

## Genetic diversity assessment through principal component analysis in potato (*Solanum tuberosum* L.)

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In order of importance for food production in comparison to 20 other major food crops, potato (*Solanum tuberosum* L.) ranks 4<sup>th</sup> in the world and 3<sup>rd</sup> in India. It produces high dry matter, minerals, vitamin C & B and carbohydrates per unit area. Besides its significance to human food security, potato is also a crop with fascinating genetic traits and cultural history (Swaminathan, 1999). For improvement in potato crop genetic diversity is required. However due to narrow genetic base in cultivated potato, in India lot of potential yet to be explore. Principal component analysis was done to estimate the variability in germplasm under study. For the principal component analysis each genotype was identified on the basis of correlation matrix as a single point in a standardized multidimensional space. The axes of this space were principal components obtained from the original data as orthogonal transformation of the original variety. In this way each principal component becomes a linear combination of the varietal scores corresponding to the original variables.

The present investigation for assessment of genetic diversity in potato (*Solanum tuberosum* L.)” was conducted at Vegetable Research Centre of the GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand during *rabi* season of 2007-08. The climate of this place is humid and subtropical and frost can be expected from last week of December to end of the January. Fifty potato genotypes and four checks were conducted in Augmented Block Design with 5 blocks. Each block contains 10 genotypes along with 4 checks and each plot contains 2 row of 2 meter long. Observations were recorded on 13 agronomical and quality traits to analyze the data by Principal Component Analysis through a software programme developed by IISR, New Delhi. Principal component analysis suggested by Hotelling (1933) after its original concept

given by Pearson (1901) and non-hierarchical Euclidean cluster analysis was used for grouping all genotypes into clusters.

### Principal Component Analysis

The principal component analysis of 54 potato genotypes based on correlation matrix of agronomic and quality traits yielded the 13 eigen roots (eigen values) and eigen vectors. These values and associated percentage of variation explained by eigen root have been presented in Table 1.

First 11 components explained 96.25 per cent variation. All these vectors were utilized for ordination. The maximum variation of 18.78 per cent was explained by first latent vector followed by 16.34 per cent (second vector) and 13.30 per cent (third vector).

The approach of Rao (1964) based on covering 90 per cent of total variation seems to be useful and has been adopted to explain the variation in the breeding material. The scales per corresponding eigen vector for principal component taking the largest element in each vector as unity has been presented in Table 1. These elements may be interpreted as the relative weight given to the variables in each component and important variables are those which possess high positive and high negative weight (Jeffers, 1967).

In the present study first principal component had high positive weight to plant height followed by specific gravity and number of tubers per plant and high negative weight to tuber length. While, the second principal component had high positive weight for tuber breadth and high negative weight for specific gravity, TSS and ascorbic acid. The third principal component had highest weight for number of stems per plant and high negative weight for dry matter.

From this result it may be concluded that important variables in potato genotypes with respect to agronomic traits were tuber yield per plant, number of tubers per

**Table 1.** Eigen vector, eigen root and associated variation for principal component in potato based on economic traits.

Sl. No.	Characters	Eigen vector												
		1	2	3	4	5	6	7	8	9	10	11	12	13
1	Emergence percentage at 30 DAP	-0.01	0.30	-0.26	0.18	0.39	0.40	0.38	0.13	0.07	0.16	-0.24	-0.20	0.42
2	Plant height (cm)	0.38	0.27	0.26	0.52	-0.22	-0.30	0.15	0.03	-0.08	0.13	0.39	-0.10	0.28
3	No. of stems per plant	-0.01	-0.03	0.28	0.02	0.20	0.10	0.22	-0.12	0.33	0.55	0.34	-0.49	-0.14
4	No. of tubers per plant	0.22	0.12	-0.39	-0.01	0.35	-0.13	-0.01	0.71	-0.21	-0.13	-0.04	0.10	0.21
5	Single tuber weight (g)	0.13	-0.34	0.16	0.20	0.02	0.27	-0.23	-0.24	0.68	-0.17	0.12	0.28	0.08
6	Tuber length (mm)	-0.66	-0.23	-0.27	0.41	-0.25	0.09	0.008	-0.07	-0.15	0.02	0.06	0.01	0.39
7	Tuber breadth (mm)	-0.30	0.53	0.11	-0.01	0.19	0.30	-0.39	-0.07	0.05	0.35	0.14	0.38	-0.13
8	Specific gravity (g/cm <sup>3</sup> )	0.23	-0.36	-0.16	0.03	0.35	0.33	-0.49	0.32	-0.36	-0.04	0.13	-0.19	0.08
9	Dry matter (%)	0.07	0.17	-0.50	0.14	0.16	-0.76	0.27	0.44	0.14	-0.24	0.33	0.42	-0.06
10	Protein(%)	-0.31	0.12	0.19	-0.17	0.07	-0.03	-0.06	-0.15	-0.02	0.58	0.54	-0.33	-0.16
11	Ascorbic acid (mg/100 g)	0.14	-0.27	0.26	-0.23	-0.10	0.30	0.45	-0.14	-0.35	0.17	0.41	0.32	0.10
12	TSS (%)	0.19	-0.36	-0.32	-0.41	-0.53	0.35	-0.14	0.01	0.13	-0.08	0.04	-0.13	0.35
13	Tuber yield (kg/plot)	-0.17	-0.11	0.11	-0.45	0.28	-0.44	-0.12	0.16	0.18	0.17	0.12	0.09	0.56
	Eigen root	2.441	2.124	1.729	1.240	1.123	0.932	0.832	0.715	0.547	0.432	0.396	0.263	0.224
	Percent variation	18.78	16.34	13.30	9.54	8.64	7.17	6.40	5.50	4.21	3.33	3.04	2.02	1.73

plant, tuber weight, plant height and number of stems per plant. The above variables might be taken into consideration for effective selection of parents during hybridization program.

**Non-hierarchical Euclidean Cluster Analysis:** Non-hierarchical Euclidean cluster analysis based on principal component analysis (Hotelling, 1933) was found to be more useful measure for estimating divergence, In the present study 54 genotypes of potato were grouped into seven non-overlapping clusters (Table 2) determined by 'F' test. The importance of genetic diversity in several crops has been studied by many workers viz., Shethe and Kale (1988), Krinshna Prasad and Singh (1993).

The intra cluster distance (D) ranged from 3.444 to 2.212 (Table 3). The maximum intra cluster distance was noted in cluster IV (3.444). II cluster accommodated thirteen genotypes and considered to be the biggest one. The second and third biggest clusters were IV and VII having ten and nine genotypes, respectively. The maximum inter cluster distance (6.385) was found between clusters III and VI, whereas

minimum distance (2.666) was found between clusters V and VII. The grouping of genotypes in clusters reflects the relative divergence of clusters and allows a convenient selection group of genotypes with their overall phenotypic similarity for hybridization programme facilitating better exploitation of germplasm.

An examination of results revealed that there was no sharp relationship between the clustering pattern of the genotypes and their geographical sources. Thus, the tendency of cultivars occurring in cluster cutting across geographical boundaries is possible due to genetic makeup of genotypes and subsequently natural selection during their development. The results obtained are in conformity with the findings of Kumar and Kang (2000) and Luthra *et al.* (2005). Contrary to this, these results are not supported by the findings of Juned *et al.* (1988) where a close relationship was noted between geographic and genetic diversity.

Genotypes present in cluster IV recorded tuber yield (20.12 kg/plot), maximum plant height (45.53 cm), maximum number of stems per plant (6.50), maximum

**Table 2.** Non-hierarchical cluster of 54 potato genotypes

Cluster number	Number of genotypes	Entry name
I	6	K.Pukhraj, J/93-159, J/92-148, J/95-242, K.Chipsona-1, Atlantica
II	13	K.Ashoka, K.Pushkar, K.Sutlej, K.Jyoti, K.Anand, J/93-186, CP-1588, MS/92-3128, MS/91-1326, J/96-238, K.Giriraj, J/9381, P.S-06-1(Pauri)
III	4	J/93-86, GM-27, Jx-576, TPS 07-1
IV	10	K.Badshah, Pant Selection-1, J/95-227, MS/95-1309, MP/91-132, MS/92-542, B-420(2), K.Surya, MS/95-1090, J/92-167
V	8	J/95-221, MS/93-1344, 91-P-86, K.Arun, K.Chipsona-3, MS/95-111, MS/92-209, Lady Roseta
VI	4	K.Chipsona-2, J/95-229, MS/95-117, P.S-06-2(Pusa)
VII	9	K.Bahar, K.Jawahar, K.Lalima, MS/94-899, MS/0-3808, J/93-4, J/93-87, MS/92-3146, 345-1

**Table 3.** Average distance of intra- and inter-cluster centriods

	I	II	III	IV	V	VI	VII
	(2.515)						
II	3.004	(2.331)					
III	4.472	4.801	(2.856)				
IV	4.340	2.730	5.140	(3.444)			
V	2.966	3.034	3.666	3.431	(2.421)		
VI	3.416	3.662	6.385	4.182	4.353	(2.305)	
VII	3.933	3.270	4.128	2.902	2.666	3.828	(2.212)

The intra cluster distances are shown in parenthesis.

tuber breadth (55.46) and highest specific gravity (2.36 g/cm<sup>3</sup>). The genotypes in cluster III recorded maximum number of tubers per plant (15.73). Similarly cluster VI recorded maximum values for single tuber weight (102.97 g), tuber length (84.7 mm) and dry matter (20.53 %). Thus, an improvement programme involving patterns of different clusters may yield transgressive and heterotic segregants, so that the previous selection history of cross compatibility can be ignored for selection of genotypes for various characters within each cluster.

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