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Genetics and Plant Breeding

Assessment of Genetic Divergence in Potato (*Solanum Tuberosum L.*) Genotypes for Yield and Yield Attributing Traits

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Abstract

Genetic diversity using Mahalanobis D-square (D^2) techniques was studied for yield and yield contributing traits for 19 potato genotypes at West Bengal. These genotypes were grouped into seven clusters. Cluster VII had maximum divergence with four genotypes followed by cluster IV having maximum five genotypes. Rest five clusters are digenotypic having two genotypes each. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession. The maximum and minimum divergence was revealed between cluster VI with IV and cluster I with III respectively. Cluster VI exhibited high mean values for characters like total tuber yield, marketable tuber yield, dry matter%, harvest index, polar and equatorial diameter of tuber. These characters combining with plant height are the major traits causing genetic divergence among the accessions. The genotypes belonging to different clusters are having maximum divergence and can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters.

Highlights

- Divergence analysis among the potato genotypes

- Identification of divergent parents for production of transgressive segregants

- Assessment of intra and inter cluster distances

Keywords: Divergence, cluster, tuber, & D^2 analysis

Potato is a major food crop of the world after rice, wheat and maize. Around 320 million tonnes of potatoes are produced yearly and this amount is estimated to be doubled by 2020 (FAO, 2008). Potato grown in India is a major source of carbohydrate in human diet. This crop is one of the most important tuber crop grown in India for its high production, high nutritional values, easy digestibility and many other industrial uses. Potato of an average size with

skin provides about 10 percent of the recommended daily intake of fibre. A single medium sized boiled potato contains about half the daily required of vitamin-C by adult and a significant amount of iron, potassium and zinc. Substantial amounts of vitamin B and essential trace elements such as manganese, chromium, selenium and molybdenum are also available from potato. The high vitamin C content enhances iron absorption. Utilization of genetic variation in potato for future breeding is a main factor for increasing the success of breeding of desired traits. An understanding of the nature and magnitude of variability among the genetic stocks is of prime importance to the breeders. Genetic diversity is one of the important tools to qualify genetic variability in both cross- and self-pollinated crops (Murty and Arunachalam 1966, Gaur *et al.,* 1978). Such a study also permits to select the genetic divergent parent to obtain the desirable recombinant in the segregating generations. The major goal of any potato breeding programme is to develop potential varieties that ensure highest and stable production in a wide range of environment. Genetic diversity is essential to meet the diversified goals of crop improvement such as breeding for high yield, disease resistance, wider adaptation, improve nutritional aspect etc. Divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal MAA, 2003). In addition to that genetic diversity is studied to identify specific parents for wider genetic variation and heterosis when they are crossed. Information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin AKM, 1985). Therefore the present experiment was formulated to study the genetic divergence and clustering pattern of the potato genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield. Hence 19 potato genotypes were undertaken to study the nature and magnitude of diversity by D^2 statistics.

Materials and Methods

The field experiment of the present study was carried out during the *Rabi* season of 2010-2011 from 17th November 2010 to 11th March 2011 at the Block Seed Farm, Adisaptagram of Hooghly district in West Bengal, India. The experimental place was situated at 22.57^0 N latitude and 88.20^0 E longitudes with an elevation of 7.8 meters from mean sea level. The climate of this region is sub-tropical humid. And the entire year can be classified into three distinct seasons namely winter, summer and rainy

Season. Occasionally late monsoon rain in the month of October causes some hazards to the planting of potato. The maximum and minimum temperature during the experiment ranged from 24.38 - 34.42 and 9.51 - 25.05 respectively. During the investigation period the maximum mean monthly temperature was 35.92 in the month of March and the minimum mean monthly temperature was 12.54 in the month of December. The daily mean temperature remained congenial to sustain crop growth and tuberization up to the middle of February and thereafter the temperature began to shoot up. Very low rainfall occurred during the investigation period. The monthly maximum and minimum relative humidity (RH) varied from 89.27–95.01 % and 40.13 – 70.11 % during the investigation period. The experiment was conducted in RBD with 19 genotypes in 3 replications.

Sowing of seed/potato tuber was done during 17-18th November 2010. K. Jyoti (Check) and K.Pukhraj (Check) were taken from farmer's field as local check varieties for West Bengal condition because both seems to be promising in West Bengal and 17 genotypes were procured from Central Potato Research Institute (CPRI), Kufri, Shimla which included both K.Jyoti and K.Pukhraj designated as seed materials from Kufri. So K. Jyoti and K. Pukhraj included twice for evaluation, as a check and as a designated materials from CPRI. For obtaining good harvest NPK was applied with a dose of 200: 150: 150 kg/ha respectively. Intercultural operations and plant protection measures were taken from time to time and as and when required. Germination was recorded after 30 days of planting. Plant height was measured from ground level to top of the highest branch at the time of 50 days of crop growth. Five plants were selected from each plot and each replication for recording plant height. Marketable yield, non-marketable yield, harvest index, total tuber yield, number of leaves/plant, leaflet/leaf, interjected leaflet, leaf angle to main axis, equatorial diameter, polar diameter and dry matter content were recorded**.**

The genetic diversity was estimated using the Mahalanobis D^2 statistics (Mahalanobis, 1936). Tracing D^2 as a generalized distance, the criterion used by Tocher as described by Rao (1952) was applied for determining the clusteration group. Average intra and inter cluster distances were determined using Genres version 3.11, 1994 Pascal Intl. Software and suggested by Singh and Chaudhary (1977). The dendrogram was made by using software IBM SPSS Statistics version 22.

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Dendrogram was made by using Ward's average linkage method. In Ward's minimum variance method, the distance between two clusters is the ANOVA sum of squares between the two clusters added up over all the variables. At each generation, the within-cluster sum of squares is minimized over all partitions obtainable by merging two clusters from the previous generation. The sums of squares are easier to interpret when they are divided by the total sum of squares to give the proportions of variance (squared semi partial correlations). Ward's method joins clusters to maximize the likelihood at each level of the hierarchy under the assumptions of multivariate normal mixtures, spherical covariance matrices, and equal sampling probabilities. Ward's method tends to join clusters with a small number of observations and is strongly biased toward producing clusters with approximately the same number of observations (Milligan, 1980).

Results and Discussion

The analysis of variance showed significant differences among the genotypes in respect of all characters and indicated high genetic variability. The D^2 values for all 190 comparisons between pairs of genotypes are given in (Table 1). On the basis of divergence, 19 genotypes under investigation have been grouped into seven clusters (Table 2), indicating wide diversity in the experimental material for majority of the characters. Distance between all pairs of genotypes was calculated using squared Euclidean distance method and the genotypes were clustered based on Tocher's method.

Among the seven clusters, cluster IV had maximum number of genotypes (5), cluster VII had 4 genotypes and rest of the clusters were digenotypic. The pattern of clustering proved the existence of significant amount of variability. It is obvious that the genotypes have grouped into different clusters irrespective of their geographical origins. It means that the genetic constitution of the varieties was more important than their origin and distribution (Rai *et al*., 2009). The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand inter cluster divergence suggests the distance (divergence) between the genotypes of different clusters. Inter and intra cluster D^2 values were worked out from divergence analysis. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation. The composition of cluster and values of inter and intra cluster

distances are given in Table 3. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession.

The intra cluster distance ranged from 3.457 to 13.540 and the inter cluster distance ranged from 7.759 to 34.964, indicating that the selected genotypes were highly divergent (Table 3). Minimum intra cluster distance has been recorded in cluster I (3.457). It indicated that these accessions were closely related in their evolutionary process and passed through similar evolutionary factor. These genotypes within the cluster were less divergent. This might be due to unidirectional selection practised in past that has resulted in uniformity and less divergent between these genotypes. Cluster VII had the highest intra cluster distance (13.540) followed by cluster IV (12.765), Cluster VI (9.611) and cluster V (9.611). The maximum inter cluster distance was observed between cluster VI and IV (34.964) followed by cluster VII and VI (30.402), suggesting that the genotypes belonging to these cluster may be used as parents for hybridization programme to develop desirable type because crosses between genetically divergent parents will generate transgressive segregants (Fig. 1).

The cluster mean values were estimated over genotypes for thirteen characters in potato related to yield, which revealed a wide range of variation (Table 4). Maximum germination percentage was observed in genotypes of cluster I followed by cluster III and II. Highest mean value for plant height was observed in cluster I. Cluster III, IV, V and VI were almost similar with regards to mean plant height. There was no significant variation for plant height among all the aforesaid clusters. Highest no. of leaves/ plant was recorded from cluster V followed by cluster II and III. Mean interjected leaflet were maximum in cluster II followed by cluster VII. The leaf angle to main axis was taken prior to harvesting to evaluate the crop ideotype before and after tuber formation. To study the erect or spreading behaviour of the crop after tuber formation can be adjudged by calculating the leaf angle to main axis/ stem. All genotypes showed similar behaviour with respect to this character. No significant changes were recorded in crop geometry. Characters such as total tuber yield and marketable tuber yield played dominant and direct role in higher yield. In the present study higher mean values for total tuber yield and marketable tuber yield were recorded in cluster VI followed by cluster III. Highest mean value for non marketable tuber yield was recorded from cluster III, which was a negatively

Table 1: Value of D² for combinations of 19 genotypes in potato

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.000	439.889	233.960	515.272	185.901	233.113	995.918	268.826	661.530	530.005	1072.468	2193.149	592.174	1747.046	688.908	529.408	101.356	336.411	485.571
2		0.000	106.760	85.492	78.493	304.192	152.672	186.327	117.948	189.723	190.272	743.903	94.526	594.738	83.517	59.062	370.915	124.084	37.047
3			0.000	97.060	76.298	112.301	360.654	77.953	170.415	203.108	489.819	1161.573	151.978	902.197	200.553	129.815	132.105	61.141	82.606
4				0.000	145.363	224.418	140.437	191.692	51.826	143.824	280.549	703.949	11.949	520.077	72.735	102.959	339.754	40.777	78.378
5					0.000	181.479	350.418	113.641	211.325	183.968	405.192	1151.740	171.951	862.981	204.867	143.807	162.790	91.398	122.994
6						0.000	575.857	92.699	334.057	193.139	740.710	1480.873	255.334	1149.055	337.666	282.282	87.429	117.339	310.425
7							0.000	409.001	102.576	247.534	91.466	270.096	115.537	205.471	73.323	136.303	751.706	253.654	155.859
8								0.000	213.188	101.354	473.578	1143.649	227.889	832.434	202.441	115.454	101.606	94.883	164.851
9									0.000	141.799	205.992	542.276	59.944	366.084	54.468	90.879	430.960	95.594	92.201
10										0.000	263.933	748.390	127.505	481.617	78.628	116.950	291.012	98.439	212.992
11											0.000	267.777	231.212	214.703	97.639	163.880	885.396	394.012	244.169
12												0.000	623.139	92.373	453.184	635.620	1759.681	933.538	722.319
13													0.000	464.341	56.327	108.849	411.853	68.920	113.487
14														0.000	310.429	487.029	1305.946	642.651	577.804
15															0.000	58.902	470.051	121.661	96.527
16																0.000	373.554	126.780	56.092
17																	0.000	161.479	357.415
18																		0.000	115.975
19																			0.000

1. J/99-48; 2. J/99-242; 3. Kufri ashoka ; 4. Kufri khyati; 5. 2001 P-26; 6. MS/1-4353; 7. MS/1-4906; 8. Kufri pushkar; 9. Kufri bahar ;10. Chipsona-1; 11. Chipsona-2; 12. Chipsona-3; 13. MP/98-71; 14. Kufri surya; 15. Kufri jyoti; 16. Atlantic; 17. Kufri pukhraj ; 18. Local check (K.jyoti); 19. Kufri pukhraj (check) .

Table 2: Clustering of Potato genotypes using Tocher's method

Cluster	Genotypes	Number of genotypes
I	Kufri khyati, MP/98-71	2
II	J/99-242, Kufri pukhraj (check)	2
III	Kufri bahar, Kufri jyoti	2
IV	J/99-48, Kufri ashoka, 2001 P-26, MS/1-4353, Local check (K.jyoti)	5
V	MS/1-4906, Chipsona-2	2
VI	Chipsona-3, Kufri surya	2
VII	Kufri pushkar, Chipsona-1, Atlantic, Kufri pukhraj	4

Table 3: Average intra (diagonal) and inter-cluster distance

Cluster	I	II	III	IV	V	VI	VII
I	3.457	9.642	7.759	15.044	13.854	24.039	14.380
II		6.087	9.877	14.734	13.629	25.684	14.131
III			7.380	17.397	10.949	20.445	14.521
IV				12.765	23.746	34.964	13.627
V					9.564	15.476	20.406
VI						9.611	30.402
VII							13.540

*Figures given the diagonal are intra cluster distance

Table 4: Cluster wise mean values of thirteen characters in potato

| Names Of Characters	I	II	III	IV	V	VI	VII
Germination % at 30 DAP	**87.308**	78.218	81.315	74.475	*57.982*	65.550	73.534
Plant heights at 50 DAP (in cm.)	**63.950**	*40.953*	49.972	48.345	48.537	47.473	43.163
No of leaves/plant at 50 DAP	*13.250*	15.667	15.100	14.680	**15.700**	13.900	13.954
Leaflet/leaf	8.033	**8.067**	7.633	8.007	7.767	*7.433*	7.771
Interjected leaflet	12.450	**14.267**	12.167	13.403	13.167	*11.933*	13.667
Leaf angle to main axis (in ^{o})	*29.500*	**34.167**	30.667	31.667	32.833	32.500	34.083
Total tuber yield (in Kg.)	20.967	*14.783*	22.883	18.873	18.017	**24.533**	22.658
Marketable tuber yield (in Kg.)	20.133	*14.250*	21.267	17.607	16.733	**23.833**	21.258
Non marketable yield (in Kg.)	0.833	*0.533*	**2.017**	1.267	1.283	0.700	1.400
Dry matter %	18.508	18.760	19.577	*16.505*	20.725	**23.195**	17.827
Harvest index	*62.333*	62.833	72.833	64.267	68.000	**73.167**	65.167
Tuber equatorial diameter (in mm.)	46.337	45.163	40.117	48.637	*36.215*	**48.838**	40.768
Tuber Polar diameter (in mm.)	56.633	52.112	48.403	60.568	*46.637*	**64.117**	58.881

Maximum and minimum values of each character are printed in bold and italics, respectively
DAP= Days after Planting.

Table 5: Percent contribution of different characters towards diversity in potato genotype

Names Of Characters	No. of times ranked 1st	Percent contribution
Germination %	2	1.1696
Plant height at 50 DAP (in cm.)	6	3.5088
No of leaves/plant at 50 DAP	0	0.0000
Leaflet/leaf	0	0.0000
Interjected leaflet	1	0.5848
Leaf angle to main axis (in $^{\text{o}}$)	0	0.0000
Total tuber yield (in Kg.)	5	2.9240
Marketable tuber yield (in Kg.)	0	0.0000
Non marketable yield (in Kg.)	2	1.1696
Dry matter %	49	28.6550
Harvest index	2	1.1696
Tuber equatorial diameter (in mm.)	11	6.4327
Tuber Polar diameter (in mm.)	93	54.3860

DAP= Days after Planting
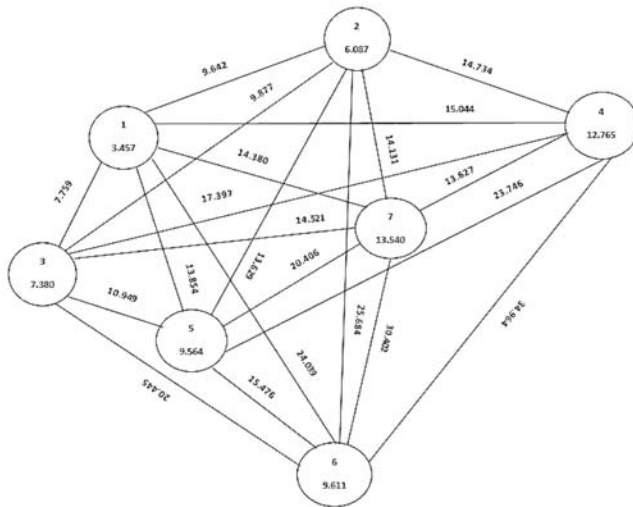
Fig. 1: Mabalanobis Euclidean distance cluster diagram (not to scale)

correlated character with yield. So the cluster having moderate to low mean non marketable yield were promising genotypes where yield is concerned. Cluster VI had highest mean value for dry matter %, harvest index, polar and equatorial diameter.

From the above study it can be concluded that the diversity in potato genotypes for yield and yield contributing characters may be due to the shape and size of potato tuber (both polar and equatorial diameter), dry matter percentage, plant height and total tuber yield. When the

above ground character like no. of leaves/plant, leaflet/leaf, interjected leaflet, plant height were more the yield was reduced and vice versa. A good quality potato tuber of oval shape will fetch good yield and optimum market potential with increasing dry matter percentage basically for the processing purpose genotypes which are best suited for chips and fry making industries.

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times, each of the yield component character appeared first in rank and its respective per cent of contribution towards genetic divergence was presented (Table 5).Among the yield contributing characters, the maximum contribution towards divergence was made by tuber polar diameter (54.38 %) followed by dry matter percentage (28. 65 %), equatorial diameter (6. 43 %), plant height (3.50%) and total tuber yield (2.92 %).

On the basis of yield performance, maximum inter cluster distance and some specialized characters, genotypes of cluster IV and VI are most diverse followed by genotypes of cluster VII and Cluster III (Fig. 2).
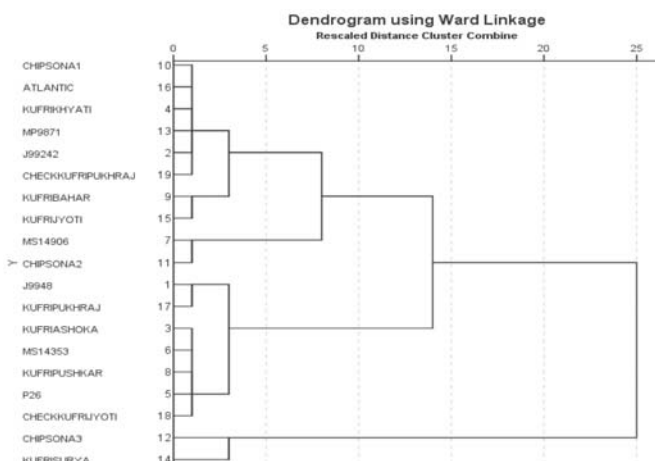
Fig. 2: Euclidean average linkage dendrogram

Conclusion

The genotypes belonging to different clusters having maximum divergence can be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production. To improve any particular trait donor for hybridization could be chosen from an appropriate cluster and that should be utilized in breeding Programme.

Acknowledgement

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