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Research Article

Genetic Variability for Yield and Yield Related Traits in Orange-Fleshed Sweetpotato Genotypes Evaluated at Hawassa, Ethiopia

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ABSTRACT

The study was conducted to determine variability for yield and yield related traits in 24 orange fleshed sweetpotato [Ipomoea batatas (L.) Lam] genotypes in the 2017 main cropping season at Hawassa Agricultural Research Center. The experiment was laid out in Randomized Complete Block Design with three replications. Data were collected on 19 traits and analysis of variance (ANOVA) was conducted. Significant differences (P≤0.05) among genotypes were observed for root yield and its components as well as morphological and qualitative traits including sweetpotato virus disease reaction (SPVD). The phenotypic coefficient of variation (PCV) ranged from 22.1 % for mature leaf size to 118.3 % for unmarketable root yield, while genotypic coefficient of variation (GCV) ranged from 20.6 % for root girth to 111.7 % for unmarketable root yield. All the traits studied showed PCV and GCV more than 20%, suggesting high variability and this could be used for selection of superior genotypes with respect to character of interest. Most traits showed high values for broad sense heritability which ranged from 66.7 to 100 %, indicating low environmental influence in the observed variation. High heritability coupled with high genetic advances as percent of mean were observed for marketable root yield, root skin color, root beta carotene content, harvest index, vine length, vine inter-node length and above ground fresh weight, implying that, these characters are governed by additive gene action and selection would be rewarding for the further improvement of such traits.

Keywords: Genotypes; Heritability; Orange fleshed sweetpotato; Variability; Yield

INTRODUCTION

Sweetpotato is an economically important crop in tropical, subtropical and warm temperate regions [1]. Chiefly, Orange fleshed sweetpotato [Ipomoea batatas (L) Lam.] has been considered as an invaluable crop in the fight against malnutrition (Vitamin A deficiency) in Africa. It is cross-pollinated (self-incompatible) and, therefore, highly heterozygous crops 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 [2].On top of this, the availability of morpho-genetic variation in agronomic characters of the crop would be of considerable importance in determining the best method to improve the crop yield.

Genetic improvement of any crop requires knowledge on the nature and magnitude of variability in the base population [3]. Also, it is necessary to generate information on the relative contribution of the various component traits to yield and the identification of superior yielding genotypes from genetically variable populations [4]. However, so far, there is little information on the variability and character association study among sweetpotato varieties in Ethiopia [5]. Therefore, this study was initiated to assess variability in orange fleshed sweetpotato genotypes to exploit the genetic potential of sweetpotato genotypes for further improvement program.

MATERIALS AND METHODS

Description of the experimental site

The experiment was conducted during the 2017 main rainy season under the rain-fed condition at Hawassa Agricultural Research Center (HwARC). HwARC is located in Hawassa city (7o04′N, 38031′E , 1700 meters above sea level, the average annual rain-fall of the area is 1141 mm, minimum/maximum air temperature is 13.1/27.1 0C respectively) the capital of Southern Nations, Nationalities, and Peoples' Regional State (SNNPRS), in the southern part of Ethiopia. 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 [6].

Experimental materials

Twenty four orange fleshed sweetpotato genotypes were used for the study, among which two released varieties in Ethiopia included as checks (Kulfo and Tula). The four genotypes are advanced lines from HwARC crosses and the rest are introduced from Kenya, Uganda and Mozambique.

Experimental design and field management

The experiment was planted using a Randomized Complete Block Design (RCBD) with three replications. The experimental plot size was

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7.2 m2, with 3 m long and 2.4 m width. Each plot consisted of four rows (ridges), with ten plants per row. The spacing between rows and between plants within row was 60 and 30 cm, respectively. The spacing between blocks was 2 meter. Ten holes per row and 40 per plot were prepared and one vine cutting of 30cm in length was planted in each hole of the row (ridge). The genotypes were planted on 8 Aug 2017. All plots received the recommended [7] cultural practices uniformly and no fertilizer was applied.

Replanting was done to substitute the dead vine after one week of planting. Earthning-up was done after the fourth week of planting and all plots were kept weed free by regular weeding and cultivation. Harvesting was done on 28 Dec 2017.

Data collection

Data collected from the two central rows excluding the two plants grown at both ends of the row and the two border rows.

Growth and Morphological Characteristics: Vine length (cm): measured by taking the vertical length of the vine from the ground level to the tip of the main shoot of the plants by using five plants randomly taken from each plot and averaged over the plants. Vine inter-nodal length (cm): is the measured value between two successive nodes. It was measured by using three internodes (node numbers) located in the middle section of the vine of five randomly selected plants in a plot and was expressed in centimetre. Mature leaf size (cm): Three leaves located in the middle section of the vine were measured from the basal lobes to the tip (apex) of the leaves and averaged over the sampled numbers per plot. Vine girth (mm): is the mean diameter of the vine from the central portion of the main shoot. The girth of each of the five sampled plants was measured by calliper and divided by number of plants. It was expressed in centimetre.

Petiole length (cm): The petiole length was measured from the base to the insertion point with the blade. Data taken from five randomly selected plants and expressed in centimetre. Ground cover: Estimations of ground cover were recorded 60 days after planting and levels were considered as low with < 50 % ground cover, medium with 50-74 % ground cover, high with 75-90 % ground cover and very high with >90 % ground cover.

Yield and Yield Related Traits: Number of storage roots per plant: is the mean number of storage roots produced by the sampled plants. Total number of storage roots from each of the sampled plants were counted and divided by the number of plants and expressed as number per plant. Storage root length (cm): is the length of storage root that was measured from distal to the proximal end on five randomly taken plants at harvest. Storage root girth: is the diameter from the middle portion of the storage root. The girth of all the storage roots of each of the sampled plants were

measured by using calliper and divided by number of storage roots from all plants sampled and expressed in centimetre.

Aboveground fresh weight (t ha-1): The weight of above ground parts of the two central rows was taken and converted to t/ha. Harvest index (HI): it was calculated as a ratio of economical yield (fresh root weight) to total weight (above ground fresh weight + fresh root weight) on fresh weight basis

Marketable yield (t ha-1): is the weight of clean, uninfected storage roots that fall in the size range of 100 g-500 g. It was taken by weighing all the storage roots collected from the harvestable plot by using beam balance and expressed as t ha-1. Unmarketable yield (t ha-1): is the weight of infested, under sized (less than 100g), over-sized (more than 500 g) bruised, or cut storage roots. It was taken by weighting all the storage roots collected from the harvestable plot by using beam balance. It was expressed as t ha-1. Total storage root yield (t ha-1): is the sum total of both marketable and unmarketable storage root yields obtained from the harvestable plot. And then it was expressed as t ha-1. Yield per hectare: this was obtained from harvestable plot (net plot) and converted in to yield per hectare by using the formula written below and was expressed as ton per hectare

Yield per hectare in tones = Yield per net plot (kg) * 10,000

Net area of the plot (m2)* 1000

Qualitative data

Sweetpotato Virus Disease (SPVD): - recorded on plot basis, using a scale of 1 to 5, where 1 = no visible symptoms, 2 = mild symptoms (a few local lesions on a few leaves), 3 = moderate symptoms (mosaic symptoms on leaves), 4 = severe symptoms (mosaic symptoms with plants showing stunted growth) and 5 = very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting. Predominant skin colour: - recorded on a scale of 1-9 as described by Huaman, where 1=White, 2 = Cream, 3 = Yellow, 4 = Orange, 5 = Brownish orange, 6 = Pink, 7 = Red, 8 = Purple red, and 9 = Dark Purple. Predominant flesh colour:- recorded in scale of 1-9 as described by Huaman, where 1 = White, 2 = Cream, 3 = Dark cream, 4 = Pale yellow, 5 =Dark yellow, 6 = Pale orange,7= Intermediate orange, 8 = Dark orange, and 9=Strongly pigmented with anthocyanin. β-carotene content: was estimated based on a colour chart developed by Burgos. Root dry matter content (RDMC):-expressed as percentage of root dry weight (g) to fresh root weight (g). 200 g samples were taken from roots of sampled plants in the plot and the samples were dried in an oven at 80 oC for 48 hours to maintain constant weight. The weight was taken by using sensitive balance and the ratio was expressed in percent.

Data analysis

All collected data were subjected to ANOVA using SAS statistical package (SAS 9.0) and Minitab software version 16. Duncan's multiple range tests was employed to compare means at 5% probability levels as described by Gomez and Gomez.

Analysis of genetic parameters

The phenotypic, genotypic and environmental variances and coefficient of variations were calculated according to the formula suggested by Singh and Chaudhury using ANOVA table of Randomized Complete Block Design (RCBD).

RESULTS AND DISCUSSION

Study setting

Analysis of Variance for 19 Traits of OFSP Genotypes

Analysis of Variance (ANOVA) showed the presence of highly significant difference ($p<0.01$) among the tested genotypes for yield and its contributing traits studied (Table 1).

Table 1: Analysis of variance for 19trais of OFSP genotypes.

No.	Traits	Mean square Replication (df=2)	Genotype (df=23)	Error (df=48)
1	GC	48.98	936.18	19.39
2	SPVD	0.38	1.57	0.22
3	VL	231.3	4640.3	167.1
4	IL	0.77	6.58	0.38

5	VD	0.51	2.72	0.26
6	PL	18.73	104.87	6.71
7	MLS	0.1	7.15	0.86
8	RL	0.97	16.51	3.92
9	RG	2.12	1.16	0.58
10	AGFW	2.14	480.94	71.21
11	HI	0	0.03	0
12	RDMC	0.14	46.27	0.39

The mean performance of the genotypes for root length ranged from 9 to 18.1 cm with over all mean of 14.7 cm. Genotype G1 (Ukr/Eju-10) showed the highest mean root length of 18.1cm while genotypes G24 (Tula) and G23 (Kulfo) showed the lowest mean root length performance of 9, 9.5 cm respectively. The high root girth values were recorded for genotypes: G19, G15, G20, G21, G10, G13, G1, G11, and G23 with average mean of more than 5.1 cm respectively . The lowest root girth values were recorded for genotypes G4, G12 and G16 with mean value of 3.4, 3.8 and 3.8 cm respectively. Genotype G14 (Mayai) and G17 (Tomulabula) showed the highest above ground fresh weight of 75.1 and 63.7 t ha-1 respectively. This suggests their potential use as a source of animal feed [8].Whereas, genotype G23 (Kulfo) had showed the lowest mean performance of 17.4 t ha-1. The highest and lowest mean values of number of roots per plant was obtained 0.7 for G19 (Melinda) and 0.2 for G24 (Tula). The highest marketable roots were obtained from genotypes G22 (Jane) and G19 (Melinda) with 23.5 and 22.0 t ha-1 respectively, indicating that these genotypes are better genotypes with less wastage.

On the other hand, the lowest marketable roots were recorded for genotypes G4 (Res/Tem-23), G23 (Kulfo) and G24 (Tula) with mean yield of 5.0, 5.0 and 5.4 t ha-1 in that order. The mean of unmarketable root yield was ranged from 0.2(G10) to 6.5 (G24) t ha-1. This genotype is not a good type for producing sweetpotato for marketing roots.

The highest total storage root yield was obtained from G10 (27.4 t ha-1) while the lowest total storage root yield was obtained from G24 (5.7 t ha-1) (Table 2. Genotypes: G10, G9, G11, G15 and G19 had the highest harvest index of 45, 44, 42, 41 and 41% respectively. The harvest index of the tested genotypes ranged from 13 % for G4 to 45 % for G10 with an average of 29 %. The harvest index showed the ratio of assimilation distribution between economic and the overall biomass [9]. High harvest index shows the efficiency of the assimilate utilization which could be seen from the high production point of view. This was confirmed by genotype G10 that offered the highest harvest index (0.45), which also had the highest storage root yield (27.4 t ha-1). However, this genotype showed low above ground fresh weight. As a result, the high HI values were not only due to its high fresh root yield but also due to its low above ground fresh weight. This suggests that high correlation between yield and HI does not necessarily imply that HI could be an effective selection criterion for high yield in all situations, as suggested by [10]. The root dry matter content was ranged from 20 to 33%. And nearly 50% of the tested genotypes expressed the root dry matter content of more than 30%. Especially, genotypes G3 (Res/Tem-14), G21 (Gloria) and G1 (Ukr/Eju-10) showed high mean dry matter contents of 33, 32.6 and 31.9%, respectively, indicating that these genotypes could solve the acceptability problem of the previously released OFSP varieties that had low root dry matter contents. This is because root dry matter content is an important and most preferred market attribute and is one of the criteria famers use in selecting sweetpotato cultivars, as suggested by [11] and [12].

	Traits								
Genotypes	RL	RG	AGFW	NRP (Kg)	MRKY	UMRKY	TYLD	HI	RDMC
	(cm)	(cm)	(t ha-1)		(t ha-1)	(t ha-1)	(t ha-1)	(%)	(%)
G1	18.1 a	5.1 bac	46.2 b	0.35 dec	12.8 egdf	3.7 ebdac	16.5 fge	0.26 gefdh	31.9 ba
G2	17.4 ba	4.5 bdac	43.1cb	0.32 dec	8 hgjfi	0.3 ef	8.3 kji	0.16 ji	30.9 bc
G3	15.8 bdac	4.8 bdac	45.7 b	0.54 bdac	15.6 bdc	2.9 e bdfc	18.5 fdec	0.28gefdc	33 a
G4	11.9ef	3.4 d	46.7 b	0.2 e	5j	1.7 e dfc	6.8 kj	0.13 j	30.6 dc
G5	15.1 ebdac	4.3 bdac	38.1 cebd	0.4 bdec	10.4 hegdfi	1.6 e dfc	11.9 gjih	0.24 gefih	27.9 g
G6	14.8 ebdac	4.1bdc	29.3 fced	0.5 bdac	11.4 hegdfi	4.1 bdac	15.5 fg	0.35 bdc	28.1fg
G7	14.3 ebdac	4.3 bdac	31.6 fcebd	0.3 de	7.2 hgji	1.1 e df	8.3 kji	0.20 gjfih	28.5 feg
G8	16.5 bac	4.6 bdac	38.5 cebd	0.6 ba	20.7 ba	1.9 e dfc	22.7 bdac	0.37 bac	30.3 dc
G9	16.9 bac	4.8 bdac	30.8 fcebd	0.5 bdac	20.1 bac	3.8 bdac	23.9 bac	0.44 ba	31.5 bc
G10	14.5 ebdac	5.3 bac	33.7 cebd	0.5 bdac	20.1ba	6.5 a	27.4 a	0.45 a	31.3 bc
G11	15.4 ebdac	5.1 bac	28.8 fced	0.5 bdac	19.2 bac	1.4 e dfc	20.6 bdec	0.42 ba	29.6 de
G12	12 edf	3.8 dc	27.8 fced	0.3 de	6.1 ji	2.1 e dfc	8.3 kji	0.23 gefih	30.5 dc
G13	16.8 bac	5.3 bac	40.9 cbd	0.5 bdac	15.7 bdc	3.6 e bdac	19.3 ebdec	0.32edf	31.9 ba
G14	15.3 ebdac	4.6 bdac	75.1a	0.4 bdec	11.9 hegdf	4.5 bac	16.5 fge	0.19 gjih	28.2 feg
G15	15.3 ebdac	5.5 ba	25.5 fed	0.5 bdac	14.8 edc	3.1 e bdfc	17.9 fgde	0.41 ba	25.7 h
G16	17.2 bac	3.8 dc	31.4 fcebd	0.5 bdac	11.5 hegdfi	5.9 ba	17.4 fghe	0.35 bdc	30.8 bc
G17	15.8 bdac	4.8 bdac	63.7 a	0.5 bdac	13.4 edf	3.1 e bdfc	16.4 fge	0.20 gjfih	28.5 feg
G18	12.5 edf	5.4 ba	47.2 b	0.3 de	9.5 hegdfi	0.4 ef	9.9 kjih	0.17 jih	30.7
G19	14.2ebdc	5.8 a	35.7 cebd	0.7 a	22 a	2.6 e dfc	24.6 ba	0.41 ba	20.1 j
G20	13.4edf	5.5 ba	38 cebd	0.4 bdec	13.5 edf	0.4 ef	13.8 fgih	0.27gefdc	29.2fe
G21	16.5 bac	5.3 bac	47 b	0.3 dec	6.9 hji	1.4 e dfc	8.4 kji	0.15 ji	32.6 a
G22	14.4 ebdac	4.9 bdac	45.8 b	0.4 bdec	23.5 a	1.2 e dfc	24.7 ba	0.35 bdc	22.3 i
G23	9.5 f	5.1 bac	17.4 f	0.3 de	5 j	2.1 e dfc	7.1kj	0.29 efdf	20.8 j

G17	15.8 bdac	4.8 bdac	63.7 a	0.5 bdac	13.4 edf	3.1 e bdfc	16.4 fge	0.20 gjfih	28.5 feg
G18	12.5 edf	5.4 ba	47.2 b	0.3 de	9.5 hegdfi	0.4 ef	9.9 kjih	0.17 jih	30.7
G18	12.5 edf	5.4 ba	47.2 b	0.3 de	9.5 hegdfi	0.4 ef	9.9 kjih	0.17 jih	30.7
G19	14.2ebdc	5.8 a	35.7 cebd	0.7 a	22 a	2.6 e dfc	24.6 ba	0.41 ba	20.1 j
G20	13.4edf	5.5 ba	38 cebd	0.4 bdec	13.5 edf	0.4 ef	13.8 fgih	0.27gefdc	29.2fe
G21	16.5 bac	5.3 bac	47 b	0.3 dec	6.9 hji	1.4 e dfc	8.4 kji	0.15 ji	32.6 a
G22	14.4 ebdac	4.9 bdac	45.8 b	0.4 bdec	23.5 a	1.2 e dfc	24.7 ba	0.35 bdc	22.3 i
G23	9.5 f	5.1 bac	17.4 f	0.3 de	5 j	2.1 e dfc	7.1kj	0.29 efdf	20.8 j
G23	9.5 f	5.1 bac	17.4 f	0.3 de	5 j	2.1 e dfc	7.1kj	0.29 efdf	20.8 j
G24	9 f	4.4 bdac	23.9 fe	0.2 e	5.4 j	0.2 f	5.7 k	0.19 gjih	20 j
Mean	14.7	4.8	38.8	0.42	12.9	2.5	15.4	0.28	28.5

Where, RL = root length, RG= root girth, AGFW =above ground fresh weight, NRP = number of roots per plant, MRKY = marketable root yield, UMRKY = unmarketable root yield, YLD =total fresh root yield, HI = harvest index, RDMC = root dry matter content.

Table 2: Mean performances for yield and yield contributing characteristics of 24 orange fleshed sweetpotato genotypes.

Mean performance of the genotypes in morphological, qualitative traits and spvd reaction

Mature leaf size varied among the genotypes from 9.7 cm for G19 (Melinda) to 14.8 cm for G17 (Tomulabula) with the overall mean of 12.1 cm. As reported by Kareem, genotypes with large leaf size can easily trap sunlight and hence carry out better photosynthesis required for carbohydrates synthesis than those with small leaf size (high water consume is also observed). Ground cover is the function of these characters and it varied among the genotypes where three genotypes (G20, G22 and G24) showed low ground cover. These genotypes showed below 50 % ground cover estimates. Conversely, genotypes: G1, G2, G3, G4, G7, G17, G18, G21, and G23 attained 50-74 % ground cover; these genotypes were considered as medium types. Twelve genotypes had showed high ground cover (75-90 %) after 35-40 day of planting. High ground cover estimate indicates early coverage of the ground and subsequent suppression of weeds (water evaporation from the soil). This has practical significance as weeds compete for light, water and nutrients. Genotype G4 had the highest mean inter-node length of 8.3 mm, whereas, genotype G24 (Tula) had the lowest mean inter-node length (1.7 mm). The longest vine length (193.2 cm) was recorded for the genotype designated as G4, which had a spreading growth habit while the shortest vine length (49.3 cm) was obtained for genotype G10, which was erect type.

This implying that in addition to storage root yield benefits obtained from these genotypes, their long vine could be used as a good source of planting material. Similar to this study, [13] indicated that sweetpotato vines used as forage for ruminants due to their richness in protein and minerals. In addition, [13] and [14] reported significant differences among sweet potato genotypes for vine length, growth rate, leaf area as well as tuber yield in sweetpotato.

The highest skin color score (9.0) was recorded for genotypes G9, G10 and G15; these genotypes had a dark purple skin color. While the lowest skin color score (2.0) was recorded for genotypes: G1, G3, G8, G12, G13, G14, G18, G19, and G21.This indicates that most of the studied genotypes had cream skin color. For flesh color, the highest mean value (8.0) was recorded for G4, G6, G11, G13 and G15, where these genotypes had dark orange flesh color indicating their high beta carotene content, this is in agreement with the study by Fekadu. Whereas, the lowest mean value (4.0) was recorded for genotypes G16 and G18. These genotypes had pale yellow flesh color. Genotypes G2, G5, G6, G12, G20, G21 and G23 showed high SPVD scores with the scores of 2.0, 2.7, 3.0, 3.7, 2.3, 2.0 and 2.3, respectively, implying their susceptibility to sweetpotato virus diseases. The remaining genotypes showed low scores of sweetpotato virus diseases, which showed their resistance/tolerance to sweetpotato virus disease. The finding is in agreement with the work of [15].

Phenotypic and genotypic coefficient of variation

The result revealed a wide range of variability among the 24 OFSP genotypes in quantitative and qualitative traits and SPVD reaction. For all traits studied, the magnitude of environmental variance was lower than the corresponding genotypic variance. This indicates that the genotypic component of variation was the major contributor to the total variation in the studied traits. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV). The PCV values ranged from 22.1 % for mature leaf size to 118.3% for unmarketable root yield. The GCV ranged from 20.6 % for root girth to 111.7% for unmarketable root yield. The lowest GCV obtained for root girth (20.0%) while the highest GCV were observed for traits such as, unmarketable root yield, root beta carotene content, skin color, marketable root yield, SPVD and total root yield, with values of 111.7, 104.97.8, 76.1, 75.4 and 72.6 % in that order. All the studied traits had PCV and GCV values higher than 20% , reflecting the presence of high variability and this could be an advantage as they can offer opportunity for selection of superior genotypes with respect to character of interest. Particularly, high GCV is an indication of low influence of environmental factors in the expression of such traits and the higher possibility to improvements through selection and hybridization [16]. In addition, Alam and Hossain reported high PCV and GCV values for vine length, number of storage roots per plant, individual root weight and storage root fresh weight. While, traits with low PCV and GCV values suggested the higher influence of environment for their expression, hence, the phenotypic basis of selection would not be effective for the improvement of the traits [17]. In addition, the present study results are in agreement with that obtained by Jones who reported considerable variances for ten storage root traits in sweet potato and a larger part was accounted by genotypic variance. Similarly, Solankey observed the maximum PCV and GCV for root yield per plant, fresh weight of root per plant and number of branches per plant, indicating the presence of wide genetic variability for morphological traits. Nevertheless, The PCV values were greater than GCV but the differences between the two values were narrow, indicating the variability due to genetic constituent of the genotypes was less influenced by environmental factors [18]. Accordingly, selection for desirable traits would be effective for sweetpotato improvement.

Estimates of heritability

In this study, except one trait almost all the traits had high broad sense heritability, where the values ranged from 66.7 to 100 %. Indicating that, the traits studied were more influenced by genetic factors [19]. Accordingly, a broad sense heritability of 100 % was recorded for a trait pre-dominant root skin colour. Moderate heritability was recorded for flesh color only. More than 91.1% heritability values were obtained for almost all traits under study except root flesh color, root girth, number of roots per plant and unmarketable root yield , which indicates that these traits were less influenced by environmental factors [20]. The result is consistent with the study of Mok who reported high heritability for number of storage root per plant and storage root weight per plant in sweetpato genotypes. However, a study of Jones suggested that in sweetpotato, a heritability estimates above 60 % are quite adequate for good selection advance. Conversely, Singh suggested that, if heritability is less than 40% selection may be difficult or virtually impractical to improve the characters due to the masking effect of the environment on the characteristics of genotype. In general, heritability estimates alone are not of any use in predicting the results about the selection unless it is accompanied by genetic advance [21-26].

Expected genetic advance as percent of mean

In the present study, the expected genetic advance expressed as a percentage of the mean by selecting the 5 % of the genotypes varied from 38.7 % for root girth to 217.1% for unmarketable root yield. This indicates that selecting 5 % of high performing genotypes from the base population could result in an advance of 38.7 % to 217.1% over the population mean. According to Johnson, the genetic advance as percent of mean is categorized as low (0 – 10%), moderate (10-20%) and high (> 20%). Accordingly, very high expected genetic advances as percent of mean (GAM) values were observed for unmarketable root yield (217.1), root beta carotene content (214.9), skin color (201.5), SPVD (201.5), vine length (141.6), marketable root yield (154.4), total root yield (147.5), inter-nodal length (120.9), harvest index (120.9) and above ground fresh weight (110.6).

High values of GAM for these traits showed that these characters are governed by additive genes and selection would be rewarding for the further improvement of such traits. In addition, high heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. Thus, in the present study, high heritability coupled with high GAM were observed for marketable root yield, root skin color, root beta carotene content, harvest index, vine length, vine inter-nodal length and above ground fresh weight. Hence, high heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals [27,28].

CONCLUSION

The significant variation among the tested genotypes revealed the presence of considerable variability for the mean performance of genotypes for vine traits, yield and its component traits as well as reaction to SPVD. Among the traits considered in this study, storage root yield, root dry matter content, root beta carotene content and reaction to SPVD were given due emphasis to select better performing genotypes. Besides, very high heritability coupled with high GAM were observed for marketable root yield, root skin color, root beta carotene content, harvest index, vine length, vine inter-node length and above ground fresh weight, implying these characters are governed by additive gene action and selection would be efficient for the further improvement of such traits. Therefore, this study demonstrated the possibility of developing high yielding OFSP varieties for release.

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