THE EXTENT OF GENETIC DIVERSITY IN DIFFERENT GENOTYPES OF POTATO

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ABSTRACT : The maximum genetic divergence for quality characters (3145.78) was observed between cluster-I and III. The highest cluster mean values for growth characters viz. shoot girth, plant height and yield (q/ha) were observed in cluster-II. While for quality characters cluster-I showed maximum cluster mean for protein content, nitrogen content, phosphorus content and specific gravity. Cluster VII showed maximum cluster mean value for specific gravity. The characters viz. plant height, leaf area, tuber weight, number of stolen per hill and number of tuber per hill contributed maximum towards diversity in descending order. There is no parallelism between geographical and genetic divergence. Thus, based on the findings of present investigation it can be concluded that good diversity and variability was present in the genotypes tested.

The cultivated potato is highly heterozygous and out breeding species which suffers from inbreeding depression. An increase in its heterozygosity results in hybrid vigour (Cubillos and Plaisted,1; Tarn and Tai, 7). Heterosis in potato perpetuates because of its vegetatively propagated nature. Therefore, selection of suitable parents to cross is crucial. Parents to be used in crossing programmes are selected as per breeding objectives. The germplasm collection constitutes a reservoir of genes and gene complex and is the raw materials for improvements of crop plants. Diverse genetic materials are, therefore, required to meet the ever-changing demands of plant improvement. Genetic divergence is assessed on the basis of field performance of genotypes. Information on genetic diversity in available germplasm collection is therefore, of paramount importance. To introduce new valuable genes from wild or primitive *Solanum spp.* and to exploit genetic variation efficiency in existing cultivars, a parental line breeding programme with suitable modifications is required (Dallaert and Vinke, 2). Therefore, considering the above facts the present study was undertaken to study the genetic diversity in different genotypes of potato.

MATERIALS AND METHODS

The experimental material for the present investigation comprised of 30 potato genotypes (Table 1) forming the part of germplasm collection from different university and research centres. The experiment was carried out in experiment field of CSSS (PG) College, Machhra, Meerut. All the thirty genotypes were grown in Randomized Block Design with three replications. All the agronomic package of practices to raise good crop were followed. All the observations were recorded on individual plant basis and averaged. Five plants per plot were selected randomly for each genotype to record various observations.

Statistical Analysis

The statistical analysis of the data was carried out on computer using the software of OPSTAT. Individual as well as pooled analysis of the data recorded and field trials for various traits was done.

D^2 Analysis

The genetic divergences in thirty genotypes were estimated by Mahalonobis "D^2" statistics (generalized distance as suggested by Rao (5) and by steps followed by Murthy and Arunachalam (4) for D^2 calculation

Group constellation

Treating D^2 as the square of generalized distance, all genotypes were grouped into a number of clusters, according to the methods described by Tocher (Rao, 5). The criterion used in clustering by this method is that two genotypes belonging to same cluster should at least on the average show a smaller D^2 value than those belonging to two different clusters. In other words, if genotypes V_1 and V_2 are close together and genotype V_3 is distant from both as shown by their generalized distances, then V_1 and V_2 form one cluster. The average D^2 values of all possible combinations of genotypes in one cluster were computed and its square roots were used to represent the statistical distance between two clusters.

Table 1: List of potato (*Solanum tuberosum* L.) genotypes screened for genetic diversity.

Sl. No.	Genotype	Sl.No.	Genotype	Sl. No.	Genotype
1.	J/95-144	11.	J/95-242	21.	Kufri Chipsona-2
2.	J/95-378	12.	J/93-139	22.	Kufri Jawahar
3.	J/92-159	13.	J/95-80	23.	Kufri Jyoti
4.	J/96-84	14.	J/95-228	24.	Kufri Pukhraj
5.	J/96-149	15.	JW-160	25.	Kufri Sutlej
6.	J/96-171	16.	PS/96-14	26.	Kufri Pushkar
7.	J/96-238	17.	Kufri Anand	27.	MS/99-1871
8.	J/95-221	18.	Kufri Ashoka	28.	J/95-226
9.	J/95-227	19.	Kufri Bahar	29.	J/95-158
10.	J/95-229	20.	Kufri Chipsona-1	30.	J/96-80

Table 2 : Clustering pattern of thirty genotypes of potato (growth parameters) on the basis of genetic divergence.

S.No.	Cluster	No. of Genotypes	Genotypes
1	I	29	J/95-144, J/95-378, Kufri Pukhraj, Kufri Chipsona -2, J/96-171, J/96-84,Kufri Bahar, J/96-149, J/96-171, J/96-238, Kufri Jyoti, J/95-221, J/95-227, J/92-159,J/95-242, J/95-80,J/93-139, J/95-228,Kufri Sutlej, JW-160, Kufri Chipsona-1, J/95-226, Kufri Anand, Kufri Jawahar,J/95-158,MS/99-1871, Kufri Anand, Kufri Ashoka, PS/96-14

Table 3 : Clustering pattern of thirty genotypes of potato (quality parameters) on the basis of genetic divergence.

S.No.	Cluster	No. of Genotypes	Genotypes
1	I	3	J/95-144, JW-160, Kufri Jawahar
2	II	9	J/96-238, Kufri Jyoti, J/95-221, J/95-227, Kufri Anand, Kufri Sutlej, J/92-159, PS/96-14,J/96-171
3	III	4	J/96-84, J/96-149, J/93-139,J/95-229
4	IV	6	J/95-228, J/95-242, Kufri Ashoka, Kufri Bahar, Kufri Pukhraj, J/95-80
5	V	5	J/95-378, J/96-80,J/95-158, J/95-226, Kufri Pushkar
6	VI	2	Kufri Chipsona -1, MS/99-1871
7	VII	1	Kufri Chipsona -2

Contribution of different characters towards divergence

The relative contribution of different characters to the total D^2 between each pair of genotypes was given a score of 1 to 20 (total number of characters) based on the magnitude of the D^2 value due to each character. A rank of 1 represented the highest contribution, while 20 the lowest percentage of contribution of character 'X' towards divergence.

Per cent contribution of character 'X'

$$= \frac{N(x)}{N\,(n-1)/2}$$

Where,

N (x) = Number of genotypic combinations, which were ranked first for character 'X' out of total genotypic combinations of N(n-1)/2; i.e.300 (for n=25).

RESULTS AND DISCUSSION

Analysis of genetic diversity

The analysis of variance revealed significant difference between all thirty genotypes for all the characters. Based on D^2 values, the constellation of genotypes into clusters was done following Tocher's method (Rao, 5).

Clustering pattern

The clustering pattern of all genotypes has been presented in Table 2 and 3.

Thirty genotypes were grouped into two clusters on the basis of growth characters (Table 2). Highest number of genotypes (29) was assembled in cluster-I

Table 4: Average intra and inter cluster D^2 values (in first row) and distance $(\sqrt{D})^2$ (in second of each cluster row) among thirty genotypes of potato for growth.

Cluster	I	II
I	1652.32	1713.02
		41.39
II		0.00

and one genotype in cluster–II. But on the basis of quality characters (Table 3) all thirty genotypes were grouped into seven clusters. The cluster–II had nine genotypes followed by cluster–IV (6), V (5), III (4), I (3), VI (2) and VII (1).

Intra and inter cluster divergence

The intra and inter cluster divergence (average D^2 values) of all clusters are presented in the Table 4 and 5. Intra-cluster average D^2 values ranged from 0.00 to 1652.32 for growth characters (Table 4). But on the basis of quality characters (Table 5), intra-cluster average D^2 values varied from 0.00 to 83.99. Cluster–III with three genotypes showed maximum intra-cluster average D^2 values, while cluster–VI and VII having single genotypes exhibited minimum intra-cluster D^2 values. The inter-cluster average D^2 values for growth characters was maximum 1713.02 between cluster–I and II, and for quality character maximum values was 3145.78 between cluster-I and III. The minimum inter-cluster average D^2 value (132.10) for quality character was obtained between cluster-II and III, followed by cluster-V and VI (146.03).

Table 5: Average intra and inter cluster D^2 values (in first row) and distance ($\sqrt{D^2}$) (in second of each cluster row) among thirty genotypes of potato for quality.

Cluster	I	II	III	IV	V	VI	VII
I	83.31	513.05	3145.78	393.03	1476.00	1439.04	153.52
		24.78	56.09	19.82	38.42	37.93	12.39
II		59.35	132.10	1137.44	244.80	377.55	2291.29
			11.49	33.73	15.65	19.43	47.87
III			83.99	1483.29	416.12	681.18	2797.42
				38.51	20.40	26.10	52.89
IV				71.97	437.59	472.05	344.36
					20.92	21.73	18.56
V					70.69	146.03	1220.51
						12.08	34.94
VI						0.00	994.55
							31.54
VII							0.00

Table 6: Cluster mean value of eleven characters (growth) in potato.

Traits → Cluster ↓	Days to 50 % emergence	No. of haulms /hill	No. of leaves /haulm	Leaf area (cm²)	Total chlorophyll (mg/100g)	No. of stolons /hill	Shoot girth (cm)	Plant height (cm)	No. of tubers /hill	Yield (q/ha)	Tuber weight (g)
I	13.33	5.22	12.80	108.45	0.81	0.75	1.55	3.21	0.62	6.25	0.44
II	11.95	4.50	14.16	126.32	0.82	0.90	1.71	3.16	0.67	6.61	0.47

Table 7: Cluster mean value of eleven characters (quality) in potato.

Traits → Cluster ↓	Specific gravity (g/cm³)	Dry matter content (%)	Total soluble solids (°B)	Ascorbic acid (mg/100g)	Vitamin A (IU)	Tuber Protein (%)	Nitrogen in tuber (mg /100 g)	Phosphorus in tuber (mg /100 g)	Potassium in tuber (mg /100 g)
I	5.02	4.34	1.04	16.28	6.78	23.47	39.87	1.91	305.50
II	5.34	4.20	1.04	15.90	6.87	23.31	32.14	1.27	203.21
III	4.92	4.64	1.06	15.82	6.33	20.70	45.34	1.22	195.89
IV	5.74	4.29	1.05	15.96	6.55	23.13	37.85	1.66	268.72
V	5.75	4.30	1.05	17.81	6.49	21.42	38.95	1.44	230.50
VI	6.29	4.70	1.04	23.35	7.50	22.40	21.50	1.46	233.00
VII	5.56	5.10	1.07	23.47	7.29	22.92	25.37	1.37	295.00

Table 8: Contribution of growth and quality characters for creating diversity in potato genotype.

Growth Characters	Contribution	Quality Characters	Contribution
Days to 50% emergence	0.33	Specific gravity (cc/cm^3)	1.00
No. of haulms/hill	0.00	Dry matter content (%)	1.33
No. of leaves/haulm	0.00	Total soluble solids (^{0}B)	0.00
Leaf area/leaf (cm^2)	28.67	Ascorbic acid (mg/100g)	1.33
Total chlorophyll (mg/100g)	0.33	Vitamin A(I.U.)	3.67
No. of stolon/hill	1.67	Tuber protein content (%)	0.67
Shoot girth	0.00	Nitrogen content (mg/100g)	8.33
Plant height (cm)	38.67	Phosphorus content (mg/100g)	0.33
No.tubers/hill	1.67	Potassium content (mg/100g)	83.33
Yield (q/ha)	0.33		
Average tuber weight (g)	10.67		

Similar findings were also given by Kumar and Kang (3).

Cluster mean for characters

The cluster means for all the characters are given in Table 6 and 7. A close perusal of these cluster means for different characters indicated considerable difference between the clusters for all the characters.

Custer–I recorded the highest cluster mean values (Table 6) for days to 50% emergence (13.33), number of leaves per haulm (12.80) and plant height (3.21). Cluster–II exhibited the highest cluster mean value for number of leaves per haulm (14.16), leaf area (126.32), total chlorophyll (0.82), number of stolon (0.90), shoot girth (1.71), number of tuber per hill (0.67), yield (6.61) and tuber weight (0.47).

For quality characters as indicated in Table 7, cluster-VI recorded the highest values for specific gravity (6.29) and vitamin A (7.50); and cluster–VII for dry matter content (5.10), total soluble solids (1.07) and ascorbic acid content (23.47). Cluster–I had the highest mean value for tuber protein (23.47), phosphorus content (1.91) and potassium content (305.50) in tuber and cluster–III for nitrogen content in tuber (45.34). Sandhu and Kang (6) evaluated 286 *andigena* potato genotypes collected from Argentina, Bolivia, Chile, Colombia and Peru for genetic diversity at Shimla and found similar findings.

Contribution of different characters towards divergence

The relative contribution of twenty different growth and quality characters under the evaluation towards the expression of genetic divergence (Table 8) showed that the contribution of growth characters in creating genetic diversity which varied between 0.00 to 38.67 per cent. The characters viz. plant height (38.67%),

leaf area (28.67%), average tuber weight (10.67%), number of stolon per hill (1.67%) and number of tubers per hill (1.67%) contributed towards diversity in descending order. For quality characters (Table 8) contribution of characters in creating genetic diversity varied between 0.00 to 83.33 per cent. The characters viz. potassium content (83.33%), nitrogen content (8.33%) and vitamin A (3.67%) contributed effectively towards genetic divergence.

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