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Genetic variability for yield and yield related traits in orange-fleshed sweet potato (*Ipomoea batatas* L.) Genotypes

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Abstract

The present investigation was undertaken to estimate the genetic variability, heritability and genetic advance for growth and yield parameters among sixteen genotypes of orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes. In a randomized block design with two replications during *rabi* 2020-21 at Regional Horticultural Research and Extension centre (RHREC), (Kumbapur Form), Dharwad. Analysis of variance revealed highly significant differences among the genotypes were observed for all the characters under study. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High (>20%) genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were observed for number of leaves per vine at 60 and 120 DAP, leaf area at 60, 90, 120 DAP, mean weight of tuber, tuber yield per vine, tuber yield per plot, tuber yield per hectare. It indicated the existence of broad genetic base, which would be amenable for further selection. High heritability (> 60%) coupled with high genetic advance as per cent over mean (>20%) were recorded for the characters such as, vine length, number of leaves per vine, leaf area, internodal length, number of tubers per vine, tuber girth, mean weight of tuber, tuber yield per vine, tuber yield per plot, tuber yield per hectare, starch content, dry matter percent and beta carotene content indicating the prevalence of additive gene action for these traits. Thus, there is ample scope for improving these characters through direct selection.

Keywords: Yucatec maya, traditional medicine, plant use, herbalist

Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam] belongs to family Convolvulaceae having its chormosome number 2n=6x=90. Its 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. 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. Presence of variability is prerequisite to the plant breeder for planning an effective breeding programme. This is useful for selecting, identifying promising variants for developing hybrids or varieties directly or through recombinant breeding. Genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweet potato improvement breeding strategy. Therefore, this research was conducted with the objective to assess the extent and nature of genetic variability and heritability among the orange fleshed sweet potato genotypes.

Materials and Methods

The experiment was conducted from September, 2020 to March, 2021 at Regional Horticultural Research and Extension Centre (RHREC), Kumbapur, Dharwad. The site is located in the agro climatic zone-8 (Northern Transition Zone) of Karnataka state. Dharwad is geographically located at 15^0 26^1 North latitude, $76^0 27^1$ East longitude and at an altitude of 678 m above mean sea level. The soil was a medium sandy loam.

Well matured healthy and disease-free cuttings of sixteen genotypes of sweet potatoes (Table 1) were procured from AICRP on Tuber crops, Dharwad, UHS, Bagalkote have been taken for investigation. The experiment was laid out in a randomized complete block design (RCBD) with three replications. The treatments in each replication were allotted randomly by using random number table. Sweet potato cuttings which have 2-3 buds were planted in each replication with 3m × 3m plot size at 60cm × 20 cm spacing. All other recommended cultural practices and irrigation were applies as needed. Plots were kept free from weeds by regular hand weeding. Five plants of each genotype from each replication were used for observations.

Statistical analysis

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1957) [10]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953) [3]. Heritability in broad sense was estimated as per Weber and Moorthy (1952) [20]. Genetic advance was estimated as per the formula proposed by Johnson *et al.*, (1955) [7]. The range of genetic advance as per cent of mean was classified as low (Less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Johnson *et al.*, (1955) [7].

Results and Discussion

Analysis of Variance

The analysis of variance for different quantitative and qualitative characters in sixteen genotypes of orange fleshed sweet potato genotypes was presented in Table 2 and 3. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz*., vine length, number of branches per vine, number of leaves per vine, inter nodal length, leaf area, number of tuber per vine, tuber length, tuber girth, tuber weight, total tuber yield per vine, total tuber yield per plot, total yield per hectare, starch content, beta-carotene, and dry matter content indicates the presence of sufficient amount of variability in all the characters under study. These findings are in line with earlier reports of Basavaraj *et al.*, (2005) [2] in potato, Engida *et al.*, (2006) [21] and Shashikanth *et al.*, (2008) [17] in sweet potato. Sharavati *et al.* (2018) [16], Narasimhamurthy *et al.* (2018) [9] in orange fleshed sweet potato and Gehan *et al.* (2019) [6].

Phenotypic and genotypic coefficient of variation

Higher magnitude of PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) (> 20%) were observed for In the present investigation high (>20%) magnitude of GCV and PCV were observed for leaf area, and number of leaves per vine both at 60 DAP, 90 DAP and 120 DAP respectively and mean weight of tuber, tuber yield per vine, tuber yield per plot, total tuber yield per hectare. Indicating wider range of variability exhibited in this traits (Table 11). Similar results were also obtained by Badu *et al.* (2017) [1] for leaf area in orange fleshed sweet potato. Singh *et al.* (2015) [18] for number of leaves per vine in sweet potato. It indicated the presence of high variability in the genotypes for selection. The differences between PCV and GCV values were minimum for most of the traits studied and indicating that, traits under study were less influenced by environment. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

The moderate phenotypic and genotypic coefficient of variations recorded for other growth parameters like vine length, number of leaves per vine and internodal length at 60 DAP, 90 DAP and 120 DAP respectively, indicates that the apparent variation is not only due to genotypes but also due to little influence of environment on the expression of character. Similar opinion was expressed by other researchers like Rangare and Rangare (2013) [14], Singh *et al.* (2015) [18], Darshan *et al.* (2017) [4], Sharavati *et al.* (2018) [16], and Gehan *et al.* (2019) [6].

Heritability

High heritability (>60%) coupled with high genetic advance (>20%) as per cent of mean were recorded for growth parameters such as vine length at 60 and 90 DAP, leaf area, number of leaves and intermodal length at 60, 90 and 120 DAP respectively, number of tubers per vine, tuber length, tuber girth, mean weight of tuber, tuber yield per vine, tuber yield per plot, total tuber yield per hectare. These results suggested that the inheritance of such traits governed mainly by additive gene effects hence selection based on phenotypic performance may performed useful (Table 11). As high heritability accompanied with high genetic advance as per cent mean indicates the prevalence of additive gene action, selection would be effective. Similar results were noticed in earlier studies by Prarthana *et al.* (2015) [12] for vine length, inernodal length, number of leaves and leaf area index in sweet potato, Badu *et al.*, (2017) [1] for vine length, number of leaves, intermodal length Ramachandra and Srinivasa (2017) [13], for leaf area in sweet potato, Sharavati *et al.* (2018) [16] in vine length, number of leaves, intermodal length in sweet potato, Narasimhamurthy *et al.* (2018) [9] for vine length and leaf area in orange fleshed sweet potato. Thus, there is an ample scope for improving these characters by direct selection. Similar results were also reported by Madawal *et al.* (2015), Badu *et al.* (2017) [1], Nasiruddin *et al.* (2017), Ramachandra and Srinivasa (2017) [13], Sharavati *et al.* (2018) [16] for traits number of tubers per vine, tuber length, tuber girth, mean weight of tuber, tuber yield per vine, tuber yield per plot, tuber yield per hectare in sweet potato. For tuber yield per vine, tuber yield per plot, results were similar to Tripathi (2018) [19] and Narasimhamurthy *et al.* (2018) [9]. The research findings of Gehan *et al.* (2019) [6], Prajapati *et al.* (2020) [11] and Seid *et al.* (2020) [15] was similar for number of tubers per plant.

Table 2: Analysis of variance (mean sum of squares) for growth parameters in orange fleshed sweet potato genotypes

Sl. No.	Source of variation/characters	Replication	Genotypes	Error		
	Degrees of freedom	2	15	30	S.Em±	CD @ 5%
A	Growth parameters					
1	Vine length (cm) at 60 DAP	255.87	1096.36*	172.13	7.57	21.87
2	Vine length (cm) at 90 DAP	282.80	1574.51*	203.94	8.24	23.81
3	Vine length (cm) at 120 DAP	423.52	1229.40*	366.06	11.04	31.9
4	Leaf area (cm^2) at 60 DAP	367262.09	2947601.11*	111174.23	192.50	555.99

5	Leaf area (cm^2) at 90 DAP	28821.18	34626000.04*	165514.82	234.88	678.39
6	Leaf area (cm^2) at 120 DAP	619507.00	7019614.08*	237667.58	281.46	812.92
7	Inter nodal length (cm) at 60 DAP	0.37	0.94*	0.11	0.19	0.56
8	Inter nodal length (cm) at 90 DAP	0.25	0.91*	0.08	0.17	0.49
9	Inter nodal length (cm) at 120 DAP	0.20	0.86*	0.09	0.18	0.52
10	Number of leaves per vine at 60 DAP	216.74	2678.75*	153.29	7.14	20.64
11	Number of leaves per vine at 90 DAP	233.16	2463.16*	315.40	10.25	29.61
12	Number of leaves per vine at 120 DAP	324.01	7002.10*	495.26	12.84	37.10
13	Number of branches per vine at 90 DAP	0.19	0.43*	0.07	0.15	0.46
14	Number of branches per vine at 120 DAP	0.55	0.93*	0.17	0.24	0.69

* Significant @ 5% DAP: Days after planting

Table 3: Analysis of variance (Mean sum of squares) for yield and quality parameters in orange fleshed sweet potato genotypes

Sl. No.	Source of variation/ characters	Replication	Genotypes	Error	S.Em±	CD @ 5%
	Degrees of freedom	2	15	30		
B	Yield parameters					
1	Number of tubers per vine	0.19	0.99*	0.06	0.15	0.43
2	Tuber length (cm)	4.00	4.98*	1.30	0.65	1.90
3	Tuber girth (cm)	0.89	19.52*	2.204	0.85	2.47
4	Mean weight of tuber (g)	702.42	17151.27*	282.86	9.71	28.04
5	Tuber yield per vine (kg)	9319.50	176725.19*	3612.13	34.69	100.21
6	Tuber yield per plot (kg/plot)	6.72	120.50*	2.89	0.98	2.83
7	Tuber yield per hectare (t/ha)	8.30	148.77*	3.57	1.09	3.15
C	Quality parameters					
8	Starch content (%)	0.84	32.83*	0.27	0.30	0.87
9	Dry matter content (%)	0.18	27.99*	0.29	0.31	0.90
10	Beta-carotene (mg/100g)	0.10	21.20*	0.04	0.12	0.37

* Significant @ 5%

Table 4: Estimates of range, mean, components of variance, heritability and genetic advance for growth attributes in orange fleshed sweet potato genotypes

Sl. No.	Character	Range	Mean	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM%
A	Growth parameter									
1	Vine length (cm) 60 DAP	96.33-178.20	132.16	303.03	361.63	13.14	14.36	83.80	32.82	24.79
2	Vine length (cm) 90 DAP	130.46-218.93	172.12	471.78	546.02	12.60	13.56	86.40	41.59	24.14
3	Vine length (cm) 120 DAP	175.06-252.46	201.23	278.81	411.08	7.95	9.66	67.82	28.32	13.50
4	Number of leaves per vine 60 DAP	69.73-175.60	122.05	841.81	892.91	23.77	24.48	94.28	58.03	47.54
5	Number of leaves per vine 90 DAP	101.13-210.53	161.37	715.92	821.05	16.58	17.75	87.20	51.46	31.89
6	Number of leaves per vine 120 DAP	134.93-307.40	210.19	2168.94	2334.03	22.15	22.98	92.93	92.48	43.99
7	Leaf area (cm^2) 60 DAP	2098.54-5510.95	3509.09	945475.62	982533.70	27.70	28.24	96.23	1964.91	55.99
8	Leaf area (cm^2) 90DAP	3338.3-6838.83	4718.17	1099028.40	1154200.01	22.21	22.77	95.22	2107.34	44.66
9	Leaf area (cm^2) 120 DAP	4208.17-9852.56	6023.11	2260648.83	2339871.36	24.96	25.39	96.61	3044.41	50.54
10	Number of branches per vine 90 DAP	3.20-4.66	3.82	0.1202	0.14	9.06	9.97	82.47	0.64	16.95
11	Number of branches per vine 120 DAP	4.83-6.60	5.51	0.2516	0.31	9.09	10.10	81.09	0.93	16.87
12	Inter nodal length (cm) 60 DAP	2.55-4.25	3.35	0.27	0.31	15.70	16.73	88.01	1.01	30.34
13	Inter nodal length (cm) 90 DAP	2.69-4.37	3.63	0.27	0.30	14.47	15.21	90.53	1.03	28.36
14	Inter nodal length (cm) 120 DAP	2.79-4.70	4.00	0.25	0.28	12.61	13.40	88.59	0.97	24.46

GV- Genotypic variance; PCV- Phenotypic co-efficient of variation; GAM- Genetic advance as percent over mean
PV - Phenotypic variance; GCV- Genotypic co- efficient of variation; GA- Genetic advance; DAP- Days after planting

Table 12: Estimates of range, mean, components of variance, heritability and genetic advance for yield attributes in orange fleshed sweet potato genotypes

Sl. No.	Character	Range	Mean	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM%
B	Yield parameter									
1	Number of tubers per vine	2.73-4.60	3.23	0.30	0.33	17.80	17.80	93.02	1.10	34.12
2	Tuber length (cm)	10.94-15.60	12.49	1.22	1.66	8.86	10.31	73.87	1.96	15.69
3	Tuber girth (cm)	12.54-21.26	16.39	5.77	6.50	14.65	15.55	88.71	4.66	28.43
4	Mean weight of tuber (g)	106.19-315.27	176.11	5622.80	5717.09	42.57	42.93	98.35	153.19	86.98
5	Tuber yield per vine (kg)	205-1027.86	536.73	57704.35	58908.39	44.75	45.21	97.96	489.76	91.24
6	Tuber yield per plot (kg/plot)	10.11-33.64	17.74	39.20	40.16	35.28	35.71	97.60	12.74	71.80
7	Tuber yield per hectare (t/ha)	11.24-37.38	19.71	48.39	49.59	35.28	35.71	97.60	14.15	71.80

GV- Genotypic variance PCV- Phenotypic co-efficient of variation PV - Phenotypic variance GCV- Genotypic co- efficient of variation GA-Genetic advance GAM-Genetic advance as percent mean

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