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Genetic advance and heritability for tuber yield and its component characters in Sweetpotato

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Abstract

Knowledge of the magnitude of genetic variability, heritability and genetic gains in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. Thirty sweetpotato genotypes were evaluated at the Teaching and Research farm, Osun State University, Ejigbo, Osun State, Nigeria, during 2018 and 2019 cropping seasons to estimate genetic variability, heritability and genetic advance of tuber yield and its component characters. Planting of 25 cm long vine was inserted at a slant, with two-third buried below the soil surface. Weeding was done 4, 6 and 8 weeks after planting, using small hoes. No herbicides or fertilizers were applied. Data were recorded on percentage of survival after 2 weeks, no of tubers per plant, tuber weight per plant, fresh tuber yield, vine length at 8 weeks after planting, foliage weight at harvest. Results show that the effect of genotype and genotype by year interaction were significant for tuber weight per plant and fresh tuber yield, while the effect of year was highly significant (P< 0.01) for all the characters. High magnitude of phenotypic and genotypic coefficient of variations as well as high heritability along with high genetic advance recorded for tuber yield, number of tubers per plant, vine length and fodder weight provide evidence that these parameters were under the control of additive gene effects and effective selection could be possible for improvement for these characters. The most outstanding accessions (Ex-Igbariam, Bath, W-151, Offa 2, Mothers delight and Ojo oba) for tuber yield could be sources of alleles that can be manipulated with other promising cultivars for higher tuber yield. © 2022 Department of Agricultural Sciences, AIOU

Keywords: Genetic advance, Genetic gain, Heritability, Sweetpotato, Tuber yield

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Introduction

Sweetpotato is the seventh most important crop plant in the world and of increasing importance in Africa. Sweetpotato is emerging from its traditional role of classic food security to a more commercialized crop. With urbanizing populations, the demand for sweetpotato has been increasing to fill gaps in cereal supply in livestock industries. As a result of its commercial potential in the Nigerian economy, sweetpotato is complementing the traditional crops such as maize (*Zea mays* L), guinea corn [*Sorghum bicolor* (L.) Moench] and millet [*Pennisetum glaucum* (L.) R. Br.] (Adedire et al., 2022). Trends in area cultivated have progressively increased over the years from 2010 to 2020 with notable increase in Africa from 1.5 to 4.5 million ha. Thus, there is significant potential to increase cultivation and yield through the use of improved cultural practices and varieties (Waqar-Ul-Haq et al., 2008). Increase in sweetpotato production in Nigeria is a reflection of the crop's comparative advantage as populations increase and demands on production system intensity.

In view of the importance of sweetpotato in Nigeria, researchers are utilizing available genetic resources to reconstruct the ideotype of the plant in order to meet the ever-increasing requirements of the population through improvement in tuber yield, other desirable agronomic and phenological characters as well as quality. The success of any crop improvement programme depends not only on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Kashiani et al., 2018). Genetic variability for agronomic characters therefore is a key component of breeding programmes for broadening the gene pool of crops (Rafique et al., 2014). Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Eckebil et al., 2007). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Su, 2019). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been stressed that heritability alone has no practical importance without genetic advance (Ngailo et al., 2019).

Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. Ramanujam and Thirumalachar (2007) reported the limitation of estimating heritability in narrow sense, as it included both additive and epistatic gene effects, and thereby suggested that heritability estimates in the broad sense will be reliable if accompanied by a high genetic advancement. Different researchers (Neguse & Saleh 2007; Rafiq et al., 2010; Rafique et al., 2014) reported high heritability and high genetic advance for different yield controlling traits in cereals. Therefore, availability of good knowledge of these genetic parameters existing in different yield contributing characters and the relative proportion of this genetic information in various quantitative traits is a prerequisite for effective crop improvement. Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance for tuber yield and its component characters in thirty (30) sweetpotato varieties to provide necessary information that could be useful in sweetpotato improvement programmes aimed at improving tuber yield.

Materials and Methods

Thirty (30) sweetpotato accessions were evaluated at the Teaching and Research (T and R) farm of Osun State University, Ejigbo Campus ((Latitude 7° 52'28.37'N and Longitude 4° 18'13.76' E) during the cropping seasons of 2018 and 2019. The experimental material used consisted of 30 accessions of sweet potato roots collected from the University of Ibadan, in Oyo state, local farmers in Offa, Kwara state and Teaching and Research Farm Osun State University, Ejigbo. The origin of the sweetpotato parents is presented in Table 1.

Soil samples collected from the trial site before cropping in 2018 and 2019 were analyzed in the Soil Science Laboratory of the Landmark University, Omu Aran, Kwara State, Nigeria for selected physical and chemical properties and presented in Table 2. The collected samples were air-dried and passed through a 2 mm sieve to remove large particles, debris and stones. The sieved samples were analyzed for pH in 1:1 soil to water ratio using the Coleman pH meter. Organic carbon was determined by Walkley and Black procedure (Bremner et al., 1965). Total Nitrogen was determined by the micro Kjeldahl method (Bray & Kurtz, 1945), while available phosphorus was extracted by Bray's P1 method (International Institute of Tropical Agriculture [IITA], 1989) and read from the atomic absorption spectrometer. Exchangeable Ca, Mg, K, Na and effective cation exchangeable capacity (ECEC) were analyzed using Atomic Absorption Spectrophotometry (Bremner et al., 1965), while textural analysis was done by hydrometer method. The soil texture was loamy and the other soil properties were not significantly different in both years at 0-15cm and 15-30cm depth. At 0-15cm depth, the approximate amounts of silt, sand and clay were 8%, 84% and 8%, respectively, with soil pH = 7.30 and ECEC = 2.83 (Cmol kg^{-1}). Rainfall data for the period of the experiment were obtained from a meteorological station in Ido-Osun, Osun State. Plantings were carried out during the growing seasons on 25th July, 2018 in the first year and 22nd July, 2019 in the second year using a randomized complete block design with three replications. The plot size used was 3m x 1 in two rows. Each plot comprised the 20 cuttings from each progeny of a cross. Planting of 25 cm long vine was inserted at a slant, with two-third buried below the soil surface. Weeding was done 4, 6 and 8 weeks after planting, using small hoes. No herbicides or fertilizers were applied. Data were recorded on percentage of survival after 2 weeks, no of tubers per plant, tuber weight per plant, fresh tuber yield, vine length at 8 weeks after planting, foliage weight at harvest.

Table 1 Description of experimental materials

S/N	Name	Source	Growth habit	Tuber skin color	Flesh color
1	Naspot 5 Bodija	UI, Ibadan	Spread	Deep Purple	Cream
2	Ladele	UI, Ibadan	Spread	Purple	Cream
3	W-151 Omini	UI, Ibadan	Spread	Purple	Cream
4	Dammy	Ejigbo	Extremely spreading	Cream	Orange
5	PK5	Offa	Spread	Purple	Cream
6	PK3	Offa	Spread	Cream	White
7	Offa 2	Offa	Spread	Purple	White
8	Offa 1	Offa	Extremely spreading	Cream	Cream
9	Ojo oba	UI, Ibadan	Extremely spreading	Cream	White
10	Doris	UI, Ibadan	Spread	Deep Purple	White

11	Bath	UI, Ibadan	Extremely spreading	Cream	Orange
12	Mothers delight	NRCRI, Iresi	Extremely spreading	Orange	Orange
13	Ex-Igbariam	UI, Ibadan	Extremely spreading	Cream	Cream
14	Shaba	UI, Ibadan	Spread	Cream	Cream
15	Sauti	UI, Ibadan	Extremely spreading	Deep Purple	Cream
16	Famgbe I	UI, Ibadan	Spread	Purple	Cream
17	TIS 80/0140	UI, Ibadan	Extremely spreading	Purple Red	White
18	440125	UI, Ibadan	Spread	cream	Cream
19	TIS 70357	UI, Ibadan	Extremely spreading	Cream	White
20	King J	NRCRI, Iresi	Spread	Cream	Orange
21	Ex Oyunga	UI, Ibadan	Spread	Cream	Orange
22	Naspot 2	UI, Ibadan	Extremely spreading	Purple	White
23	440034	UI, Ibadan	Spread	cream	Orange
24	Naspot 3	UI, Ibadan	Extremely spreading	Purple	Orange
25	TIS 2532	UI, Ibadan	Spread	Purple	White
26	Bleshbok	UI, Ibadan	Spread	Red	Orange
27	TIS 86/0356	UI, Ibadan	Spread	purple	white
28	Resisto	UI, Ibadan	Extremely spreading	purple	Orange
29	Ak wide	UI, Ibadan	Extremely spreading	Purple red	White
30	Benue	UI, Ibadan	Extremely spreading	Purple	White

Table 2 Physical and chemical properties of soil in the experimental sites

	Values	
Properties	2018	2019
Sand %	69	73
Clay %	5	6
Silt %	20	21
Textural class	Sandy clay loam	Sandy clay loam
pH (H$_2$0)	4.2	5.7
Organic matter %	1.4	1.7
Nitrogen %	0.05	0.07
Phosphorus (mg/kg)	-2	8.8
Ca^{2+} (cmol/kg)	1.5	1.72

Statistical analysis

Combined analysis of variance and means over years were computed using PROC GLM model of SAS (2007) for the sweetpotato accession with respect to tuber yield and other agronomic characters. The mean values were compared using least significant difference (LSD) procedure as laid down according to Steel et al. (1980). The linear statistical model was used as described by Fehr (1987):

Yijk = μ + βj + ʎk + (GE)ij + Ɛijk

Where

Yijk = the observation made in the ith genotypes on the jth replication, in the kth year; μ = the overall mean of the character; βj = the effect of the jth replication; ʎk = the effect of the kth year; (GE)ij = sum of interaction terms of the genotypes and year, and ijkƐ = the residual effects. The form of the analysis of variance indicating sources of variation, mean squares and their expected values are shown in Table 3.

Components of variance were estimated using the method described by Fehr (1987). The form of the estimation of the variance components obtained by equating the mean square for a source of variation to its expectation and solving for the unknown is presented in Table 4.

Where: δ^2g, δ^2gy and δ^2e are components of genotype, genotype by environment interaction and variance for error respectively. M_1, M_2, and M_3 are the observed values of the mean squares for the error, interaction and genotype, respectively (Eckebil et al., 1977).

The phenotypic variance (δ^2 p) was calculated as δ^2 p = δ^2 g+(δ^2 gy/y) + (δ^2 e/ry).

Where y, g and r are number of years, genotypes and replications, respectively. δ^2 g and δ^2 e are components of variance for genotypes and error, respectively (Eckebil et al., 1977).

Broad sense heritability (H_2) for pooled data across years was estimated as described by Allard (1960).

H2 (%) = (δ^2 g / δ^2 p) x100 Genetic Advance (GA) and Genetic Gain (GG) values were determined as described by Burton (1952)

GA = (K)(δA) (H). Where, K = 2.063 (selection differential at 5%),

δA = phenotypic standard deviation of the mean yield of the n original lines and H = Broad sense heritability.

Genetic gain (GG) was determined from genetic advance (GA) expressed as a percentage of the population mean (x) Genotypic and phenotypic coefficients of variations were estimated by the formula suggested by Ajala & Olaoye (2009) given as:

GCV = (√ δ2 g/Ū) x100 and PCV = (√ δ2 ph/Ū) x100

Where Ū = mean value of the particular character.

Table 3 Form of combined analysis of variance with mean squares and their expected values

Source of variation	Df	Mean square	Expected mean square
Year	y-1	M5	
Rep(year)	r-1(y)	M4	
Genotype	g-1	M3	δ2e + rδ2gy + ryδ2g
Genotype x year	(g-1) (y-1)	M2	δ2e + rδ2gy
Pooled error	(r-1) (g-1)y	M1	δ2e

Table 4 Mean squares from combined analysis of variance for tuber yield and other related characters among 30 accessions of sweetpotato evaluated in 2018 and 2019 at Ejigbo

Variance components	Method of determination
Genotype (δ2 g)	M3-M2/yr
Genotype x Year (δ2 gy)	M2-M1/yr
Pool Error (δ2 e)	M1

Results and Discussion

Rainfall amount and distribution that was higher and favourable in the year 2019 compared to 2018 might have contributed significantly to the differences observed between the years for these traits as differences in environmental conditions varied from year to year (Fig. 1).

Analysis of Variance Combined analysis of variance indicated that the effect of year was highly significant (P< 0.01) for all the characters (Table 5). Rainfall amount and distribution that was higher and favorable in the year 2019 compared to 2018 might have contributed significantly to the differences observed between the years for these traits as differences in environmental conditions varied from year to year (Fig. 1). Mean squares due to accessions and genotype x year interaction were significant for weight of tuber per plant and fresh tuber yield indicating presence of genetic variability for these two traits in the accessions material studied and they were highly influenced by environmental factors. This also indicated that there was significant amount of phenotypic variability, and that all the accessions differed from one another with regard to weight of tuber per plant and fresh tuber yield offers way for further improvement through simple selection.

However, the interaction of the year with accessions is very important in this study. The effect of genotype by year interaction was highly significant for weight of tuber per plant and fresh tuber yield. This indicates the diversity of the accessions and their differences in environmental responses across the two years for these traits. This invariably suggests that sweetpotato fresh tuber yield could be genetically manipulated for its improvement. The mean performances across the two years for fresh tuber yield and related characters of the Accession are presented in Table 6. The results showed significant differences among the accessions for growth, yield and yield components. The most outstanding accessions for fresh tuber yield are Ex-Igbariam (231.84 t/ha), Bath (31.11t/ha), W-151 (28.02t/ha), Offa 2 (26.08), Mothers delight (23.93t/ha) and Ojo oba (20.91t/ha) in descending order with yield ranging from 31.84-20.91t/ha, while Naspot 5 had the lowest value of fresh tuber yield (1.82t/ha) over the two years.

The wide variability observed for tuber yield as a quantitatively inherent character among the accession means that there is ample opportunity for selection in the accession for improvement of this important economic character. This variability could be heritable and exploited in the process of selection in the breeding programmes.

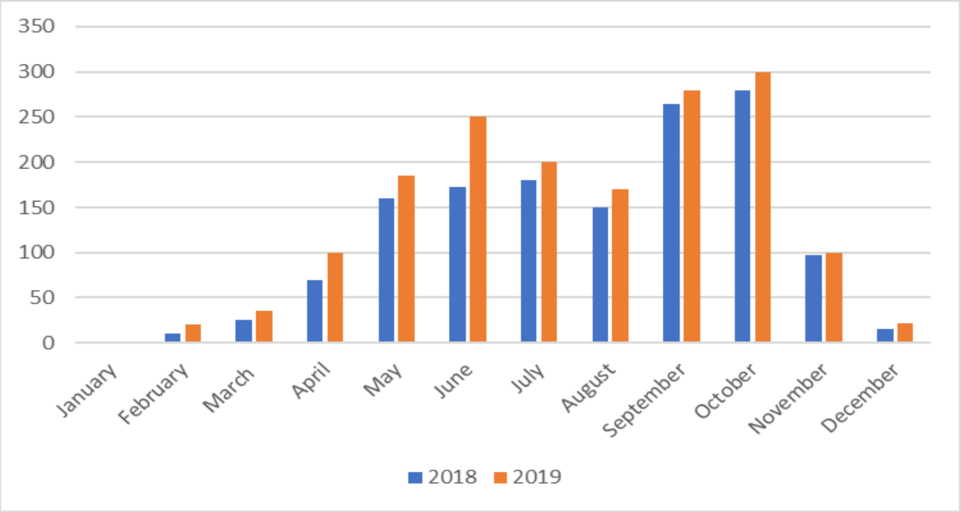

Fig. 1 Monthly rainfall distribution pattern in Ejigbo for 2018 and 2019

Table 5 Mean squares from combined analysis of variance for tuber yield and other related characters among 30 accessions of swetpotato evaluated in 2018 and 2019 at Ejigbo

Source of variation	Degree of freedom	% Survival	Vine length (M)	Foliage weight (Kg)	No. of tuber per plant	Tuber weight per plant (G)	Tuber yield (t/ha)
Year	1	23.45**	34.55**	12.68* *	23.58**	92.48**	202.48**
Rep(year)	4	31.45	7.38	5.43	9.78	9.86	4.54
Genotype	29	12.6	1.43	3.58	10.58	82.58**	166.32**
Genotype x year	29	10.59	1.54	4.76	13.70	93.58**	111.54**
Pooled error	116	33.45	2.78	7.39	5.73	17.54	93.4

** shows significant at p< 0.01 mean performance of the sweetpotato accessions

Table 6 Combine mean performance of 30 accession of sweetpotato for tuber yield and related character evaluated in 2018 and 2019 at Ejigbo (Nigeria) (Tuber yield)

S/N	Accession	% Survival	Vine length (M)	Foliage weight (Kg)	No. of tuber per plant	Tuber weight per plant (G)	Fresh tuber weight (t/ha)
1	Naspot 5	35.7	2.13	3.64	4	54.6	1.82
2	Ladele	47.2	1.06	17.68	3	242.83	8.84
3	W-151	87.5	3.36	56.04	3	548	28.02
4	Dammy	55.8	1.00	16.74	2	452.25	8.37
5	PK5	57.9	1.04	17.46	2	385	8.73
6	PK3	91.3	2.19	36.52	3	335.5	18.26
7	Offa 2	98.5	3.12	52.16	3	261.8	26.08
8	Offa 1	56.85	1.36	22.74	3	153.4	11.37
9	Ojo oba	99.3	2.51	41.82	3	341.17	20.91
10	Doris	57.05	1.37	22.82	4	442.14	11.41
11	Bath	85.7	3.73	62.22	5	700.54	31.11

12	Mothers delight	85.3	2.87	47.86	4	613.75	23.93
13	Ex-Igbariam	94.5	3.82	63.68	4	703.33	31.84
14	Shaba	52.2	0.72	11.98	4	260.7	5.99
15	Sauti	88.9	2.13	35.56	2	103.7	17.78
16	Famgbe I	42.5	0.63	10.52	2	94	5.26
17	TIS 80/0140	48.3	1.16	19.32	4	54.67	9.66
18	440125	52.2	1.25	20.88	6	533.43	10.44
19	TIS 70357	73.7	1.77	29.48	9	416.5	14.74
20	King J	26.3	0.63	10.52	5	179.83	5.26
21	Ex Oyunga	79.5	1.91	31.8	6	533.43	15.9
22	Naspot 2	22.6	0.54	9.04	4	119.71	4.52
23	440034	43.45	1.04	17.38	5	265.25	8.69
24	Naspot 3	25.55	0.61	10.22	2	139.27	5.11
25	TIS 2532	65.3	2.47	41.12	2	649.25	20.56
26	Bleshbok	43.45	1.04	17.38	4	260.7	8.69
27	TIS 86/0356	53.2	0.55	10.3	1	18	0.23
28	Resisto	60	1.26	21.75	2	110.09	0.6
29	Ak wide	60	1.67	50.55	3	153.54	3.97
30	Benue	65	2.00	52.35	4	374.5	11.48
	Mean	61.825	1.7	28.7	3.6	316.7	12.65
	SD	22.18	0.98	17.66	1.6	316.7	9.25
	Max	99.3	3.82	63.68	9	703.33	31.84
	Min	22.6	0.54	3.64	1	18	0.23

Phenotypic and genotypic coefficients of variation

Since most of the economic characters (tuber yield) are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, the study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection (Kwartenf et al., 2020). The reliability of a parameter to be selected for a breeding programme among other factors is dependent on the magnitude of its coefficient of variations (CV) especially the GCV. However, the differences between genotypic and phenotypic coefficient of variability indicate the environmental influence (Mahmood et al., 2004). While a lower value of CV generally depicts low variability among the tested sample; a high proportion GCV to the PCV is desirable in breeding works. The results given in Table 7 depicted that phenotypic variance (σ 2 p) and PCVs were slightly higher than genetic variances (σ^2 g) and GCVs for all the characters, suggesting the least influence of environment in the expression of these characters Similar results have also been reported by Aziz et al. (2008). Also, estimates of genotype x year interaction variance (σ^2 gy) for the traits in most instances were low. This result tends to support the notion that greater heterozygosity confers a buffering effect or stability over a wide range of environments (Gibson et al., 2008). High genetic variability for tuber yield in the accession over years recorded in the accession used suggested that it could be further exploited through improvement and selection programmes (Wannows et al., 2010). High values of PCV and GCV observed in tuber yield followed by tuber weight per plant not only show that the selection can be effective for these traits but also indicate the existence of substantial variability, ensuring ample scope for their improvement through selection. These observations are in confirmation with the findings of Nigussie & Saleh (2007); Ajala et al. (2009). On the other hand, very low values of PCV and GCV recorded for survival percentage, vine length, foliage weight and number of tubers per plant revealed that low variability among the accession was very low for these characters.

Heritability and Genetic Advance High magnitude of broad sense heritability estimated in all the characters except foliage weight (Table 8). This implied the possibility of effective selection for genetic improvement of these traits. High heritability estimates for sweetpotato tuber yield (Grunerberg et al., 2005) tuber weight per plant, number of tubers per plant, vine length and percentage survival Afolabi et al. (2020), observed in the present study were in agreement with the findings of earlier worker (Grunerberg et al., 2004). High heritability estimates coupled with high estimates of genetic advance expected in the next generation in tuber yield, tuber weight per plant, number of tubers per plant indicate the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. This also provides the evidence that a larger proportion of phenotypic variance has been attributed to genotypic variance, and reliable selection could be made for these traits on the basis of phenotypic expression. These results find support from the earlier studies by Kashiani et al. (2008) that there was greater magnitude of broad sense heritability and high genetic advance in tuber yield plant, number of tubers per plant and tuber weight per plant. The authors suggested that these parameters were under the control of additive genetic effects. Sumath et al. (2005) also suggested that these parameters could be manipulated according to requirements, and worthwhile improvement could be achieved through selection. Kriegner (2001) concluded that the selection at an early segregating generation will prove beneficial for selecting superior varieties of sweetpotato. However, high heritability and low genetic advance were observed for vine length which may be attributed to non-additive gene action governing this trait, and this character could be improved through the use of hybridization and hybrid vigour. High heritability accompanied with low genetic advance had earlier been reported by Hussain et al. (2011). Foliage weight exhibited low heritability with low genetic advance indicating non-additive genetic effects governing this trait. However, care must be taken while breeding for this complex trait as it is considerably influenced by environmental factors such as rainfall or soil fertility. It seems a limited scope of improvement could be achieved for this trait within this group of accession. Sweetpotato tuber yield and tuber weight per plant can be improved by selection, as these characters exhibited moderate genotypic and phenotypic coefficients of variations.

Table 7 Estimate of genetic variance (δ2 g) genotype × year interaction (δ^2gy) variance, phenotypic variance (δ^2 p), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) for tuber yield and other related character among 30 accessions of sweetpotato evaluated in 2018 and 2019 at Ejibgo, Nigeria

Character	δ^2 p	PCV	δ^2gy	GCV	δ2 g	ECV
% Survival	7.42	6.88	7.42	6.35	15.58	17.04
Vine length (m)	9.55	13.08	6.42	13.82	13.68	24.83
Foliage weight (kg)	11.73	9.03	10.62	12.25	15.73	28.06
Number of tubers per plant	9.64	10.38	8.79	11.45	12.64	23.81
Tuber weight per plant (g)	149.55	127.21	136.42	120.55	4.68	7.03
Fresh tuber weight (t/ha)	181.58	112.68	114.62	110.89	210.38	13.83

Table 8 Estimate of heritability (H2) and genetic advance for tuber yield and other related characters among 30 accessions of sweetpotato evaluated in 2018 and 2019 at Ejibgo, Nigeria

Source of variation	% Survival	Vine length (M)	Foliage weight (Kg)	No. of tuber per Plant	Tuber weight per plant (G)	Tuber yield (t/ha)
Heritability	76.48	78.74	9.74	84.32	61.79	98.16
Genetic Advance	7.65	8.43	8.68	8.14	8.53	29.58

Conclusion

This study revealed that information about the extent of variation, estimates of heritability and expected genetic advance in respect of sweetpotato tuber yield and yield contributing characters constitutes the basic requirement for a crop improvement programme. Broad sense heritability is useful for measuring the relative importance of the additive portion of genetic variance that can be transmitted to the offspring. The preponderance of additive gene effects controlling a trait usually resulted in both high heritability and genetic advance, while those governed by non-additive gene actions could give high heritability with low genetic advance. However, in the present research, expected genetic advance values were based on broad sense heritability, which integrates an additive portion of the total phenotypic variance. Effective selection for superior accession is possible considering tuber yield and tuber weight per plant could be used as target traits to improve sweetpotato tuber yield. The most outstanding accessions (Ex-Igbariam, Bath, W-151, Offa 2, Mothers delight and Ojo oba) for tuber yield could be sources of alleles that can be manipulated with other promising cultivars for higher tuber yield.

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