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Genetic variability of Sweet Potato on yield and yield related traits at werer Agricultural Research Center, Ethiopia.

Muluken Demelie[1] and Abiyot Aragaw[2]

Ethiopian Institute of Agricultural Research (Werer Center), P.O. Box: 2003, Addis Ababa Ethiopia[1]
International Potato Center – Ethiopia (CIP), .PO Box 10059 Addis Ababa, Ethiopia[2]

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Abstract

Sweet potato [*Ipomoea batatas* (L.) Lam.] is important food security root crop in tropical and subtropical regions. It can tolerant of a wide range of edaphic and climatic conditions and grown with limited inputs.Genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweetpotato improvement breeding strategy. Therefore, the objectives to determine genetic variability and to estimate the association of agro-morphological trait in sweet potato genotypes. Filed experiment was conducted at Were Agricultural Research Center using three varieties and eight accessions in Randomize Complete Block Design (RCBD) with three replications. Data were collected from twelve agro-morphological traits. This analysis of variance revealed significant ($p<0.05$) among sweet potato genotypes for all traits except stand count at sprout which showed non significant among sweet potato genotypes. Genotypes showed total tuber yield ranged from 123.67 to 370.04 with mean of 231.04 qt/ha while root weight 100 to 263 with mean of 168.04 gm. Newly released variety Ma'e gave highest yield. Genotypic coefficients of variation lower in magnitude than phenotypic coefficient of variation all agro-morphological traits. Genotypic coefficient of variation ranged from 0.77 (stand count at sprout) to 33.93 (unmarketable tuber yield) while phenotypic coefficient variation ranged between 3.47 (stand count at sprout) to 39.36 (unmarketable tuber yield).Heritability in broad sense was recorded for twelve traits ranged between 4.99% (stand count at sprout) to 86.45% (vine internode length). Genetic advance as percent mean ranged from 7.42% (stand count at harvest) to 60.27 (unmarketable tuber yield). Genotypic correlation higher in magnitude than corresponding phenotypic correlation for most of the traits. Genotypic correlation ranged from -0.56 (unmarketable and vine inter node length) to 0.98 (marketable and total tuber yield) while phenotypic correlation ranged from -0.56 (unmarketable and vine inter node length) to 0.97 (marketable and total tuber yield). This result suggested the importance of further collection to exploit the genetic variability between varieties and accessionsfor variety development of sweet potato in the country.

Key words: phenotypic and genotypic coefficient of variation, heritability, genetic advance

Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam.], being under the Convolvulaceae family,It is a globally important root crop, ranked second most important tropical and subtropical staple root crop in area and production after cassava (Boney, 2014, FAOSTAT, 2014).It is widely adapted in the tropics, sub-tropical and warm temperate regions where it is grown by smallholder farmers on marginal land with minimal inputs (Bashasha*et al*., 1995; Kapinga *et a*l., 1995, Wassu *et al*., 2015). Sweet potato is tolerant of a wide range of edaphic and climatic conditions and grown with limited inputs. It grows best at the pH of 6but alkaline soils result in poor yields and very acid soils (pH under 5) will not be withstood (FAO, 2006; Wassu *et al*., 2015).In Ethiopia, sweet potato has been cultivated for the last several years. Sweet potato ranks third after Enset [*Ensete ventricosum* (W.) Cheesman] and Potato [*Solanum tuberosum* (L.)] as the most important root crops produced in the country (Wassu *et al*., 2015).Sweet potato research and its production is very limited to specific regions, like that of South Nation Nationalities and Peoples, Oromia, Harerghe and Amhara regions (Birhanu*et al*., 2014).

Genetic variability studies are important in the selection of parents for hybridization (Chaudhary and Singh, 1982) as sound crop improvement depends upon the magnitude of genetic variability in the base population (Adebisi *et al*., 2001). Once geneticvariability has been ascertained in a crop, improvement is possible through the use of appropriate selection method. Genetic variability is the principal foundation of any breeding program. Determining the level of variation and identifying the variants within the collected species is invaluable for genetic improvement and conservation of the crop (Lin *et al*., 2007; Clark and Hoy, 2006, Boney, 2014).Genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweetpotato improvement breeding strategy (Wassu *et al*., 2015).However, the genetic variability of agro-morphological traits within and between varieties and accessions was not determined.Therefore, this research was conducted with the objectives to assess the nature and extentgenetic variability and to estimate the association of agro-morphological trait in sweet potato genotypes.

Materials and Methods

Experimental Site, Materials and Design

Sweet potato genotypes were planted at Were Agricultural Research Centerwhichis 280 km in the northeast of Addis Ababa with altitude 740 m.a.s.l. The center has total annual rainfall of 564 mm and total annual average evapotranspiration of 2050 mm. The soil is light textured alluvial and black soil with a pH of 8.4. The mean annual temperature is 34.1 °C with a minimum of 18.9 °C and maximum of 38 °C (WARC, 2007).

Eleven sweet potato genotypes namelythree released varietiesMa’e, Koka-12 and Fallaha and eight accessions CN-2054-6, CN-2066-1, TIS-9068-7, TIS-82-0602-6, 1870004-2, CN-2065-7, TIS-9068-4 and CN-1753-1Bwere evaluated in randomized complete block design (RCBD) with three replications. Sweet potato cutting which have 2-3 buds were planted in each replication with 5 m X 6 m plot size and spacing were used 0.4 mx 1.0 m. All other recommended cultural practices and irrigation were applied as needed.

Data Collected

Data were collected from total, marketable and unmarketable tuber yields, green top weight, vine length, vine internode length, vine internode diameter, average number of roots/plant, average root weight, stand count at sprout and harvestwere collected.

Data Analysis

Data were subjected to analysis of variance (ANOVA) using SAS version 9.1 (SAS, 2004) to test the presence of significant differences among genotypes. The phenotypic and genotypic coefficient of variation was computed using the formula suggested by Burton and de Vane (1953). Broad sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996). Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al*. (1955).

Results and Discussion

Analysis of Variance and Mean Performance of Genotypes

The analysis of variance computed for 12 agro-morphological traits revealed the presence highly significant differences ($p< 0.01$) on vine internode length, green top weight, vine length, number of roots per plant, unmarketable tuber yield(qt/ha), marketable tuber yield (qt/ha) and total tuber yield (qt/ha). On other hand genotypes showed significant difference ($p<0.05$) on number of braches per plants, stand count at harvest, vine internode diameter (mm) and root weight (gm)among accessions.However, non significant differencewas observed on stand count at sprout among sweet potato genotypes (Table 1). This analysis of variance result indicated the presence of variability among sweet potato genotypes studied traits which can be exploited through selection to improve the crop for desired traits for further sweet potato breeding program. This result is in agreement with Boney (2014) who reported the presence significant difference among sweet potato genotypes.

The mean performance of sweet potato genotypes showed wide range of means for studied agro-morphological traits except a few traits which revealed narrow mean range of variation among tested genotypes. In these study genotypes showed narrow range of variation on stand count at sprouting ranged from 104 to 120 with mean of 112.18, number of branches per plant 2 and 4.6 with mean of 2.99, Vine internode length 2.5 to 5.85 with mean of 4.26 cm, vine internode diameter ranged from 3.2 to 7.4 with mean of 5.22 mm, number of roots per plants ranged between 3.6 to 13.6 with mean of 6.95.While this study analysis revealed that wide range of mean performance for stand count at harvest between 70 to 112 with mean of 88.88, green top weight ranged between 120 to 500 with mean of 306 qt/ha, vine length ranged between 59.6 to 263 with mean of 138.01 cm, root weight 100 to 263 with mean of 168.04 gm, unmarketable tuber yield ranged from 20.5 to 87.97 with mean of 48.2qt/ha, marketable tuber yield ranged from 100.52 to 319.47 with mean of 182.84 qt/ha and total tuber yield between 123.67 to 370.04 with mean of 231.04 qt/ha.

Estimation of Genetic Variance Component Genotypic and Phenotypic Variation

Genetic variability estimates including genotypic and phenotypic variance, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability, and genetic advance as percent mean for 12agro-morphological raits in sweet potato genotypes are presented in (Table 2). Estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean indicating the presence of variation and genotypes were diverse materials (Wassu *et al*., 2014).

Genotypiccoefficients of variation lower in magnitude than phenotypic coefficient of variation all agro-morphological traits. Genotypic coefficient of variation ranged from 0.77 (stand count at sprout) to 33.93 (unmarketable tuber yield) while phenotypic coefficient variation ranged between 3.47 (stand count at sprout) to 39.36 (unmarketable tuber yield). According to Sivasubramaniah and Menon (1973) PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. Based on this delineation PCV and GCV recorded in this study, unmarketable (qt/ha), vine length (cm), number of roots per plant, total tuber yield (qt/ha) and green top weight (qt/ha) had higher value both at GCV and PCV. This find agreed with Solankeyet *al*., (2015) who reported that PCVandGCVwerehigher ontuberyield. This result is supported by Tsegaye*et al*.(2007) andThiyagu *et al*.(2013) who reported that high GCV and PCV indicatingthepresenceofwidegeneticvariabilityformorphologicaltraits Medium GCV and higher PCV value recorded from number of branches per plant, vine internode length (cm) and root weight (gm) scored. On other hand vine internode diameter had medium value for both GCV and PCV. This find disagreed with Solankeyet *al*., (2015) who reported that PCVandGCVwere higher for fresh weight of tubers per plant,and number of branches per plant. However stand count at sprouting and harvesting had lowest value both at GCV and PCV.Higher magnitude of difference between phenotypic and genotypic coefficient were observed in root weight (gm), number of branches per plant, vine internode diameter (mm), green top weight (qt/ha) and number of roots per plant in decreasing orders. The observed moderate to high differences between phenotypic and genotypic coefficient of variations noticed for most of the traits indicating higher sensitivity to environmental modifications which might be difficult to improve traits through selection of high performing accessions (Wassu *et al*.,2015).On other hand remaining trait lower difference between phenotypic and genotypic coefficient of variation which differ only slightly indicating little influence of the environmental factors and traits can be improve through selection. This observation was in conformity with that ofAddisu *et al*., (2013).

Estimate broad sense heritability

Heritability in broad sense was recorded fromtwelvetraits ranged between 4.99% (stand count at sprout) to 86.45% (vine internode length). This is disagreed with Boney *et al.*, 2014 who reported heritability estimates varied from -0.375% for total tuber yield to 66.3% for scab assessment.According to Robinson *et al.* (1955) heritability in broad sense is categorized as low (0-30%), moderate (31-60%) and high > 60%. Accordingly, heritability estimate in broad sense was low value was recorded for stand count at sproutwhile moderate heritability was registered for root weight (gm), vine internode diameter (mm), stand count at harvest and number of branches per plant.Very low broad sense heritability reveals the ineffectiveness of direct selection for the improvement of the traits while moderate heritability suggests improvement through selection (Obilana and Fakorade 1980) and Snowder *et al.*, 2005). High heritability was recorded from remaining seven tout of twelve traits. This result is in agreement with Jones *et al*., (1986)andThiyaguetal., (2013)who foundthatvine length and root size hadhighheritability.If heritability of a character is very high around 80% or more, selection for such character is fairly easy. This indicates there would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotype expression of the trait (Singh *et al*, 1990).

Estimate of Genetic advance

Genetic advance as the percentage of mean (GAM) at 5% selection intensity is presented (Table 2). This study result genetic advance as percent mean ranged from 7.42% (stand count at harvest) to 60.27 (unmarketable tuber yield). This result disagreed with Boney*et al*., 2014 who reported that genetic advance as percent of mean varied from -8.2% for total yield (tonnes/ha) to 44.6% for scab assessment.Genetic advance as percent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al*.,1955). As per this suggestion, the lowest (<10%) genetic advance was observed for stand count at harvest. Moderate genetic advance as the percentage of the mean were recorded from vine internode diameter (mm), root weight (gm) and number of branches per plant.This study finding disagreed with Boney*et al*., (2014) who reported moderate genetic advance as percent of mean for marketable tuber yield. While the highest genetic advance as the percentage of the meanrecorded from eight out of twelve agro-morphological traits. This result is supported by Boney*et al*., (2014) who reported that genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to predict the rate of improvement that can be achieved in different characters (Singh andNararayanan, 1993;Thiyagu*et al.*, 2013)

Estimate of heritability along with genetic advance as percent of mean: Johnson *et al*. (1955) suggested that heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. This study analysis revealed that vine internode length, green top weight, vine length, number of roots per plant, unmarketable tuber yield, marketable tuber yield and total tuber yield scored high heritability along with high genetic advance as percent of mean. This result is supported by Boney*et al*., (2014) who reported that high heritability together with high genetic advance is vital tool for selection of the best individuals and for successful genetic improvement. On other hand, moderate heritability and genetic advance as percent of mean recorded fromnumber of branches per plant, vine internode diameter and root weight. This result confirm with Falconer and Mackay, (1996) who reported that moderate genetic advance together with moderate heritability noticed for marketable tuber yield indicated the presence of intra and inter allelic interactions in the appearance of these characters. This result also showed that low heritability and high genetic advance was recorded from stand count at sprout and medium heritability with low genetic advance was scored from stand count at harvest but there is low scored at heritability and high genetic advance. This result agreed with Chahal and Gosal, (2010, Wassu *et al*., (2015) who reported that both heritability and expected genetic advance values were low, indicated that selection might be considerably difficult to improve the crop through selection due to the masking effect of environment on the genotypic effect.

Genotypic and Phenotypic Correlations

Correlation of tuber yield with other agro morphological traits

Yield in generally, isa complex polygenic trait and difficult to improve directly. Estimating its genotypic and phenotypic correlation coefficients with yield related traits is important to utilize the available variability through selection. Root weight is of primary importance, and thus associations with it are particular interest (Jones, 1970). This study result showed that genotypic correlation higher in magnitude than corresponding phenotypic correlation for most of the studied traits.This result supported by Solankey*et al*.(2015) who reported that genotypic correlation is greater in magnitude than corresponding phenotypic correlation which indicated that most of the association existed between total storage root yield and other traits were controlled by genetic factor.

This study analysis revealed that genotypic correlation ranged from -0.56 (unmarketable and vine inter node length) to 0.98 (marketable and total storage root yield). Stand count, vine internode length and green top weight hand negative non significant genotypic correlation withtotal storage root yield while number of branches per plant, stand count at harvest and vine internode length hand positive non significant genotypic correlation coefficient with total storage root yield. This result disagreed with Yohannes *et a*l. (2010) who reported that non-significant positive correlation of total storage root yield with rootdiameter, marketable storage root yield and average storage root weight.Total storage root yield hand positive and highly significant genotypic correlation with number of roots per plant, unmarketable root yield and marketable root yield. However vine length hand negative highly significant genotypic correlation with total storage root yield.This find confirm with Yohannes *et a*l. (2010) who reported that total storage root yield had significant genotypic correlation with only unmarketable storage root yield. However, disagree with negative correlation between root length and total storage root yield.

This study analysis revealed phenotypic correlation ranged from -0.56 (unmarketable and vine inter node length) to 0.97 (marketable and total tuber yield). Root tuber yield hand negative and non significant phenotypic correlation with stand count and vine internode length.While number of branches per plant, stand count at harvest, green top weight, vine internode diameter and root weight hand positive and non significant phenotypic correlation coefficient with root tuber yield.Root tuber yield hand positive and highly significant phenotypic correlation with vine length, number of roots per plant, unmarketable root yield and marketable root yield. This finding supported by Solankey*et al*. (2015) who reported that positive and highly significant association was existed between total storage root yield and unmarketable storage root yieldbut disagreed with positive and significant phenotypic correlation was observed for fresh weight of tuber per plant with number of tubers per plant and root length had negative and significant correlation with total storage root yield at phenotypic level.

Conclusion

This analysis of variance revealed significant ($p<0.05$) among sweet potato genotypes for all traits except stand count at sprout which showed non significant among sweet potato genotypes which indicates the existence of notable genetic variability. There were less coefficients of variation in all of the characters indicating good precision of the experiment. The result of this study revealed that most studied traits had high genotypic and phenotypic coefficient of variation,high heritability, high genetic advance as percent of mean and high heritability along with high genetic advance as percent of means indicating successful genetic improvement of sweet potato genotypes. Total tuber yield will be improved simultaneously with number of roots per plant; unmarketable root yield and marketable root yield while the reverse true for vine length. This result suggested the importance of further collection to exploit the genetic variability between varieties and accessionsfor variety development of sweet potato in the country.

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Table 1. Mean squares from analysis of variance for agro-morphological traits of 11 sweet potato genotypes at Werer Agricultural Research Center

Traits	SE	Genotype	Error	CV	Range	Mean
Stand Count at Sprout	3.79	16.62^{ns}	14.36	3.38	104 -120	112.18
No of Branches	0.50	0.82*	0.25	16.85	2 - 4.6	2.99
Vine Internode Length (cm)	0.34	2.28**	0.11	7.89	2.5 -5.85	4.26
Stand Count at Harvest	6.65	125.15*	44.17	7.48	70 -112	88.88
Green Top Weight (qt/ha)	60.10	21165.82**	3612.45	19.64	120 - 500	306.00
Vine Internode Diameter (mm)	0.74	1.56*	0.55	14.25	3.2 - 7.4	5.22
Vine Length (cm)	17.82	5682.95**	317.40	12.91	59.6 - 263	138.01
Root Weight (gm)	33.64	2772.12*	1131.98	20.02	100 - 263	168.04
Roots per Plant	1.35	11.15**	1.82	19.41	3.6 -13.6	6.95
Unmarketable Yield (qt/ha)	9.61	894.91**	92.36	19.94	20.5-87.97	48.20
Marketable Yield (qt/ha)	33.06	7292.40**	1092.82	18.08	100.52-319.47	182.84
Total Yield (qt/ha)	36.48	11338.63**	1330.69	15.79	123.67-370.4	231.04

Table 2: Genotypic and phenotypic coefficient of variances, heritability and genetic advance in 11 sweet potato genotypes for 10 agro morphological traits

Traits	σ2g	σ2p	GCV%	PCV%	H %	GA%
Stand Count at Sprout	0.75	15.12	0.77	3.47	4.99	35.64
No of Branches	0.19	0.44	14.45	22.20	42.37	19.37
Vine Internode Length (cm)	0.72	0.84	19.94	21.45	86.45	38.19
Stand Count at Harvest	26.99	71.16	5.85	9.49	37.93	7.42
Green Top Weight (qt/ha)	5851.12	9463.57	25.00	31.79	61.83	40.49
Vine Internode Diameter (mm)	0.34	0.89	11.09	18.06	37.69	14.02
Vine Length (cm)	1788.52	2105.92	30.64	33.25	84.93	58.17
Root Weight (gm)	546.71	1678.70	13.91	24.38	32.57	16.36
Roots per Plant	3.11	4.93	25.35	31.93	63.03	41.46
Unmarketable Yield (qt/ha)	267.52	359.88	33.93	39.36	74.34	60.27
Marketable Yield (qt/ha)	2066.53	3159.35	24.86	30.74	65.41	41.42
Total Yield (qt/ha)	3335.98	4666.67	25.00	29.57	71.49	43.54

Table.3. Phenotypic above and genotypic below correlation coefficients of 12 traits of 11 sweet potato genotypes evaluated at Werer

	SCE	NB	VInL	SCH	GTW	VInD	VLe	RW	NRPt	UMY	MY	TY
SCE		0.13	0.01	0.23	0.04	0.22	0.17	0.08	0.08	0.12	-0.15	-0.09^{ns}
NB	0.21		-0.39	0.11	-0.13	0.04	-0.29	-0.16	0.08	0.04	0.09	0.09^{ns}
VInL	0.21	-0.49		0.09	0.48	0.30	0.82	0.06	0.43	-0.56	0.49	-0.57^{ns}
SCH	0.42	0.28	0.10		0.46	0.36	0.02	0.08	0.09	0.38	0.26	0.33^{ns}
GTW	0.52	-0.23	0.56	0.55		0.41	0.39	0.04	0.11	0.07	0.02	0.04^{ns}
VInD	0.82	0.06	0.42	0.65	0.65		0.30	0.03	0.11	0.04	0.04	0.05^{ns}
VLe	0.13	-0.39	0.94	0.08	0.57	0.44		0.08	0.27	-0.43	-0.44	0.49^{*}
RW	-0.30	-0.50	0.21	0.04	0.11	-0.21	0.18		0.48	0.10	-0.03	0.00^{ns}
NRPt	-0.03	0.12	-0.44	0.12	-0.06	0.05	-0.37	-0.71		0.53	0.44	0.52^{**}
UMY	-0.16	-0.13	-0.56	0.37	0.15	-0.09	-0.50	0.00	0.61		0.44	0.65^{**}
MY	-0.12	0.09	-0.58	0.44	-0.17	0.04	-0.54	0.09	0.43	0.62		0.97^{**}
TY	-0.14^{ns}	0.04^{ns}	-0.62^{ns}	0.46^{ns}	-0.10^{ns}	0.00^{ns}	-0.58^{**}	0.07^{ns}	0.52^{**}	0.78^{**}	0.98^{**}	