic breeding.

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). Hence, consideration of quantitative approaches for exploitation of the extensive genetic variability available in sweet potato is of paramount importance, which in turn is dependent on good estimates of the genetic parameters. Estimates of genetic parameters serve

as a base for selection and hybridization as the degree of variability for a given character is a basic prerequisite for its improvement. Although several sweet potato germplasm accessions have been introduced to Ethiopia from International Potato Center (CIP), International Institute for Tropical Agriculture (IITA), Asian Vegetable Research and Development Center (AVRDC) and a considerable amount have been collected from farmers field for evaluation and utilization, information on the nature and extent of variability among these collections for traits of economic importance is lacking. Thus, this study was undertaken to estimate the nature and magnitude of variability for yield and yield related characters with the help of genetic parameters as such as phenotypic as well as genotypic coefficients of variation, heritability and genetic advance.

### MATERIALS AND METHODS

**Experimental site:** The study was carried out at Awassa Agricultural Research Center, Ethiopia, during 2003/04 growing season under rainfed condition. Awassa lies at 7° 04' N and 38° 31' E, at an elevation of 1700 masl. The average annual rainfall of Awassa is 1033.6 mm with a

minimum/maximum mean air temperature of 13.2/27.4°C. The soil is volcanic in origin and is classified as Vitric Andosol. The textural class is a well-drained sandy loam with a pH of 7 and CEC 22.6 meq per 100 g.

**Experimental materials, design and management:** Thirty sweet potato genotypes randomly taken from the germplasm collection of materials introduced from CIP, IITA and AVRDC over different years and maintained at Awassa Agricultural Research Center were used for this study. The experiment was arranged in a randomized complete block design with four replications. Each genotype was planted on 3 m long and 2.4 m wide plot consisting of four rows, which accommodated ten plants per row and thus forty plants per plot. A distance of 1m was maintained between the plots. Vine cuttings from the top portion of 3-4 months old mother plants were taken for planting. The vine cuttings were then cut into 30 cm length and thereafter planting was done on 29th July 2003 with a spacing of 60 cm between rows and 30 cm between plants. Earthing up was done twice, 45 and 75 days after planting. Fertilizers were not applied during the course of the experiment. During the course of this experiment, no serious disease or insect pest infestations were noticed and thus crop protection measures were not employed.

**Data collection:** For each character under study, data were recorded on five randomly taken plants from the middle two rows of each plot and expressed on per plant basis. The mean of five plants was used for statistical analyses. Total storage root yield per plot was recorded as weight of storage roots harvested from the middle two rows of each experimental plot. The following sixteen characters were measured during the course of this study: Vine length (cm), vine internode length (cm), vine internode diameter (mm), leaf area (cm<sup>2</sup>), above ground fresh weight per plant (g), above ground dry matter content (%), above ground dry weight per plant (g), storage root number per plant, storage root length (cm), storage root diameter (cm), individual storage root weight (g), harvest index per plant (on dry weight basis), storage root fresh yield per plant (g) storage root dry matter content (%), storage root dry yield per plant (g) and storage root fresh yield per plot (kg).

**Statistical analysis:** The mean values of each character under the study were computed and subjected to analysis of variance following the procedures described by Gomez and Gomez (1984) using MSTAT computer software. Phenotypic and genotypic variances were calculated by the methods suggested by Burton and Devane (1953):

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad \sigma_g^2 = MS_g - MS_e/r$$

where:

- $\sigma_p^2$  = Phenotypic variance,
- $\sigma_g^2$  = Genotypic variance,
- $\sigma_e^2$  = Environmental variance (error mean square).

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated according to the procedure outlined by Johnson *et al.* (1955):

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

where,  $\bar{x}$  = grand mean  $GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$ . Broad sense heritability and the genetic advance expected under selection, assuming the selection intensity of 5% were calculated as suggested by Allard (1960):

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where:

$H^2$  = Heritability in broad sense (in percentage).

$$G_s = (K) \sigma_A (H^2)$$

where:

- $G_s$  = Expected genetic advance,
- $K$  = Selection differential (2.06 at 5% selection intensity),
- $\sigma_A$  = Phenotypic standard deviation.

Genetic advance as percent of mean (GAM) was calculated using the following formula:

$$GAM = \frac{G_s}{\bar{x}} \times 100$$

## RESULTS AND DISCUSSION

The analysis of variance showed that there were highly significant ( $p < 0.01$ ) differences among the genotypes for all the characters (Table 1). This may be attributed to the existence of large variability among genotypes maintained at Awassa Agricultural Research Center, the germplasm collected from diverse collections at CIP, IITA and AVRDC.

The estimates of genotypic and phenotypic variances along with the phenotypic (PCV), genotypic coefficients of variation (GCV), broad sense heritability,

Table 1: Analysis of variances for 16 characters in 30 sweet potato genotypes grown at Awassa, 2003

Character	MS <sub>e</sub> (3) <sup>‡</sup>	MS <sub>e</sub> (29)	MS <sub>e</sub> (87)
Vine length (cm)	493.78	2745.21**	138.20
Vine internode Length (cm)	0.42	1.94**	0.20
Vine internode diameter (mm)	0.82	1.20**	0.14
Leaf area (cm <sup>2</sup> )	66.14	332.21**	32.70
Aboveground fresh weight plant <sup>-1</sup> (g)	2904.06	21894.29**	1482.65
Above ground dry matter content (%)	32.12	652.68**	42.70
Aboveground dry weight plant <sup>-1</sup> (g)	7.96	4.64**	1.59
Storage root number plant <sup>-1</sup>	0.52	6.92**	0.62
Storage root length (cm)	16.46	18.22**	3.14
Storage root diameter (cm)	1.39	2.26**	0.44
Individual storage root weight (g).	966.66	8171.93**	573.47
Harvest index plant <sup>-1</sup> (%)	24.34	317.73**	25.50
Storage root fresh yield plant <sup>-1</sup> (g)	7842.13	86373.10**	10239.28
Storage root dry mater content (%)	18.77	47.04**	4.58
Storage root dry yield plant <sup>-1</sup> (g)	530.27	3431.91**	853.23
Storage root fresh yield plot <sup>-1</sup> (kg)	3.93	12.22**	1.10

MS<sub>e</sub> = replication mean square MS<sub>e</sub> = mean square due to genotypes, MS<sub>e</sub> = Error mean square, <sup>‡</sup>Figures in parenthesis indicate the degree of freedom, \*\* \* Significant at 1% and 5% probability levels, respectively

Table 2: Estimates of components of variance, broad sense heritability, GA and GA as percent of the mean for 16 characters in sweet potato genotypes evaluated at Awassa, 2003

Character*	$\sigma_g^2$	$\sigma_p^2$	GCV	PCV	Heritability	Genetic advance	GA as (%) of the mean
VL	651.751	789.957	33.47	36.85	82.50	47.77	62.63
VIL	0.435	0.630	26.20	31.52	69.11	1.13	44.87
VID	0.266	0.402	11.73	14.41	66.22	0.87	19.66
LA	74.887	107.581	23.07	27.65	69.60	14.87	39.65
AGFW	5012.910	6585.557	40.29	45.77	77.49	129.53	73.06
AGDMC	0.762	2.352	5.30	9.31	32.40	1.02	6.21
AGDW	152.494	195.197	42.28	47.83	78.12	22.49	76.98
SRN	1.576	2.191	28.67	33.81	71.92	2.19	50.09
SRL	3.768	6.911	13.37	18.12	54.53	2.95	20.35
SRD	0.455	0.896	14.37	20.16	50.84	0.99	21.11
ISRW	1899.615	2473.086	31.69	36.16	76.81	78.69	57.21
HI	73.057	98.559	10.45	12.13	74.13	15.16	18.65
SRFY	19033.455	29272.738	24.48	31.36	65.02	229.18	40.67
SRDMC	10.615	15.198	13.10	15.68	69.84	5.61	22.56
SRDY	644.671	1497.900	18.52	28.23	43.04	34.31	25.03
SRFYP	2.791	3.841	31.33	36.75	72.67	2.93	55.02

VL = Vine Length (cm), VIL = Vine Internode Length (cm), VID = Vine Internode Diameter (mm), LA = Leaf Area (cm<sup>2</sup>) AGFW = Aboveground Fresh Weight Plant<sup>-1</sup> (g), AGDW = Aboveground Dry Weight Plant<sup>-1</sup> (g), AGDMC = Aboveground Dry Matter Content (%), SRN = Storage Root Number Plant<sup>-1</sup>, SRL = Storage Root Length (cm), SRD = Storage Root Diameter (cm), ISRW = Individual Storage Root Weight (g), HI = Harvest Index Plant<sup>-1</sup> (%), SRFY = Storage Root Fresh Yield Plant<sup>-1</sup> (g), SRDMC = Storage Root Dry Mater Content (%) SRDY = Storage Root Dry Yield Plant<sup>-1</sup> (g), SRFYP = Storage Root Fresh Yield Plot<sup>-1</sup> (kg)  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and GA = genetic advance

genetic advance and genetic advance as percent of the mean for sixteen characters in thirty sweet potato genotypes are presented in Table 2. The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. In all the traits a large portion of the phenotypic variance was accounted for by the genetic component except for above ground dry mater content and storage root dry yield per plant in which the contributions of genetic variance to phenotypic variance were only 32.4 and 43.04%, respectively. Generally, in vine traits 32.4 to 82.5% of the observable variability was due to the genetic variation while in root traits this value ranged from 43.04% for storage root dry yield per plant to 76.81% for individual storage root weight. This is an indication for the existence

of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection and hybridization programs. These results are in conformity with the results obtained by Jones *et al.* (1969) who investigated considerable phenotypic variance among ten storage root traits in sweet potato and in every case a large part of this variance was accounted for by the genotypic variance.

Both phenotypic and genotypic coefficients of variation were highest for above ground dry weight per plant followed by above ground fresh weight per plant and vine length. In addition to these three traits, six other traits had PCV and GCV higher than 20% (Table 2) and thereby indicating high variability and great scope for

improvement. These findings are in agreement with the works of Alam *et al.* (1998) and Hossain *et al.* (2000) who investigated high GCV and PCV for vine length, number of storage root per plant, individual root weight and storage root fresh yield per plant. The GCV was relatively moderate for storage root dry yield per plant, harvest index, storage root dry matter content, vine internode diameter, storage root length, storage root diameter and low for above ground dry matter content. While the PCV was moderate for vine internode diameter, storage root length, storage root dry matter content, harvest index and low for above ground dry matter content.

For all characters under the study PCV values were greater than GCV values. However, in most cases the two values differed in narrow indicating that the variability due to the genetic constitution of the genotypes was more than the variability exerted by environmental factors. Hence, selection for desirable traits on these highly variable characters would be effective in sweet potato improvement programs. The moderate to high value of genotypic coefficients of variation for all characters except above ground dry matter content indicated that most of these traits might be further improved through clonal selection.

**Estimates of heritability in broad sense:** Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. As stated by Burton (1952) the genotypic coefficient of variation along with heritability estimates provide reliable estimate of the amount of genetic advance to be expected through phenotypic selection. The results of the present study indicated that except for above ground dry matter content, moderate to high heritability values were recorded for all characters (Table 1). The heritability estimates were higher for vine length, above ground dry weight, individual storage root weight, above ground fresh weight, harvest index, storage root fresh yield per plant, storage root number, vine internode length, leaf area, vine internode diameter, storage root dry matter content and storage root fresh yield per plot indicating the lesser influence of environment on them. These results were in agreement with the findings of Jones (1969) who reported high heritability for vine length, vine internode length and vine internode diameter; Mok *et al.* (1997) for number of storage roots per plant, storage root weight per plant, storage root dry matter content, root size and harvest index; Kamalam (1977) for foliage weight and individual storage root weight. Hence, satisfactory, progress can be achieved by selection on these characters. Moderate

heritability estimates were also observed in storage root length, storage root diameter and storage root dry yield. The heritability of above ground dry matter content was the least suggesting that this trait was greatly influenced by environmental factors. As yield is a complex character liable to have more environmental influences, compared to all other traits except above ground dry matter content, the heritability of storage root dry yield per plant (43.04%) was lower. Nevertheless, Jones *et al.* (1986) suggested that in sweet potato, a heritability estimates above 60% are quite adequate for good selection advance and estimates as low as 40% by variance-covariance analysis could be considered favorable provided that the selection techniques have enough precision. Thus, although the heritability value recorded on storage root dry yield *per se* was the second from the least, it can be considered as favorable to achieve satisfactory progress by selection.

**Estimates of expected genetic advance:** Even though heritability estimates provide the basis for selection on the phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously as high heritability will not always be associated with high genetic advance (Johnson *et al.*, 1955). The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus the heritability estimates will be reliable if accompanied by a high genetic advance. The expected genetic advance values for 16 characters of sweet potato genotypes evaluated is presented in Table 2. These values are also expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. Progress that could be expected from selecting the top 5% of the genotypes ranged from 6.21% for above ground dry matter content to 76.98% for above ground dry weight (Table 2). For all characters except for above ground dry matter content the genetic advance values were considered moderate to high. Comparatively, the highest genetic advance as per cent of the mean was recorded for above ground dry weight followed by above ground fresh weight and vine length. This indicates that selecting the top 5% of the genotypes could make an advance of 76.98% in above ground dry weight, 73.06% in above ground fresh weight and 62.63% in vine length (Table 2).

High heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. In the present

investigation, high heritability along with high genetic advance as per cent of the mean were obtained for above ground fresh as well as dry weight, vine length, individual storage root weight, storage root fresh yield per plot, storage root number, vine internode length, leaf area and storage root fresh yield per plant. This findings is in agreement with that of Hossain *et al.* (2000) and Choudhary *et al.* (1999) who reported high estimates of both heritability and genetic advance for number of roots per plant and storage root fresh yield per plant. Kamalam (1977) and Hossain *et al.* (2000) also observed high heritability coupled with high genetic advance for individual storage root weight whereas Alam *et al.* (1998) obtained similar result for vine length. As stated by Panes (1957), high heritability associated with equally high genetic advance is chiefly due to additive gene effect but if the heritability is mainly due to dominance and epistasis, the genetic gain would be low. Hence, selection for these characters would prove quite effective since the characters seemed to be governed by additive genes action.

On the other hand, characters such as vine internode diameter, storage root dry matter content and harvest index exhibited relatively moderate genetic advance. However, their heritability estimates were high. The presence of high heritability and moderate genetic advance is the effects of equal contribution of additive and non-additive gene action (Shelby, 2000). Storage root length, storage root diameter, storage root dry yield per plant also showed relatively moderate genetic advance along with moderate heritability.

High GCV along with high heritability and genetic advance will provide better information than a single parameter alone (Sahao *et al.*, 1990). Hence, in this study above ground fresh as well as dry weight, vine length, individual storage root weight, storage root fresh yield per plot, vine internode length, storage root fresh yield per plant, leaf area and storage root number exhibited high genotypic coefficient of variation, high heritability together with high genetic advance indicating that these characters would be very useful as a base for selection in sweet potato improvement programs. Alam *et al.* (1998) and Hossain *et al.* (2000) also found high genotypic coefficients of variation coupled with high heritability and genetic advance for the traits vine length, number of roots per plant and individual root weight. Thus, from the present investigations it is concluded that future improvement of the crop plant should exploit the genetic variability available in the germplasm collection at Awassa Agricultural Research Center from which the test genotypes were sampled at random.

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