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Studies on Genetic Variability, Heritability, Genetic Advance, Correlation Coefficient and D² Analysis in Sweet Potato (*Ipomoea batatas* L.)

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ABSTRACT

Thirty six diverse genotype of sweet potato collected from different location of India were evaluated for nineteen quantitative and qualitative characters in Randomized Block Design with three replications at Main Experiment Station, Department of Vegetable Science, NDUAT, Kumarganj, Faizabad(UP) during October, 2011 to March, 2012. On the basis of mean data, the existence of very high degree of variability was observed in the germplasm. The genotypes, NDSP-65 (375g) followed by SP-594 (354g), 187017 (336), NDSP-1-4 (333) and NDSP-1-3 (324g) were the best yield performer for tuber yield per plant. High genotypic coefficient of variability and phenotypic coefficient variability were estimated for number of branches per vine followed by internodal length, length of vine, number of leaf per vine, girth of tuber and acidity. High heritability coupled with high genetic advance in percent of mean were recorded for number of branches per vine, internodal length, length of vine, number of leaf per vine, acidity, average weight of tuber, number of tubers per vine, TSS and width of leaf. Tuber yield (q/ha) followed by tuber weight, internodal length, specific gravity and tuber length showed positive significant correlation with tuber yield per plant while, TSS and moisture per cent showed negative significant correlation with tuber yield per plant. Path coefficient analysis revealed that, tuber weight followed by tuber per vine, tuber yield (q/ha) showed higher value of positive direct effect on tuber yield per plant while, tuber yield followed by specific gravity via tuber weight and branches per vine, length of vine and laves per vine via tuber per vine, vine length and leaves per vine showed positive indirect effect on tuber yield per plant. Total of 36 genotype were grouped in to seven cluster. The highest intra cluster distance was found in cluster V and inter cluster distance between cluster IV and VI. Internodal length (31.59%) number of branches per vine (21.90%) and acidity (21.11%) were found as the important traits in clustering the genotype with different groups. Based on above finding it might be concluded that these are existing sufficient variability in the available germplasm. Genotype (NDSP-65 followed by SP-594, 187017, NDSP-1-4 and NDSP-1-3) may be exploited in future after further evaluation for stability test.

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1. Introduction

Tropical root and tuber crops are considered as third important crop after cereal and legumes. They contribute six percent of the average daily calorific intake of human beings. The tropical roots and tuber crops are of utmost importance for the world food security (Navaleet *et al.*, 2016). The sweet potato (*Ipomoea batatas* L. Lam.) belongs to the family Convolvulaceae, is one of the important tuber crop of tropical and sub tropical regions of the world. In India it is mainly cultivated in Orissa, Bihar, Uttar Pradesh, Madhya Pradesh, Maharashtra, and Karnataka and approximately 80% of sweet potato is grown in Asia while, China is the forefront with respect to sweet potato cultivation among sweet potato growing countries (George, 2012). The annual production of sweet potato is estimated to be 110.7 MT from an area of 8.2 M ha with a productivity of 13.5 t h⁻¹. India comes ninth in production which about 1.3 MT from an area of 0.11 M ha with a productivity of 10.2 t ha⁻¹ where, Odisha state contributed maximum (Aswathy *et al.*, 2015). Sweet potato constitutes the staple diet of tribal Indian population due to hardiness and adoptability in to diversified farming system. Its tubers are used both for direct human consumption and manufacture of industrial products such as starch, glucose pectin, sugar and alcohol. It is rich source of carotene, ascorbic acid, thiamine, riboflavin and protein. The yellow or orange fleshed varieties of sweet potato contain high level of beta-carotene a precursor of vitamin A. It was found in study the weekly intake of 100g orange fleshed sweet potato could remake vitamin A deficiency in children, pregnant women and lactating mothers. The food security of the increasing population is in danger owing to the inability and insufficiency of the cereals and pulses to cope up with the situation. There is a need to look for alternate sources of foods and it is here that the tropical tuber crops come in handy to alienate the food security crises as they can supply cheap source of energy especially to weaker section (Krishnakumar, 2013).

Improvement of any crop depends upon the magnitude of genetic variability present in the economic characters in modern farming system. Only a few high yielding varieties dominant in such system which obtain leads to genetic homogeneity resulting in genetic vulnerability to biotic and abiotic stresses. Emphasized that genetic diversity and location specific varieties are essential for achieving sustainable advances in productivity of any crop breeding programme. The extent of transmission of a quantitative characters from parent to

offspring depends upon the heritability of a particular character. Most of the agronomical characters including yield are polygenically controlled and are highly influenced by environmental factors. Since yield is a complex character which depend on several components. Selection on yield checks it alone is not likely to be efficient. Path coefficient analysis which determines the cause and effect relationship has been found useful in splitting the correlation coefficient in to direct and indirect effect contributing to yield. To meet the challenges, there is need for concerted and dedicated efforts on research and development towards harnessing the potential of sweet potato for livelihoods.

2. Materials and Methods

The present investigation was carried out at Main Experiment Station, Department of Vegetable Science, NDUAT, Kumarganj, Faizabad (UP) during 2011-2012. The experimental materials were comprised of 36 genetically divergent indigenous genetic stocks of sweet potato collected from different part of India. The experiment was carried out in Randomized Block Design with three replications. Each genotype was planted in a plot comprising of 2.4 x 1.8m. size with the spacing of 60x 20 cm. Proper spacing between the plot was also maintained to avoid the crowd of vine between the germplasm. Length of 25 cm. vine cuttings were planted cross on the ridges exposing of both the side. The recommended dose of fertilizers were applied as on recommended time to grow healthy crop. Other agronomical practices were done to maintain the crop. Five competitive plants from each plot were randomly selected for recording observations for all the characters *viz.* days to initiation of buds, size of leaves (length and width in cm.), length of vine (cm), number of branches per vine, number of leaves per vine, inter nodal length (cm), length of tubers (cm), girth of tubers (cm), number of tubers per vine, average weight of tuber (g), yield per plant (kg), yield per hectare (q), specific gravity, pH, T.S.S., moisture per cent, acidity and ascorbic acid. The experimental data collected in respect of 19 characters of 35 sweet potato genotypes and 1 check were compiled by taking the mean values of selected plants in each plot and subjected to following statistical analysis *viz.* the variability was worked out using formula suggested by Burton and de Vane (1953), heritability in broad sense by Hanson *et al.* (1956), genetic advance in per cent of mean suggested by Johnson *et al.* (1955), correlation coefficient by Al-Jibouriet *et al.* (1958) and genetic divergence analysis by Mahalanobis' D² statistic (1936) followed by Rao (1952).

Table 1. Estimates of range, grand mean, phenotypic, genotypic, environmental, coefficients of variation, heritability in broad sense (h^2_{bs}) and genetic advance in per cent of mean (GA) for 19 characters in sweet potato germplasm

S. No.	Characters	Range		Grand mean	PCV (%)	GCV (%)	ECV (%)	Heritability (%) (h^2_{bs})	GA in % of Mean
		Lowest	Highest						
1.	Days to bud initiation	7.49	10.00	8.66	11.04	8.20	7.40	55.09	16.06
2.	Length of leaf (cm)	4.31	7.82	6.07	13.25	11.89	5.86	80.46	28.15
3.	Width of leaf (cm)	3.50	7.40	5.15	0.82	0.71	0.11	86.44	31.43
4.	Length of vine (cm)	28.80	103.40	49.83	33.05	32.69	4.88	97.81	85.35
5.	No. of branches per vine	1.40	8.20	3.60	49.84	49.57	5.17	98.92	130.15
6.	No. of leaves per vine	18.40	71.20	36.18	29.53	28.62	7.24	93.99	73.27
7.	Internodal length (cm)	1.40	6.84	2.83	44.27	44.05	4.42	99.00	115.71
8.	Length of tuber (cm)	11.52	28.12	18.71	18.54	16.71	8.03	81.23	39.76
9.	Girth of tuber (cm)	1.50	6.90	4.47	28.71	27.07	9.56	88.90	67.38
10.	No. of tuber per vine	3.00	7.20	5.22	20.20	18.64	7.78	85.17	45.42
11.	Average weight of tuber (g)	37.50	88.05	59.67	22.92	22.56	4.06	96.85	58.62
12.	Yield per plant (g)	240.00	375.00	307.50	11.09	9.59	5.56	74.84	21.91
13.	Yield per hectare (q)	160.80	251.25	201.00	11.60	9.28	6.96	63.99	19.60
14.	Specific gravity	0.98	1.02	1.00	1.14	1.01	0.53	78.43	2.36
15.	pH	5.90	6.91	6.51	6.23	3.40	5.22	29.76	4.90
16.	T.S.S	6.80	14.50	9.36	19.44	17.29	8.88	79.12	40.61
17.	Moisture percent	69.20	78.00	74.35	3.90	2.65	2.86	46.25	4.76
18.	Acidity (mg)	0.11	0.28	0.20	25.05	24.62	4.65	96.55	63.89
19.	Ascorbic acid (mg)	21.80	27.90	24.33	9.32	4.72	8.04	25.0	6.32

3. Result and Discussion

The success of breeding programme depends upon quantum of variability present in the available germplasm which are undertaken for study. The analysis of variance indicated that, the differences due to genotype were highly significant for all the characters. This indicates sufficient genetic variability could be exploited in a breeding which are reflected in broad sense observed for each traits. Genotype NDSP-65 planted as check, showed high mean performance for most of the yield component over all the genotypes. The experimental materials consisted of thirty six genotypes including check (NDSP-65) of sweet potato were observed in terms of range, grand mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance (Table 1). The range of variation was observed higher for the character yield per plant (240 to 375g) followed by yield (160.80 to 251.25) tones per hectare. A better hypothesis can be gained by comprising the relative amount of coefficient of phenotypic and genotypic variances for the actual strength of variability. The estimates of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied, although the differences were recorded

narrow between PCV and GCV implying that, variability was due to genetic factor. Higher PCV and GCV were observed for number of branches per vine followed by internodal length and length of vine, while minimum was observed in width of leaves. The result further revealed that, the characters under study exhibited high degree of PCV revealing close relationship between phenotypic and genotypic coefficient of variation and these characters are not influenced by environment, hence improvement for these characters are easy. Similar reports have also been put forward by Sen and Goswami (1991) and Pandey *et al.* (1996). The estimates of heritability in broad sense (h^2_b) showed considerable variation for different characters. It indicates the possibility and extent to which improvement is possible through selection. Maximum heritability was recorded for all the characters except ascorbic acid (25.00) and pH (29.76) while days to bud initiation (55.09) and moisture percent (46.25) showed moderate heritability. Selection will be more effective in case of characters showing high heritability while, selection will be difficult in case of low heritability, since the genotypes are affected by the environment in such case. The highest estimates of genetic advance along with high heritability clearly indicates the possibility of improvement through selection. Genetic advance in per cent of mean exhibited considerable variation

Table 2. Estimates of phenotypic and genotypic correlation coefficient of 19 characters in sweet potato germplasm

Clusters		Leaf length (cm)	Leaf Width(cm)	Vine length(cm)	Branches / vine	Leaves/vine	Internodal length (cm)	Tuber length (cm)	Tuber girth(cm)	Tuber/vine	Tuber weight (g)	Tuber yield (q/ha)	Specific gravity	pH	TSS	Moisture (%)	Acidity (g)	Ascorbic acid (g)	Tuber yield/plot (g)
Days to bud initiation	P	-0.073	-0.014	0.087	0.136	0.161	0.129	-0.020	-0.105	0.071	-0.140	-0.154	-0.152	-0.009	0.305**	0.138	0.085	-0.182	-0.072
	G	-0.168	-0.004	0.124	0.164	0.234	0.154	-0.062	-0.140	0.099	-0.183	-0.122	-0.165	-0.209	0.482	0.485	0.100	-0.280	-0.187
Leaf length (cm)	P		-0.142	0.056	0.195*	-0.087	0.087	-0.056	-0.106	0.151	-0.132	-0.016	-0.237*	-0.139	-0.153	-0.030	0.073	0.153	-0.001
	G		-0.180	0.069	0.217	-0.097	0.101	-0.058	-0.152	0.199	-0.173	-0.004	-0.317	-0.136	-0.211	-0.112	0.090	0.302	-0.014
Leaf width	P			0.218*	-0.011	-0.018	0.178	0.065	0.133	0.044	0.056	0.105	-0.047	-0.021	0.088	0.071	-0.075	-0.118	0.098
	G			0.234	-0.005	-0.025	0.195	0.079	0.165	0.020	0.051	0.108	-0.023	0.055	0.168	0.044	-0.083	-0.228	0.116
Vine length	P				0.148	0.232*	0.232*	0.079	0.087	0.286**	-0.242*	0.065	-0.213*	0.010	0.118	-0.083	0.206*	0.005	0.059
	G				0.153	0.236	0.240	0.083	0.096	0.319	-0.251	0.078	-0.231	0.069	0.125	-0.115	0.211	-0.028	0.081
Branches / vine	P					0.393**	0.197*	0.129	-0.065	0.316**	-0.296**	0.035	-0.226*	0.012	0.113	-0.035	-0.279**	0.049	0.044
	G					0.415	0.121	0.145	-0.065	0.343	-0.304	0.050	-0.241	-0.031	0.125	-0.065	-0.290	0.077	0.045
Leaves/vine	P						0.217*	0.313**	0.133	0.257	-0.226*	0.058	0.089	0.202*	0.105	0.082	0.014	0.130	0.030
	G						0.228	0.356	0.147	0.287	-0.233	0.056	0.134	0.436	0.140	0.158	0.014	0.276	0.073
Internodal length (cm)	P							0.245*	0.212*	0.096	-0.007	0.307**	-0.004	0.003	-0.029	-0.072	-0.062	0.072	0.333
	G							0.207	0.234	0.108	-0.007	0.402	-0.007	-0.021	-0.020	-0.104	-0.066	0.159	0.383
Tuber length (cm)	P								0.287**	0.031	0.066	0.252**	0.309**	-0.060	0.031	-0.000	-0.075	0.130	0.249
	G								0.371	0.057	0.063	0.306	0.364	-0.122	0.024	0.057	-0.091	0.126	0.306
Tuber girth	P									0.19*	-0.143	0.170	0.297**	0.244*	0.033	0.276**	-0.099	-0.035	0.160
	G									0.230	-0.146	0.190	0.382	0.423	0.017	0.450	-0.108	0.075	0.195
Tuber/vine	P										-0.848**	-0.028	-0.206*	0.100	0.199*	0.211*	-0.121	0.123	-0.026
	G										-0.924	-0.050	-0.252	0.270	0.255	0.334	-0.127	0.235	-0.050
Tuber weight (g)	P											0.357**	0.266**	-0.071	-0.301**	-0.272**	0.055	-0.089	0.378
	G											0.466	0.297	-0.147	-0.351	-0.408	0.066	-0.139	0.449
Tuber yield (q/ha)	P												0.176	-0.008	-0.342**	-0.189	-0.025	0.178	0.742
	G												0.300	0.183	-0.419	-0.382	-0.036	0.397	1.188
Specific gravity	P													0.088	-0.300**	0.143	0.082	0.242*	0.251
	G													0.335	-0.353	0.262	0.093	0.437	0.247
Ph	P														0.076	0.087	0.148	0.067	0.063
	G														0.130	0.639	0.267	0.482	0.102
TSS	P															0.245	-0.056	-0.206*	-0.331
	G															0.409	-0.060	-0.386	-0.423
Moisture (%)	P																-0.040	-0.047	-0.249

for different characters. The genetic advance in percent of mean ranged from number of branches per vine (130.15) to specific gravity (2.36). The estimates of genetic variability and genetic advance in per cent of mean for most of the characters under study are in accordance with earlier reports have also been put forward by Vimala and Lakshmi (1991) Engida *et al.* (2007) and Singh *et al.* (2015). Correlation studies exhibited tuber weight, internodal length, specific gravity and tuber length showed positive association with tuber yield per plant (Table 2). TSS and moisture content showed strong and negative association with tuber yield per plant. Leaf length had highly significant positive correlation with number of tuber per vine and significant positive correlation with leaves per vine, internodal length and acidity while, significant negative correlation with tuber weight and specific gravity. Branches per vine showed significant positive correlation with internodal length where, non-significant positive correlation were found with tuber length, tuber yield per hectare, pH, TSS, ascorbic acid and tuber yield per plant but it was negative with tuber girth and moisture per cent. In general genotypic correlations were higher in magnitude from the corresponding phenotypic values. Similar results have been reported by Pillai *et al.* (1995) Sahu *et al.* (2005), and Singh *et al.* (2015) Path coefficient analysis is a tool to partition the observed correlation into direct and indirect effects of yield components on tuber yield provides clearer picture of character association for formulating efficient selection strategy (Table 3). A very high positive direct contribution to tuber yield per plant was exerted by tuber weight. Tuber per vine, tuber yield (q/ha) were also major direct contribution to the tuber yield per plant. Branches per vine, length of vine, leaves per vine and tuber per vine exerted high order positive indirect effects on tuber yield per plant. Path correlation coefficient analysis revealed that tuber weight (0.662) showed maximum positive direct effect on tuber per vine (0.551) followed by tuber yield per hectare showed higher value of positive direct effect tuber yield per plant. Thus it revealed that tuber weight major positive role yield traits, while negative direct effect was exhibited by moisture per cent (-0.123) followed by leaves per vine (-0.094) and TSS (0.056) at phenotypic level. The results of path analysis obtained under present study are also in close agreement with the result of Sahu *et al.* (2005), Singh *et al.* (2015) in sweet potato while, Chand *et al.* (1987) reported in colocasia and Rekha *et al.* (1991) reported in cassava.

The D² analysis grouped 36 genotypes into seven different non-overlapping clusters. This indicated considerable diversity among the germplasm evaluated in

the present study (Table 4). Cluster I had 14 out of 36 entries which were characterized by highest cluster means followed by Cluster IV (8) cluster V (4) and cluster VII (4). Cluster II, III, and IV having 2 genotypes each. The seven clusters in aforesaid genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although the genotypes originated in the same place or geographic region were also found to be grouped together in same cluster. The instance of grouping of genotypes of different origin or geographic region in the same cluster were observed in case of all the seven clusters. This indicated presence of substantial genetic diversity in the evaluated genotypes. This result is highlighting by Ahmad *et al.* (2000), Teshome *et al.* (2003) and Singh *et al.* (2017) in sweet potato. The intra and inter cluster distance were observed which represent the index of genetic diversity among the traits as shown in Table 5. Table showed greater inter cluster distance than intra-cluster distance in maximum clusters revealing considerable amount of genetic diversity among the genotypes. The highest intra cluster distance was recorded in cluster V (898.39) where, cluster IV had minimum (305.20). In relation to inter cluster distance, cluster IV recorded greater divergence with cluster VI (5160.45) which indicates the members of these two clusters are genetically very diverse to each other. Genotypes observed under above clusters could be applied for crop improvement through intercrossing. Minimum inter-cluster distance was observed between cluster VI and VII (741.38) which showed close relationship among the genotypes. A perusal showed that cluster V means for different traits indicated considerable difference between the cluster. All clusters from I and VII had in general medium mean performance for most of the characters exhibiting extreme cluster means for. Maximum cluster mean for tuber yield per hectare (320.25) was observed in cluster VII followed by cluster IV and V where lowest was observed in cluster III. Likewise, cluster III exhibited maximum mean value for tuber length (20.88), tuber girth (6.37), tubers per vine (6.20), TSS (6.72), moisture content (11.25) and Acidity (76.35). Other important character such as maximum weight of tubers (70.74) observed in cluster VI. As per the observation of important traits and fulfilling the breeding objectives, the potential lines to be selected from different cluster as parents to use in hybridization programme should be based on genetic distance. These findings are in agreement with Teshome *et al.* (2003) reported that the clustering pattern could be utilized in selecting the parents for making the combinations to generate possible variability through crossing for economic traits. Similar result in sweet potato have been put forwarded by Singh *et al.* (2017).

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Table 4. Clustering pattern of 36 genotypes on the basis of Mahalanobis D² statistics

Cluster No.	No. of genotypes	Genotypes
I	14	SP-594, IGSP-11, NDSP1-2, RS-47, RNSP, NDSP1-4, IGSP-5, SI-14, Kalmegh, 440127, NDSP1-6, RS-92, DOP-93-19, NDSP1-
II	2	S-1281, 42027
III	2	440038, Sri Bhadra
IV	2	SV-362, CROSS-4
V	4	187017, RS-35, RS-43, RS-5
VI	8	S-61, SV-98, IGSP-14, CIPWA-2, S-1156, NDSP1-3, DOP-92-93, X-29
VII	4	IGSP-10, NDSP1-1, NDSP1-7, NDSP-65

Table 5. Average of intra and inter- clusters D² values for seven clusters

Cluster number	I	II	III	IV	V	VI	VII
I	472.90	877.60	1043.46	2893.14	1460.99	944.88	768.64
II		340.31	981.04	1886.31	2007.54	2109.88	1696.37
III			440.82	1350.68	1268.16	2633.22	1556.63
IV				470.83	1910.00	5160.45	3210.81
V					898.39	2309.89	1162.97
VI						305.20	741.38
VII							389.35

Table 6. Cluster mean for different characters in sweet potato genotypes

Clusters	Leaf length (cm)	Leaf width (cm)	Vine length (cm)	Branches / vine	Leaves/vine	Internodal length (cm)	Tuber length (cm)	Tuber girth (cm)	Tuber/vine
I	8.54	6.37	5.16	49.97	3.88	35.64	2.27	18.33	4.43
II	9.00	6.55	4.09	38.00	7.00	40.00	2.19	18.15	1.90
III	8.00	5.78	5.28	71.50	4.70	47.50	2.96	20.88	6.37
IV	9.50	5.56	5.92	51.80	7.60	52.70	5.26	19.58	5.67
V	8.75	6.26	5.44	72.80	3.50	36.07	4.83	20.70	4.35
VI	8.63	5.66	4.99	39.29	1.90	30.20	1.95	18.05	4.19
VII	8.87	5.89	5.27	41.60	1.93	34.40	3.61	18.19	5.12

Cont.....

Clusters	Tuber weight (g)	Tuber yield (q/ha)	Specific gravity	pH	TSS	Moisture (%)	Acidity (g)	Ascorbic acid (g)	Tuber yield/plot	Leaf length (cm)
I	5.77	53.21	298.72	200.14	1.00	6.51	8.97	74.04	0.21	24.50
II	5.05	57.24	286.50	191.96	1.00	6.25	9.85	72.05	0.17	24.85
III	6.20	44.98	274.50	183.92	1.01	6.72	11.25	76.35	0.14	24.20
IV	5.95	53.49	318.00	213.06	1.00	6.65	9.50	76.00	0.19	24.10
V	4.88	65.48	315.00	211.05	1.00	6.39	9.68	72.45	0.23	23.95
VI	4.25	70.74	289.88	194.22	1.01	6.55	9.65	75.11	0.25	24.10
VII	4.88	66.01	320.25	214.57	1.01	6.55	8.88	75.15	0.17	24.53