

*Full Length Research Paper*

# Morphological characterization of potato (*Solanum tuberosum* L.) germplasm under rainfed environment

M. Fareed Khan\*, Najma Tabassum, Anila Latif, Abdul Khaliq and Mansoor Malik

Department of Plant Breeding and Molecular Genetics, Faculty of Agriculture, Rawalakot, University of Azad Jammu and Kashmir, Pakistan.

Accepted 11 May, 2012

In this study, 11 potato cultivars were assessed based on their genetic variability of different morphological parameters, including emergence percentage (%), date of flowering, plant height (cm), number of leaves per plant, average leaf area, number of flowers per plant, number of stems per plant, and number of fruits per plant. All of these characters showed a high level of variation among all the varieties. Locally developed advanced line SH-19 showed maximum emergence percentage (92.33%). Among other characters, Asterix, Smeengi and SH-19 produced considerable amount of flowers per plant (37.39). Romeo touched the line, indicating three stems per plant and was grouped into a separate group 'A'. Cultivars Smeengi and Aziza, Leonardo and Avalanche carried 2.67 and 1 stem per plant respectively. Moreover, the 11 cultivars were ranked and grouped into 5 groups (A to E). For number of fruits/plant, means were not very much different from one another. The pyramid of variety Asterix was the highest, indicating that this genotype is efficient in bearing fruits. Variation was observed for tuber yield among all the cultivars and was not significantly high between replications of all varieties. Overall, there was highly significant variation for this character among all the potato cultivars. All the 11 varieties were grouped into seven homogeneous groups (A to G) in which the means are not significantly different from one another. Almost every variety was in a different group. Average yield for all the varieties ranged from 22 to 7 kg. Pyramid height for Desiree was highest, indicating that maximum yield (22 kg) was produced by this variety.

**Key words:** Germplasm, potato, *Solanum tuberosum* L. Rawalakot, Azad Kashmir.

## INTRODUCTION

Potato (*Solanum tuberosum* L.) ranks as the most important food crop in the world after rice, wheat and maize (Akkale et al., 2010). Improvement in potato crop is essential as it is one of the most important cash crops of the country. It is widely cultivated over an area of 2024.9 thousand hectares, with an average yield of 18.1 tons per hectare (Anonymous, 2009). Because of nutritional value and broad adaptability, its consumption is increasing day by day. Unfortunately, potato production in Pakistan is much lower than the other potato growing

countries because of the low yield of the adapted varieties. A narrow genetic base of the germplasm used for development of cultivars is another reason for the low yield of potato varieties grown in this region.

Knowledge about germplasm diversity and genetic relationships among potato germplasm could be a valuable aid in crop improvement strategies. A number of methods are currently available for analysis of genetic diversity in germplasm accessions, breeding lines and segregating populations. These methods have mostly relied on pedigree data, morphological data, agronomic performance data, biochemical data, and molecular (DNA-based) data (Mohammadi and Prasanna, 2003). Molecular markers can be used for detection of relationships among different germplasm lines in seed banks, search of

\*Corresponding author. E-mail: [drmfareedkhan@yahoo.com](mailto:drmfareedkhan@yahoo.com).  
Tel: 05824 4443718.

**Table 1.** Analysis to estimate variation among 11 potato cultivars for emergence percentage.

Source	Degree of freedom	Sum of square	Mean square	F-value (cal.)	F-value (tab.)
Variety	10	2225.52	222.552	19.61**	2.35
Replication	2	10.97	5.485		
Error	20	227.03	11.352		
Total	32	2463.52			

\*Highly significant.

promising heterotic groups for hybrid breeding, identification of duplicates in seed banks, and assessment of the level of genetic diversity present in germplasm pool and its flux over time (Schulman, 2006). The analysis for rapid amplified polymorphic DNA (RAPD) markers is quick and simple, although results are sensitive to laboratory conditions. There is increasing number of reports where RAPDs have been successfully used to estimate genetic variability in potato cultivars (Chimote et al., 2007; Jaime et al., 2007; Sayed et al., 2008). Markers have also been used in the *Solanum* genus for the analysis of biodiversity and phylogenetic studies (Ritter, 2000; Spooner et al., 2005).

The aims of the present study were to estimate diversity among commercial cultivars grown under Azad Jammu and Kashmir (AJK) agro-climatic conditions using morphological markers and determine the genetic relationships existing among these cultivars.

## MATERIALS AND METHODS

### Breeding materials

The analysis was made on 11 commercial potato cultivars including one advanced breeding line (SH-19). Tubers of cultivar Cardinal (01) Romeo (02), Asterix (03), Leonardo (04), Smeengi (05), Avalanche (06), VDW-004 (07), Folva (08), Aziza (09), Desiree (10), and SH-19 (11) were collected from Potato Breeding Research sub-Station, Murree, Pakistan. The experiment was conducted in research fields of Faculty of Agriculture, Rawalakot, Azad Kashmir. Date of sowing was 12/04/2010 and harvesting was done on 09/08/2010, with a temperature range of 20 to 25°C.

### Statistical analysis

Experiment was designed according to randomized complete block design (RCBD) with three replications for each of the cultivar. Data for each of these characters were recorded at different growth stages and subjected to statistical analysis.

### Cluster analysis

Data from all the replications for each character were ordered against each of the cultivar. These data were used to calculate the Pearson's correlation coefficients using statistical computer software SPSS version 10. These correlation coefficients were taken as similarity coefficients and a rectangular similarity matrix was established. This similarity matrix was then used to generate a

dendrogram based on morphological characters using unweighted pair group method with averages (UPGMA) clustering method and employing sequential, agglomerative hierarchic and non-overlapping (SAHN) clustering, a sub program of Numerical Taxonomy and Multivariate Analysis System, version 2.1 (Rohlf, 2001).

## RESULTS

### Morphological parameters

#### *Emergence percentage*

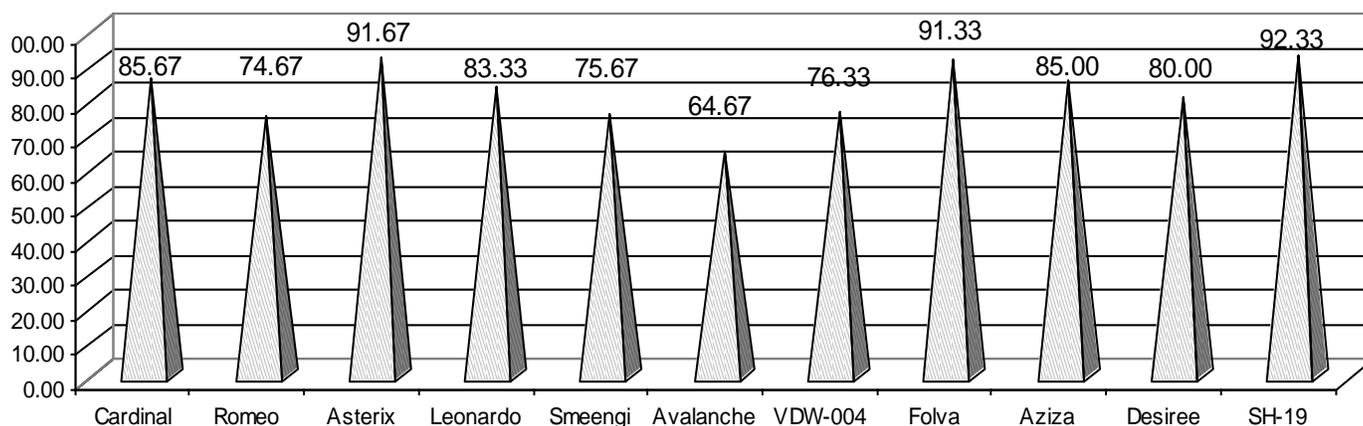
Most of the potato cultivars showed a considerable variation for this trait. Varieties were compared for their emergence percentage by subjecting their mean values for this trait to least significant difference test (LSD) and all the varieties were grouped into five homogenous groups, where the means were not significantly different from one another (Tables 1 and 2). SH-19 and Asterix were in group 'A' by producing highest number of seedlings and this was also visible from the heights of pyramids for these varieties (Figure 1). Romeo, Smeengi and VDW-004 appeared in the same group 'C'. Overall, emergence for all these varieties, except few, was reasonable. By using ANOVA (Table 1), phenotypic and genotypic variances and heritability estimates were computed. This trait showed a high value (95%) for heritability. Phenotypic and genotypic variances were 22.26 and 21.12, respectively, while genetic advance was 9.47 (Table 3).

#### *Plant height (cm)*

All potato cultivars showed variation for this character. Variation within replications was less as compared to between replications for each cultivar. Varieties Romeo and SH-19 showed maximum uniformity. All the varieties were grouped into four homogeneous groups (A to D), and among these groups, the means were not significantly different (Table 4). Pyramids for varieties Smeengi, Avalanche, VDW-004, Folva and Aziza attained almost similar heights, indicating that these are identical for plant height. All the aforementioned varieties also acquired the same homogeneous group 'C'. Average

**Table 2.** LSD all-pair wise comparison test of emergence percentage for potato varieties.

Variety	Mean	Homogeneous group
11	92.33	A
3	91.66	A
8	91.33	AB
1	85.66	BC
9	85.00	C
4	83.33	C
10	80.00	CD
7	76.33	D
5	75.66	D
2	74.66	D
6	64.66	E

**Figure 1.** Emergence percentage recorded after 50% shoot emergence.**Table 3.** Variance estimates based on emergence % age of potato cultivars.

Component	Symbol	Value
Phenotypic variance	$\sigma_p^2$	22.26
Genotypic variance	$\sigma_g^2$	21.12
Heritability	$h^2$	95%
Genetic advance	AG	9.47
Coefficient of variation	CV	4.11%
LD at 0.05 alpha	LSD	5.7

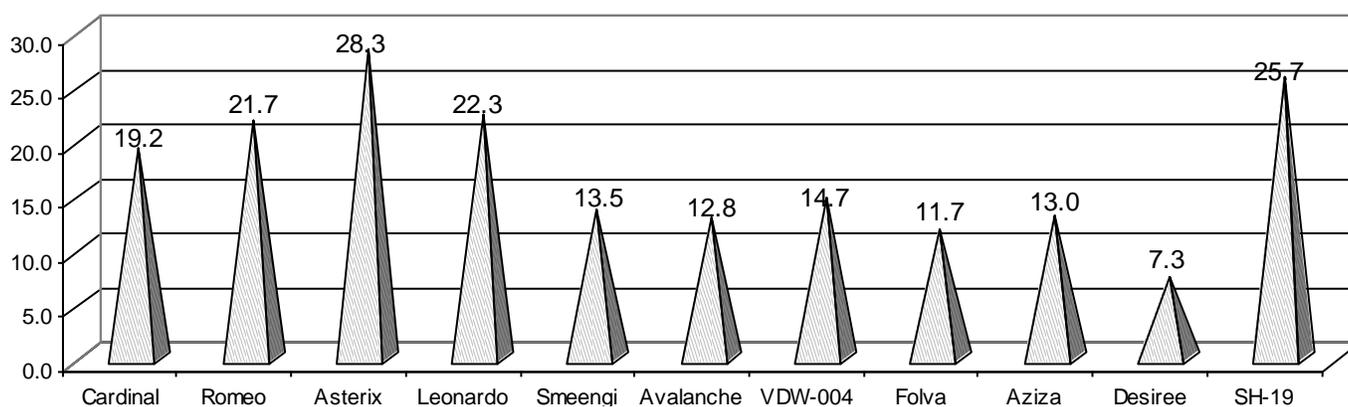
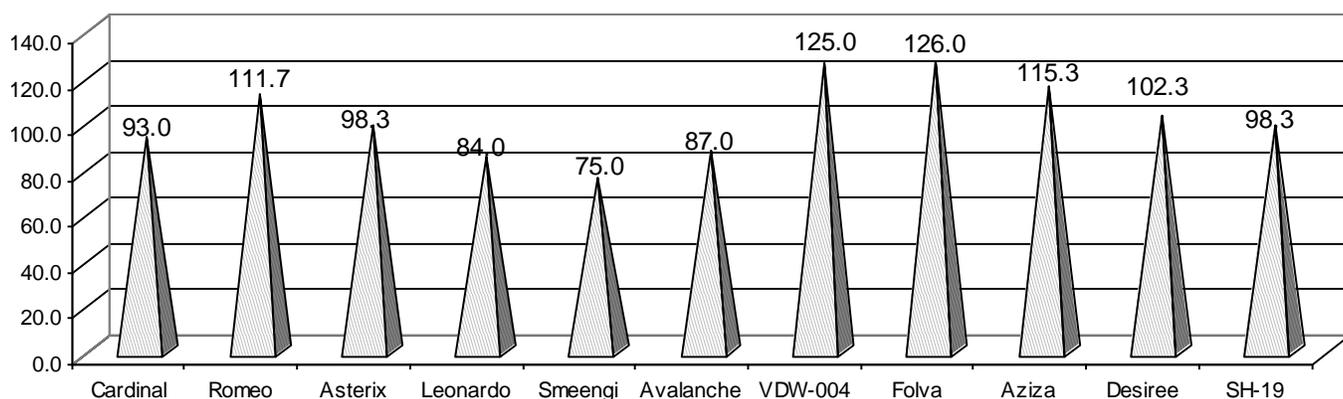
plant height for these varieties varied from 14.66 to 11.6 cm only. Two varieties Asterix and SH-19 from group 'A' attained maximum height also visible from their pyramids in Figure 2. Furthermore, the genotypic and phenotypic variances for average plant height were 12.58 and 12.92, respectively. Heritability of this character was found to be maximum (97%) and genetic advance was 7.31.

#### **Number of leaves per plant**

All the 11 varieties were grouped into five homogeneous groups (A to E) in which the means were not significantly different from one another. Varieties Folva and VDW-004, Leonardo and Avalanche, Asterix and SH-19 appeared to be similar in their pyramidal height, indicating almost

**Table 4.** LSD all-pair wise comparison test of plant height for potato varieties.

Variety	Mean	Homogeneous group
3	28.33	A
11	25.66	A
4	22.33	B
2	21.66	B
1	19.23	B
7	14.66	C
5	13.50	C
9	13.00	C
6	12.83	C
8	11.66	C
10	7.33	D

**Figure 2.** Average plant heights in centimeters of the 11 potato cultivars.**Figure 3.** Average number of leaves per plant of 11 potato cultivars.

similar number of leaves per plant for these varieties (Figure 3). Range of means (126-75) for number of leaves per plant indicates considerable variability among

these cultivars (Table 5). This trait was used to calculate the phenotypic and genotypic variances, heritability, genetic advance and coefficient of variation. Phenotypic

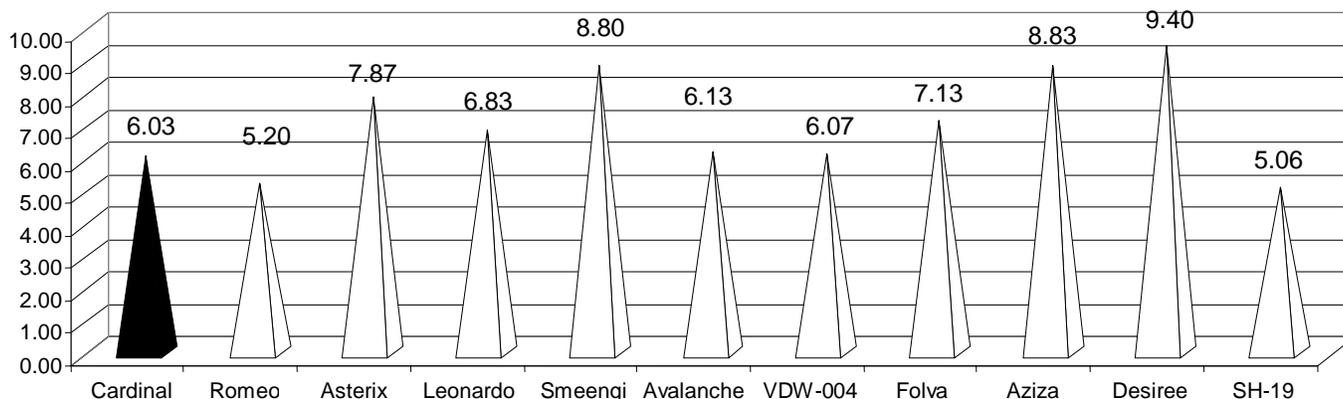
**Table 5.** LSD all-pair wise comparisons test of number of leaves per plant for potato varieties.

Variety	Mean	Homogeneous group	Variety	Mean	Homogeneous group
8	126.00	A	11	98.33	BC
7	125.00	A	1	93	C
9	115.33	AB	6	87	CD
2	111.67	AB	4	84	D
10	102.33	BC	5	75	E
3	098.33	BCD			

Probability at 5% level.

**Table 6.** LSD All-pair wise comparisons test of average leaf area.

Variety	Mean	Homogeneous group	Variety	Mean	Homogeneous group
10	9.40	A	6	6.13	DE
9	8.83	A	7	6.06	E
5	8.80	A	1	6.03	E
3	7.86	B	2	5.20	F
8	7.13	BC	11	5.06	F
4	6.83	CD			

**Figure 4.** Average leaf area in (cm<sup>2</sup>) of potato cultivars.

and genotypic variance exhibited the values of 82.77 and 71.76, respectively. A high level of heritability (87%) was found for this character and genetic advance was 17.45.

#### Average leaf area (cm<sup>2</sup>)

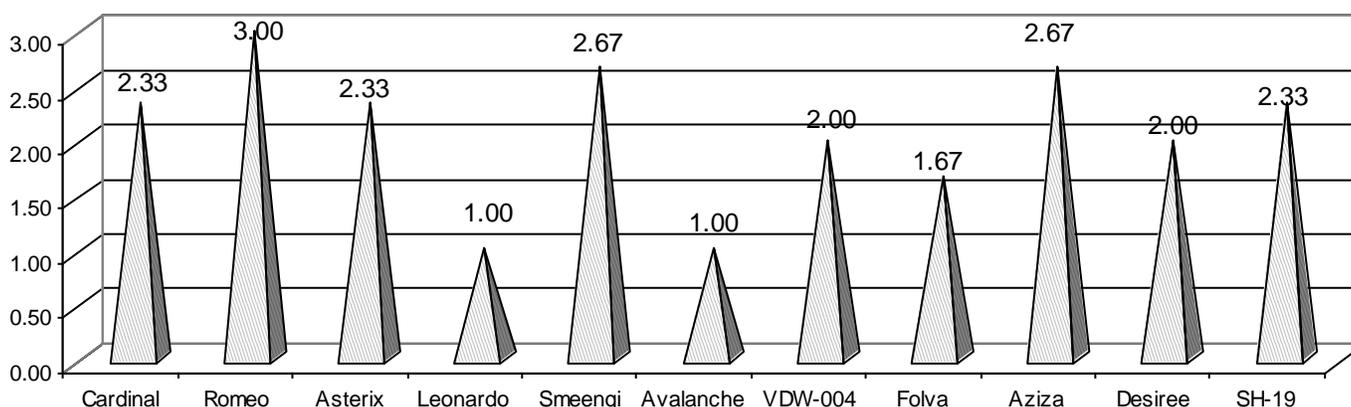
Leaf area for all the varieties was measured using leaf area meter and means for each replication were computed. These mean values for leaf area was used to find out the variation for this trait among all the potato varieties. Within replication, the variation for this trait was extremely low; indicating the reliability of the experiment

and a low value for coefficient of variation confirmed this. All the varieties were grouped into six homogenous groups in which means were not significantly different from one another (Table 6). Three varieties Smeengi, Aziza and Desiree occupied group 'A'. Desiree showed maximum leaf area (9.40 cm<sup>2</sup>). Lowest pyramid height for average leaf area was observed for SH-19 (Figure 4.).

In further analysis, phenotypic and genotypic variances, heritability and genetic advance were calculated. Heritability for this trait was found to be 97% with phenotypic and genotypic variances of 0.68 and 0.66, respectively, while genetic advance was determined as 0.75.

**Table 7.** LSD All-pair wise comparisons test of number of stems per plant.

Variety	Mean	Homogeneous group	Variety	Mean	Homogeneous group
2	3.00	A	7	2.00	BC
5	2.66	AB	10	2.00	BC
9	2.66	AB	8	1.66	CD
1	2.33	ABC	4	1.00	D
3	2.33	ABC	6	1.00	D
11	2.33	ABC			

**Figure 5.** Pyramids indicating mean values for number of stems per plant.

### Number of stems/plant

Variation for this character was found in almost all the 11 potato cultivars (Table 7). It was found that the variation between replications was higher as compared to within replications. Within replication again the variation was higher as compared to other characters. All the varieties were ranked and grouped into four groups with non-significant differences. Pyramid for cultivar Romeo touched the line, indicating three stems per plant (Figure 5) and were grouped into a separate group 'A'. Cultivars Smeengi and Aziza, Leonardo and Avalanche carried 2.67 and 1 stem per plant, respectively. Among other estimates, the phenotypic and genotypic variances were computed to be 0.13 and 0.11, respectively. Moreover, the heritability estimates remained at 85%, indicating higher heritability of this trait. The genetic advance for number of stems per plant was 0.58.

### Number of fruits/plant

Analysis was conducted to evaluate the genetic diversity among 11 potato cultivars based on fruiting. There was much less variation within replication as compared to between replications. Varieties Asterix and Avalanche showed minimum variation within their replications. All

the 11 cultivars were ranked and grouped into 5 groups (A to E) in which the means were not very much different from one another. LSD values revealed that all the means were separated by just a figure of 0.49 (Table 8). Pyramid of variety Asterix was the highest, indicating that this genotype is efficient in bearing fruits (Figure 6) and was grouped into a separate group 'A'. Five varieties Cardinal, Romeo, Avalanche, Aziza and SH-19 showed similar heights and were grouped into group 'A'.

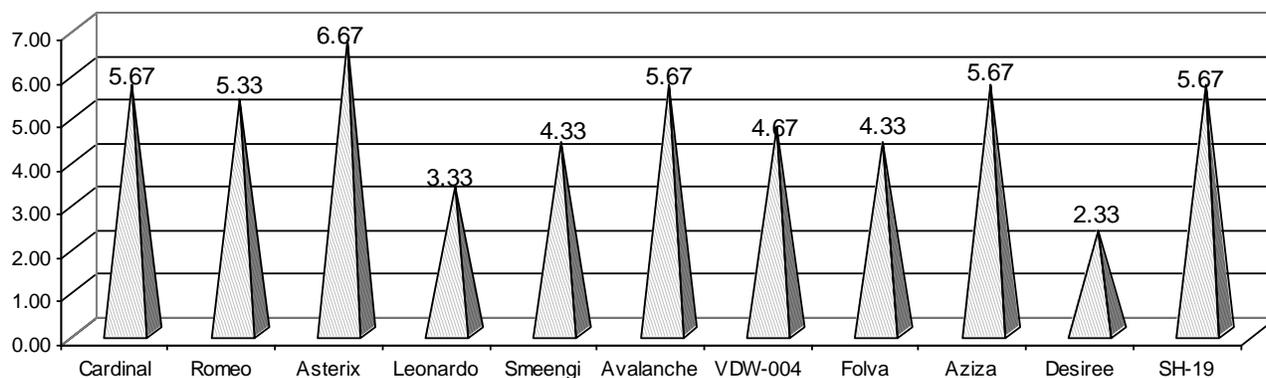
Other estimates to assess the contribution of this trait toward yield were also made. Genotypic and phenotypic variances were calculated to be 0.43 and 0.46, respectively. Heritability estimate was found to be 92% with genetic advance of 1.35.

### Tuber yield (kg/ha)

Tuber yield was analyzed statistically, and variation was observed for this trait among all the cultivars, which was not significantly high between replications of all varieties. Varieties were grouped into 7 homogeneous groups (A to G) in which the means were not significantly different from one another. Almost every variety was in a different group. Average yield for all the varieties ranged from 7 to 22 kg (Table 9 and Figure 7). Pyramid height for Desiree was highest, indicating that maximum yield (22 kg) was

**Table 8.** LSD All-pair wise comparisons test of number of fruits per plant.

Variety	Mean	Homogeneous group	Variety	Mean	Homogeneous group
3	6.66	A	7	4.66	BC
1	5.66	AB	5	4.33	CD
6	5.66	AB	8	4.33	CD
9	5.66	AB	4	3.33	DE
11	5.66	AB	10	2.33	E
2	5.66	BC			

**Figure 6.** Number of fruits/plant for potato cultivars.**Table 9.** LSD All-pair wise comparisons test for average yield of 11 potato cultivars.

Variety	Mean	Homogeneous groups	Variety	Mean	Homogeneous gGroup
10	22.00	A	4	14.00	DE
9	19.00	B	6	13.33	E
8	17.00	BC	5	12.33	EF
11	17.00	BC	1	10.33	F
7	15.66	CD	2	7.00	G
3	14.33	DE			

produced by this variety. Also the tuber size and weight of tuber per plant was highest for this variety which contributed its high yield. Phenotypic and genotypic variance obtained the values 5.09 and 4.91, respectively. A high level of heritability (96%) was found for this character and genetic advance stayed at 4.57.

### Cluster analysis

Data for all the morphological characters were subjected to Pearson's correlation coefficient and the correlations among these varieties were calculated. These correlation values were used to generate similarity matrixes which consequently led to a development of a dendrogram following UPGMA clustering method using a computer prog-

ram NTSysPC 2.1. All the varieties were clustered into four groups (I, II, III and IV) at a similarity coefficient of 0.81, indicating a reduced level of diversity among genotypes (Figure 8). Group I appeared to be the largest and can be further subdivided into two subgroups (from top to down). First subgroup contained three varieties, Cardinal, Desiree and Avalanche. The former two varieties appeared similar at 0.98 similarity level, indicating high level of similarity between these two. A local advanced line (SH-19) developed at Potato Research Station, (substation Murree) was clustered into the second subgroup group along with Aziza within group I.

Cultivar Smeengi which produced maximum weight of potato tubers was clustered into group III along with Leonardo at similarity coefficient of 0.82. Groups II and IV also comprised two varieties each. Group IV, including

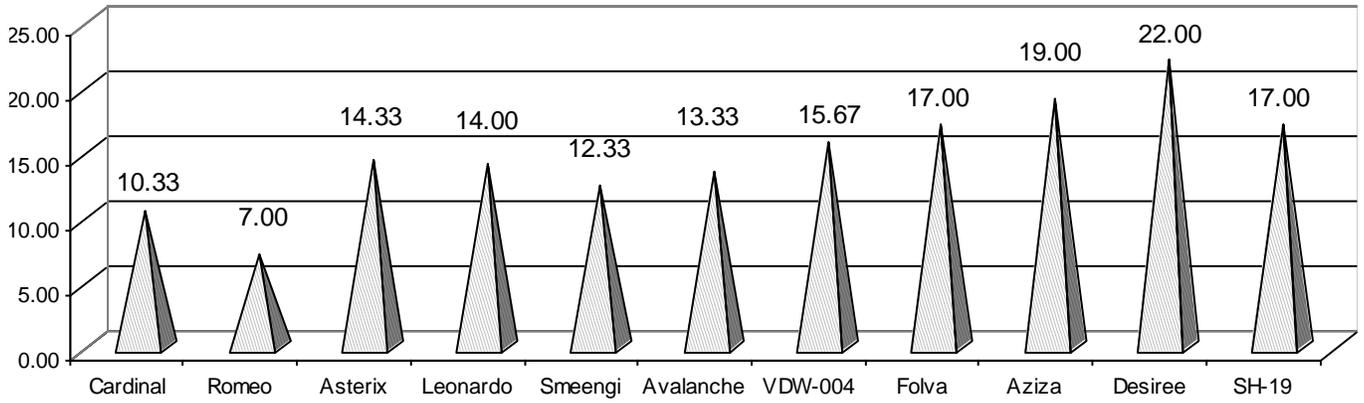


Figure 7. Tuber yield of potato cultivars.

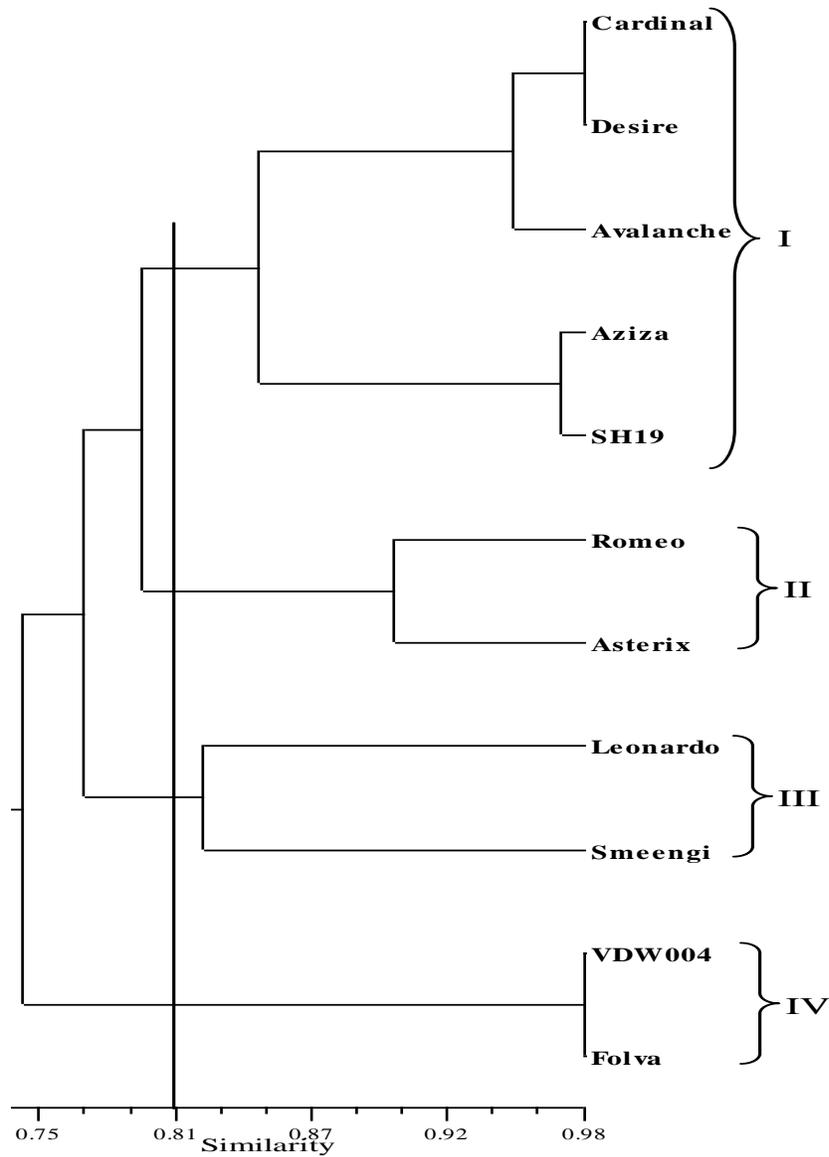


Figure 8. Morphologically dendrogram of potato cultivars for their phylogenetic analysis.

Folva and VDW-004, had a similarity coefficient of 0.74 from the rest of the varieties and 98% similarity with each other. The former variety showed maximum dissimilarity (53%) with Cardinal. Similarity of advanced line SH-19 ranged from 58 (with Asterix) to 98% (with Cardinal).

## DISCUSSION

Morphologically, all the 11 potato cultivars were evaluated for 13 characters which comprised of emergence percentage, date of flowering, plant height, number of leaves/plant, average leaf area, number of flowers/plant, number of stems/plant, number of fruits/plant and tuber yield. Different tools such as morphological characters (Gaur et al., 1999), RAPD (Pattanayak et al., 2002 and Chakrabarti et al., 2001) and simple sequence repeat (SSR) (Chimote et al., 2004) have previously been employed to study genetic diversity in potato varieties. Different views regarding genetic base of potato varieties have been analyzed. Morphological parameters have also been used in combined analysis to evaluate potato varieties for diversity studies (Jaime et al., 2007).

In the present study, 11 potato cultivars were characterized for genetic divergence based on different phenotypic parameters. Similar type of results were reported by Key van et al., (2008) previously. Emergence percentage ranged from 92.33 to 64.33%. Most of the varieties showed good emergence with maximum emergence from SH-19 (92.33%) followed by Asterix (91.66%) and Folva (91.33%). Khaliq (2002) reported 95% emergence percentage in cultivars Ultumash and 80% in cardinal. Moreover, plant height analysis in this study revealed a high level of variation among the 11 potato cultivars. The parameter ranged from 7.33 cm for Desiree to 28.3 cm for Asterix, giving a wide range of variation in between. These results are similar to those reported by Ahmed (1984) while characterizing local genotypes of *Hippophae rhamnoides* and screening of exotic germplasm for yield and growth in potato respectively. In addition, variation for the number of leaves per plant was observed among all the varieties. This character has more importance in case of tuber crops like potato. Photosynthesis in such crops results in the increased tuber size, which in turn increases the final yield. In the current analysis, Folva and VDW-004 produced maximum number of leaves (126 and 125). Average number of leaves ranged from 126 to 75. However, phenotypical variation (82.77) was more as compared to the genotypic variation (71.76). High heritability has been achieved for number of leaves per plant (Sarwar, 1972; Bashir, 1991). Leaf area also showed a high level of variation among all the cultivars. Mean values for average leaf area ranged from 9.40 to 5.06 cm<sup>2</sup>. Desiree produced maximum leaf area, followed by Aziza and Asterix (Table 4). Similar results were reported by Sarwar (1972) and Khaliq (2002).

Furthermore, a high level of variation was observed for number of stems per plant. Mean values for this trait varied from 3 to 1. However, among replications, up to 5 tillers per plant was observed. On average, Romeo produced the highest number of tillers, followed by Smeengi and Aziza, each producing pyramids showing a value of 2.67 (Figure 5). Khaliq (2002) reported 5.55 number of stems per plant for the variety Cardinal and 2.66 for Ultumash. Phenotypic and genotypic variances showed a low value for each. Heritability value was reasonable for number of stems per plant among the genotypes investigated. The number of fruits per plant revealed a considerable amount of variation among all the cultivars. Mean values ranged from 6.66 to 2.33, indicating a high level of variation for this trait. Asterix lead by producing 6.66 numbers of fruits per plant. It was followed by the Cardinal, Avalanche, Aziza and SH-19, attaining a height of 5.67 fruits per plant (Figure 6). Homogeneous grouping of the cultivars indicated that most of the cultivars appeared similar by same grouping. These findings agree with those of Sarwar (1972). Moreover, average yield was found to have variation for all the varieties ranging from 22.00 to 7.00 kg. Desiree performed best from rest of the cultivars by producing 22 kg of yield. These results are in comparison with those reported earlier by Estevez et al. (1982) and Khaliq (2002).

When cluster analysis was performed, all the varieties were grouped into seven groups. Dendrogram was generated by calculating simple matching similarity coefficients using UPGMA clustering method and employing sequential, agglomerative, hierarchic and non-overlapping (SAHN) clustering technique (Figure 8). Ahmed et al. (2010) and Isaacs et al. (2003) used a similar kind of clustering analysis while examining genetic diversity among wheat and sunflower, respectively. The results of genetic similarity analysis showed that a moderate level of divergence did exist among the varieties. In current analysis, morphological similarity values ranged from 0.53 to 0.98. In an earlier report, Key van et al. (2008) found that similarity values ranged from 0.55 to 1.00 while screening the potato cultivars for salt tolerance. In another diversity analysis, Sayed et al. (2008) observed 0.48 to 0.83 similarity values.

In general, the low values for the coefficients of variation for almost all the trait studied indicate that the errors contributed by the experimental parameters were not significant. There is need to characterize potato germplasm grown under AJK agro-climatic conditions and the genotypes best responding should be selected. This will also be useful for developing descriptors for potato crop grown in AJK.

## REFERENCES

- Ahmed M (1984). Relationship of stem density with seed size and weight in four potato cultivars. *J. Agric. Res.*, 232(A):309-312.

- Ahmed MF, Iqbal M, Masood MS, Rabbani MA, Munir M (2010). Assessment of genetic diversity among Pakistani wheat (*Triticum aestivum* L.) advanced breeding lines using RAPD and SDS-PAGE. *Elect. J. Biotech.* 13(3):213-223.
- Akkale C, Yildirim Z, Yildirim MB, Kaya C, Öztürk G, Tanyolaç B (2010). Assessing genetic diversity of some potato (*Solanum tuberosum* L.) genotypes grown in Turkey by using AFLP marker technique. *Turk. J. Field Crops* 15(1):73-78.
- Anonymous (2009). Economic Survey of Pakistan, Economic Advisor's Wing Finance Division, Government of Pakistan, Islamabad.
- Bashir A (1991). Screening of exotic germplasm for yield and growth in potato. Thesis (M.Sc), Department of Horticulture, University of Agriculture, Faisalabad.
- Chakrabarti SK, Pattanayak D, Naik PS (2001). Fingerprinting Indian potato cultivars by random amplified polymorphic DNA (RAPD) markers. *Potato Res.* 44:375-387.
- Chimote VP, Pattanayak P, Naik PS (2004). Semi-automated simple sequence repeat (SSR) analysis reveals narrow genetic base in Indian potato (*Solanum tuberosum* L.) cultivars. *Biol. Plant* 48:517-522.
- Chimote VP, Pattanayak D, Naik PS (2007). Molecular and morphological divergence studies in Indian potato varieties. *Ind. J. Biotech.* 6(4):216-223.
- Estevez A, Arzuga J, Correa S (1982). Study of characters related to yield in potato. *Cult. Tropicales* 4(3):549-558.
- Gaur PC, Naif PS, Kaushik SK, Chakrabarti SK (1999). Indian potato varieties, Technical Bulletin-51, Central Potato Research Institute, Shimla, pp. 1-38.
- Isaacs SM, Manivannan N, Muralidharan V (2003). Genetic diversity analysis using RAPD marker in inbred lines of sunflower (*Helianthus annuus* L.). *Helia*, 26(39):59-66.
- Jaime SS, Ulloa DM, Rodríguez LA (2007). Molecular description and similarity relationships among native germplasm potatoes (*Solanum tuberosum* ssp. *tuberosum* L.) using morphological data and AFLP markers. *Elect. J. Biotech.* 10(3):115-120.
- Key van A, Ehsanpour AA, Balai G, Mostajeran A (2008). *In vitro* screening of potato (*Solanum tuberosum* L.) cultivars for salt tolerance using physiological parameters and RAPD analysis. *American-Eurasian J. Sust. Agric.* 3(2):159-164.
- Khaliq A (2002). Genetic characterizations of cultivated potato (*Solanum tuberosum*) varieties by cyto-morphic and molecular techniques under agro-climatic conditions of district Poonch, Azad Kashmir. A thesis submitted to Deptt. Of Plant Breeding and Genetics, University College of Agriculture Rawalakot, Azad Jammu and Kashmir.
- Mohammadi SA, Prasanna BM (2003). Analysis of genetic diversity in crop plants salient statistical tools and considerations. Review and interpretation. *Crop Sci.* 43:1235-1248.
- Pattanayak D, Chakrabarti SK, Naik PS (2002). Genetic diversity of late blight resistant and susceptible Indian potato cultivars revealed by RAPD markers. *Euphytica* 128:183-189.
- Ritter A (2000). Aplicacion de la biotecnologia a la mejora genetica de la patata 2000. Vitoria-Gasteiz, Espana. p. 8.
- Rohlf FJ (2001). NTSYS-pc. Numerical taxonomy and multivariate analysis system, version 2.1. Exeter Software, New York.
- Sarwar M (1972). Evaluation of some important exotic cultivars of potato (*Solanum tuberosum* L.). MSc Thesis Department of Horticulture, University of Agriculture, Faisalabad.
- Schulman AH (2006). Molecular markers to assess genetic diversity. *Springer Sci. Bus.* 10:1222-1226.
- Sayed JA, Rasool G, Shah SRU, Iqbal A. (2008). Analysis of Genetic Diversity in Pakistani Potato Cultivars by Using Randomly Amplified Polymorphic DNA (RAPD) Primers. *American-Eura. J. Sust. Agric.* 2(1):50-53.
- Spooner DM, Mclean K, Ramsay G, Waugh R, Bryan GAJ (2005). Single domestication for potato based on multilocus amplified fragment length polymorphism genotyping. *Proceedings of the National Academy of the United States of America*, 102(41): 14694-14699.