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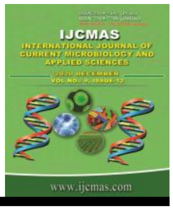

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Variability and Diversity Analysis in Genotypes of Potato (*Solanum tuberosum* L.) for Yield and Yield Attributing Traits

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A B S T R A C T

The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the characters studied except foliage senescence percent recorded highly significance, which is indicating that the genotypes were widely variable. The phenotypic variance was in general higher than the genotypic variance for all the characters. High heritability coupled with high genetic advance was recorded for the traits *viz.* number of leaf plant^{-1}, marketable tuber yield, tuber rottage, total tuber yield. Hence, these characters were predominantly governed by additive gene action and can be improved through simple selection. Genotypes were grouped into five distinct clusters depending upon the similarities of their D2 values. The maximum numbers of five genotypes were included in cluster-IV and maximum genetic divergence 4.008 was noted between cluster II and III. The highest cluster mean values recorded for premium characters *viz.* Number of leaf plant^{-1} in cluster-I, plant height in cluster-II, Seed weight plat^{-1}, in cluster III, % emergence in cluster IV, foliage senescence in Cluster I, marketable tuber yield in cluster-V, minimum tuber rottage in cluster II, tuber dry matter in cluster IV, Haulm dry matter in cluster IV and Total tuber yield in cluster V. Hence, genotypes having maximum distances should be selected from different clusters and can be utilized in hybridization programme for producing more desirable segregants for seed yield.

Keywords

Variability, Diversity, Potato (*Solanum tuberosum*), Yield, Attributing traits

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Introduction

Potato (*Solanum tuberosum* L.) is one of the most important staple food crops among the vegetables; which is utilized throughout the year in India. Potato (*Solanum tuberosum* L.) belonging to Solanaceae family and having Chromosome no. 2n = 48 is the most important food crop of the world. Potatoes are rich in carbohydrates (60-80% is starch). The protein content is 1-1.5 % in freshly harvested with a very negligible fat content (0.09%) and it is also rich in several micronutrients, especially vitamin C, foliate, pantothenic acid and riboflavin and minerals such as potassium, phosphorus and magnesium. In India, the major potato growing states are Himachal Pradesh, Punjab, Uttar Pradesh, Madhya Pradesh, Gujarat, Maharashtra, Karnataka, West Bengal, Bihar and Assam. In India, the area and production of potato is 2179 million and 5260000 ton. In

Chhattisgarh potato is cultivated in 45435 ha area, production around 682342 metric ton ha^{-1} in average productivity of potato 15.02 ton ha^{-1}, respectively (Anonymous, 2018). In the past the cultivation area for the potato has increased but there is lack of suitable cultivars for this State, therefore it is an urgent need to evolve the potato genotypes suitable for Chhattisgarh Plains. Genetic variability and genetic diversity it is very helpful for effective selection in crop improvement of Potato.

Materials and Methods

The experiment material of eighteen potato genotypes were conducted at Research Cum Instructional, Department of Horticulture, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) grown in a the randomized complete block design with four replication of plot size 4.8 m^{2}(3.0 x 2.4) with recommended dose of fertilizer 150:100:0100 NPK, 60 cm x 20 cm spacing during *Rabi* 2018-19. All the recommended package of practices were adopted for the raising a good crop. The crop was harvested at maturity and observations were recorded on five randomly selected competitive plants in each genotypes in each replication and the means were calculated. Data were subjected to analysis of variance (ANOVA) as per (Panse and Sukhatme 1968). The genetic parameters like GCV and PCV were estimated according to (Burton, 1952), heritability as suggested and genetic advances as percentage of mean as given by (Johnson, *et al.*, 1955). The genetic divergence was estimated by Mahalanobis' 1928, D^{2} statistics as described by (Rao 1952).

Results and Discussion

Based on overall findings of mean performance for various yield and its components for potato (table 2.) the genotypes *viz.* K. Khyati and K Pukhraj possessed the highest no. of leaf plant^{-1}; K. Lavkar and K. Mohan possessed highest plant height; MS/6-2196 and K Khyati had used maximum seed weight plot^{-1}; MS/08-1565 and K. Lavkar possessed highest percent emergence; PS/06-88 and PS/5-75 possessed the foliage senescence percent; MS/6-1947 and K. Lalit for maximum marketable tuber yield plant^{-1}; PS/5-75 and K. Lavkar observed lowest tuber rottage; PS/8-31 and K. Pukjraj recorded highest tuber dry matter percent; MS/08-1565 and MS/6-2196 recorded highest haulm dry weight percent; MS /6-1947 and K. Lalit recorded maximum tuber yield kg plaot^{-1}. Similar findings were also reported by Sharma 1999 and Barik *et al.*, (2009).

The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the characters studied except foliage senescence percent recorded highly significance, which is indicating that the genotypes were widely variable (table 1). In the present study, the phenotypic variance was in general higher than the genotypic variance for all the characters (table 2). Among different yield attributing characters studied, tuber rottage, seed weight plat^{-1}, marketable tuber yield and total tuber yield had the highest magnitude of PCV (83.55 33.85, 26.68 and 25.49 per cent) and GCV (97.48, 35.36, 26.96 and 25.86 per cent). The estimates of heritability revealed that, characters namely for Number of leaf plant^{-1}, Plant Height seed weight, marketable tuber yield, tuber rottage, total tuber yield were recorded with high heritability. The highest genetic advance as percentage of mean was recorded for number of leaf plant^{-1}, seed weight, marketable tuber yield, tuber rottage, total tuber yield. High heritability coupled with high genetic advance was recorded for the traits *viz.* number of leaf plant^{-1}, marketable tuber yield, tuber rottage, total tuber yield.

Table.1 Analysis of variance for yield and its attributes in potato genotypes

Sources	d.f.	No. of leaf plant^{-1}	Plant height (Cm)	Seed Wt./ plot (kg)	% Emergence	Foliage Senescence (%)	Marketable tuber yield(kg/plot)	Tuber rottage (kg/plot)	Tuber dry matter (%)	Haulm dry wt. (%)	Total tuber yield (kg/plot)
Replication	3	2.18	7.9	3.50	4.52	31.79	2.73	9.88	0.46	0.41	3.38
Treatment	17	95.57**	91.12**	7.68**	7.01**	22.57	138.96**	0.679**	5.96**	4.01**	141.88**
Error	51	4.9	2.73	0.171	1.92	14.29	7.37	5.93	1.45	0.56	1.04

Table.2 Mean performance of different potato genotypes

Genotypes	No. of leaf plant^{-1}	Plant height (Cm)	Seed Wt./plot (kg)	% Emergence	Foliage Senescence (%)	Marketable tuber yield(kg/plot)	Tuber rottage (kg/plot)	Tuber dry matter (%)	Haulm dry wt. (%)	Total tuber yield (kg/plot)
PS/06-88	36.82	52.50	3.75	89.95	25.25	25.30	0.22	18.35	11.56	26.48
PS/5-75	42.07	54.50	3.75	88.60	24.50	12.28	0.16	19.47	11.47	13.65
MP/6-39	45.42	52.90	3.88	89.20	23.75	14.61	0.22	17.72	11.57	15.76
MS/8-1148	43.38	49.47	4.62	88.88	24.00	26.39	0.82	18.61	11.81	28.08
MS/6-1947	38.53	43.18	5.67	90.91	21.75	34.28	0.92	18.89	12.72	36.20
PS/8-31	42.53	48.00	2.43	93.25	22.00	22.71	0.29	20.75	12.39	23.76
PS/9-9	38.88	47.37	2.45	88.57	18.57	22.92	0.17	20.31	11.51	24.90
PS/7-7	48.50	49.65	2.45	88.97	21.50	26.42	0.28	19.00	13.14	27.18
MS/08-1565	41.50	50.90	2.60	91.34	21.75	27.12	0.32	19.37	14.35	28.25
MS/6-2196	42.90	54.78	6.11	90.28	21.25	18.16	0.85	18.24	13.96	19.43
MCIP/9-11	37.85	42.62	5.80	88.68	16.25	13.98	0.85	18.89	11.52	15.23
K Khyati	50.50	54.97	5.85	90.79	20.75	24.38	0.32	18.67	10.85	15.63
K Mohan	37.62	55.25	5.70	89.54	19.50	20.99	0.35	20.57	11.49	21.73
K Garima	37.62	55.18	5.07	90.93	18.25	16.43	1.75	19.72	12.12	18.52
K Lalit	35.08	53.82	3.95	88.00	23.25	28.24	0.29	17.75	10.77	29.28
K pukhraj	49.78	43.68	2.95	89.79	22.50	15.72	0.79	17.12	11.66	16.69
K. Lavkar	35.88	60.10	2.43	91.19	22.00	20.62	0.16	16.50	12.81	21.05
K lalima	35.68	52.45	2.42	89.02	24.25	26.08	0.38	20.75	13.04	27.32

Table.3 Genetic parameters of variation for tuber yield, its components characters in genotypes of potato

Characters	**Mean ($\bar{X}$)**	**Range**		**GCV (%)**	**PCV (%)**	**Heritability ‘h^2(bs)’ (%)**	**Genetic advance (GA)**	**Genetic advance as percentage of mean (%)**
		Min.	Max.					
No. of leaf plant^{-1}	41.14	35.08	50.50	11.57	12.78	81.90	8.87	21.56
Plant height (Cm)	51.18	42.62	60.10	9.18	9.74	89.00	9.13	17.84
Seed Wt./plot (kg)	4.04	2.42	6.11	33.85	35.36	91.60	2.70	66.83
% Emergence	89.80	88.57	91.34	1.26	1.99	39.80	1.47	1.64
Foliage Senescence (%)	21.73	16.25	25.25	6.62	18.61	12.70	1.05	4.83
Marketable tuber yield(kg/plot)	22.03	12.28	34.28	26.68	26.96	97.90	11.98	54.38
Tuber rottage (kg/plot)	0.78	0.08	1.72	83.55	97.48	73.50	0.71	91.03
Tuber dry matter (%)	18.92	16.50	20.77	5.61	8.49	43.70	1.45	7.66
Haulm dry wt. (%)	12.15	10.77	13.96	7.63	9.82	60.40	1.48	12.18
Total tuber yield (kg/plot)	23.28	13.65	36.20	25.49	25.86	97.10	12.05	51.76

Table.4 Estimate average intra and inter cluster distance for eight clusters in potato genotypes

Clusters	**I**	**II**	**III**	**IV**	**V**	**No. of genotypes**	**Genotypes**
I	1.689					3	PS/5-75, MP/6-39 and K. Pukhraj
II	3.463	1.918				3	PS/06-88, K Lalit and K. Lavkar
III	3.467	4.008	2.286			4	MS/6-2196, MCIP/9-11, K Mohan and K Garima
IV	3.750	3.083	3.711	2.146		5	PS/8-31, PS/9-9, PS/7-7, MS/08-1565 and K lalima
V	3.856	3.193	3.382	2.957	2.219	3	MS/8-1148, MS/6-1947 and K Khyati

Table.5 Cluster mean for tuber yield, its attributes characters in potato genotypes

Characters	I	II	III	IV	V
No. of leaf plant^{-1}	45.76	35.92	39.00	41.42	44.13
Plant height (cm)	50.36	55.47	51.96	49.67	49.21
Seed Wt./plot (kg)	3.86	3.38	5.67	2.47	5.38
% Emergence	89.20	89.71	89.86	90.23	90.19
Foliage Senescence (%)	23.58	23.50	18.81	21.65	22.17
Marketable tuber yield(kg/plot)	14.20	24.72	17.39	25.05	28.35
Tuber rottage (kg/plot)	0.39	0.22	0.95	0.29	0.68
Tuber dry matter (%)	18.10	17.53	19.36	20.04	18.72
Haulm dry wt. (%)	11.57	11.72	12.27	12.89	11.79
Total tuber yield (kg/plot)	15.37	25.60	18.73	26.26	29.97

Hence, these characters were predominantly governed by additive gene action and can be improved through simple selection. These results are also supported by the findings of Desai 1997, Sharma 1999, Luthra *et al* 2005, Barik, 2010, Tripura *et al* 2016, Rangare and Rangare 2017, Patel *et al.,* 2018 for genetic variability, heritability and genetic advance.

In genetic diversity analysis the breeding programmes depends on the genetic diversity present among genotypes for its accomplishment. Clustering and divergence analysis are prerequisite to know the expansion of diversity among genotypes. It is measured in the form of phenotypic and genotypic diversity out of which genetic divergence is of enormous importance for choosing the parents for further use in hybridization programme for obtaining desirable genetic combination. Genetic divergence gives an idea about more genetically divergence genotypes and help in their identification and selection. Genetically diverse parents can be further used in any crop improvement programme for obtaining desirable segregants. Degree of genotypic diversity was measured with the help of Mahalanobis $D^2$and also reveals pattern of clustering due to difference in geography. The genotypes used for analysis of divergence set forth within different clusters exhibited sufficient inter cluster and intra cluster distance. Genetic distance plays a significant role in efficient selection of parents for future breeding programmes. Hence, genotypes belonging distant clusters may helpful to develop potent genotypes with broad genetic base through various breeding programmes. The traits with maximum percentage contribution towards divergence should be given priority while selection will operated. Based on the D^2 analysis, all the forty four genotypes were grouped into five clusters. The maximum numbers of five genotypes were included in cluster-IV and maximum genetic divergence 4.008 was noted between cluster II and III. The highest cluster mean values recorded for premium characters *viz.* Number of leaf plant^{-1} in cluster-I, plant height in cluster-II, Seed weight plat^{-1}, in cluster III, % emergence in cluster IV, foliage senescence in Cluster I, marketable tuber yield in cluster-V, minimum tuber rottage in cluster II, tuber dry matter in cluster IV, Haulm dry matter in cluster IV and Total tuber yield in cluster V.

In inter and intra cluster distances mean values of inter and intra cluster D^2 are shown in table 4. Five clusters were formed based on D^2 values where, intra cluster distance varied from 0.00 to 4.08 Distance between clusters had higher value than distance within cluster.

Cluster III showed highest intra cluster value (2.286), followed by cluster V (2.219), IV (2.146), II (1.918) and I (1.689). Distance between cluster II and cluster III was found highest other than these clusters, cluster I and cluster V (3.856), cluster I and cluster IV (3.750), cluster III and cluster IV (3.711), cluster II and cluster I (3.463), cluster I and cluster III (3.467), cluster III and cluster V (3.382), cluster II and cluster V (3.193), cluster II and IV (3.083) showed diverse inter clusters distances in a consecutive decreasing manner. This analysis indicated high variability present in these clusters.

Cluster Mean

We have showed value for cluster mean for the different clusters obtained in the table 5. Broad ranges of variations were obtained for all the characters under this study. In case of No of leaf plant^{-1} cluster I and cluster IV showed maximum value of 45.76 and 44.13 respectively and cluster II showed minimum 35.92. The characters plant height Cluster II and III showed maximum 55.47 and 51.96 and minimum 49.67 cluster mean value was observed for cluster IV. Seed weight plot^{-1} had maximum in cluster III, 5.67 and minimum in cluster II, 3.38 respectively. Percent emergence exhibited maximum in cluster IV, 90.23 and minimum in cluster I, 89.20, while foliage senescence percent showed maximum in cluster I, 23.58 and minimum in cluster III, 18.81. Marketable tuber yield showed maximum in cluster V, 28.35 and minimum in cluster I, 14.20. The mean value for tuber rottage were recorded maximum in cluster III, 0.95 and minimum in cluster II, 0.22.Tuber dry matter percent showed maximum in cluster IV, 20.04 g and minimum in cluster II, 17.53. Haulm dry weight showed maximum in cluster IV, 12.89, whereas minimum in cluster I, 11.57. For total tuber yield cluster V showed maximum 29.97 kg plot^{-1} and cluster III showed minimum 15.37 kg plot^{-1}. Clustering pattern and D^{2} values of genotype indicate presence of genetic diversity but we found some of the similarity among different clusters which we have observed. Hence, genotypes having maximum distances should be selected from different clusters and can be utilized in hybridization programme for producing more desirable segregants for seed yield.

The similar finding were reported in diversity among potato genotypes has also been suggested by Desai and Jaimini 1997, Joseph *et al.*, 2005, Luthra *et al* 2005, Barik *et al.*, 2010, Satter *et al* 2011, Rangare and Rangare 2017 and Patel 2018 in potato.

In conclusions the analysis of variance observed highly significance for all the characters studied except foliage senescence percent, which is indicating that the genotypes were widely variable. High heritability coupled with high genetic advance was recorded for the traits *viz.* number of leaf plant^{-1}, marketable tuber yield, tuber rottage, total tuber yield. Hence, these characters were predominantly governed by additive gene action and can be improved through simple selection. Genotypes were grouped into five distinct clusters depending upon the similarities of their D2 values. The maximum numbers of five genotypes were included in cluster-IV and maximum genetic divergence 4.008 was noted between cluster II and III. Hence, genotypes having maximum distances should be selected from different clusters and can be utilized in future hybridization programme.

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