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Analysis of genetic divergence in potato

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Abstract

The experimental material comprised of 86 F₁C₂ clonal progenies of potato with four check varieties were grown in randomized block design with three replications. The present investigation was conducted under AICRP on potato, Department of Genetics and Plant Breeding at Horticultural Research Farm, College of Agriculture, I.G.K.V., Raipur (C.G). The multivariate analysis by using Mahalanobis's D² statistics was carried out to assess the genetic diversity in the study material revealed the clustering of clonal genotypes into separate clusters. Based on the relative magnitude of D² values, the 86 F₁C₂ clonal progenies were grouped into seven clusters. No relationship was found between genetic divergence and geographic distribution. The highest intra cluster distance were recorded for cluster VI and inter cluster distance in between cluster I and VI. Based on the mean performance the genotypes viz., CIP 30340-8-3-2 of cluster I; CIP 304146-12-4 and CIP 398203-8-2 of cluster II; CIP 303139-9-4 and CIP 304102-11-1 of cluster III; CIP 302024-3-3 of cluster IV; CIP 398068-4-2 of cluster V; CIP 398068-7-3 and Kufri Ashoka of cluster VI; Kufri Surya and CIP 398203-2-2 of cluster VII possessing superiority for the characters. Highest per cent contribution of characters viz, tuber weight plant⁻¹, number of shoots plant⁻¹, number of branches plant⁻¹, plant height, marketable tuber yield plant⁻¹ and number of tubers plant⁻¹ towards total divergence in potato. Hence, while formulating breeding programme, these traits be given priority to exploit the diversity in population.

Keywords: Potato, divergence, clonal progenies

Introduction

Potato is a major food crop of the world after rice, wheat and maize. Potato grown in India is a major source of carbohydrate in human diet. In addition, potato is one of the few major food crops that give high yields of edible energy and good quality protein per unit area and per unit time with a short vegetative cycle that can fit in to intensive cropping systems (Gebremedhin *et al.*, 2008b) [5]. 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.

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) [15, 16]. 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) [17]. 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) [18]. 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.

Material and methods

Eighty six clonal progenies (39 F₁C₁) obtained from genetic stock of AICRP on potato, Department of Genetics and Plant Breeding, COA, IGKV, Raipur (C.G.) were evaluated using Completely Randomized Block Design with three replications at Horticulture Research Farm of college of Agriculture, Indira Gandhi Krishi vishwavidyalaya, Raipur, (C.G.). Each progeny was accommodated in two rows of 1 m length. The row to row spacing of 60 cm and plant to plant spacing of 20 cm was adopted. The recommended packages of practices were followed for twelve traits were recorded on five randomly selected plants of each progeny and yield

contributing traits like Plant emergence (%), Plant height (cm), Number of leaves plant⁻¹, Number of branches plant⁻¹, Number of shoots plant⁻¹, Dry matter content of shoots (%), Dry matter content of tubers (%), Number of tubers plant⁻¹, Tuber weight plant⁻¹ (kg), Marketable tuber yield plant⁻¹ (kg), Unmarketable tuber yield plant⁻¹ (kg) and Number of eyes tuber⁻¹. The multivariate analysis (D² statistic) was carried out following to Mahalanobis (1936). Grouping of genotypes into different clusters was carried out following Tocher's procedure (Rao, 1952) [11] and the relative contribution of different characters towards total divergence was calculated as per Singh and Choudhary (1985) [14].

Results and Discussions

The analysis of variance showed significant differences among the genotypes in respect of all characters and indicated high genetic variability. Based on the D² analysis, all the eighty six F₁C₂ clonal progenies were grouped into seven clusters (Table 1.). The clustering pattern of genotypes in the divergence studies revealed that out of 86 maximum of 20 progenies were accommodated in cluster I, followed by 15 in cluster V, 13 in cluster III, 12 in cluster II, 11 in cluster VI, 8

progenies in cluster IV and lowest 7 progenies in cluster VII. The clustering pattern of genotypes showed that genotypes from the same geographical area did not necessarily belong to the same cluster. These group constellations indicated that geographical diversity was not related to genetic diversity, which may be attributed to distribution of different gene constellations into a geographical region (Bergale *et al.*, 2001) [20]. It means that the genetic constitution of the varieties was more important than their origin and distribution (Rai *et al.*, 2009) [19].

The estimates of intra and inter cluster revealed that the highest intra cluster distance was observed for the cluster VI (3.170) followed by cluster VII (3.001), cluster III (2.808), cluster II (2.427), cluster V (2.400), cluster I (2.243) and cluster IV (1.808) (Table 2).

The data on intra cluster distance, suggesting that genotypes in cluster VI were relatively more diverse. The minimum intra-cluster distance exhibited by cluster IV indicated limited genetic diversity among the constituents genotypes. These findings are in agreement with the findings of Singh (2008) [13], Chandrakar (2007) [3] and Desai and Jaimini (1997b) [4] and Joseph *et al.* (2005) [6].

Table 1: Clustering pattern in F₁C₂ clonal progenies of potato

Cluster	No of genotypes included	Genotypes
I	20	CIP 304012-1-4, CIP 304012-7-3, CIP 304012-12-4, CIP 303405-4-2, CIP 303405-5-3, CIP 303408-6-3, CIP 303408-8-2, CIP 303408-8-3, CIP 303408-3-2, CIP 304146-11-2, CIP 304014-8-4, CIP 398181-7-4, CIP 304124-2-5, CIP 304124-7-2, CIP 304124-8-3, CIP 304124-1-4, CIP 304124-4-3
II	12	CIP 398203-5-3, CIP 398203-8-2, CIP 302024-2-3, CIP 302024-3-4, CIP 302024-6-2, CIP 302431-3-2, CIP 302431-4-1, CIP 303405-8-3, CIP 303405-6-2, CIP 304146-12-4, CIP 304146-11-3, CIP 304146-1-4
III	13	CIP 302024-5-1, CIP 302434-2-1, CIP 302431-5-3, CIP 302431-6-4, CIP 304012-9-2, CIP 304102-11-1, CIP 304102-4-2, CIP 304102-4-5, CIP 398181-9-3, CIP 398181-17-2, CIP 398181-14-5, CIP 398181-10-1, CIP 303139-9-4
IV	8	CIP 398203-6-1, CIP 398203-7-4, CIP 302024-3-3, CIP 304012-6-1, CIP 304012-6-2, CIP 304014-5-4, CIP 303139-8-3, CIP 303139-10-3
V	15	CIP 304102-9-3, CIP 304102-7-1, CIP 304146-2-2, CIP 398201-7-2, CIP 398201-5-3, CIP 304014-2-6, CIP 304014-1-3, CIP 304014-12-2, CIP 304014-9-2, CIP 398181-16-5, CIP 303139-4-4, CIP 303139-2-2, CIP 398068-15-3, CIP 398068-3-2, CIP 398068-4-2
VI	11	CIP 302031-2-3, CIP 303405-9-1, CIP 398201-3-3, CIP 398201-15-4, CIP 398201-11-6, CIP 398201-2-2, CIP 398068-9-4, CIP 398068-7-3, KufriJawahar, KufriAshoka, KufriPukhraj
VII	7	CIP 398203-2-2, CIP 398203-4-1, CIP 303405-3-1, CIP 303405-7-4, CIP 303139-9-2, CIP 398068-1-5, Kufri Surya

Table 2: Inter and intra cluster distances in F₁C₂ clonal progenies of potato

Cluster	I	II	III	IV	V	VI	VII
I	2.243	2.514	2.579	2.690	3.245	5.330	4.993
II		2.427	2.939	2.460	3.021	4.056	4.527
III			2.808	2.857	2.652	4.510	4.147
IV				1.808	2.857	4.729	4.794
V					2.400	2.868	3.574
VI						3.170	3.900
VII							3.001

Diagonal bold values indicate intra cluster distances

The highest inter-cluster distance was observed between cluster I and VI (5.330) followed by cluster I and VII (4.993), cluster IV and VII (4.794), cluster IV and VI (4.729), cluster II and VII (4.527), cluster III and VI (4.510), cluster III and VII (4.147) and cluster II and cluster VI (4.056). The minimum inter cluster distance was observed between cluster II and IV (2.460). Inter-cluster distance is the main criterion for selection of genotypes on the basis of D² analysis. Genetic diversity is the most important tool to select prospective parents for improvement programmes. The genotypes belonging to the cluster separated by high estimated distance

could be utilized in hybridization programmes for obtaining wide variation among the segregants.

Mean performance of individual cluster for different yield attributing traits are presented in the Table 3. Results revealed that, cluster mean for plant emergence per cent in cluster VI exhibited the highest mean value (87.27%) whereas, cluster I was found to exhibit the lowest value (75.83%). The highest mean value for plant height was observed in cluster VII (49.42 cm) and the lowest mean value in cluster I (32.58 cm). For number of leaves plant⁻¹, the highest mean value was observed in cluster VII (35.68), whereas, cluster I exhibits the lowest mean value (25.38). Similarly, the number of branches plant⁻¹ was highest in cluster VII (16.01) and lowest in cluster II (8.56). Similarly, number of shoots is concerned, genotypes of cluster VII was found highest (6.65) than genotypes of other clusters and the lowest in cluster III (3.26). Per cent dry matter content of shoots observed highest in cluster VI (15.82%) and lowest in cluster IV (12.72%). Similarly, the highest dry matter content of tubers was observed in cluster VI (17.62%) followed by cluster III (17.52%), cluster V (17.44%) and cluster IV (17.19%) whereas, the lowest dry matter content of tubers was observed in cluster II (15.73%). The maximum and minimum number of tubers plant⁻¹ was

exhibited by cluster VII (9.90) and cluster I (6.17), respectively. For tuber weight plant⁻¹, cluster VI exhibited the highest tuber weight of 0.43 kg whereas, the minimum tuber weight was observed in cluster I (0.30kg).

The highest marketable tuber yield plant⁻¹ was observed in cluster VI (0.38kg) whereas, cluster IV (0.25 kg) and cluster VII (0.25 kg) was found to be the lowest with respect to marketable tuber yield. Similarly, the unmarketable tuber yield plant⁻¹ was recorded highest in cluster III (0.09 kg) and lowest in cluster I (0.04 kg) and cluster II (0.04 kg). The number of eyes tuber⁻¹ was recorded highest cluster mean value in cluster IV (12.32) followed by cluster V (10.53), cluster VI (10.02), cluster II (10.01), cluster VII (9.98), cluster I (9.73) and the lowest cluster mean value was recorded in cluster III (8.62).

Based on mean performance, it can be concluded that intercrossing among the genotypes of genetically diverse clusters showing superior mean performance may be helpful for obtaining desirable segregants with higher yield.

In this study, the genotype *viz.* CIP 303408-3-2 of cluster I; CIP 304146-12-4 and CIP 398203-8-2 of cluster II; CIP 303139-9-4 and CIP 304102-11-1 of cluster III; CIP 302024-3-3 of cluster IV; CIP 398068-4-2 of cluster V; CIP 398068-7-3 and KufriAshoka of cluster VI; Kufri Surya, CIP 398203-2-2 of cluster VII possessing superiority for more than two characters may be utilized as parents in hybridization programme for obtaining desirable combinations. The better genotypes selected for all the characters under consideration are presented in Table 4 and revealed that, the highest mean performance of genotypes for plant emergence per cent was observed in cluster II, cluster VI and Cluster VII and in genotypes *viz.*, CIP 304146-12-4 (93.33%), CIP 398201-3-3 (93.33%) and Kufri Surya (93.33%), respectively. The genotype CIP 398203-2-2 (54.67) of cluster VII possessed the highest mean value for plant height. For character number of leaves plant⁻¹, the highest mean value was exhibited by the genotype CIP 398203-2-2 (39.53) in cluster VII.

The highest number of branches plant⁻¹ was observed in genotype CIP 398203-2-2 (18.20) of cluster VII. Similarly, highest number of shoots plant⁻¹ was observed in genotype CIP 398068-7-3 (7.80) of cluster VI. The genotypes CIP 398068-4-2 (21.18%) of cluster II possessed the highest mean value for dry matter content of shoots. The highest mean for dry matter content of tubers was recorded in genotype Kufri Surya (22.00%) of cluster VII. The highest number of branches plant⁻¹ was observed in genotype CIP 398203-2-2 (18.20) of cluster VII. Similarly, highest number of shoots plant⁻¹ was observed in genotype CIP 398068-7-3 (7.80) of cluster VI.

The genotypes CIP 398068-4-2 (21.18%) of cluster II possessed the highest mean value for dry matter content of shoots. The highest mean for dry matter content of tubers was recorded in genotype Kufri Surya (22.00%) of cluster VII.

The genotype CIP 398068-4-2 (16.80) of cluster V showed maximum number of tubers plant⁻¹. For character tuber weight plant⁻¹, the highest mean value was exhibited by the genotype KufriAshoka (0.52 kg) of cluster VI. The highest marketable tuber yield plant⁻¹ was observed in genotype KufriAshoka (0.47 kg) of cluster VI. The genotype CIP 304124-7-2 (0.017 kg) included in cluster I was found superior having the lowest unmarketable tuber yield plant⁻¹. The lowest number of eyes tuber⁻¹ was observed in genotype CIP 398181-17-2 (7.2) of cluster III. The similar trend in

divergence have also been reported by Chandrakar (2007)^[3] and Singh (2008)^[13], Barik *et al.* (2010)^[11]

Table 5: Percentage contribution of characters towards divergence in F₁C₂ clonal progenies of potato

S. No.	Character	Contribution by each character (%)
1	Plant emergence (%)	1.78
2	Plant height (cm)	8.62
3	Number of leaves Plant ⁻¹	4.70
4	Number of branches Plant ⁻¹	9.24
5	Number of shoots Plant ⁻¹	11.03
6	Dry matter content of shoots (%)	4.32
7	Dry matter content of Tubers (%)	0.25
8	Number of tubers Plant ⁻¹	7.82
9	Tuber weight Plant ⁻¹ (kg)	37.07
10	Marketable tuber yield Plant ⁻¹ (kg)	7.93
11	Unmarketable tuber yield Plant ⁻¹ (kg)	3.97
12	Number of eyes tuber ⁻¹	3.25

The per cent contribution of the characters towards total divergence is presented in Table 5. The contribution of various characters towards the total divergence was recorded the highest for tuber weight (37.07) followed by number of shoots plant⁻¹ (11.03), number of branches plant⁻¹ (9.24), plant height (8.62), marketable tuber yield plant⁻¹ (7.93) and number of tubers plant⁻¹ (7.82). Rest of the traits recorded low contribution to the total divergence. Hence, while formulating breeding programme, these traits be given priority to exploit the diversity in population. The similar trend in divergence has also been reported by Desai and Jaimini (1997b)^[4], Chandrakar (2007)^[3], Barik (2007)^[2], Singh (2008)^[13], Sattar *et al.* (2011)^[12], Panigrahi *et al.* (2014)^[8, 9], Panigrahi and Baisakh (2014)^[8, 9] and Rangare and Rangare (2017)^[10].

Table 3: Mean performance of clusters for tuber yield and its components in F₁C₂ clonal progenies of potato

Cluster No.	Number of genotypes included	Plant emergence (%)	Plant height (cm)	Number of leaves Plant ⁻¹	Number of branches Plant ⁻¹	Number of shoots Plant ⁻¹	Dry matter content of shoots (%)	Dry matter content of Tubers (%)	Number of tubers Plant ⁻¹	Tuber weight Plant ⁻¹ (kg)	Marketable tuber yield Plant ⁻¹ (kg)	Unmarketable tuber yield Plant ⁻¹ (kg)	Number of eyes tuber ⁻¹
I	20	75.83	32.58	25.38	10.13	3.63	13.93	16.60	6.17	0.30	0.26	0.04	9.73
II	12	85.28	41.02	26.45	8.56	3.30	14.82	15.73	8.45	0.32	0.28	0.04	10.01
III	13	76.67	40.33	30.12	10.87	3.26	13.05	17.52	7.57	0.33	0.26	0.09	8.62
IV	8	81.67	41.53	28.37	8.67	3.28	12.72	17.19	6.61	0.32	0.25	0.07	12.32
V	15	76.67	44.92	31.92	11.78	4.20	14.54	17.44	6.86	0.38	0.32	0.05	10.53
VI	11	87.27	47.00	33.73	11.36	5.70	15.82	17.62	9.68	0.43	0.38	0.05	10.02
VII	7	81.43	49.42	35.68	16.01	6.65	15.21	16.88	9.90	0.31	0.25	0.06	9.98

Table 4: Desirable genotypes for important traits of F₁C₂ clonal progenies of potato on individual clusters

S. No.	Character	Cluster						
		I	II	III	IV	V	VI	VII
1	Plant emergence (%)	CIP 304146-11-2	CIP 304146-12-4	CIP 302024-5-1, CIP 302431-5-3	CIP 3303139-8-3	CIP 304146-2-2, CIP 398201-5-3	CIP 398201-3-3, KufriPukhraj	Kufri Surya
2	Plant height (cm)	CIP 303405-4-2	CIP 302024-3-4	CIP 398181-9-3,	CIP 398203-7-4	CIP 304102-7-1	CIP 398068-3-3	CIP 398203-2-2
3	Number of leaves Plant ⁻¹	CIP 304012-12-4	CIP 302024-3-4	CIP 304102-4-5,	CIP 302024-3-3	CIP 304014-12-2	KufriPukhraj	CIP 398203-2-2
4	Number of branches Plant ⁻¹	CIP 303408-3-2, CIP 304146-11-2	CIP 304146-12-4	CIP 303139-9-4	CIP 304014-5-4	CIP 304102-7-1, CIP 304014-12-7	CIP 398201-15-4	CIP 303405-7-4
5	Number of shoots Plant ⁻¹	CIP 303408-3-2	CIP 303405-8-3	CIP 398181-17-2	CIP 303139-10-3	CIP 303139-4-4	CIP 398068-7-3	Kufri Surya
6	Dry matter content of shoots (%)	CIP 304124-2-5	CIP 398203-8-2	CIP 304102-11-1	CIP 303139-8-3	CIP 304014-2-6	KufriPukhraj	Kufri Surya
7	Dry matter content of Tubers (%)	CIP 304124-4-3	CIP 302024-3-4	CIP 398181-9-3	CIP 303139-10-3	CIP 304102-7-1	KufriAshoka	CIP 398203-2-2
8	Number of tubers Plant ⁻¹	CIP 303408-4-5	CIP 302024-3-4	CIP 303134-9-4	CIP 398203-7-4	CIP 398068-4-2	CIP 398201-15-4	CIP 303405-3-1
9	Tuber weight Plant ⁻¹ (kg)	CIP 303408-4-5, CIP 304124-4-3	CIP 302024-2-3, CIP 303405-8-3, CIP 3303405-6-2	CIP 302431-2-1, CIP 304102-11-1	CIP 3304012-6-1	CIP 398201-7-2	KufriAshoka	CIP 303405-3-1
10	Marketable tuber yield Plant ⁻¹ (kg)	CIP 303408-4-5	CIP 303405-8-3	CIP 302431-2-1, CIP 304102-11-1, CIP 304102-4-2	CIP 304012-6-1	CIP 398201-5-3	KufriAshoka	CIP 303139-9-2
11	Unmarketable tuber yield Plant ⁻¹ (kg)	CIP 303408-2-1	CIP 302431-4-1	CIP 302024-5-1	CIP 302024-3-3	CIP 398181-16-5, CIP 398068-13-3	CIP 398068-9-4	CIP 398203-2-2
12	Number of eyes tuber ⁻¹	CIP 304124-2-5	CIP 303405-8-3, CIP 304146-1-4	CIP 303139-9-4	CIP 302024-3-3	CIP 303139-4-4	KufriAshoka	CIP 398203-2-2, CIP 303405-7-4

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