Original Research Article

Genetic variability, heritability and genetic advance in Sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes

ABSTRACT

Sweet potato [*Ipomoea batatas*(L.) Lam.] is one of the important tuber crops of tropical and sub-tropical regions of the world. Studies on mean performances of 51 sweet potato genotypes~~ was~~were carried out at Vegetable Research Centre, Regional Horticultural Research and Extension Centre (RHREC), Dharwadduring rabi, 2019-20 and 2020-21.Thedata wascollected on 20 characters. High estimates of PCV, GCV, heritability ~~coupled with~~and high genetic advance as percent of mean were recorded fortuber yield per vine, thenumber of leaves per vine, themean weight of tuber per vine, vine length and tuber yield per hectare.

Keywords: Sweet potato; genetic variability; genetic advance; heritability

1. INTRODUCTION

Sweet potato [*Ipomoea batatas* (L.) Lam.] is an important tuber crop of tropical and sub-tropical regions of the world and it forms the sixth most important food crop after rice, wheat, potato, maize and cassava. It is native to South America and it belongs to the family *Convolvulaceae*. The family includes 55 genera and~~ contains~~ more than 1000 species (Watson and Dallwitz, 2000). It is popularly known as *'white potato'* or *'Irish potato'* in thesouthern part of theUnited States of America, while in India, it is commonly called as *sakarkand*.The total area of sweet potatoes in the world is about 77 lakh hectares, with a production of 918 lakh tonnes and productivity is 11.92 t ha^{-1}. China is the leading producer of sweet potatoes in the world, followed by Nigeria and Uganda. India is at 9th position in production (Anon., 2019a). In India, it is cultivated in an area of 1.07 lakh hectares with a production of 11.10 lakh tonnes(Anon., 2022). The major states cultivating this crop in India are Orissa, West Bengal, Bihar, Uttar Pradesh, Madhya Pradesh, Maharashtra and Karnataka. ~~Orissa~~Odisha is the leading state in area and production, followed by West Bengal and Uttar Pradesh, while Andhra Pradesh holds the record for thehighest productivity (Anon., 2019c). In Karnataka state, sweet potato is grown in an area of about 2,730 hectares with a production of 32,866 tonnes and productivity of 12.04 t ha^{-1} (Anon., 2019b).

Sweet potato (hexaploid: $2n=6x=90$) is a perennial, dicot and a vegetatively propagated tuber crop, but it is cultivated as an annual crop for tuber production and biannual/perennial for foliage production (Ravi and Indira, 2010). Sweet potato genotypes are broadly grouped into the bush, intermediate and vining types, which may vary greatly in branching pattern and overall stem length. Latex is present in all parts of the plant. Leaves are spirally arranged and have long petioles measuring 5 to 30 cm. They are broad, entire or lobed with a more or less pronounced leaf incision. The flowers are cymose and hermaphrodite, having violet or white colour. Seeds have a hard seed coat and develop within a capsule. The plants usually set few viable seeds, many genotypes do not readily flower, others are sterile and most are self-incompatible (Onwueme, 1978).

In any crop improvement programme, thegermplasm evaluationto assess the existing variability is a preliminary step. Since theenvironment greatly influences quantitative characters, it is necessary to separate the variability into heritable and non-heritable components. Genotypes exhibiting high variability for desirable characters that contribute to the yield are to be selected in such a programme of evaluation. Sweet potato is cross-pollinated and heterozygous crop with wide variability. The presence of variability is a pre-requisite for any crop improvement programme to make selections and harness the variability for thebetterment of the crop. Efficient utilization of the genetic potential held in germplasm collections requires detailed knowledge about genotypes. Thus, it is important to consider the quantitative approaches for exploitation of the extensive genetic variability available in sweetpotato and this is dependent on the reliable or accurate estimates of the genetic parameters. Thus, this study was undertaken to estimate the nature and magnitude of variability for morphological, yield and yield component characters with the help of genetic parameters, such as phenotypic as well as genotypic coefficients of variation and estimate of heritability in broad-sense

2. MATERIAL AND METHODS

The current study was undertaken in AICRP on tuber crops, Vegetable Research Centre, Regional Horticultural Research and Extension Centre (RHREC), Dharwad (University of Horticultural Sciences, Bagalkot) during rabi, 2019-20 and 2020-21. Totally 51 genotypes were collected from different sources and evaluated. The geographical site of experimental fields is located in the Northern Transitional Zone (Zone VIII) of Karnataka state, situated at 150 26’ North latitude, 750 07’ East longitude with an altitude of 678 m above the mean sea level. The experiment was laid out in a randomized block design (RBD) with two replications. Each replication's treatments were allotted randomly using a random number table. Sweet potato cuttings with 2-3 buds were planted in each replication with 3 m × 3 m plot size at 60 cm × 20 cm spacing. The crop was raised by following the recommended package of practices of theUniversity of Horticultural Sciences, Bagalkot. Observations were recorded on five randomly selected plants in each replication for quantitative traits viz., vine length, number of branches per vine, number of leaves per vine, inter-nodal length, leaf area, tuber length, tuber diameter, number of tubers per vine, mean weight of tuber, tuber yield per vine, total tuber yield per plot, yield per hectare, harvest index, reducing sugar, non-reducing sugar, total sugar, starch content, β-carotene content and dry matter content, The data were presented in Table 1.

3. RESULTS AND DISCUSSION

3.1 Genetic variability

The efficiency in improving any crop would depend on the magnitude of genetic variability present and the extent to which it is heritable for the desired traits. There are different ways through which this kind of variability can be created and utilized. Examining readily available variability in the germplasm of the given species is also an important avenue for the breeder. The first step in aplant breeding programme is to determine the extent of variability for the traits under improvement and to divide this variability into genetic and environmental components. The phenotypic and genotypic coefficient of variance was calculated for all the characters (Table 1 and Fig. 1). The results ~~obtained~~ showed that the phenotypic coefficient of variance was,~~in general~~,generallyhigher than the genotypic coefficient of variance for all the characters. It is due to ~~presence of~~ substantial influence of environmental factors besides the genetic variation for expression of these traits.

In the present investigation, high magnitude of GCV and PCV were observed for β carotene content (GCV=125.71 %; PCV=125.77 %), leaf area (GCV=40.63 %; PCV=40.97 %), number of leaves per vine (GCV=35.01 %; PCV=35.03 %), tuber length (GCV=34.19 %; PCV=34.28 %), mean weight of tuber per vine (GCV=33.68 %; PCV=33.72 %), tuber yield per plot (GCV=32.07 %; PCV=32.09 %), tuber yield per hectare (GCV=32.07 %; PCV=32.09 %), inter-nodal length (GCV=27.14 %; PCV=27.40 %), tuber diameter (GCV=24.80 %; PCV=24.96 %) and vine length (GCV=23.15 %; PCV=23.19 %). Moderate estimates of PCV and GCV were registered for number of tubers per vine (GCV=17.12 %; PCV=17.13 %), harvest index (GCV=16.31 %; PCV=16.34 %), reducing sugar (GCV=16.19 %; PCV=16.33 %), starch content (GCV=16.13 %; PCV=16.60 %), dry matter content (GCV=12.77 %; PCV=12.96 %) and number of branches per vine (GCV=12.62 %; PCV=13.36 %). While lower estimates of thecoefficient of variations were observed for non-reducing sugar, shelf life of tubers and total sugar.

The above findings indicated that the characters with moderate and high magnitudes of GCV and PCV indicated the existence of variability in the population for these characters. Therefore, selection for theabove traits can also be beneficial for improvement. The observed higher estimates of phenotypic and genotypic coefficients of variation for theabove characters indicated the existence of adequate variability among the genotypes. Thus, a simple selection could help bring further improvement. These findings follow the findings by Sasmal*et al.* (2015) for β carotene; Babu *et al.* (2017) for leaf area; Tripathi *et al.* (2016) for thenumber of leaves per vine; Sharavati*et al.* (2018) for tuber length and tuber diameter; Asemie and Ali (2021) for themean weight of tuber per vine; Rahajeng*et al.* (2020) for tuber yield per plot, tuber yield per vine, tuber yield per hectare and Narasimhamurthy*et al.* (2018) for inter-nodal length, tuber diameter and vine length.

3.2 Heritability

From the study, it is observed the higher heritability of cent per cent for non-reducing sugar, the number of leaves per vine, number of tubers per vine, tuber yield per vine, tuber yield per plot, and tuber yield per hectare were all 99.90 per cent heritable, mean weight of tuber per vine and vine length each had 99.80 per cent heritability, harvest index (99.70 %), tuber length (99.50 %), tuber diameter (98.80 %), leaf area (98.40 %), reducing sugar (98.40 %), inter-nodal length (98.20 %), dry matter content (97.20 %), total sugar (96.40 %), starch content (94.50 %), theshelf life of tuber (94.30 %) and number of branches per vine (89.40 %).The observed high heritability aligns with earlier workers for the characters *viz.*, number of leaves per vine (Cheema *et al*., 2007), total sugar and inter-nodal length (Alam*et al*., 2015), leaf area and dry matter content (Tripathi *et al*., 2016) (Table 1).

3.3 Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The genetic advance was worked out as apercentage of themean for tuber yield and its components ~~which is~~ presented in Table 1. Genetic advance is important to find out the genetic gains likely to be achieved in subsequent generations. The success of genetic advance under selection depends on genetic variability, heritability and selection intensity.The higher genetic advance was recorded for tuber yield per vine (284.93 %), number of leaves per vine (164.03 %), mean weight of tuber per vine (77.42 %), vine length (71.30 %), leaf area (33.60 %), tuber yield per hectare (20.58 %) and harvest index (20.02 %). The observed results on high genetic advance are in line with previous researchers for the characters *viz.*, tuber yield per vine (Solankey*et al*., 2015 and Tripathi *et al*., 2016); number of leaves per vine (Cheema *et al*., 2007); mean weight of tuber per vine (Bhadauriya*et al*., 2018); vine length (Solankey*et al*., 2015) and leaf area (Tripathi *et al*., 2016).

The moderate values of genetic advance were recorded for tuber yield per plot (18.52 %). Similar results were also observed by Narasimhamurthy*et al.* (2018).

3.4 Genetic advance as per cent of mean

Very often, heritability, in abroad sense, is not the true indicator of theinheritance of traits, since only anadditive component of genetic variance is transferred from generation to generation. Therefore, heritability, in a broad sense, may mislead in judging the effectiveness of selection for the trait. Considering heritability broadlyand genetic advances over per cent mean may reveal the prevalence of specific components (additive or non-additive) for the trait more accurately.

In the present study, high heritability coupled with high genetic advance as per cent over mean was recorded for the characters *viz.*, β carotene (258.85 %), leaf area (83.04 %), number of leaves per vine (72.08 %), tuber length (70.28 %), mean weight of tuber (69.34 %), tuber yield per vine (66.03 %), tuber yield per plot (66.03 %), tuber yield per hectare (66.03 %), inter-nodal length (55.40 %), tuber diameter (50.79), vine length (47.63 %), number of tubers per vine (35.26 %), harvest index (33.55 %), reducing sugar (33.08 %), starch content

(32.30 %), dry matter (25.94), number of branches per vine (24.60 %) and non-reducing sugar (20.55 %). These results are in agreement with Solankey*et al.* (2015) for fresh weight tuber per plant, β carotene content, tuber yield per plot, starch content and total sugar content; Tripathi *et al*. (2016) for leaf area and yield per plant, and Bhadauriya*et al*. (2018) for number of branches per vine, inter-nodal length, length of vine, number of leaves per vine, theaverage weight of tuber and number of tubers per vine (Table 1).The above findings indicated that the characters with high and moderate heritability and high genetic advance could be considered for direct selection for improvement.

4. CONCLUSION

The results showed that the phenotypic coefficient of variance was generally higher than the genotypic coefficient of variance for all the characters. The higher magnitude of GCV and PCV were observed for β carotene content, leaf area, number of leaves per vine, tuber length, mean weight of tuber, tuber yield per plot, tuber yield per hectare, inter-nodal length of vine, tuber diameter and vine length. It is observed the higher heritability for non-reducing sugar, number of leaves per vine, number of tubers per vine, tuber yield per vine, tuber yield per plot, tuber yield per hectare, mean weight of tuber and vine length, harvest index, tuber length, tuber diameter, leaf area, reducing sugar, inter-nodal length of vine, dry matter content, total sugar, starch content, shelf life of tuber and number of branches per vine. Thereby denoting that direct selection for these characters could improve recognition of superior genotypes in sweet potatoes. The highest genetic advance was recorded for tuber yield per vine, number of leaves per vine, mean weight of tuber per vine, vine length, leaf area, tuber yield per hectare and harvest index. It states that these characters are controlled by additive gene effects and their selection will contribute to the development of these characters.

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Table 1. Mean, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean for various characters of sweet potato genotypes

Sl. No.	Characters	Mean	Range		Variance		Coefficient of variation		Heritability (%)	Genetic advance (%)	Genetic advance as per cent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	$\mathbf{x_{1}}$	149.68	96.41	246.70	1201.58	1205.33	23.158	23.19	99.70	71.30	47.63
2	$\mathbf{x_{2}}$	06.94	4.74	08.71	0.77	00.86	12.628	13.36	89.40	1.71	24.60
3	$\mathbf{x_{3}}$	227.57	111.00	410.59	6348.27	6356.08	35.012	35.03	99.90	164.03	72.08
4	$\mathbf{x_{4}}$	04.60	2.75	07.35	01.56	01.59	27.142	27.40	98.20	2.55	55.40
5	$\mathbf{x_{5}}$	40.46	19.67	93.39	270.34	274.74	40.638	40.97	98.40	33.60	83.04
6	$\mathbf{x_{6}}$	11.83	4.95	18.09	16.38	16.46	34.197	34.28	99.50	08.32	70.28
7	$\mathbf{x_{7}}$	05.80	2.52	09.35	02.07	02.09	24.806	24.96	98.80	02.94	50.79
8	$\mathbf{x_{8}}$	03.94	2.54	05.46	0.46	00.46	17.124	17.13	99.90	01.39	35.26
9	$\mathbf{x_{9}}$	111.66	28.53	207.58	1414.91	1417.26	33.689	33.72	99.80	77.42	69.34
10	$\mathbf{x_{10}}$	59.67	32.94	77.46	94.73	95.06	16.312	16.34	99.70	20.02	33.55
11	$\mathbf{x_{11}}$	431.52	126.57	661.30	19152.83	19174.45	32.071	32.09	99.90	284.93	66.03
12	$\mathbf{x_{12}}$	28.05	08.23	42.99	80.93	81.02	32.072	32.09	99.90	18.52	66.03
13	$\mathbf{x_{13}}$	31.17	09.14	47.76	99.90	100.01	32.07	32.09	99.90	20.58	66.03
14	$\mathbf{x_{14}}$	00.53	00.39	00.70	00.01	00.01	16.192	16.33	98.40	00.17	33.08
15	$\mathbf{x_{15}}$	02.61	02.18	03.24	00.07	00.07	09.977	09.98	100.00	00.54	20.55
16	$\mathbf{x_{16}}$	03.11	02.58	03.44	00.06	00.06	07.987	08.14	96.40	00.50	16.16
17	$\mathbf{x_{17}}$	00.48	00.35	00.63	00.01	00.01	16.133	16.60	94.50	00.15	32.30
18	$\mathbf{x_{18}}$	00.32	00.02	02.33	00.16	00.16	125.713	125.77	99.90	00.83	258.85
19	$\mathbf{x_{19}}$	28.31	16.79	35.53	13.08	13.46	12.773	12.96	97.20	07.34	25.94
20	$\mathbf{x_{20}}$	23.83	18.83	29.86	05.65	05.99	09.973	10.27	94.30	04.76	19.96

Note:

$\mathbf{X_{1}}$ - Vine length (cm)
$\mathbf{X_{2}}$ - Number of branches per vine
$\mathbf{X_{3}}$ - Number of leaves per vine
$\mathbf{X_{4}}$ - Inter-nodal length (cm)
$\mathbf{X_{5}}$ - Leaf area (cm²)

$\mathbf{X_{6}}$ – Tuber length (cm)
$\mathbf{X_{7}}$ - Tuber diameter (cm)
$\mathbf{X_{8}}$ - Number of tubers per vine
$\mathbf{X_{9}}$ - Mean weight of tuber
$\mathbf{X_{10}}$ - Harvest index (%)

$\mathbf{X_{11}}$ - Tuber yield per vine (g)
$\mathbf{X_{12}}$ - Tuber yield per plot (kg/plot)
$\mathbf{X_{13}}$ - Tuber yield (t/ha)
$\mathbf{X_{14}}$ - Reducing sugar (%)
$\mathbf{X_{15}}$ - Non-reducing sugar (%)

$\mathbf{X_{16}}$ - Total sugar (%)
$\mathbf{X_{17}}$ - Starch content (%)
$\mathbf{X_{18}}$ - β carotene content (%)
$\mathbf{X_{19}}$ - Dry matter content (%)
$\mathbf{X_{20}}$ - Shelf life of tuber

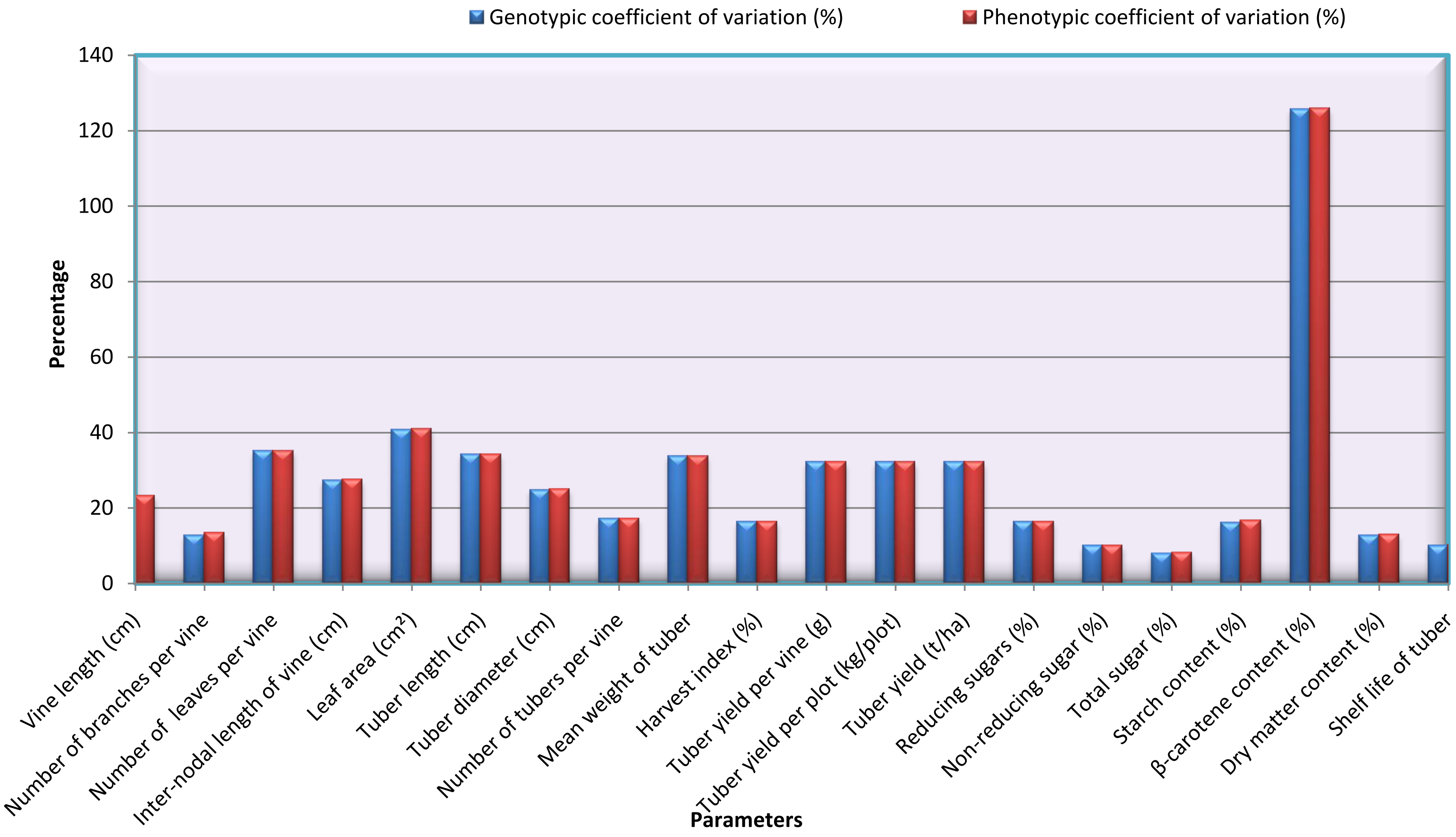

Fig. 1. Estimates of genotypic and phenotypic coefficient of variation for twenty characters of sweet potato genotypes