



## RESEARCH PAPER

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## Estimation of phenotypic diversity among locally available potato germplasm

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### Abstract

In the present study 12 different genotypes of *Solanum tuberosum* were acquired from Potato Program, NARC, Islamabad and compared for their agromorphological traits. The study was conducted to check the phenotypic and genotypic diversity among locally available potato germplasm. The experiment was conducted in a randomized complete block design with three replication and data were recorded. Cultivar Harmes produced best result regarding number of branches/plant (8.0a), number of leaves/plant (503.77a), number of tubers/plant (19.76a) and tuber mass/plant (0.833a), leaf area (41.667a) and yield (41.66a t/ha) followed by Melanto for number of tuber/plant (14.8ab), tuber mass (0.733ab), and number of branches/plant (2.9000b). A UPGMA cluster, grouped the 12 *Solanum tuberosum* genotypes into two major clusters on the basis of agro morphological data. Euclidian distance for morphological traits ranged from 1.17 to 7.79. Minimum distance between *Safari* and *Desiree* (1.17) and *Flamba* and *Santay* (1.43) were observed showing great similarity with each other. Highest dissimilarity was found between *Harmes* and *Triplo* (7.79). Euclidian distances obtained from a dendrogram could help breeders to choose the diverse parents for a breeding program aimed at varietal improvement. In the present study, *Santay*, *Kuroda*, *Desiree* and *Harmes* were found to be promising genotypes on the basis of specific gravity and dry matter tests showed that these genotypes may satisfy the industrial requirements. Thus, this study revealed the presence of sufficient phenotypic diversity among varieties in the country that can be exploited for germplasm enhancement.

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## Introduction

Potato (*Solanum tuberosum* L.) is an annual crop belongs to the family solanaceae, genus solanum and species tuberosum. It's chromosome number is  $2n = 48$ . It is an auto-tetraploid and heterozygous plant (Roodbar *et al.*, 2008). Potato is the most important non-cereal food crop of the world. In monetary terms it ranks fourth in the world after wheat, rice and maize (Akkale *et al.*, 2010). The cultivated potato types grown for world trades are collectively designated *Solanum tuberosum*. In total, there are seven cultivated species (including *Solanum tuberosum*), with seven subspecies, according to the latest comprehensive taxonomic treatment of Hawkes (1990). Today, over 7,500 different potato varieties are produced around the world (Hamester and Hills 2003). The introduction and development of new potato cultivars (*Solanum tuberosum* L.) has been an important strategy to increase crop productivity of this important staple food, fourth after rice, wheat and corn.

Genetic diversity is essential to study the taxonomic relationships present among germplasms and also to identify the sources of genes for a particular trait from the existing germplasms (Haydar *et al.*, 2007; Arslanoglu *et al.*, 2011; Abebe *et al.*, 2013) and to sort out parental lines with complementary features that can enhance breeding progress (Cartea *et al.*, 2002; Saljoghianpour *et al.*, 2007). Genetic diversity analysis of genotypes can be carried out using various procedures with morphological characterization being the earliest (Smith and Smith, 1989). This system relies on the recording and description of phenotypic and agronomic characteristic that cover the leaf, floral parts and the yield and yield component attributes. In potato, morphological characterization techniques have been used in the taxonomic classification of cultivated and wild species (Hawkes, 1994), the characterization of local genotypes (Arslanoglu *et al.*, 2011), and the evaluation of genetic diversity among cultivars (Ahmadzadeh and Felenji, 2011). Genetic divergence is a useful tool for an efficient choice of parents for hybridization to develop high yield potential cultivars.

Morphological characterization is the first step in description and classification of genetic resources (Smith and Smith, 1989).

The potato is a highly heterozygous outcrossing crop with ploidy levels ranging from the diploid to the pentaploid level (Haan *et al.*, 2013). Information on genetic divergence is essential for sustained genetic improvement of a crop (Chimote *et al.*, 2007).

Since most of the present day potato (*Solanum tuberosum* L.) varieties are derived from crossing and selection of few lines of *S. tuberosum* subspecies *andigena* introduced into temperate world around 300 years back, it is known to have narrow genetic base (Mendoza and Haynes, 1974; Love, 1999). Evaluation of genetic divergence is important to know the source of genes for a particular trait within the available germplasm (Williams *et al.*, 1990; Kawchuk *et al.*, 1996). From the late 1920s till the early 1990s, potato collection expeditions by American (Correl, 1962), Dutch (Hermsen and Schatgraven, 1974), English (Hawkes, 2003), Peruvian (Ochoa, 2003; Vargas, 1949; Vargas, 1956) and Russian (Loskutov, 1999) scientists, among researchers from many other nationalities, have contributed to the establishment of important ex situ collections that are currently maintained in gene banks around the world.

The signature of the Convention of Biological Diversity (CBD) in 1992 and the adoption of national regulatory frameworks for access to genetic resources.

These ex situ collections continue to provide valuable genetic diversity to potato breeding programs around the world in order to continue to deliver bred cultivars adjusted to a changing world in its climatic, as well as human dimensions. At the same time, interventions designed to support in situ conservation have increased (Scott, 2011).

In the present investigation, an attempt has been made to evaluate phenotypic variation in 12 genotypes of *Solanum tuberosum* and subsequently interpret their phylogeny and affinities in the context of an efficient breeding partner selection.

## Materials and methods

This Research Trail was conducted for the evaluation of promising potato clones for different agronomic and processing traits at National Potato Program, HRI, NARC, Islamabad, during 2014, for varieties; Zina red, Triplo, Safari, Harmes, Melanto, Flamba, Aestrix, Amarin, Santay, Kuroda, Desiree and Stemster. Each plot had 3 rows, 75 cm apart and 2.75 meters long (with an area of 6.18 m<sup>2</sup>). The field was prepared following the traditional practices used to grow a potato crop from tuber seed. When the field attained proper moisture conditions for ploughing, a recommended dose (250:125: 125 NPK kg/ha) of ½ N and full P & K was applied uniformly. The remaining half of nitrogen was applied at earthing-up. Plant to plant distance of 20 cm and row to row distance of 75 cm was maintained. Seed was cut in pieces to break dormancy and lower the cost of production. More than one eye was kept on each seed tuber piece to attain proper crop stand. The planting of trial was done on 11<sup>th</sup> January 2014 and harvesting was carried out on May 15, 2014. The following parameters were recorded during the study were germination (%), plant height, Number of branches/plant, Leaf area, No. of leaves/plant, Number of tubers/plant, Average

tuber weight, Variety Evaluation for Processing Traits (Specific Gravity and Dry Matter).

## Statistical analysis

Statistically data were analyzed by using Statistix 8.1 and Excel software. Analysis of Variance was applied for comparison among different Potato species. Unweighted pair group method with an arithmetic average (UPGMA) cluster analysis was used to infer genetic relationships and phylogeny among 12 genotypes of potato by using the NTSYS-pc, Version 2.2 package (Rohlf, 2005; Rabbani, *et al.* 2008).

## Results and discussion

### Germination Percentage

Results regarding germination percentage were significant at five percent level as shown by (Table 1). *Harmes*, *Aestrix* and *Kuroda* gave maximum germination percentage (94.66a, 93.33a & 93.33a) respectively followed by Melanto and Zina Red (91.33ab). Poor germination percentage was noted in Stemster (76.66d). Similar results were recorded by Khaliq (2002) who reported 95% to 80% variation in emergence percentage among tested cultivars.

**Table 1.** Phenotypic diversity among locally available potato germplasm.

Genotypes	Germination%	Leafarea (cm <sup>2</sup> )	NumberofBranches/plant	PlantHeight (cm)	No.ofLeaves	No.ofTuber	Tuber weight (Kg)	Yield/hectare
ZinaRed	91.00ab	2000.0ede	2.9000 b	361.00a	183.20b	766.7b	0.4000be	2000.0ede
Triplo	80.33cd	1333.3e	2.2000b	38.36ed	164.77b	556.7b	0.2667e	1333.3e
Safari	80.00ed	1333.3e	2.5333b	37.833 a	205.00b	920.0ab	0.2333e	1333.3e
Harmes	94.66a	4166.7a	8.0000a	37.43de	503.77a	197.67a	0.8333a	4166.7a
Melanto	91.33ab	3500.0ab	2.9000 b	49.800a	246.33b	1480.0ab	0.7333Ab	3500.0ab
Flamba	90.00Abe	2166.7ede	2.3333b	33.067a	263.57b	111.00ab	0.4667Abe	2166.7ede
Aestrix	93.33a	2666.7be	2.3667b	43.00a	237.33b	1353.3ab	0.5000Abe	2666.7be
Amarin	90.00Abe	2500.0ed	3.3333b	40.26e	244.57b	12.467ab	0.6000Abe	2500.0ed
Santay	85.00Abed	2333.3ed	2.5333b	33.633a	270.90b	12.433ab	0.4667Abe	2333.3ed
Kuroda	93.33a	2166.7ede	2.2000b	38.56ed	203.67b	12.000ab	0.5000Abe	2166.7ede
Desiree	81.3300Bed	1666.7de	2.9000b	37.46de	238.37b	109.00ab	0.3000e	1666.7de
Stemster	76.66da	1333.3e	2.2333b	34.800a	218.33b	9.100ab	0.3000e	1333.3e

### Plant Height (cm)

Effect of potato cultivars on plant height was significant at the one percent level (Table 1). Cultivar Melanto gave highest (49.43a) followed by Harmes (43.76b) and allocated as a longest cultivars compare to others.

Lowest plant height produced by cultivar 9. This difference in plant height may be attributed to genetic difference in varieties in term of length and number of internodes between stem node (Ranjbar and Khan, 2012).

**Table 2.** Euclidian distance between Potato germplasm.

Euclidean Distance											
Variety	ZINA-RED	TRIPLO	SAFARI	HARMES	MELANTO	FLAMBA	AESTRIX	AMARIN	SANTAY	KURODA	DESIREE
ZINA-RED	0.00										
TRIPLO	2.02	0.00									
SAFARI	1.47	1.77	0.00								
HARMES	6.66	7.79	6.75	0.00							
MELANTO	4.45	6.02	4.94	5.15	0.00						
FLAMBA	1.99	2.71	2.14	6.30	5.18	0.00					
AESTRIX	2.44	4.08	2.75	5.88	3.79	2.19	0.00				
AMARIN	2.26	3.83	2.62	5.02	2.77	2.60	1.65	0.00			
SANTAY	2.18	2.53	2.05	5.74	4.74	1.43	2.79	2.43	0.00		
KURODA	1.53	3.16	2.29	6.04	3.45	2.04	1.65	1.52	2.06	0.00	
DESIREE	1.68	2.60	1.17	6.32	4.89	1.50	1.93	2.33	1.99	2.09	0.00
STEMSTER	2.80	1.68	2.04	7.01	5.73	2.96	4.26	3.67	2.06	3.40	2.86

#### Number of branches per plant

Data related to number of branches/plant showed highly significant results (Table 1). Number of branches per plant is highest (8.00a) in Harmes followed by Amarin (3.13b). However, lowest number of branches was observed in Triplo and Kurado (2.200b). This increase in number of branches per plant might be attributed to better growth and vigor of these entries. The difference between the numbers of branches/plant dependent to the number of days from planting to emergence and flowering time. Similar results were earlier reported for growth periods in table potato cultivars by Kumar *et al.*, 2008. Reported that branch density has positive correlation with tuber number and size.

#### Number of leaves/plant

Analysis of variance for number of leaves revealed highly significant difference among cultivars of potato evaluated (Table 1). Number of leaves was highest (503a) in Harmes followed by (270.90b). Lowest number of leaves was noted in (164.77c) in Triplo followed by Zina Red (183.20). Khan *et al.*, (2013).

#### Leaf area (cm<sup>2</sup>)

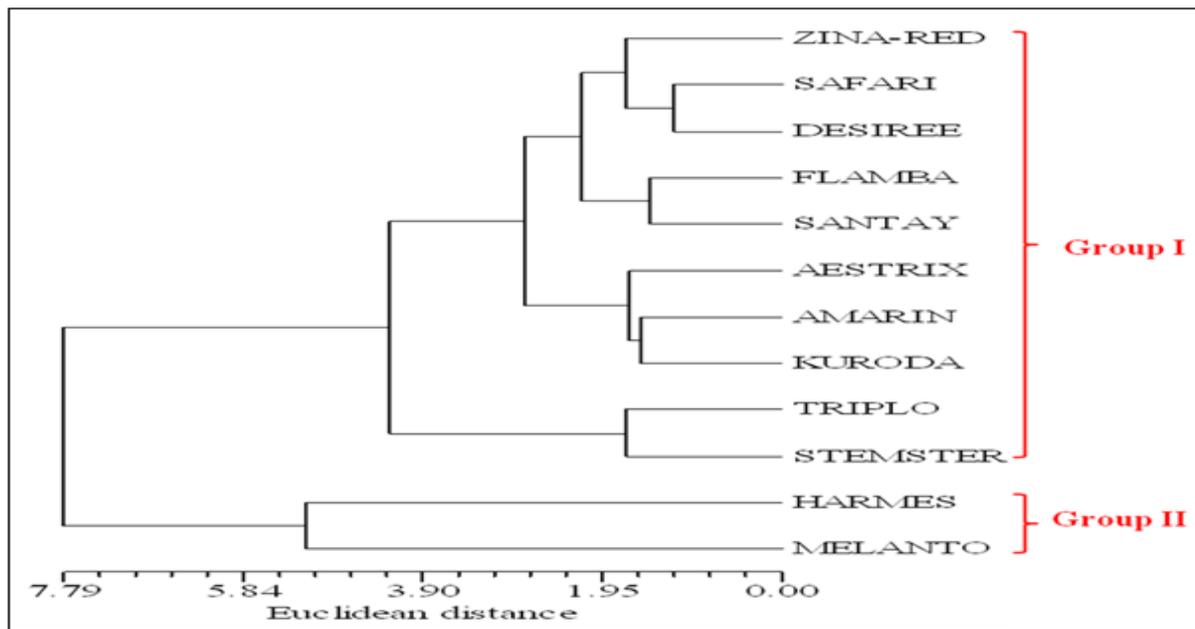
Average leaf area was measured according to the standard procedure. Results regarding leaf area were nonsignificant at five percent level as shown by (Table 1). Results showed that there was a great variation among different genotype, Harmes shown maximum leaf area 41.667a while Triplo, Safari and stemster shows minimum leaf area 13.333e. Khan *et al.*, (2013).

#### Number of tuber per plant

The results regarding tuber/plant of the different potato varieties are presented in (Table 1). Maximum number (19.76a) of tuber\plant was attained by Harmes followed by (14.80ab) in Melanto and (13.53abc) in Aestrix. Minimum (5.56d) number of tuber was found in Triplo followed by Zina Red (7.67cd). Tuber yield in potato is influenced by genotype (Patel *et al.*, 2008), such varietal response was also observed by Pandey (2004) Gupta *et al.*, (2009) Singh and Ahmad (2008).

#### Tuber Weight (gm)

The results indicated that tuber weight differed significantly among different potato cultivars (Table 1). Weight of tubers has a vital role in potato production and yield. It is obvious from the results that the highest tuber weight (0.833a) was gained by Harmes followed by Melanto (0.733ab), Amarin (0.600bc). Whereas lowest tuber weight was attained by Safari (0.233f) and Triplo (0.266ef). Ravikant and Chandha (2009) reported significant variations among different cultivars while analyzing average tuber weight, number of tubers/plant and yield. Tuber yield in potato is influenced by genotype (Patel *et al.*, 2008), such varietal response was also observed by Pandey (2004) Gupta *et al.*, (2009) Singh and Ahmad (2008).



**Fig. 1.** UPGMA Cluster observed in 12 genotypes of Potato on the basis of morphological characterization.

#### *Yield (t/ha)*

The results regarding yield (t/ha.) of different potato varieties are presented in (Table 1). The results indicated that yield differed significantly among different potato varieties. It is obvious from the results that the higher yield 41.66a t/ha was shown by Harmes which was significantly higher than all other varieties. It shows better adoptability of variety Harmes in the area of Islamabad during spring season. Second high yielding variety in this study was found Melanto with values of 35.00ab t/ha. The Poorest performance was shown by Triplo, Safari and Stemster with the value of 13.33e t ha<sup>-1</sup>. This low yield was due to poor emergence as well as low stems and poor soil coverage.

In Bangladesh, CIP clone 88163 and variety Provento produced 30.8 and 31.0 t/ha compared to 28.8 and 27.3 t/ha yield in Cardinal and Diamont respectively Behjati *et al.*, (2013).

#### *Cluster and principal component analysis*

Cluster and principal component analysis for the phenotypic relationship among the Potato cultivars was assessed by the unweighted Pair Group Method with an Arithmetic average (UPGMA). The UPGMA cluster analysis diagram grouped the 12 genotypes of potato into two major clusters, I and II, having additional sub-clusters within the both clusters (Figure 1).

The genotypes were closely related with each other within the first group, whereas relatively diverse within the second group. Group-I consisted of 10 genotypes which showed clear division into two subgroups; I and II. Subgroup I comprised of genotypes named as Zina red, Safari, Desiree, *Flamba*, *Santay*, *Aestrix*, *Amarin* and *Kuroda*. Genotypes Triplo and Stemster were included into sub group II. Group II comprised of only 2 cultivars including Harmes and Melanto, without additional sub groups. The cluster analysis placed most of the high yielding genotypes (Harmes and Melanto) with greater number of branches/plant, number of leaves/plant, number of tubers/plant and tuber mass/plant together, showing a high level of genetic association among these cultivars. The dendrogram showed that the genotypes that were derivatives of genetically similar type, clustered together. In this study, a number of traditional and improved cultivars originally from various regions, did not form distinct groups. These were interspersed with each another in the cluster analysis, which confirmed no association between the cultivars growth patterns and their geographic origin under investigation. Das *et al.*, (2010) also use cluster analysis to find the diversity among thirty genotypes of *Solanum tuberosum*.

Haan *et al.*, (2013) reported the comparative genetic composition of ex- and in-situ landrace cultivar populations from a potato diversity hotspot in the Andes and UPGMA clustering method applying NTSYS-pc 2.2 software. Carputo *et al.*, (2013) study the 12 potato species, and realizing the importance of diversity not only to choose the best parents for breeding, but also to design proper crossing schemes and selection strategies. The phenotypic diversity of 25 potato varieties was examined by Abebe *et al.*, (2013) and they grouped 25 varieties were grouped into three main clusters based on the distance matrix following the hierarchical agglomerative clustering method known as UPGMA (unweighted pair group method with arithmetic mean). Cluster I, which was the largest, contained 18 varieties followed by clusters II and III, with 3 and 4 varieties, analysis of the average taxonomic genetic distance based on 18 qualitative characteristics using the Euclidean distance function revealed considerable divergence (genetic distance value ranged from 0.24 to 0.72) among the studied varieties.

In the present study, Euclidian distance for morphological traits ranged from 1.17 to 7.79. Lowest Euclidean distances among *Safari* and *Desiree* depicts their highest similarity (98.83% with each other respectively) followed by *Flamba* and *Santay* (98.57 %). Highest dissimilarity was found between *Harmes* and *Triplo* (92.21%).

The data presented in the current study showed great phenotypic and biochemical diversity among the potato genotypes collected from different agro-ecological zones of Pakistan. Relating to phenotypic diversity to origin/collecting sites of the germplasm indicated the potential for future exploration mission in the area and taking samples with maximum genetic distance to assemble broad based genetic resources of potato for future use. Potato could be a good nutritional alternative to meet the challenges of food crises.

### Conclusion

In conclusion, we have presented some characteristics of local potato genotypes grown in Pakistan and have not been characterized.

An analysis of morphological and agronomic traits showed that genetic variation was high among the locally available potato genotypes sampled. Clusters obtained in this study may provide a basis for further study, and it could be selected separately for each in terms of traits investigated further as potato breeding programs. These evaluations could assist breeders to select and identify genotypes with desirable characteristics for inclusions in variety breeding programs.

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