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Genetic diversity analysis among *Solanum tuberosum* genotypes of potato under Indo-Gangetic plain

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Abstract

A Research, titled "Genetic diversity analysis among *tuberosum* genotypes of potato under Indo-Gangetic plain" was conducted at the Potato Research Farm, TCA Dholi, Bihar, during the Rabi season of 2023-2024. Understanding the nature and extent of genetic divergence helps plant breeders in selecting and hybridizing suitable parents to develop superior genotypes with improved quality traits. The primary objective was to assess the genetic diversity and identify genotypes with superior traits for various breeding programs. The material consisted of 26 *tuberosum* genotypes used in a RBD with 3 replications. Tocher's method of clustering grouped the 26 *tuberosum* genotypes into seven distinct clusters. Cluster I contained the more number of genotypes (13), followed by Cluster III with 5 genotypes, while Cluster II had three genotypes. Clusters V, VI, and VII were mono-genotypic. Clusters I and V has the lowest inter-cluster distance (196.41) whereas between cluster IV and VII highest inter cluster distance 1180.82 was governed. Maximum contribution to total genetic diversity was recorded for the number of tubers per plant. Cluster III of the *tuberosum* genotypes showed the highest mean values for important traits such as tuber yield, number of compound leaves per plant, and plant height. CP1215, CP1157 and CP1596 genotypes can be used for the early maturing variety breeding programs. Genotypes such as CP2298, CP3674, and CP4404 from Cluster III were identified as potential donor parents for hybridization programs aimed at improving potato yield under Indo-Gangetic plain conditions.

Keywords: Cluster analysis, genetic diversity, *Solanum tuberosum*, selection and tuber yield

Introduction

Potato (*Solanum tuberosum* L.) is the fourth most important food crop globally, after wheat, rice, and maize [1]. It serves not only as a staple vegetable but also as a key raw material for various processed food products. In addition, potatoes are utilized in industries for the production of starch and alcoholic beverages. Developing varieties with desirable agronomic traits and good keeping quality remains a major challenge for potato breeders. Potato is a highly heterozygous crop, and greater heterozygosity contributes to increased hybrid vigor [2]. Crosses made between genetically diverse parents tend to produce progenies with higher heterotic expression [3]. In any plant breeding program, maintaining a pool of diverse and desirable donor parents is essential for enhancing productivity [4]. Genetic diversity in crop plants is essential to sustain the level of high productivity [5]. The most effective approach to enhance crop productivity is through genetic improvement [6]. The success of any plant breeding relies on the degree of existing genetic diversity within the species, as greater variability offers wider opportunities for effective selection and improvement [7]. Genetic diversity serves as an important tool for assessing genetic variability in both cross-pollinated and self-pollinated crops [8]. Therefore, the present study was undertaken to assess the genetic divergence and clustering pattern among potato genotypes for identifying suitable parents to be used in hybridization programs and to evaluate genetic parameters contributing to yield. Accordingly, 26 potato genotypes were analyzed to determine the nature and magnitude of genetic diversity using D^2 statistics.

Materials and Methods

The research was carried out in a Randomized Block Design (RBD) with three replications. Treated tubers were planted on ridges spaced 60 cm × 20 cm apart on 10th November 2023

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at the farm of TCA, Dholi, Bihar. The experimental material comprised 26 potato genotypes. The 26 potato genotypes includes CP-2298, CP-1424, CP-2148, CP-2132, CP-7701, CP-1157, CP-4242, CP-2150, CP-3674, CP-1596, CP-1544, CP-1215, CP-4404, CP-1162, CP-7783 CP-3433, CP-7183, CP-3168, CP-3593, CP-1214, CP-1735, CP-3426, CP-1329, CP-2354, Kufri jyoti and Kufri girdhari. Data for each trait were recorded from randomly selected 5 plants per plot and expressed on a per-plant basis. The mean values of these five plants were used for statistical analysis. The recorded traits comprised plant height, percentage of plant emergence, number of shoots and compound leaves per plant, tuber count per plant, days to maturity, harvest index, tuber dry matter content, specific gravity (g/cm^3), reducing and non-reducing sugar contents (mg/100g), and tuber yield per plant (kg). The genetic diversity or degree of divergence among the cultivars was computed using D^2 statistics had been suggested by [9].

Results and Discussion

Significant differences among genotypes for all traits indicated substantial genetic diversity within the germplasm. Twelve characters were evaluated, and significance tests confirmed variation among genotypes. Using Wilks' (1932) criterion, multivariate significance was assessed for correlated traits (10). D² analysis was conducted by transforming correlated variables into standardized, uncorrelated ones. The D² value between two genotypes (i and j) was computed as the sum of squared differences of their mean values across traits and tested against tabulated χ^2 values. Genotypes were grouped using Tocher's method (11-12). Intra and inter-cluster distances were calculated from average D² values, with inter-cluster distances obtained by averaging all possible pairwise distances between clusters. Cluster diagrams illustrated genetic relationships, and genetic distances were derived as the square root of mean D² values. Based on D² analysis, 26 genotypes were grouped into seven distinct clusters using Tocher's method. The cluster I had the highest number of genotypes (thirteen), which were CP1424, CP2150, CP7701, CP7183, CP1162, CP7783, CP1735, CP3433, CP4242, CP3168, CP1544, CP3426 and CP2354. After that in cluster III had five entries *viz*; CP2298, CP3674, CP4404, Kufri Jyoti and Kufri Girdhari. whereas cluster II contain three genotypes such as CP1215, CP1157 and CP1596 and the cluster IV contains two genotypes such as CP2132, CP1214.The cluster V (CP3593), cluster VI (CP1329) and cluster VII (CP2148), were observed monogenotypic, containing only one genotype each.

The average D² values for the clusters are presented in Table 4.9. According to the table, the lowest inter-cluster distance (196.41) was observed between clusters I and V, while the highest inter-cluster distance (1180.82) was recorded between clusters IV and VII. Maximum inter-cluster distance, measured at 1180.82 between cluster IV and cluster VII, followed by cluster IV and cluster VI at 1093.53, cluster II and cluster VI at 1036.46. Minimum inter-cluster distance measured at 196.41 between clusters I and V. Similar kind of results were also obtained by (13-14). Eight cluster‘s average intra-cluster distance values were displayed in Table Due to the mono-genotypic nature of clusters V, VI and VII the intra cluster distance value in those clusters was 0. The highest intra-cluster D 2 value was found in cluster III (146.31), followed by cluster II (138.54). Each attribute was graded based on its percentage contribution to overall genetic diversity between two entries (di = yit - yjt) in all genotypic combinations.

Regarding the cluster means of the traits, the trait plant height (PH) exhibited its maximum value in cluster III (47.77) and its minimum in cluster II (27.64). The values for plant emergence ranged from 95.5 (cluster VII) to 82.21 (cluster V). The number of shoots per plant showed its highest value in cluster V (6.27) and lowest in cluster IV (4.24). For the number of compound leaves (NCL), the maximum value was observed in cluster III (46.35) and the minimum in cluster V (26.55). The trait number of tubers per plant (NTP) ranged from 7.39 in cluster IV to 3.12 in cluster V. Days to maturity (DTM) had its highest value in cluster V (116.98) and lowest in cluster II (92.81). The harvest index (HI) exhibited a maximum value of 78.65 in cluster VII and a minimum of 64.38 in cluster V. For dry matter (DM), values ranged from 23.96 (cluster VII) to 17.42 (cluster V). Specific gravity (SG) showed the highest value in clusters II and III (1.13), while the lowest value was observed in clusters VI and VII (1.07). The trait reducing sugars (RS) had its maximum value in cluster V (307.05) and minimum in cluster VI (176.48). The number of reducing sugars (NRS) ranged from 428.79 in cluster VI to 241.40 in cluster V. Lastly, tuber weight per plant (TWPP) exhibited its highest value in cluster III (0.23) and its lowest in cluster II (0.13).

Contribution towards genetic diversity

The trait contributing most to genetic diversity was the number of tubers per plant, with a contribution of 35%, followed by the number of compound leaves, contributing 30.5%, number of shoots per plant 7.4%, reducing sugar 5%, plant height 4.8%, non reducing sugar 4.4%, harvest index 3.1%, days to maturity 2.8%, specific gravity 1.2%, plant emergence at 30 days after planting 0.95% and dry matter 0.90%.

Table 1: Pattern of clustering in tuberosum genotypes

Cluster no.	No. of Genotypes	Genotypes
I	13	CP1424 , CP2150 , CP7701 , CP7183 , CP1162 , CP7783 , CP1735 , CP3433 , CP4242 , CP3168 , CP1544, CP3426, CP2354
II	3	CP1215, CP1157,CP1596
III	5	CP2298, CP3674, CP4404, Kufri Jyoti , Kufri Girdhari
IV	2	CP2132,CP1214
V	1	CP3593
VI	1	CP1329
VII	1	CP 2148

Table 2: Average inter and intra-cluster distances among seven clusters of tuberosum

Cluster Number	cluster I	cluster II	cluster III	cluster IV	cluster V	cluster VI	Cluster VII
I	108.82	324.62	256.83	575.38	196.41	375.57	282.01
II		138.54	680.48	766.51	240.42	1036.46	196.49
III			146.3108	381.98	475.55	458.04	724.05
IV				117.09	834.47	1093.53	1180.82
V					0	716.88	223.21
VI						0	737.8
VII							0

Table 3: Cluster means for twelve yield contributing traits in tuberosum potato genotypes

Trait/cluster	PH	GP.	NSP	NCL	NTP	DTM	HI.	DM	SG	RS	NRS	TWPP
cluster I	37.11	92.98	5.25	33.67	4.21	105.78	70.38	18.4	1.08	191.64	329.77	0.15
cluster II	27.64	90.55	4.42	27.54	4.38	92.81	65.83	20.63	1.1	223.23	381.72	0.13
cluster III	47.77	94.66	5.22	46.35	7.35	98.69	73.02	21.81	1.13	216.12	266.86	0.23
cluster IV	30.64	84.99	4.24	36.91	7.39	101.85	69.85	18.15	1.13	225.16	337.35	0.15
cluster V	40.75	82.21	6.27	26.55	3.12	116.98	64.38	17.42	1.09	307.05	241.4	0.13
cluster VI	33.72	94.99	5.54	44.41	3.89	94.18	74.12	18.24	1.07	176.48	428.79	0.15
Cluster VII	35.63	95.55	5.4	34.35	4.56	93.52	78.65	23.96	1.07	186.22	424.6	0.16

Conclusion

Considerable variation was observed among cluster means for the studied traits. Cluster IV recorded the highest mean values for the number of tubers per plant and specific gravity of tubers. Cluster VII exhibited the highest means for plant emergence, harvest index, and dry matter content. Cluster III showed superior performance for tuber weight per plant, specific gravity, number of compound leaves, and plant height. Therefore, genotypes such as CP2298, CP3674, and CP4404 from Cluster III can be utilized as donor parents in hybridization programs aimed at improving potato yield under Indo-Gangetic Plain conditions. CP1215, CP1157 and CP1596 genotypes can be used for the early maturing variety breeding programs since these cluster genotypes showed very less days to maturity. Additionally, genotypes CP7701, CP2150, CP3433, and CP3148, characterized by high dry matter and low reducing sugar content, can be suitable for developing processing-quality breeding programs.

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