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Research Article

Analysis of genetic diversity in Indian potato genotypes by using Principal Component Analysis

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Abstract

Determination of the best selection criteria is the most important aim in potato breeding programmes. In order to evaluate and classify morphological and morpho-physiological traits of potato genotypes, 30 cultivars were sown in randomized block design with three replications. Principal component analysis indicated that two important components accounted for about 84 percent of the total variation among traits in potato genotypes. The first component assigned 70 percent of total variation between traits and was significantly related with tuber yield and its components. Therefore, the selection should be done according to the first component and will helpful for a good hybridization breeding programme. Other components accounted for 13 percent of variation between traits. Based on the bi-plot figures Kufri Surya, Kufri Chipsona-3, PH-1, PH-3, MM-12, V1-121, Kufri Jyoti, Kufri Sutlej and V2-645 were identified as the best genotypes, therefore it can be stated that these cultivars can be used for exploitation of good hybridization breeding programme.

Keywords: Yield, diversity, principal component, potato

Introduction

In order of importance for food production in comparison to 20 other major food crops, potato (*Solanum tuberosum* L.) ranks 4th in the world and 3rd in India (Lohani *et al.*, 2012). It is an important calorie rich crop having potentiality to reduce food deficit for ever growing population in the world (Pradhan *et al.*, 2011). The potato is a crop which has always been a ‘poor man’s friend’. For vegetable purpose it has become one of the most popular crops in India as well as in the world. It can be used for several industrial purposes such as for the production of starch and alcohol (Haydar *et al.*, 2009). Besides its significance to human food security, potato is also a crop with fascinating genetic traits and cultural history (Swaminathan, 1999). Determination of the best selection criteria is the most important aim in potato breeding programme. Many researchers believed that genetic improvement of crop yield must be done via genetic improvement of physiological traits (Beheshtizadeh *et al.*, 2013). In determining the potentiality of genetically different lines and cultivars, breeders have to observe many different characters that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction (Tadesse and Bekele, 2001). Principal component analysis helps researchers to distinguish significant relationship between traits. This is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent factors (Beheshtizadeh *et al.*, 2013).

Using genetic diversity there can be vast improvement in potato crop. However due to narrow genetic base in cultivated potato, in India lot of potential yet to be explore. So, the present investigation was conducted in order to determine the dependence relationship between yield, yield components and some agro-morphological characters of potato cultivars using principal component analysis.

Materials and Methods

In this present investigation, 30 potato genotypes were collected from All India Coordinated Research Project (AICRP) on Potato Crop, Kalyani Centre, Bidhan Chandra Krishi Viswavidyalaya, Kalyani, West Bengal, India and evaluated at Agricultural farm of Government of West Bengal, Adisaptogram, Hoogly, West Bengal, India, where the research of university was permitted for AICRP on Potato. This area having a sub-tropical climate with regular visiting of South-West monsoon generally from the month of June to September. The materials were sown in Randomized Block Design with three replications, maintaining 30 cm row to row and 20 cm plant to plant distance. The plot size for individual genotype was 6 m^2 (3m x 2m) and recommended cultural practices were followed prior to sowing or during the vegetative to reproductive stages of crop growth. Thirty genotypes were planted in the field on 3rd week of November and harvested on 3rd week of February (2011-12, 2012-

13). In this experiment observations were recorded on 12 agro-morphological traits like percent of plant emergence, plant height (cm) (60 DAP), number of branches/plant, number of leaves/plant, number of interjected leaflets/leaf, length of leaf(cm), length of lateral leaflets/ leaf(cm), length and breadth ratio of terminal leaflet/leaf, girth of stem (cm), average tuber weight (g), total number of tubers/plant as well as tuber yield/plant(kg), respectively on 10 normal plants randomly selected from each plot.

After recording observations data were subjected to analyze to principal component analysis using SPSS software version 16.0 and XLSTAT of 2014 version 16.5.02 Computer programme for all the traits of potato genotypes. The PC was used to determine the extent of genetic variation. Eigen-values were obtained from PC, which were used to determine the relative discriminative power of the axes and their associated characters.

Results and Discussion

Principal Component Analysis: In principal component analysis, out of twelve, only the first two component axes (Table.1) in the PCA analysis had Eigen values up to 1.0, presenting cumulative variance of 84.1 %. Principal component one (PC1), with Eigen value of 8.504, contributed 70.8% of the total variability, while PC2, with Eigen value of 1.590 accounted for 13.2% of total variability observed among the 30 potato genotypes. The first PC was more related to tuber yield/plant, number of tubers/plant, tuber weight, plant height, plant emergence and leaves/plant and it was cleared from the values of PC1 (Table.1). In the second PC, characters like girth of stem and number of interjected leaflets/leaf were observed. Number of interjected leaflets/leaf was of more importance as it had negative effect with yield as observed by Pradhan *et al*., (2011). So, selection towards negative direction should be considered for interjected leaflets.

Though correlation analysis helps in determination of effective traits in order of indirect selection of superior genotypes but on the other hand, principal component analysis is suitable multivariate technique in identifying and determining of independent principal components that are effective on plant traits separately. Therefore, principal component analysis also helps breeders for genetic improvement of traits such as yield that have low heritability specifically in early generations via indirect selection for traits effective on yield (Leilah and Al-Khateeb, 2005 and Golparvar *et al*., 2006).

From this result it may be concluded that the important variables considered in present investigation with respect to agronomic traits were tuber yield/plant, number of tubers/plant, tuber weight, plant height, plant emergence and leaves/plant. These above variables might be taken into consideration for effective selection of parents during hybridization program for broadening the genetic base in the population as well as to develop elite lines. Furthermore, selection of the genotypes with the highest amounts of tuber yield and its components should be recommend as one of the best breeding strategy for genetic improvement of tuber yield in potato. These results have been emphasized by many researchers like Haydar *et al*., (2007), Mondal *et al*., (2007), Sattar *et al*., (2011) Ahmadizadeh and Felenji, (2011) as well as Lohani *et al*., (2012).

PCA is a technique which identifies plant traits which contributed most to the observed variation within a group of genotypes and it had a practical application in the selection of parental lines for breeding purpose (Ahmadizadeh and Felenji, (2011). The cumulative variance of more than 84% by the first two axes with Eigen values of more than 1.0 indicated that the identified traits within this axes exhibited great influence on the phenotype of the cultivars and could effectively be used for selection among them. Cardi *et al*., (2002) identified ten major components with 98.9% justification amount by means of analyzing tetralpoid potato cultivars into major components. Tairo *et al*., (2008) also used PCA to study the variability among Tanzanian landraces and found low genetic variability among them. Lahoni *et al*., (2012) observed that first 11 components explained 96.25 % variation. The maximum variation of 18.78 % was explained by first latent vector followed by 16.34 % (second vector) and 13.30 % (third vector).

Principal Component Bi-plot: Scree plot: Scree plot explains the percentage of variance associated with each principal component obtained by drawing a graph between Eigen values and PC. The PC scree plot is shown Figure 1 clearly showed the highest variation in PC 1 to explain maximum variation in the data set, so the selection of genotypes from this PC will be useful.

After principal components analysis was drawn to reviewing relationships between variables based on bi-plot first and second components (Figure 2), so that the horizontal axis was related to first component and the vertical axis was related to the second component . Based on the component values, the location of genotypes and their grouping were determined in top of bi-plot (Figure 3). Therefore, according to bi-plot figures Kufri Surya, Kufri Chipsona-3, PH-1, PH-3, MM-12, V1-

121, Kufri Jyoti, Kufri Sutlej as well as V2-645 identified as the best genotypes as these genotypes grouped in positive part of the bi-plot. Bi-plot had been used by many researchers such as Ahmadizadeh and Felenji, (2011) in potato, Afuape *et al.*, (2011) and Sethuraman *et al*., (2007) in sweet potato.

Thus, from the above investigation it can be concluded that Principal component analysis in potato cultivars facilitates in identifying desirable traits and their relationship with yield and reliable classification of genotypes. Relatively more variations were evident in the traits which were located on the first component. The above variables might be taken into consideration for effective selection of parents during hybridization program. A good hybridization program can be initiated by the selection of cultivars from the bi-plot figures, with which we can identify core genotypes and relationship with morphological traits with possible utility for specific breeding purposes. Thus, an improvement programme involving such different cultivars 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 these cultivars.

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References

Afuape, S. O., Okocha, P. I. and Njoku, D. 2011. Multivariate assessment of the agro-morphological variability and yield components among sweetpotato (*Ipomoea batatas* (L.) Lam) landraces. *African J. Plant Sci*., **5**(2): 123-132.

Ahmadizadeh, M. and Felenji, H. 2011. Evaluation diversity among potato cultivars using agro-morphological and yield components in fall cultivation of Jiroft area. *American-Eurasian J. Agric. & Environ. Sci*., **11**(5): 655-662.

Beheshtizadeh, H., Resaie, A., Resaie, A. and Ghandi, A. 2013. Genetic variability assessment in bread wheat (*Triticum aestivum* L.) cultivars using multivariate statistical analysis. *Int. J. Farm and Alli. Sci*. **2** (16): 520-523.

Cardi, T., Mazzei, M. and Frusciante, L. 2002. Field variation in a tetraploid progeny derived by selfing a *Solanum commersonii* (+) *S. tuberosum* somatic hybrid: A multivariate analysis. *Euphytica*, **124**(1): 111-119.

Golparvar, A. R., Ghasemi-Pirbalouti, A. and Madani, H. 2006. Genetic control of some physiological attributes in wheat under drought stress conditions. *Pak. J. Bio. Sci*. **9**(8): 1442-1446.

Haydar A, Uddin, M. S., Khokani, T. A., Khalequzzaman, K. M., and Hoque, A. (2009). D^2 -analysis and selection criteria in potato. *Int. J. Sustain. Crop Prod.* **4**: 91-93.

Haydar, A., Ahmed, M. B., Hannan, M. M., Razvy, M. A., Mandal, M. A., Salahin, M., Karim, R. and Hossain, M. 2007. Analysis of genetic diversity in some potato varieties grown in Bangladesh. *Middle-East J. Sci. Res.*, **2**(3-4): 146-148.

Leilah, A. A. and Al-Khateeb, S.A. 2005. Statistical analysis of wheat yield under drought conditions. *J. Arid. Environments*. **61**: 483- 496.

Lohani, M., Singh, D. and Singh, J. P. 2012. Genetic diversity assessment through principal component analysis in potato (*Salamun tuberosun* L.). *Vegetable Sci.*, **39** (2): 207-209.

Mondal, M. A. A., Hossain, M. M., Rasul, M. G. and Uddin, M. S. 2007. Genetic diversity in potato *(Solanum tuberosum* L.). *Bangladesh J. Bot*., **36**(2): 121-125.

Pradhan, A. M., Nanadeshwar, B. C., Sarkar, K. K. and Konar, A. 2011. Estimation of genetic parameters and association of traits related to yield in potato *(Solanum tuberosum* L.). *J. Crop and Weed*, **7**(2): 229-231.

Sattar, M. A., Uddin, M. Z., Islam, M. R., Bhuiyan, M. K. R. and Rahman, M. S. 2011. Genetic divergence in potato *(Solanum tuberosum* L.). *Bangladesh J. Agril. Res*., **36**(1): 165-172.

Sethuraman, S. P., Ray, R. C., Panda, S. H. and Naskar, S. K. 2007. Application of principal components analysis for sensory characterization of sweet potato curd. *J. Root Crops*, **33**(1): 62-66.

Swaminathan, M. S. 1999. Potato for global food security. In: Potato: Global research and development, Vol. 1, S.M. Paul Khurana, G. S. Shekhawat, B. P. Singh, S. K. Pandey (Eds.), Indian Potato Assoc., p. 8-12.

Tadesse, W. and Bekele, E. 2001. Factor analysis of yield in grasspea (*Lathyrus sativus* L.). Lathyrus Lathyrism Newsletter. **2**: 416-421.

Tairo, F., Mneney, E. and Kullaya A. 2008. Morphological and agronomical characterization of sweet potato [*Ipomoea batatas* (L.). Lam.] germplasm collection from Tanzania. *Afr. J. Plt. Sci*., **2**(8): 77-85.

Table 1. Eigen value, factor scores and contribution of the first four principal component axes to variation in potato germplasm

Sl.No.	Characters	PC I	PC II
1.	% Plant emergence	0.983	0.042
2.	Plant height(cm)(60DAP)	0.969	0.021
3.	Number of branches plant^{-1}	0.095	-0.636
4.	Number of leaves plant^{-1}	0.973	0.009
5.	Number of interjected leaflets leaf^{-1}	0.023	0.761
6.	Length of leaf(cm)	0.982	-0.034
7.	Length of lateral leaflet(cm)	0.897	-0.065
8.	Ratio(l:b) of terminal leaflet	0.985	-0.030
9.	Girth of stem(cm)	0.141	0.773
10.	Average tuber weight(g)	0.984	0.002
11.	Number of total tubers plant^{-1}	0.977	-0.011
12.	Total yield plant^{-1} (kg)	0.980	-0.006
	Roots/ Eigen values	8.504	1.590
	% of total variation accounted for	70.868	13.248
	% of cumulative variation	70.868	84.116

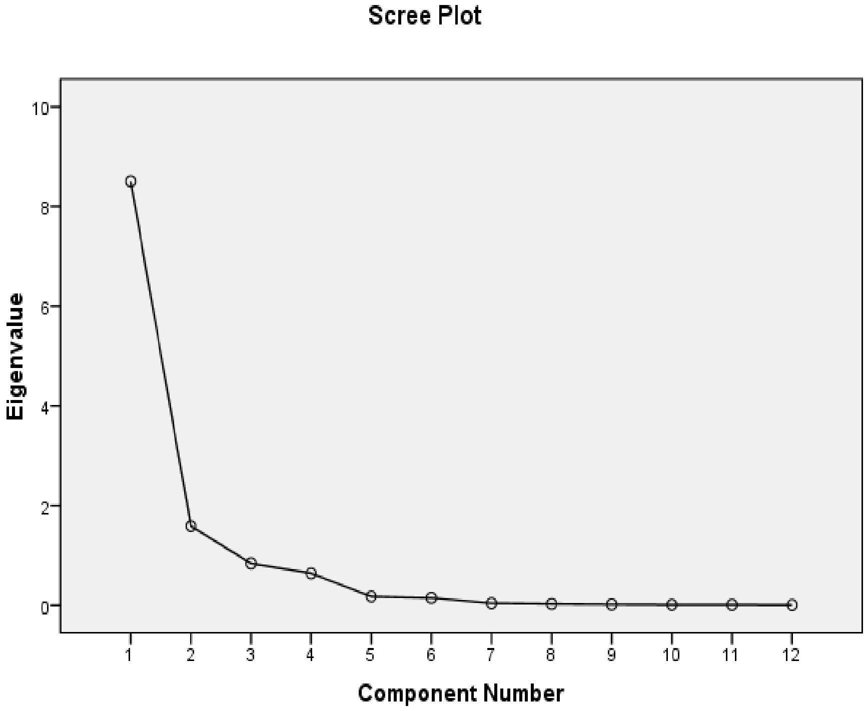
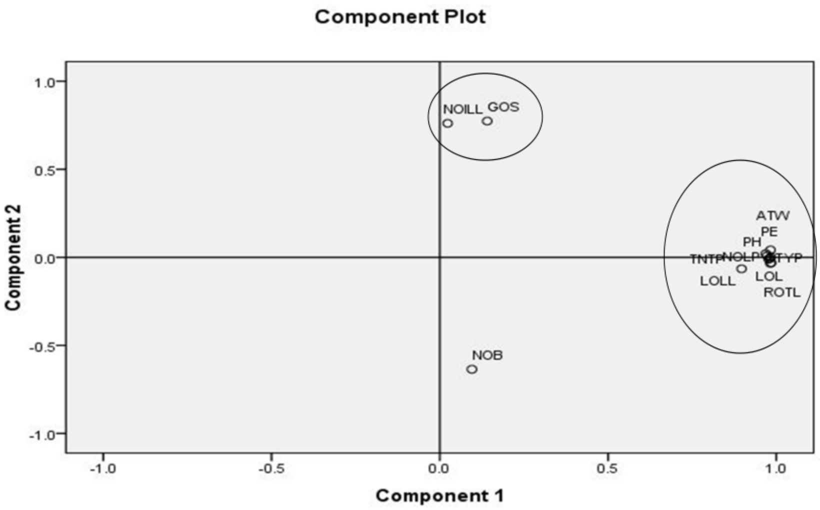


Figure 1. Principal scree plot between component number and Eigen values



Here, PE=% of plant emergence, PH= Plant height(cm)(60DAP), NOB= Number of branches plant^{-1}, NOLP= Number of leaves plant^{-1}, NOILL= Number of interjected leaflets leaf^{-1}, LOL= Length of leaf(cm), LOLL= Length of lateral leaflet(cm), ROTL= L:B ratio of terminal leaflet, GOS= Girth of stem(cm), ATW= Average tuber weight(g), TNTP= Total number of tubers plant^{-1}, TYP= Total yield plant^{-1} (kg).

Figure 2. Principal component bi-plot between 12 morphological characters

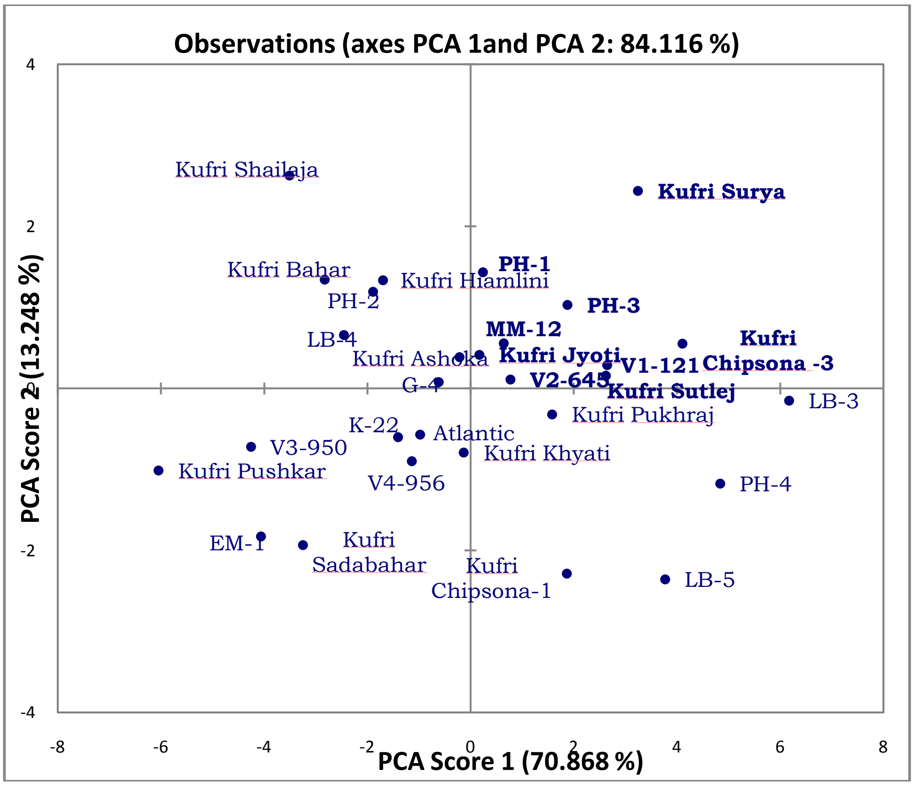


Figure 3: Principal component bi-plot of 30 potato genotypes