Plant Archives Vol. 25, No. 2, 2025 pp. 551-554 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.075

GENETIC DIVERSITY ANALYSIS AT MORPHOLOGICAL LEVEL IN GENOTYPES OF POTATO (*SOLANUM TUBEROSUM* L.)

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(Date of Receiving-16-06-2025; Date of Acceptance-22-08-2025)

ABSTRACT

A breeding experiment using 35 diverse genotypes of Potato was conducted in Randomised Block design with three replications at Horticulture Research Centre of SVP University of Agriculture & Technology, Meerut, during *Rabi* season 2023-24. The findings showed that the differences among the genotypes were highly significant for several traits, *viz.* days to germination, number of leaves at 30 and 60 days, respectively, plant height after 65 days, number of branches per plant, number of stem per plant, length of leaf cm, leaves defoliation in days, days to tuber harvesting, number of tubers per plant, length of inter node, tuber size, single tuber weight and tuber yield plant. On the bases of Mahalanobis D^2 statistics 35 genotypes of Potato were grouped into five clusters. The cluster II comprised maximum 13 genotypes and minimum 3 genotypes comprised in Cluster IV. The range of intra-cluster distance was from 2.643 to 3.192. The maximum intra-cluster distance was recorded in cluster IV (3.192) and minimum intra cluster distance was found in cluster I(2.643).The maximum inter-cluster distance was observed in cluster I and IV and the minimum inter-cluster distance was found in cluster II and V.

Key words : Potato, Genetic divergence, Cluster analysis, D^2 statistics.

Introduction

Potato (*Solanum tuberosum* L.) (2n=4x=48) is one of the most significant food and industrial crops and Peru is the origin's centre of South America. It belongs to Solanaceae family (Tolessa, 2018). Modified stem is called a tuber. Potato rank fourth among all food crops and are eaten as staples in over 40countries worldwide (Solomon and Barker, 2001). In India the potato major crop and cultivation in Uttar Pradesh at the large scale follow by West Bengal, Bihar, Gujarat Madhya Pradesh, Punjab Assam, Chhattisgarh, Jharkhand and Haryana.Kharif crop in several states like Maharashtra, Uttarakhand, Karnataka, Himachal Pradesh and Tamil Nadu. All India production of Potato in 2023-24 is estimated to be 53.60 million tons (N.H.B 2023-2024). The problem of food security is getting worse every day. These problems can hardly be addressed by the stagnating yield of conventional grains and pulses. According to Singh and Rana (2013), potatoes' wholesome character, low calorific values, higher biological values, greater food output per unit of space and time, wider regional adaptation, and higher reactions to inputs can all help to address the pressing problem of food security. Potato is a good source of energy and excellent source of minerals, vitamins of the human diet and carbohydrates. 20.6%, 1.87% protein, 0.3%fat, 1.1% crude fibre and 0.9% a share all present in them.

The breeder needs to select the suitable parental genotypes on the basis of genetic divergence for the hybridization therefore, Mahalanobis D^2 statistic technique based onquantitative Traits is a powerful tool as it measures the degree of divergence among the genotypes in various groups. It also points the suitable genotype for their utilization in hybridization Programme (Rao, 1952).

Materials and Methods

The present investigation was conducted on 35 genotypes of potato in Randomized Block Design with three replicationsat Horticulture Research Centre, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.) during the *Rabi* season of 2023-24. Observation was recorded like days to germination, number of leaves at 30 and 60 days respectively, plant height after 65 days, number of branches per plant, number of stem per plant, length of leaf cm, leaves defoliation in days, days to tuber harvesting, number of tubers per plant, length of inter node, tuber size, single tuber weight, and tuber yield plant. Divergence was analysison the bases of Mahalanobis D^2 statistics

Results and Discussion

The result revealed that significant the highest mean value was observed in Cluster IV (21.78), followed closely by Cluster II (21.67), Cluster V (20.37), Cluster III (20.33) and the lowest in Cluster I (19.93). In case of number of leaves at 30 days on Cluster IV showed the highest mean (26.04), followed by Cluster V (24.82), Cluster III (24.31), Cluster I (23.84) and the lowest in Cluster II (22.91). The result revealed that number of leaves at 60 days on Cluster IV recorded the maximum mean (590.49), followed by Cluster V (521.48), Cluster III (447.45), Cluster II (425.64) and Cluster I (412.39). In case of plant height at 65 days on, Cluster I had the highest mean value (43.55), followed closely by Cluster IV (42.95), Cluster II (33.15), Cluster III (31.71) and the lowest in Cluster V (29.73). In case of number of branches per plant Cluster III exhibited the highest mean (12.50), followed by Cluster IV (10.93), Cluster V (10.62), Cluster II (10.59) and the lowest in Cluster I (9.84). The result revealed that number of stems per plant was highest in Cluster IV (5.89), followed by Cluster V (5.29), Cluster I (4.96), Cluster III (4.91), and the lowest in Cluster II (4.62). In case of leaf length, Cluster III had the greatest value (8.89), followed by Cluster IV (8.56), Cluster I (8.51), Cluster V (8.36) and the lowest in Cluster II (7.51). In terms of days to leaf defoliation Cluster II recorded the highest mean (81.88), followed by Cluster V (79.21), Cluster IV (76.53), Cluster III (60.48), and the lowest in Cluster I (60.24). The result revealed that days to tuber harvesting, the maximum value was in Cluster II (94.72), followed by Cluster V (92.52), Cluster IV (91.69), Cluster I (75.41), and the lowest in Cluster III (74.84). Regarding number of tubers per plant Cluster IV recorded the highest mean (8.82), followed by Cluster III (7.71), Cluster II (7.57), Cluster I (7.03) and the lowest in Cluster V (6.53). The highest length of inter node was noted in Cluster I

Table 1 : Means of Intra-cluster groups for 14 characters in potato (*Solanum tuberosum* L.).

Clusters		DG	NL 30 at days	NL 60 at days	PH 65 at days	NBPP	NSPP	LL	DLD	DTH	NTPP	LIN	TS	STW	TYPP
I	Mean	19.93	23.84	412.39	43.55	9.84	4.96	8.51	60.24	75.41	7.03	4.04	4.54	72.54	390.22
	SE±	1.29	0.78	49.30	6.29	1.17	0.56	0.90	4.93	8.28	1.13	0.82	0.27	14.77	71.89
II	Mean	21.67	22.91	425.64	33.15	10.59	4.62	7.51	81.88	94.72	7.57	2.84	4.35	76.79	500.10
	SE±	0.70	1.21	61.31	7.69	1.67	0.94	1.01	7.73	6.92	0.81	0.66	0.46	11.75	59.00
III	Mean	20.33	24.31	447.45	31.71	12.50	4.91	8.89	60.48	74.84	7.71	2.38	4.66	80.21	656.59
	SE±	1.03	1.27	83.87	5.47	1.18	0.45	1.09	3.57	4.93	0.64	0.60	0.49	19.43	134.68
IV	Mean	21.78	26.04	590.49	42.95	10.93	5.89	8.56	76.53	91.69	8.82	2.56	3.65	82.82	537.84
	SE±	1.25	0.86	33.58	20.55	0.47	1.25	1.45	8.10	6.66	0.73	0.14	0.11	25.08	85.07
V	Mean	20.37	24.82	521.48	29.73	10.62	5.29	8.36	79.21	92.52	6.53	3.36	4.89	83.04	507.68
	SE±	0.89	0.75	85.39	5.19	1.63	0.25	0.98	5.38	5.62	1.08	0.83	0.35	16.98	81.11

DG = Days to germination, NL= No of Leaves, PH= Plant height (cm), NBPP= No of Branches per plant, NSPP= No. of Stem per plant, LL= Length of leaf(cm), DLD= Days to Leaves defoliation, DTH = Days to Tuber harvesting, NTPP= No of tubers per plant, LIN= Length of inter node, TS= Tuber size (cm), STW= Single tuber weight (gm), TYPP = Tuber yield per plant (gm).

Table 2 : Average intra and inter-cluster D^2 values for five clusters in *Potato* (*Solanum tuberosum* L.).

Clusters	I	II	III	IV	V
I	**2.643**				
II	3.862	**2.929**			
III	3.808	3.817	**2.888**		
IV	5.149	4.175	4.516	**3.192**	
V	3.575	2.927	3.521	4.189	**2.696**

Table 3 : Clustering pattern of 35 genotypes of potato (*Solanum tuberosum* L.) based on Mahalanobis' D^2 statistics.

Cluster	Numbers	Genotypes
I	6	K. Pushkar, K. Pukhraj, K. Lalit, K. Thar 1, K. Ashoka, and K. frysona
II	13	K. Chipsona 3, K. Sinduri,K. Anand, sK. Lohit, K. Lima, K. Thar 3, K. R- 507, K. Chipsona 4, K. Mohan, K. Kiran, K. Lalima, K. Dakash and K. Chipsona 1
III	7	K. khyati, K. Lavkar,K. Surya,K. Arun,K. Garima, K. Bohar and K. Jyoti
IV	3	K. Neelkanth, K. Badshah and K. Gaurav
V	6	K. Ganga, K.Sadabahar,K. Chandramukhi,K. Sangam, K. Thar 2 and K. Uday

(4.04), followed by Cluster V (3.36), Cluster II (2.84), Cluster IV (2.56), and the lowest in Cluster III (2.38). For tuber size Cluster V exhibited the highest mean (4.89), followed by Cluster III (4.66), Cluster I (4.54), Cluster II (4.35), and the lowest in Cluster IV (3.65). The result revealed that in single tuber weight the highest mean was observed in Cluster V (83.04) followed by Cluster IV (82.82), Cluster III (80.21), Cluster II (76.79), and the lowest in Cluster I (72.54). Finally, for tuber yield per plant Cluster III showed the highest performance (656.59), followed by Cluster IV (537.84), Cluster V (507.68), Cluster II (500.10) and the lowest in Cluster I (390.22). These results suggest that Cluster III and Cluster IV harbor the most promising genotypes for yield and yield-contributing traits, indicating their potential use in future breeding programs.

Intra and inter-cluster distance

The average intra- and inter-cluster distances (D^2 values) among five potato clusters are presented in Table 4.9. The range of intra-cluster distance was from 2.643 to 3.192. The intra-cluster distance was lowest in Cluster I (2.643), followed by Cluster V (2.696), Cluster II (2.929), Cluster III (2.888) and Cluster IV, which had the highest intra-cluster distance (3.192). The inter-cluster distances revealed that the most divergent clusters were Cluster I and Cluster IV, with the maximum distance of (5.149), followed by the distance between Cluster IV and Cluster III (4.516), Cluster IV and Cluster V (4.189), and Cluster IV and Cluster II (4.175). The smallest inter-cluster distance was observed between Cluster II and Cluster V (2.927). Previous reports of similar findings were also made by Prabha *et al*. (2019).

Cluster pattern

Based on Mahalanobis D^2 statistics, the 35 potato (*Solanum tuberosum* L.) genotypes were classified into five distinct clusters, as shown in Table 2. This clustering highlights the presence of considerable genetic diversity among the genotypes. Cluster II emerged as the largest group, containing 13 genotypes - K. Chipsona 3, K. Sinduri, K. Anand, K. Lohit, K. Lima, K. Thar 3, K. R-507, K. Chipsona 4, K. Mohan, K. Kiran, K. Lalima, K. Dakash and K. Chipsona 1. Cluster III followed with 7 genotypes, including 'K. Khyati, K. Lavkar, K. Surya, K. Arun, K. Garima, K. Bohar and K. Jyoti. and Clusters I and V were each composed of 6 genotypes. Cluster I comprised K. Pushkar, K. Pukhraj, K. Lalit, K. Thar 1, K. Ashoka and 'K. Frysona, while Cluster V consisted of K. Ganga, K. Sadabahar, K. Chandramukhi, K. Sangam, K. Thar 2 and K. Uday. Cluster IV was the smallest, consisting of only 3 genotypes-K. Neelkanth, K. Badshah and K. Gaurav.The point of view has been supported by Seid *et al*. (2021).

Conclusion

The characters that contribute most to the D^2 values are given greater importance when determining clusters, as they play a key role in guiding future breeding improvement programs.

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