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Genetic diversity studies in potato (*Solanum tuberosum* L.) genotypes

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Abstract

An experiment on genetic diversity studies in potato (*Solanum tuberosum* L.) genotypes was conducted during *kharif* 2018-19 under AICRP (Potato) MARS, UAS, Dharwad. Analysis of variance indicates the existence of large variability among the genotypes. Thirty genotypes were grouped into eight distinct clusters depending upon their similarities in D^2 values. Cluster I includes the maximum number of genotypes (18), Cluster II had six genotypes and while, remaining six clusters (III, IV, V, VI, VII and VIII) had single genotype in each cluster (monogenic groups). The maximum intra cluster distance was recorded in Cluster II (95.89) and maximum inter cluster D^2 was reported between cluster VI had VII (510.78). The higher inter cluster distance was recorded between the cluster VI and cluster VII. The genotypes from these clusters P-41 (cluster VI) and C-18 (cluster VII), are suggested to include in hybridization programme for getting advantageous and superior combinations.

Keywords: Potato, genotype, genetic diversity, cluster analysis, cluster composition

Introduction

Potato (*Solanum tuberosum* L.) is a member of family Solanaceae, which comprises about 2000 species. Out of these, only two tuber bearing species *viz.*, *Solanum tuberosum* and *Solanum andigenum* have been commercially exploited throughout the world while, *Solanum tuberosum* is widely cultivated in large scale. It is native of Central Andean region of South America.

Potato is one of the most prevalent staple foods and occupies fourth largest food crop in terms of food and nutritional security, after rice, wheat and maize among ever-increasing population. It is very nutritious, readily digestible wholesome food with a good source of carbohydrates, vitamins, proteins, minerals and dietary fiber.

In recent years, the per capita utilization of potato is increasing day by day, hence there is need to evolve high yielding cultivars having better storage and processing qualities. It could be achieved by crop improvement programme by identifying genetically diverse parents for yield and its components. The use of genetically divergent parents in crop improvement is expected to give desirable and superior segregates following the hybridization programme (Bhatt, 1973) [1].

Genetic diversity in a population is a pre-requisite for an effective breeding programme. It has been regarded as major factor in hybridization to achieve good outcomes with high yielding and superior progenies. The D^2 analysis is widely followed to estimate the genetic distance among the lines and also to find traits contributing for genetic divergence. This information can be taken up to compute the genetic divergence so as to identify genetically diverse parents for further breeding programme. Hence, to get the information on the nature and degree of genetic diversity of potato genotypes for selection of parents for hybridization the study was undertaken.

Materials and methods

The investigation was conducted under AICRP (Potato), Department of Horticulture, MARS, UAS, Dharwad during *kharif* 2018-19. Thirty genotypes were evaluated using randomized block design (RBD) and list of genotypes are in given in Table 1. Each progeny was accommodated in five rows of 3 m length. The row to row spacing of 60 cm and plant to plant spacing of 20 cm was adopted. The recommended package of practices was followed. Five plants were selected randomly from each replication and data were recorded for the characters *viz.*, days to fifty per cent plant emergence, plant emergence percentage (%), plant height (cm)

number of primary shoots per plant, diameter of main stem (cm), number of compound leaves per plant, leaf area, fresh weight of shoots per plant (g plant^{-1}), dry weight of shoots per plant (g plant^{-1}), weight of tubers per plant (g plant^{-1}), number of tubers per plant, total tuber yield per plot (kg plot^{-1}), marketable tuber yield per plot (kg plot^{-1}), unmarketable tuber yield per plot (kg plot^{-1}), total tuber yield per hectare (t ha^{-1}), marketable tuber yield per hectare (t ha^{-1}), unmarketable yield per hectare (t ha^{-1}), harvest index (%), dry matter content (%), moisture content (%), starch content (%), total soluble solids (TSS) ($^{\circ}$ Brix), chips colour score and yield of chips (g). The multivariate analysis (D^2 statistics) was carried out using Mahalanobis (1936) [5]. Grouping of genotypes into different clusters was carried out following Tocher's method (Rao, 1952) [7]. And the relative contribution of various characters

towards total divergence was computed as per Singh and Choudhary (1977) [8].

Results and Discussion

The analysis of variance indicates significant variation among 30 potato genotypes for all the characters studied. This indicated that ample variability existed among the genotypes and the analysis of genetic divergence is reasonable. On the basis of D^2 analysis, 30 genotypes were grouped into eight clusters (Table 2). The highest number of genotypes were present in cluster I which comprises of eighteen genotypes, cluster II with six genotypes and remaining six clusters (III, IV, V, VI, VII and VIII) had single genotype in each cluster (monogenic groups).

Table 1: List of genotypes used for the experiment

S. No.	Name of Genotype	S. No.	Name of Genotype	S. No.	Name of Genotype
1.	P-1	11.	P-30	21.	P-46
2.	P-4	12.	P-33	22.	PH-3
3.	P-7	13.	P-34	23.	RH-2
4.	P-9	14.	P-36	24.	C-8
5.	P-12	15.	P-39	25.	C-10
6.	P-14	16.	P-40	26.	C-11
7.	P-22	17.	P-41	27.	C-14
8.	P-24	18.	P-42	28.	C-15
9.	P-25	19.	P-43	29.	C-18
10.	P-28	20.	P-45	30.	C-20

Table 2: Cluster composition of potato genotypes

Cluster No.	No. of genotypes	Genotypes
I	18	P-1, P-4, P-7, P-9, P-14, P-24, P-25, P-28, P-33, P-34, P-36, P-39, P-40, P-43, P-45, RH-2, C-8 and C-11
II	6	P-12, P-22, P-42, P-46, C-10 and C-15
III	1	PH-3
IV	1	C-20
V	1	P-30
VI	1	P-41
VII	1	C-18
VIII	1	C-14

The estimates of intra and inter cluster distances represented by D^2 values has been presented in Table 3 and Fig 1. The maximum intra cluster distance was recorded in Cluster II (95.89), while the minimum inter cluster distance was reported in Clusters III, IV, V, VI, VII and VIII.

The maximum inter cluster D^2 was reported between cluster VI had VII (510.78), while the cluster IV and cluster VII recorded minimum (88.39) inter cluster D^2 values. These results reflect the findings of previous researchers Joseph *et al.* (1999) [3], Kaushik *et al.* (2014) [4], and Prabha *et al.* (2018) [6], in potato.

Table 3: Intra (diagonal) and inter cluster distances in potato genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	70.53	124.5	119.46	281.99	120.29	140.74	250.61	294.1
Cluster II		95.89	141.48	149.77	157.95	220.39	140.78	179.29
Cluster III			0	282.31	148.14	152.06	309.41	263.17
Cluster IV				0	311.73	509.01	88.39	194.77
Cluster V					0	223.19	289.02	324.23
Cluster VI						0	510.78	486.11
Cluster VII							0	106.47
Cluster VIII								0

Cluster means for various parameters

The cluster means for various parameters are given in Table 4 & 5. Observed the significant differences between clusters for all the twenty characters studied.

The highest cluster mean value of number of days to fifty per cent field emergence was reported in genotype of cluster V with mean value of 30.00 and minimum value of 11.50

recorded for genotypes in cluster IV. Cluster IV reported highest plant emergence percentage with mean value of 90.75 and lowest value of 59.50 was recorded in cluster V.

Highest plant height (59.51) showed in cluster IV and lowest (28.27) was reported in cluster VI. Highest number of primary shoots per plant (5.59) was noticed in cluster VIII and lowest (2.92) in cluster VI.

Highest diameter of main stem (3.68) was recorded in cluster VII and lowest (3.50) was reported in cluster V. Highest number of compound leaves per plant (19.75) in cluster VII and lowest (13.10) in cluster VI.

The genotypes found in cluster IV had highest leaf area (428.83), while cluster VIII had lowest leaf area (358.13). Highest fresh weight of shoots was recorded in genotypes of cluster II with cluster mean value of 156.05 and lowest value (94.44) was recorded for genotypes in cluster V. Greater dry weight of shoots was recorded in genotypes in cluster VII with a cluster mean value of 22.17 and lowest value (17.29) was recorded for the genotypes in cluster V.

Cluster IV recorded highest yield per hectare with mean value of 33.37 and lowest value (10.56) in cluster IV. Cluster IV recorded maximum marketable yield per hectare with mean value of 32.50 and minimum value (9.24) in cluster VI.

Highest unmarketable yield per hectare (1.68) was recorded in cluster III and lowest (0.87) was reported in cluster IV. Highest weight of tubers per plant (259.55) was recorded in cluster IV and lowest (96.33) in cluster III.

Maximum number of tubers per plant was observed (6.84) in cluster IV and minimum (2.38) was reported in cluster III. Highest harvest index (72.43) was recorded in cluster IV and lowest (42.98) in cluster III.

Cluster III recorded highest tuber dry matter content with mean value of 23.73 and lowest value (15.75) in cluster I. Cluster VII recorded maximum tuber moisture content with mean value of 81.40. While, minimum value (67.16) in cluster VI.

Highest TSS was recorded (7.08) in cluster VI and lowest (5.38) was reported in cluster IV. Highest chips colour score (5.5) in cluster VII while the lowest (1.0) in cluster III.

Cluster VIII recorded yield of chips with mean value of 37.52 and lowest value (14.19) in cluster VI.

Among the clusters, cluster IV was diverse with higher for total tuber yield per hectare, marketable tuber yield per hectare, weight of tubers per plant, number of tubers per plant, harvest index, plant emergence, plant height, number of shoots per plant, leaf area and lesser number of days for fifty per cent of plant emergence. The genotypes in cluster VII had highest diameter of stem, number of leaves, dry weight of shoots and moisture content. The genotypes in cluster VIII had higher starch content. Genotypes in cluster II had maximum fresh weight of shoots. Genotypes coming under cluster VI had higher TSS content. While, genotypes belong to cluster III shown lower chips colour score.

The per cent contribution of the characters towards total divergence of thirty genotypes of potato are presented in Table 6 and the data reveals that the contribution of various characters towards the total divergence was noticed for total tuber yield per hectare (35.86 %) followed by tuber dry matter content (20.46 %); yield of chips (20 %); number of tubers per plant (11.26 %); days to fifty per cent field emergence (6.21 %); fresh weight of shoots (2.07 %); marketable tuber yield per hectare (2.07 %); plant height (0.92 %); TSS (0.46 %); number of primary shoots (0.23 dry weight of shoots (0.23 %) and chip colour score (0.23 %), while, rest of the characters recorded low or negligible contribution to the total divergence. From the study, it is noticed that the characters which are contributed towards diversity are in conformity with dry matter content of tuber (Gunjan, 2008) [2], and Sunidhi (2016) [9], for tubers number per plant, fresh weight of shoots and total tuber yield.

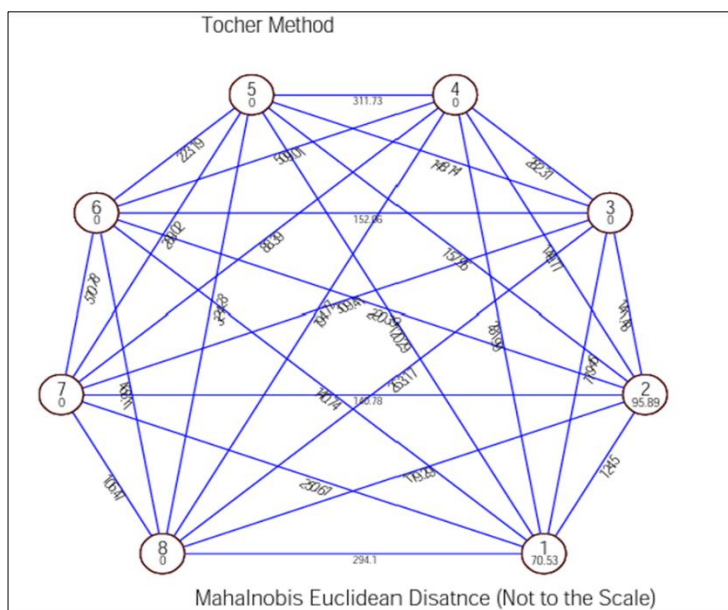


Fig 1: Intra and inter-cluster (D^2) values in potato genotypes

Table 4: Mean performance of clusters for various characters in potato genotypes

Character/ Clusters	x1	x2	x3	x4	x5	x6	x7	x8	x9	x10
Cluster I	18.13	74.85	46.39	4.16	3.60	14.45	382.43	115.90	20.20	13.47
Cluster II	15.79	82.88	45.38	4.04	3.62	15.58	383.15	156.05	20.85	23.65
Cluster III	17.50	85.25	53.61	5.06	3.60	18.73	396.61	102.17	21.11	11.09
Cluster IV	11.50	90.75	59.51	5.55	3.55	15.96	428.83	98.75	18.46	33.37
Cluster V	30.00	59.50	52.08	4.21	3.50	16.47	422.59	94.44	17.29	18.08
Cluster VI	15.50	78.00	28.27	2.92	3.58	13.10	364.37	142.02	21.61	10.56
Cluster VII	13.50	89.5	51.94	4.86	3.68	19.75	421.98	116.533	22.17	32.34
Cluster VIII	14.50	86.00	50.70	5.59	3.61	17.09	358.13	107.75	18.45	31.04

Note: x1- No. of days to fifty per cent field emergence, x2- Per cent plant emergence (%), x3- Plant height (cm), x4- No. of primary shoots per plant, x5- Diameter of main stem (cm),

x6- No. of compound leaves per plant, x7- Leaf area (cm²), x8- Fresh weight of shoots (g plant⁻¹), x9- Dry weight of shoots (g plant⁻¹) and x10- Total yield per hectare (t ha⁻¹).

Table 5: Mean performance of clusters for various characters in potato genotypes

Character/ Clusters	x11	x12	x13	x14	x15	x16	x17	x18	x19	x20
Cluster I	12.43	1.04	128.83	3.21	47.27	15.75	71.09	6.52	3.69	20.28
Cluster II	22.19	1.47	202.20	5.44	52.58	19.95	74.95	6.50	3.33	21.38
Cluster III	9.41	1.68	96.33	2.38	42.98	23.73	76.07	5.60	1.00	27.14
Cluster IV	32.5	0.87	259.55	6.84	72.43	22.40	78.40	5.38	2.00	14.19
Cluster V	16.86	1.22	156.19	4.01	56.30	20.74	67.86	6.55	4.50	17.85
Cluster VI	9.24	1.32	150.05	3.91	47.36	20.03	67.16	7.08	3.50	24.85
Cluster VII	30.82	1.52	255.86	6.68	64.17	16.13	81.40	6.85	5.50	21.09
Cluster VIII	30.03	1.01	252.97	6.71	66.09	17.48	73.78	6.28	2.00	37.52

Note: x11- Marketable yield per hectare (t ha⁻¹), x12- Unmarketable yield per hectare (t ha⁻¹), x13- Weight of tubers per plant (g plant⁻¹), x14- No. of tubers per plant, x15-

Harvest index (%), x16- Tuber dry matter content (%), x17- Tuber moisture content (%), x18- TSS (⁰ Brix), x19- Chips colour score and x20- Yield of chips (%).

Table 6: Contributions of characters towards diversity in potato genotypes

Sl. No.	Character	No. of times ranked first	Contribution (%)
1	No. of days fifty per cent field emergence	27	6.21
2	Per cent plant emergence (%)	0	0
3	Plant height (cm)	4	0.92
4	No. of primary shoots per plant (cm)	1	0.23
5	Diameter of main stem of the plant (cm)	0	0
6	No. of compound leaves per plant	0	0
7	Leaf area (cm ²)	0	0
8	Fresh weight of shoot (g plant ⁻¹)	9	2.07
9	Dry weight of shoot (g plant ⁻¹)	1	0.23
10	Total yield per hectare (t ha ⁻¹)	156	35.86
11	Marketable yield per hectare (t ha ⁻¹)	9	2.07
12	Unmarketable yield per hectare (t ha ⁻¹)	0	0
13	Weight of tubers per plant (g plant ⁻¹)	0	0
14	No. of tubers per plant	49	11.26
15	Harvest index (%)	0	0
16	Tuber dry matter content (%)	89	20.46
17	Tuber moisture content (%)	0	0
18	TSS (⁰ Brix)	2	0.46
19	Chips colour score	1	0.23
20	Yield of chips (%)	87	20

The higher inter cluster distance between the cluster VI and cluster VII was recorded by Mahalanobis's method of clustering. Therefore, genotypes from these cluster viz., P-41 (cluster VI) and C-18 (cluster VII), are suggested to include in hybridization activities for getting advantageous and superior combinations.

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