

GENETIC DIVERGENCE AND ITS RELATIONSHIP WITH HETEROSIS IN POTATO*

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ABSTRACT : The present study was conducted to assess the genetic divergence (Mahalanobis D²) in 29 potato genotypes (parental lines) based on 20 characters and to find out relationship between genetic diversity and heterosis for tuber yield. Results showed that the parental lines though morphologically diverse had narrow genetic base and could be grouped into four clusters. Observed morphological diversity was not related to geographical as well as taxonomic diversity. Genetic divergence (D values) had a positive relationship with heterosis for tuber yield in the 120 progenies derived from 24 x 5 (line x tester) matings of the parents. Selection of parents based on genetic divergence followed by progeny test is suggested for effective exploitation of heterosis in potato breeding programmes.

INTRODUCTION

The success of potato breeding programmes depends mainly on the identification of promising parental lines for making desired crosses and selection of superior genotypes from the progenies. Distantly related lines are assumed to be more complementary and produce superior heterotic progenies (6, 10, 12). Heterosis as a function of genetic divergence is known to have only a moderate effectiveness in predicting tuber yield of potato progenies and for this too parents need to be evaluated under conditions where progenies from these parents are to be subjected to selection (4). In the present investigation, genetic divergence among 29 potato genotypes (parents) and performance of 120 progenies generated from these parents were evaluated under similar conditions to identify diverse parents and verify relationship between genetic divergence and performance (progeny mean and heterosis) of progenies for tuber yield.

MATERIALS AND METHODS

Plant material: Twenty nine potato genotypes

with diverse background were drawn from the germplasm collection of Central Potato Research Institute, Shimla (**Table 1**). CP2366 (7XY.1) is a *neo-tuberosum* clone developed from short day adapted *andigena*. Advanced hybrids MS/86-84, MS/86-89 and MS/90-542 had *andigena* in their ancestry, and Kufri Swarna- a Cyst Nematode resistant variety had *Solanum vernei* in its pedigree. Remaining hybrids/varieties belong to *Solanum tuberosum* ssp. *tuberosum*.

Hybridization: The twenty nine genotypes were grown and crossed during the summer (May- August) of 1995-1997 at the Central Potato Research Station, Kufri, Shimla (32° N 77° E, 2500 m above sea level) in a 24 x 5 (females x males) mating design using CP2366, CP3197, JN2231, MS/90-512 and MS/91-1325 as males because of their high pollen fertility and broad genetic base.

Evaluation trials: Twenty genotypes of each of 120 progenies from the above mentioned parents (24 females x 5 males) produced in line x tester mating design (7) were evaluated at Central Potato Research Institute Campus,

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Table 1. Details of parental material used in the study

S.N.	Parents	Original name/number	Origin	Parentage
Females				
1	CP1085	Not known	Not known	An exotic number*
2	CP1588	Cosima	Germany	An exotic number*
3	CP1998	Michoacan	Mexico	An exotic number*
4	CP2332	AL-204	Ethiopia	An exotic number*
5	CP2334	AL-575	Ethiopia	An exotic number*
6	CP3111	Huaycha	Peru	An exotic number*
7	CP3204	MF-II	Peru	An exotic number*
8	JI1857	Advanced hybrid	India	Kufri Alankar x Kufri Jyoti
9	Kufri Ashoka	PJ-376	India	EM/C-1021 x CP1468
10	Kufri Bahar	E-3797	India	Kufri Red x Gineke
11	Kufri Jyoti	SLB/Z-389(b)	India	3069d (4) x 2814a (1)
12	Kufri Sutlej	JI-5857	India	Kufri Bahar x Kufri Alankar
13	Kufri Swarna	PCN/79-110	India	Kufri Jyoti x (VTn) ² 62.33.3
14	MS/79-10	Advanced hybrid	India	Kufri Jyoti x Dekama
15	MS/83-279	Advanced hybrid	India	Kufri Jawahar x JN2231
16	MS/86-84	Advanced hybrid	India	AB286 x MS/78-62
17	MS/86-89	Advanced hybrid	India	AB286 x MS/78-62
18	MS/89-60	Advanced hybrid	India	ON1645 x MS/78-79
19	MS/89-1095	Advanced hybrid	India	Kufri Jawahar x MS/78-62
20	MS/90-542	Advanced hybrid	India	AB286 x Kufri Jyoti
21	MS/92-2658	Advanced hybrid	India	MS/78-46 x Kufri Jyoti
22	MS/92-3128	Advanced hybrid	India	MS/82-638 x MS/80-758
23	MS/92-3178	Advanced hybrid	India	MS/82-638 x MS/80-758
24	SLB/U-125	Advanced hybrid	India	Not known
Males				
1	CP2366	7 XY.1	Peru	An exotic number*
2	CP3197	TS-4	Peru	An exotic number*
3	JN2231	Advanced hybrid	India	JF4928 x CP1463
4	MS/90-512	Advanced hybrid	India	MS/84-1169 x MS/78-79
5	MS/91-1325	Advanced hybrid	India	MA/83-27 x CP1673

*Parentage not known.

Modipuram, Meerut, U.P. (29°N and 76°E; 222 m above sea level) in second clonal generation (SCG) along with 29 parents during autumn 1999-2000. The parents were also evaluated during autumn 1997-1998. The experiments were conducted in completely randomised block design with 3 replications and plot size of 3.6m² with intra- and inter-row spacing of 20 and 60 cm, respectively. Normal manural and cultural schedules were followed. Haulm cutting was done 90 days after planting.

Data recording: Observations on 5 random plants of each parental line were recorded for 20 characters (Table 4) and on all progenies for tuber yield. Foliage characters were recorded 75 days after planting. All leaf

characters were recorded on fourth leaf from top. Tuber yield components were recorded at harvest on plot basis and averaged to per plant.

Statistical analysis: Data of parental lines were subjected to multivariate D² analysis (9) to quantify genetic divergence (11). Heterosis for tuber yield of progenies over mid-parental values was computed following Kempthorne (7). Simple correlation coefficients between genetic divergence *vs* progeny mean, genetic divergence *vs* heterosis and progeny mean *vs* heterosis for tuber yield were calculated following Searle (13). Software SPAR1 (Indian Agricultural Statistics Research Institute, New Delhi) was used for computing genetic divergence and heterosis.

RESULTS AND DISCUSSION

Genetic divergence: The analysis of variance revealed highly significant differences among the 29 potato genotypes for the 20 characters studied. The multivariate analysis by 'V'-statistic, which in turn utilizes Wilk's criterion was used as simultaneous test of differences between mean values of 20 correlated variables. Calculated 'V'-statistic (1349.01) was highly significant (Table Chi-Square value for $P < 0.001$ is 667.646 at 560 d.f.). Hence, further analysis was done to estimate the D^2 values corresponding to all possible 406 combinations involving paired comparisons among 29 genotypes.

The D^2 values ranged from as small as 14.02 between genotypes JI1857 and Kufri Sutlej to as large as 397.46 between Kufri Swarna and JN2231. Based on D^2 values, 29 genotypes were grouped into four clusters (Table 2). Intra- and inter-cluster distances are given in Table 3. As expected, intra-cluster distances were lower than the inter-cluster distances. The maximum inter-cluster distance (316.52) was observed between cluster II and IV. Cluster I was the largest containing 22 genotypes including 17 genotypes of Indian origin. Cluster II was comprised of 4 genotypes namely Kufri Swarna, CP2334, CP2366 and

Table 2. Distribution of 29 genotypes of potato in different clusters

Cluster number	Number of genotypes	Genotype (s)
I	22	CP1085, CP1998, CP2332, CP3197, CP3204, JI1857, Kufri Ashoka, Kufri Bahar, Kufri Jyoti, Kufri Sutlej, MS/79-10, MS/83-279, MS/86-84, MS/89-60, MS/89-1095, MS/90-512, MS/90-542, MS/91-1325, MS/92-2658, MS/92-3128, MS/92-3178 and SLB/U-125,
II	4	CP2334, CP2366, CP3111 and Kufri Swarna
III	2	MS/86-89 and CP1588
IV	1	JN2231

Table 3. Average intra- cluster (bold) and inter-cluster D^2 values in potato genotypes

Clusters	I	II	III	IV
I	78.76	124.00	144.18	191.86
II		90.45	168.21	316.52
III			116.04	183.90
IV				0.00

CP3111. Cluster III had only two genotypes MS/86-89 and CP1588 and cluster IV had only one advanced hybrid i.e. JN2231.

The grouping pattern showed that exotic and Indian genotypes (Table 2) were grouped together in various clusters as reported earlier (1, 3) confirming thereby that morphological diversity is not related to geographical diversity. Taxonomic divergence as judged from the genetic background of the various hybrids/varieties too seems to be not related to morphological diversity, as Kufri Swarna with *Solanum vernei* in its pedigree was grouped together with *neo-tuberosum* clone CP2366, and *tuberosum* genotypes CP2334 and CP3111 in cluster II. Similarly, hybrids MS/86-84 and MS/90-542 with *andigena* background [from one (AB286) of their parents] were grouped in cluster I along with those having only *tuberosum* background. Genotype JN2231, with both parents of *tuberosum* origin, and placed in cluster IV was morphologically more distant (D^2 : 191.86, Table 3) from cluster I, which had other *tuberosum* genotypes compared to cluster II (D^2 : 124.0) which had genotypes Kufri Swarna and CP2366 having *Solanum vernei* and *neo-tuberosum* backgrounds, respectively.

The material in the present study, in general, represents the advance breeding lines/varieties developed by crossing *tuberosum* to *tuberosum*, *andigena* or wild species at some stage of the potato breeding programme. However, after several cycles of crossing and selection, most of them have the features of *tuberosum* group. Due to this all hybrids/lines

could be grouped in just 4 clusters and intra- and inter-group morphological distances did not correspond to the differences in the pedigree of various genotypes as enumerated above. This also indicates that genetic differences among various hybrids/lines as revealed by morphological diversity, though significant, actually had very narrow genetic base. The narrow genetic base of the genotype though placed in different clusters is also reflected by the fact that two full sib hybrids MS/86-84 and MS/86-89 were placed into different clusters (cluster I and III, respectively). Simmonds (14), Gaur *et al.* (1) and Gopal (3) also pointed to the narrow genetic base of most of the cultivated potato varieties resulting from a very limited number of breeding clones which may be inter-related through common ancestors (5). The poor progress made in the improvement of *tuberosum* can, therefore, be largely attributed to a low level of diversity in the base population.

Relative importance of various characters to genetic divergence: For all the combinations (i.e. $n(n-1)/2 = 406$, in this case) each character was ranked on the basis of differences in the means of a pair of genotypes (i.e. d_i values). Rank 1 was given to the highest mean differences and rank p (p = number of characters, i.e. 20 in this case) to the lowest mean differences. Per cent contribution based on the number of times each character appeared first in ranking was calculated (Table 4). Maximum contributions to genetic divergence were of dormancy period followed by average tuber weight, plant type, tuber colour and number of tubers. Tuber yield, the main character of economic importance contributed only 2.22% to the total genetic divergence. The reason for low contribution by tuber yield to genetic diversity may be due to the fact, that genotypes had been subjected to selection for this character and out of 29 genotypes, 20 were improved potato hybrids or varieties released by CPRI, which possess

Table 4. Contribution of different characters to total divergence

Characters	Appeared first in ranking		Rank total
	Number of times	Per cent times	
Plant vigour (score1-very poor to 5-very high)	7	1.72	4843
Plant type (score: 1-erect to 3-prostrate)	57	14.04	3308
Plant height (in cm)	7	1.72	4089
Number of stems (per plant)	6	1.48	4397
Number of leaves (per plant)	1	0.25	5473
Leaf length (in cm)	2	0.49	4579
Leaf width (in cm)	16	3.94	4666
Leaf index (leaf length/leaf width)	0	0.00	5471
Tuber yield (g/plant)	9	2.22	4509
Number of tubers (per plant)	32	7.88	4120
Average tuber weight (g/plant)	60	14.78	3520
Number of eyes (per tuber)	12	2.95	4405
Tuber colour (score: 1-white to 5 purple)	46	11.33	3513
Tuber shape (score: 1-compressed to 5-long oblong)	8	1.97	4176
Tuber eye depth (score: 1-protruding to 5-very deep)	5	1.23	4095
Tuber colour uniformity (score1-very low to 5-very high)	25	6.16	3765
Tuber shape regularity (score1-very low to 5-very high)	9	2.22	4601
General impression (score1-very low to 5-very high)	1	0.25	5006
Tuber dry matter (%)	17	4.19	3845
Dormancy period (weeks)	86	21.18	2878

good yield potential in the North Indian Plains. This confirms earlier reports (1, 3) that characters not subjected to selection contribute more to genetic divergence.

Relationships between genetic divergence, progeny mean and heterosis: Progeny means and heterosis estimates of tuber yield of 120 crosses in second clonal generation were correlated with D values of the parental combinations of the crosses (Table 5). Tuber yield, the most sought after trait by any potato breeder was thought to be the most appropriate character for this purpose because it is dependent on many component characters and is the juridicator of economic productivity of a genotype.

i) *Genetic divergence vs progeny mean for tuber yield:* The results showed that genetic divergence did not have any significant ($r = 0.02$) relationship with progeny mean in SCG (Table 5). Loisele *et al.* (8) also found no relationship between genetic divergence based on agronomic data and progeny means for tuber yield and other vigour related traits. Lower correlation coefficients between genetic divergence and progeny mean in the present study as compared to those reported by Gopal and Minocha (4) may be due to narrow genetic base of the parents used in this study.

ii) *Genetic divergence vs heterosis for tuber yield:* Correlations between D values of parental combination and real value of heterosis (+ ve and - ve) were positively significant in SCG (Table 5). For tuber yield, potato breeder looks

for positive heterosis only. Therefore, relationship between genetic divergence and heterosis (real) for tuber yield as found in the present study ($r=0.35^{**}$) would be of practical importance. The results indicated that genetic distances could be used as a parameter of moderate effectiveness to predict heterosis for tuber yield. These findings were further supported by the fact that distantly grouped genotypes had resulted in heterotic crosses. In all, 18 crosses out of 120 evaluated were found to have significantly positive heterosis for tuber yield. Thirteen of these 18 heterotic bi-parental crosses involved parents from different clusters. These findings thus support the assumption (6, 10, 12) that selecting parents based on their genetic divergence can generate heterotic crosses. Though, D values had poor association with progeny mean in the present study, most of the heterotic crosses were high yielding.

(iii) *Progeny mean vs heterosis for tuber yield:* Correlation coefficient ($r=0.55^{**}$) between progeny mean and heterosis was also highly significant though of moderate magnitude (Table 5). Thus, inter-mating of parents based on genetic divergence is expected to produce heterotic progenies having reasonably high yield. As correlation coefficient ($r=0.35^{**}$) between D values and heterosis (real value) was of low magnitude, it would be desirable to go for progeny test of the population generated by crossing diverse parents from different clusters in desired combinations. Bigger populations of the selected progenies then can be raised to identify the superior clones within progeny (2).

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Table 5. Correlation coefficients between genetic divergence vs progeny mean, genetic divergence vs heterosis and progeny mean vs heterosis for tuber yield in 29 parents and 120 progenies

Genetic divergence vs progeny mean	Genetic divergence vs heterosis	Progeny mean vs heterosis
0.02	0.35**	0.55**

** Significant at $P < 0.01$.

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