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Ashish Narayan
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

K Dileep
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

T Alam
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

RS Singh
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

GS Giri
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

R Prasad
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

PP Singh
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

Corresponding Author:
Ashish Narayan
AICRP on Tuber Crops, Tirhut College of Agriculture, Dholi, Dr. Rajendra Prasad Central Agricultural University, Bihar, India

Genetic diversity in sweet potato (*Ipomea batatas* **L.**)

Ashish Narayan, K Dileep, T Alam, RS Singh, GS Giri, R Prasad and PP Singh

Abstract
A study was undertaken on genetic variability by evaluating 20 genotypes of colour fleshed sweet potato considering fourteen quantitative characters *viz.* vine length(cm) at 60 and 120 dap, number of branches/plant at 60 and 120 dap, internode length(cm) at 60 and 120 dap, leaf area index, number of tubers/plant, total tuber yield/plant(g), tuber weight(g), tuber length(cm), tuber girth(cm), biological yield/plant(g) and harvest index (%). The analysis of variance revealed that mean squares due to genotypes were highly significant for all the studied characters. Wide range of variability was observed for the characters such as biological yield/plant, vine length, leaf area index, average tuber weight, harvest index and tuber yield/plant. The phenotypic coefficient of variation was more than genotypic coefficient of variation for all the characters studied. High heritability estimates coupled with high genetic advance as percent of means were observed for characters like vine length, leaf area index, number of tubers/plant, tuber yield/plant, average tuber weight, tuber girth, biological yield/plant and harvest index indicating effectiveness of selection for these traits. Divergence studies categorized the 20 sweet potato genotypes into 4 distinct clusters. Cluster-I was the largest cluster having 10 genotypes followed by cluster-II with 8 genotypes and cluster-III and IV were mono-genotypic. Among four clusters, cluster-II showed maximum intra-cluster diversity ($D^2 = 7.58$) followed by cluster I ($D^2 = 7.37$). However, maximum inter cluster distance was exhibited between cluster II and III (17.78), followed by cluster II and IV (16.60) and cluster I and II (12.54) exhibiting sufficient genetic diversity among the genotypes of these clusters.

Keywords: Sweet potato, characters, variability, heritability, genetic diversity

Introduction
Tuber crops are the third most important food crop following cereals and grain legumes. It is a common food for approximately 20 percent of total world's population. Among tuber crops, Sweet potato (*Ipomoea batatas* L.*)* is an important tuber crop of the tropical and sub-tropical countries and in warmer regions of temperate countries. It is mainly grown in tropic countries because they are known for its drought resistance, vigorous growth and productivity with minimum inputs (Rahaman *et al.*, 2015) [1].
Sweet potato is an herbaceous, dicotyledonous, perennial vine which bears alternate palmately lobed leaves and it is belonging to the convolvulaceae family and it is auto-hexaploid in nature. The origin of sweet potato is tropical regions of America. This crop is highly cross pollinated and heterozygous cultivars with continuous variation for various traits. Because of its extreme heterozygous nature, there is an extensive variability in this species. The edible tuber of sweet potato is generally cylindrical to round in shape which tapered toward the ends with smooth skin and its colour ranges from red, brown, orange, purple and yellowish and its flesh colour also contain variability as white, cream, purple, orange and yellow. It can grow extensively under wide range of agro-climatic conditions. It is grown in environment ranging from 40 ^{0}N to 33 ^{0}S and approximately 2000 meters above the mean sea level. and it generally grows best at temperature of about 24 ^{0}C. The average rainfall required is about 800-1000 mm. Sweet potato used to grow in drained sandy loam soils on nearly neutral pH. It can be stored for six months at a relative humidity of 85-90 percent at 13-16 °C (55-61°F).
The genetic distance values and grouping of genotypes based on D^2 analysis for different traits which contribute to tuber yield and its quality parameters would be useful in planning the sweet potato improvement and further breeding programme. As variation is limited in colour fleshed sweet potato, therefore, there is an urgent need to evaluate the genetic diversity among existing germplasm conserved at Tirhut College of Agriculture, Dholi (Bihar). Due to potentiality of sweet potato, there is a prime need for developing suitable genotypes to cover specific ecological conditions. A detailed knowledge of amount of genetic variation that exists

in a particular crop for different characters is important in a crop species before the breeding work has been initiated. Genetic divergence study is essential to know the variation of heritable characters present in a crop species.

Materials and Methods
The experiment was conducted at Dholi research farm of Tirhut College of Agriculture under Dr. Rajendra Prasad Central Agricultural University, Bihar. The research farm is situated near Burhi Gandak river of Bihar having humid sub-tropical climate and an elevation of 51.2 m above from sea level. The experimental area had sandy loam soil type with uniform topography and normal fertility status. The experiment was carried out during 2019-20 by using randomized block design with three replications. Fourteen quantitative traits were selected for present study *viz.* Length of vine (cm) at 60 and 120 days after planting, Number of branches/plant at 60 and 120 days after planting, Internode length (cm) at 60 and 120 days after planting, Leaf Area Index, Number of tubers/plant, Total tuber yield/plant (g), Tuber weight (g), Tuber length (cm), Tuber girth (cm), Biological yield/plant (g) and Harvest index (%). The twenty genotypes selected were namely CIPSW-2, SV-98, Kamala Sundari, 440038, 440127, ST-14, 362-7, TSP-16-3, TSP-16-10, RS-92, TSPV-1, TSPV-2, TSPV-3, TSPV-4, TSPV-5, TSPV-6, TSPV-7, TSPV-8, TSPV-9 and TSPV-10. Standard

statistical procedures were used for analysis and interpretation of results.

Results and Discussion
Sound genetic information has been an indispensable prelude for suggesting suitable cultivar and genetic improvement in a genotype. Genetic variability and heritability which measure the relationship between genotypic and phenotypic appearance for the success of a breeding programme is essential and pre-requisite for an effective improvement in any crop species. It is well-known that the selection is based on phenotypic observation and the success would naturally depend upon the relationship between phenotype and the genotype. Hence, the estimates of heritability and genetic advance are also useful in prediction of genetic improvement following selection and deciding suitable breeding procedures for sweet potato improvement. The purpose of the present investigation was to extract the basic information which can throw light on the strategies to be adopted for sweet potato improvement with reference to Bihar regions.

The mean squares due to genotypes were found highly significant for all the characters showing suitability of the selected material for genetic variability studies in colour fleshed sweet potato. The analysis of variance showed that there were highly significant differences among genotypes for all characters (Table 1).

Table 1: Analysis of variance (mean squares) for different growth and yield parameters

Sl. No	Sources of variation/characters	Replication	Treatments (genotypes)	Error	S.EM±	C.D (5%)
	Degrees of freedom	2	19	38		
A.	**Growth Parameters**					
1.	Vine length@60 days	29.37	1188.88	126.14	6.32	18.56
2.	Vine length@120 days	62.73	2137.17	85.13	5.19	15.25
3.	Number of Branches@60 days	1.40	2.34	0.27	0.29	0.87
4.	Number of Branches@120 days	5.43	3.38	0.68	0.46	1.36
5.	Internode length@60 days	0.08	1.38	0.21	0.25	0.75
6.	Internode length@120 days	0.24	2.03	5.50	0.34	1.01
7.	Leaf Area Index	7.28	139.78	5.07	0.26	3.72
B.	**Tuber Parameters**					
1.	Number of tubers per plant	1.80	3.41	0.33	0.32	0.95
2.	Total tuber yield per plant	959.78	30865.2	1456.0	21.47	63.07
3.	Average tuber weight	126.87	1311.94	76.25	4.91	14.43
4.	Tuber length	1.26	4.91	1.29	0.64	1.88
5.	Tuber girth	0.51	5.908	0.42	0.36	1.07
6.	Biological yield per plant	94.49	55661.37	367.21	10.78	31.67
7.	Harvesting index	6.90	774.72	29.46	3.05	8.97

In the present study, wide range of variability was observed for all the characters such as biological yield per plant, vine length, leaf area index, average tuber weight and harvesting index (Table- 2). Similarly, wide range of variability for different characters were observed by Engida *et al.* (2007) [2], Singh *et al.* (2017), Bhadauriya *et al* (2018) and Narayan *et al.* (2018) [5] in different tuber crops.

The phenotypic coefficient of variation was more than genotypic coefficient of variation for all the characters studied. Higher magnitude of GCV and PCV were also observed for harvesting index, vine length@60 days, number of branches@60 days, number of branches@120 days, internode length@60 days, leaf area index, number of tubers per plant, total tuber yield per plant and these traits indicate the worth for selecting sweet potato genotypes in breeding programme. Low PCV and GCV were recorded for characters like tuber length, tuber girth indicating the existence of

limited variability in the germplasm evaluated for the trait indicating low genetic variability in the germplasm stock studied. This necessitates need for generation of new variability for these characters. Moderate PCV and GCV were recorded for the characters like internode length@120 days, average tuber weight.

Heritability estimates were high for characters like vine length @ 60 and 120 DAP, leaf area index, number of tubers per plant, total tuber yield per plant, average tuber weight, tuber girth, biological yield per plant, harvesting index number of branches per plant. Heritability estimates were moderate for internode length. These results indicated that characters were least influenced by environmental effect and were effectively transmitted to progeny.

The genetic advance over per cent of mean was low for characters like tuber length and tuber girth. This situation arises when the heritability for the character is low. Vine

length, number of branches, average tuber weight were showing moderate to low genetic advance per cent of mean indicating the operation of non additive gene action for these traits. In the present investigation, high heritability estimates (> 60%) with high genetic advance over mean (> 20%) were exhibited by characters like vine length, leaf area index, number of tubers per plant, tuber yield per plant, average tuber weight, tuber girth, biological yield per plant and harvest index indicating effectiveness of selection for these traits. However, high heritability (< 60%) with moderate genetic advance over mean (10-20%) was observed for tuber length. A low heritability with low genetic advance was observed in number of branches per plant, internode length, tuber length. Similar results of high heritability with genetic advance over mean were reported by Teshome *et al.* (2004) [6], Engida *et al.* (2007) [2], Sharavati *et al.* (2018) [7] and Bhadauriya *et al* (2018).

Table 2: Variability parameters for 14 characters in sweet potato:

Sl. No	Characters	Mean	Range	GV	PV	PCV	GCV	h²(%)	GA	GA (% of Mean)
1.	Vine length@60 days	111.75	76.50-137.70	354.24	480.392	19.614	16.843	73.7	33.29	29.795
2.	Vine length@120 days	153.42	105.29-195.28	684.01	769.147	18.076	17.47	88.9	50.80	33.116
3.	Number of Branches@60 days	4.105	2.433-5.70	0.689	0.967	23.955	20.226	71.3	1.444	35.180
4.	Number of Branches@120 days	6.140	3.78-7.38	0.902	1.584	20.494	15.466	57.0	1.477	24.045
5.	Internode length@60 days	3.555	2.533-5.033	0.393	0.602	21.832	17.632	65.2	1.043	29.333
6.	Internode length@120 days	5.766	4.53-7.13	0.554	0.924	16.67	12.912	60.0	1.188	20.604
7	Leaf Area Index	33.68	23.27-46.03	44.903	49.977	20.985	19.891	89.8	13.08	38.840
8.	Number of tubers per plant	5.190	3.42-7.69	1.026	1.36	22.466	19.516	75.5	1.813	34.924
9.	Total tuber yield per plant (g)	469.5	286.08-612.77	9803.0	11259.1	22.6	21.088	87.1	190.3	40.535
10.	Average tuber weight (g)	145.5	121.13-218.90	411.89	488.152	15.184	13.948	84.4	38.40	26.393
11.	Tuber length (cm)	11.81	9.93-14.77	1.205	2.5	13.379	9.289	48.2	1.570	13.286
12.	Tuber girth (cm)	10.54	8.8-14.8	1.829	2.251	14.228	12.825	81.2	2.511	23.813
13.	Biological yield per plant (g)	751.3	570.05-1028.01	18431.3	18798.6	18.249	18.07	98.0	276.9	36.859
14.	Harvest index (%)	63.93	34.37-102.13	248.422	277.882	26.071	24.651	89.4	30.69	48.013

GV – Genotypic Variance
GCV – Genotypic Co-efficient of Variance
h² – Broad Sense Heritability
GAM - Genetic Advance as percent of Mean.

PV – Phenotypic Variance
PCV- Phenotypic Co-efficient of Variance
GA – Genetic Advance

Table 3: Distribution of 20 genotypes of sweet potato in different clusters as per the Tocher's method:

Cluster	No. of genotypes	Name of Genotypes
I	10	TSPV-1, TSPV-2, TSPV-3, TSPV-4, TSPV-5, TSPV-6, TSPV-8, TSPV-10, CIPSW-2, and TSP-16-10
II	8	TSPV-7,TSPV-9, SV-98, Kamala Sundari, 440127, ST-14, 362-7 and TSP-16-3
III	1	440038
IV	1	RS-92

Twenty sweet potato genotypes were evaluated for 14 quantitative characters and the data obtained was subjected to D² statistics (Mahalanobis, 1936) to assess the genetic divergence. All genotypes were grouped into four clusters which had considerably high intra and inter cluster D² values. The distribution of genotypes in different clusters irrespective of their geographical locations of selection as depicted by Cluster-I having maximum 10 genotypes (TSPV-1, TSPV-2, TSPV-3, TSPV-4, TSPV-5, TSPV-6, TSPV-8, TSPV-10, CIPSW-2, and TSP-16-10) followed by cluster II with 8 genotypes (TSPV-7, TSPV-9, SV-98, Kamala sundari, 440127, ST-14, 362-7 and TSP-16-3) indicated that genetic divergence among genotypes was not associated with geographical distribution might be due to their common ancestry during their course of evolution. Similar results were obtained earlier by Bhadauriya *et al* (2018) and Singh *et al.* (2017) during clustering the genotypes of sweet potato.

The cluster distance indicated genetic diversity among the genotypes on the basis of studied characteristics. In the present sweet potato genotypes, four cluster were formed consisting only first two clusters with ten and eight genotypes, respectively. Among these two clusters, intra cluster distance were found almost at the same level, therefore genotypes present in each cluster having same level of resemblance. However, zero intra cluster value for cluster III and IV indicated that these two clusters are having single genotype.

For inter cluster distances, highest divergent clusters like II and III which was closely followed by cluster II and cluster IV indicated high level of genetic diversity among these cluster combinations as compared to other inter cluster distances and therefore may be utilized for development of recombinant combinations through transgressive breeding programmes. Similar findings were advocated earlier by Teshome *et al.* (2004) [6], Sattar *et al.* (2011) [8] and Mohanty *et al.* (2017) [9] in potato and sweet potato.

Table 4: Intra and Inter-cluster distances amongst genotypes of Sweet potato

Cluster	I	II	III	IV
I	7.37	12.54	10.70	11.62
II		7.58	17.78	16.60
III			0.00	8.90
IV				0.00

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