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Genetic variability, heritability and genetic advance for growth, yield and quality parameters among sweet potato [*Ipomoea batatas* (L.) lam.] genotypes

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Abstract
The investigation was conducted at AICRP on Tuber Crops, Regional Horticultural Research Station, ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, during *Rabi* 2017-18 with forty four sweet potato genotypes. This was to study genetic variability, heritability and genetic advance as per cent mean for several economic characters to identify promising cultivars suitable for the South Gujrat conditions. Data collected on eighteen characters exhibited significant differences among genotypes in respect of all the characters studied. Phenotypic coefficient of variation (PCV) was higher than Genotypic coefficient of variation (GCV) for all the traits, indicated a low environmental influence on expression of these traits. High heritability coupled with high genetic advance as per cent mean was observed yield per plot followed by β-carotene, non-reducing sugars, yield per plant, leaf area, vine length, petiole length, number of tubers per plant, number of branches per plant, ash content, tuber girth, internode length, total sugars, reducing sugars, tuber girth, starch except moisture content under study indicated that the characters are controlled by additive gene action and selection would be effective. These characters with high GCV, PCV, heritability and genetic advance as per cent mean should be considered as reliable selection criteria for crop improvement for yield and yield attributing characters.

Keywords: Components of variance, genetic advance, heritability, sweet potato genotypes

Introduction
Sweet potato belongs to family Convolvulaceae, 2n=6x=90 [*Ipomoea batatas* (L.) Lam] is a starchy root crop grown throughout the tropics, subtropics and warmer temperate regions. It produces higher yield per unit area per unit time even in marginal lands (Nedunchezhiyan and Byju, 2005) [11]. It's origin is South America. It is herbaceous perennial but cultivated as annual and it is vegetatively propagated by vine cuttings taken from freshly harvested vines grown in secondary nursery (Selvakumar, 2014) [13]. Sweet potato is a cross pollinated and highly heterozygous crop resulting in large variability for crop improvement, knowledge on genetic diversity helps the breeder in choosing desirable parents for use in the breeding program. The diverse genotypes or accessions can be crossed to produce superior high yielding hybrids possessing resistance to various abiotic and biotic stresses. This family includes about 55 genera and more than 1000 species. Collections of any crop are 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. In the present scenario, there is an urgent need to evaluate the available sweet potato accessions for the extent of genetic diversity. Genetic variability available within the sweet potato genotypes has not been fully explored and screened. Crop improvement largely depends on existence of genetic variability. Improvement in any crop is based on the extent of genetic variation present in it and the degree of improvement depends on magnitude of the available, beneficial genetic variability. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisites for formulating effective breeding methods as the genetic improvement of any crop depends on magnitude of genetic variability and the extent of heritability of economically important characters, though the part played by environment in the expression of such character also needs to be taken into account.

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Materials and Methods

The present investigation was carried out at AICRP on Tuber Crops, Regional Horticultural Research Station, ASPEE College of Horticulture and Forestry, Navsari Agricultural University, Navsari, (20^0 57' North latitude and 72^0 54' East longitude at an altitude of about 11.98 meter above the mean sea level) Gujrat (India). Forty four genotypes of sweet potato, representing native as well as foreign collected from different parts of India, were maintained and used for the present study was arranged in a Randomized Complete Block Design, with three replications. Planting was done at a distance of 60 cm between two rows and 20 cm within the row. The cuttings obtained from apical and middle portion of vine have been found to produce larger number of sprouts and higher yield of tubers than basal cuttings were planted by keeping 2 nodes beneath the soil surface and two nodes above the soil surface on 27th of November, 2017. The mean of five plants used for statistical analyses. Observation on vine length (cm), internode length (cm), petiole length (cm), number of branches per plant, leaf area (cm^2), tuber girth (cm), tuber length (cm), yield per plot (kg), number of tubers per plant, yield per plant (kg), moisture content (%), ash content (%), reducing sugars (%), total sugars (%), non-reducing sugars (%), dry matter (%), starch (%) and β-Carotene (mg/100g) were recorded.

Statistical Analysis: Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952) [3]. Heritability in broad sense was estimated as per Allard (1960) [1]. Genetic advance was estimated as per the formula proposed by Johnson et al. (1955) [6].

Results and Discussion
Analysis of Variance

The present experimental material showed a wide range of variation and highly significant varietal differences for all the traits investigated (Table: 1). This suggest that there is ample scope to identify high yielding and early genotypes with resistance to insect pest and disease to improve different characters simultaneously, provided that the material is subjected to judicious selection pressure. These are agreement with earlier investigations of Kamalam et al. (1977) [7], Kamalam, (1990) [8], Vimala and Lakshmi, (1990) [16], Engida et al. (2007), Mohanty et al. (2015) [9] and Badu et al. (2017) [2].

The high magnitude of PCV and GCV observed for yield per plot followed by β-carotene, non-reducing sugars, yield per plant, leaf area, vine length, petiole length, number of tubers per plant, number of branches per plant, ash content, tuber girth, internode length total sugars, reducing sugars, tuber girth and starch (Table: 2). This high magnitude of PCV and GCV for above characters suggested greater phenotypic and genotypic variability indicated and that these characters can be improved through phenotypic selection, which is in accordance with findings by Sankari et al. (2001) [12], Teshome et al. (2004) [14], Engida et al. (2007), Wera et al. (2014) [17], Badu et al. (2017) [2] and Gurmu et al. (2017) [4]. Moderate PCV was observed for tuber dry matter is in

agreement with the conclusion of Hossain et al. (2000) [5] and Engida et al. (2007) content indicated that the presence of additive gene action governing the inheritance of these traits and offers the best possibility of improvement through simple selection procedures. Low PCV and GCV were observed for moisture content.

Higher heritability was exhibited by yield per plot followed by vine length, leaf area, β-carotene, yield per plant, petiole length, non-reducing sugars, internode length, number of branches per plant, tuber girth, tuber length, number of tubers per plant, ash content, reducing sugars, total sugars, dry matter and starch. These findings was in agreement with Sankari et al. (2001) [12] and Engida et al. (2007) for vine length, Badu et al. (2017) [2], for internode length, Thiyagu et al. (2013) [15] for petiole length, Vimala and Lakshmi (1999) for number of branches per plant, Engida et al. (2007) and Thiyagu et al. (2013) [15] for leaf area, Vimala and Lakshmi (1999), Sankari et al. (2001) [12], Teshome et al. (2004) [14] and Badu et al. (2017) [2] for tuber girth, for beta carotene, starch, total sugars, Sankari et al. (2001) [12], Hossain et al. (2000) [5], Engida et al. (2007) for yield per plant, Wera et al. (2014) [17] for tuber yield. Higher values of heritability of these characters expressed that they were less influenced by the environmental factors. It reflected that the phenotypes were the near representative of their genotypes and selection based on phenotypic performance would be reliable. Estimates of heritability were recorded moderate for tuber moisture content indicates the role of both additive and non-additive gene action governing the inheritance of this trait and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects.

Higher genetic advance as per cent of mean was exhibited by yield per plot followed β-carotene, non-reducing sugars, yield per plant, leaf area, vine length, internode length, petiole length, number of branches per plant, tuber girth, tuber length, number of tubers per plant, ash content, reducing sugars, total sugars, dry matter and starch indicates high response to selection. Similar results were reported by Sankari et al. (2001) [12], Teshome et al. (2004) [14], Engida et al. (2007), Wera et al. (2014) [17].

High heritability coupled with high genetic advance as per cent of mean (Table: 3) for yield per plot followed by β-carotene, non-reducing sugars, yield per plant, leaf area, vine length, petiole length, number of tubers per plant, number of branches per plant, ash content, tuber girth, internode length, total sugars, reducing sugars, tuber girth, starch except moisture content under study indicated that the characters are controlled by additive gene action and selection would be effective. These findings was in agreement with Sankari et al. (2001) [12], Teshome et al. (2004) [14], Engida et al. (2007), Thiyagu et al. (2013) [15], Wera et al. (2014) [17], Badu et al. (2017) [2] for above characters. Moderate heritability along with low genetic advance was observed for moisture content indicating high influence of environment and consequently its selection may not be effective.

Table 1: Analysis of variance showing mean sum of squares for 18 characters in 44 genotypes of sweet potato

S. No	Source of variation	Replications	Genotypes	Error	S.Em.±	C.V. %
1.	Degrees of freedom	2	43	86		
2.	Vine length (cm)	256.14	9888.85**	108.33	5.94	6.81
3.	Internode length (cm)	0.66	6.13**	0.24	0.28	8.87
4.	Petiole length (cm)	2.19	238.48**	3.19	1.02	7.33
5.	Number of branches per plant	0.35	13.58**	0.22	0.27	7.11

6.	Leaf area (cm^2)	152.23	9477.84**	101.56	5.75	8.4
7.	Tuber girth (cm)	0.59	40.34**	1.94	0.79	10.5
8.	Tuber length (cm)	4.28	56.39**	3.33	1.04	9.72
9.	Yield per plot (kg)	0.066	33.26**	0.18	0.24	11.96
10.	Number of tubers per plant	1.65	41.07**	1.26	0.64	10.38
11.	Yield per plant (g)	0.004	0.17**	0.002	0.03	12.03
12.	Tuber moisture content (%)	5.11	61.56**	14.82	2.2	5.04
13.	Ash content (%)	0.08	0.88**	0.03	0.09	8.46
14.	Reducing sugars (%)	0.005	0.62**	0.01	0.06	5.62
15.	Total sugars (%)	0.04	3.85**	0.07	0.15	6.73
16.	Non-reducing sugars (%)	0.05	4.38**	0.06	0.13	11.87
17.	Tuber dry matter (%)	3.7	55.82**	1.58	0.72	5.06
18.	Starch (%)	2.2	22.18**	1.48	0.69	9.29
19.	β-Carotene (mg/100mg)	0.21	17.67**	0.16	0.23	11.72

Table 2: Estimates of range, mean, variability, heritability (bs) and genetic advance as per cent of mean for different characters in sweet potato genotypes

S. No	Characters	Range	Mean	Components of Variance			GCV %	PCV %	ECV %	H$^2_{bs}$ %	G.A % of mean
				σ ^2_g	σ ^2_p	σ ^2_e					
1.	Vine length (cm)	31.77-274.37	152.81	3260.17	3368.50	108.32	37.36	37.98	6.81	97	75.73
2.	Internode length (cm)	2.80-8.23	5.56	1.96	2.21	0.24	25.20	26.72	8.87	89	48.96
3.	Petiole length(cm)	6.93-40.33	24.37	78.43	81.62	3.19	36.34	37.07	7.33	96	73.38
4.	No. of branches/plant	2.47-12.27	6.55	4.45	4.67	0.22	32.21	32.99	7.11	95	64.80
5.	Leaf area (cm^2)	36.80-279.93	119.94	3125.43	3226.98	101.56	46.61	47.36	8.40	97	94.50
6.	Tuber girth (cm)	4.00-20.36	13.26	12.80	14.74	1.94	26.99	28.96	10.50	87	51.81
7.	Tuber length (cm)	11.05-28.30	18.78	17.69	21.02	3.33	22.40	24.42	9.72	84	42.34
8.	Yield per plot (kg)	0.13-12.83	3.57	11.03	11.21	0.18	92.98	93.75	11.96	98	189.98
9.	No. of tubers/ plant	2.00-18.67	10.8	13.27	14.53	1.26	33.75	35.31	10.38	91	66.45
10.	Yield per plant (g)	0.13-1.08	0.396	0.055	0.057	0.002	59.35	60.56	12.03	96	119.83
11.	Moisture content (%)	64.77-81.18	76.34	15.58	30.40	14.82	5.17	7.22	5.04	51	7.62
12.	Ash content (%)	1.05-3.40	1.96	0.28	0.31	0.03	27.14	28.43	8.46	91	53.37
13.	Reducing sugars (%)	1.24-3.28	1.86	0.20	0.21	0.01	24.06	24.71	5.62	95	48.27
14.	Total sugars (%)	1.66-8.23	3.82	1.26	1.33	0.07	29.40	30.16	6.73	95	59.03
15.	Non-reducing sugars (%)	0.26-6.08	1.98	1.44	1.50	0.06	60.75	61.90	11.87	96	122.83
16.	Tuber dry matter (%)	17.30-35.98	24.86	18.07	19.66	1.58	17.10	17.84	5.06	92	33.80
17.	Starch (%)	6.44-17.75	13.08	6.90	8.38	1.48	20.07	22.12	9.29	82	37.52
18.	β-Carotene (mg/100g)	0.32-8.60	3.46	5.83	6.00	0.16	69.72	70.70	11.72	97	141.64

Table 3: Comparison of different variability parameters in respect of eighteen characters in sweet potato

Characters	GCV			PCV			H$^2_{bs}$ %			GAM		
	L	M	H	L	M	H	L	M	H	L	M	H
Vine length (cm)	-	-	+	-	-	+	-	-	+	-	-	+
Internode length (cm)	-	-	+	-	-	+	-	-	+	-	-	+
Petiole length(cm)	-	-	+	-	-	+	-	-	+	-	-	+
No. of branches/plant	-	-	+	-	-	+	-	-	+	-	-	+
Leaf area (cm^2)	-	-	+	-	-	+	-	-	+	-	-	+
Tuber girth (cm)	-	-	+	-	-	+	-	-	+	-	-	+
Tuber length (cm)	-	-	+	-	-	+	-	-	+	-	-	+
Yield per plot (kg)	-	-	+	-	-	+	-	-	+	-	-	+
No. of tubers/ plant	-	-	+	-	-	+	-	-	+	-	-	+
Yield per plant (g)	-	-	+	-	-	+	-	-	+	-	-	+
Moisture content (%)	+	-	-	+	-	-	-	+	-	+	-	-
Ash content (%)	-	-	+	-	-	+	-	-	+	-	-	+
Reducing sugars (%)	-	-	+	-	-	+	-	-	+	-	-	+
Total sugars (%)	-	-	+	-	-	+	-	-	+	-	-	+
Non-reducing sugars (%)	-	-	+	-	-	+	-	-	+	-	-	+
Dry matter (%)	-	+	-	-	+	-	-	-	-	-	-	+
Starch (%)	-	-	+	-	-	+	-	-	+	-	-	+
β-Carotene (mg)	-	-	+	-	-	+	-	-	+	-	-	+

+ Presence, - Absence

GCV, PCV and GAM   **Heritability**
Low= 1-10   Low= 0-30
Medium = 10-20   Medium = 30-60
High = >20   High = >60

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