MOLECULAR AND MORPHOLOGICAL EVALUATION OF POTATO GENOTYPES CULTIVATED IN SANDY SOIL

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Potato (Solanum tuberosum L.) is considered as an important crop worldwide and it comes after the cereal crops in the economical importance (Mahgoub et al., 2015). Over the years, potato has become an important crop for both farmers and consumers worldwide. In Egypt, potato was introduced on the small scale during the nineteenth century, it is nowadays the second most important vegetable crop after tomato; and Egypt is one of the largest producers and exporters of potatoes in Africa (Ramadan, 1981). Potatoes are grown in Egypt for local consumption, export and processing industries (Abd-Elgawad and Youssef, 2008). Furthermore, beside carbohydrates it is a good source of vitamins, mainly B and C complexes and mineral salts.

Production of potato (Solanum tuberosum L.) takes a very important
place in the world agriculture, with a potential production of about 270 million tons which harvested from 12.2 million hectares of planted area. The cultivated potato area was increased in Egypt especially in the new lands under new irrigation systems by adding the organic fertilizers and pesticides to the irrigation water. Moreover, Potato is one of the main crops in Egypt where the production is about 4.80 million tons which harvested from 0.178 million hectare (FAOSTAT, 2013). The success of potato breeding programs is depending on identification of the amount and distribution of genetic diversity in the gene pool, to identify the gaps in germplasm collections and to develop effective conservation and management strategies (Esfahani et al., 2009). The correct identification, characterization and evaluation of conserved genotypes are fundamentally important for genetic improvement programs and for detecting duplicates in germplasm banks (Goncalves et al., 2008; Sudre et al., 2010; Abdellatif et al., 2012). The genetic deviation can be evaluated based on agronomic, morphological, biochemical, physiological and molecular characteristics (Goncalves et al., 2008). Studies with molecular markers have made significant contributions for understanding the genetic diversity. When compared with other types of markers, they present a greater number of polymorphic loci, which allows distinguishing between accessions that may have similar to the morphological and agronomical traits (Abouzied et al., 2013).

Several methods were recommended for potato cultivar identification such as RAPD (McGregor et al., 2000), AFLP (Van Treuren et al., 2004), SSR (Ghislain et al., 2004) and ISSRs (Miz et al., 2008; Aguilera et al., 2011; Hardiganl et al., 2014). ISSR marker is often chosen to perform these studies considering the advantages regarding high speed and polymorphism (Abdellatif and Soliman, 2013), therefore, it clearly shows genetic variations among studied potato cultivars (Mahfouz et al., 2012). The superiority of ISSR marker over other techniques has been identified in several studies. Prevost and Wilkinson (1999) found that five ISSR primers were adequate to distinguish among 35 varieties of potatoes. Aversano et al. (2009) and Mumtaz et al. (2010) identified thirteen ISSR primers to investigate the broad variability in cytoplasmic and nuclear DNA of Solanum genotype regenerated plantlets and emphasized that ISSR markers, due to its fast, high reproducibility and low cost, it offered useful information, and suitable for the analysis of genetic variations in this method of proliferation.

This study was conducted to investigate the genetic relationships among 26 potato (Solanum tuberosum L.) genotypes grown in Egyptian sandy soil using both morphological characteristics and molecular markers. The potato growth, yield
and tuber quality were evaluated in this study.

**MATERIAL AND METHODS**

**Plant material**

Twenty-six potato genotypes including five cultivated genotypes (Spunta, Desiree, Sophie, Red Sun and Safari) have been kindly obtained from HZPC and DE NIJS potato companies (Table 1). These potato genotypes were used for both morphological and molecular experiments.

**Morphological experiment**

Two field experiments were carried out during the two growing seasons of 2014 and 2015 at the farm of Environmental Studies and Research Institute, University of Sadat City, Minoufiya, Egypt. The morphological experiments were carried out in order to study the characteristics of yield and its components and quality of tubers under sandy soil conditions to evaluate these twenty-six potato genotypes. The physical and chemical analyses of the soil are presented in Table (2). The twenty-six potato genotypes were cultivated in a randomized complete block design (RCBD) with three replications. Each genotype was planted in three rows of 3 m long and 0.9 m wide. Tubers from each genotype were sown at the end of January in the two growing seasons (2014 and 2015) and spaced at 25 cm apart. The normal agricululture practices for growing potato plants were applied whenever required.

**Total yield and tuber quality**

After 120 days of planting, tubers from each plot were harvested, weighted, counted and graded for recording the following data; number of tubers/plant, average weight of tuber (g), average yield of tubers/plant (g), total yield/plot and then calculated as ton/ Feddan. The potato tubers were graded into four sizes: grade 1 (more than 70 mm in diameter); grade 2 (55 to <70 mm in diameter); grade 3 (35 to >55 mm in diameter); and grade 4 (less than 35 mm in diameter). Tubers of each grade were weighted and its percentage from the total marketable yield was calculated.

**Morphological Statistical analysis**

The recorded morphological data were subjected to statistical analysis of variance as described by Snedecor and Cochran (1967) to identify significant treatments and/or interaction effects using ‘F test’ by the SAS program. The means of the treatments were compared by the Student’s Least Significant Difference (LSD) value at a 5% of probability level. The averages of the morphological traits were calculated for each genotype (the averages of the two seasons and the three replications). The averages of the morphological data were used for constructing the two-way hierarchical analysis using JMP IN 7 software (Lehman et al., 2005; SAS, 2003).
Molecular marker analysis

1. DNA extraction

About a 100 mg of the tubers of each genotype was grounded in liquid nitrogen using a pestle and mortar to the fine powder. The grounded samples were used for DNA isolation using the DNA extraction kit (iNtRON Biotech., Inc.) according to their manufacturer instruction and the concentration was adjusted at 25 ng/µl.

2. PCR amplification and electrophoresis

Ten random 10-mer primers were used for RAPD analysis (Table 3). The PCR reaction was contained a 50 ng DNA template, 7.5 µl of PCR master mix (iNtRON Biotech., Inc.) and 0.25 µm of the primer. The volume was adjusted up to 15 µl using ddH2O. The PCR program consisted of an initial denaturation step at 94°C for 5 min., followed by 35 cycles of a template denaturation step at 94°C for 40 seconds, primer annealing step at 32°C for 35 seconds and primer extension step at 72°C for 40 seconds, followed by storage at 10°C. The products were separated on a 1.5% agarose gel electrophoresis and then gels were photographed for analysis.

Ten ISSR primers were used to perform ISSR analysis (Table 3). PCR reaction was performed in a 15 µl of reaction volume containing 7.5 µl of master mix, 50 ng (2 µl) of DNA template and 0.25 µm of the primer. PCR program was carried out for 36 cycles at 94°C for 45 seconds, 49°C for 50 seconds and 72°C for 45 seconds. A primary denaturation step at 94°C for 5 min. and a final extension step at 72°C for 7 min were applied. PCR products were separated on a 2% agarose gel electrophoresis, and then gels were photographed for analysis.

3. Data handling and cluster analysis

Both RAPD and ISSR gels were scored for presence or absence of the amplified fragments for each primer as 1 or 0, respectively. The scored data of both ISSR and RAPD markers were used to generate dendrograms. Similarity matrices were calculated using Jaccard coefficient’s algorithm (Sokal and Sneath, 1963) and used to construct dendrograms using UPGMA method (Rohlf, 1998). Dendrogram was used to determine the genetic relationships among the different investigated genetic material under study. The analysis was conducted using NTSYS-pc software (Rohlf, 1998).

RESULTS AND DISCUSSION

Morphological experiment of yield and its components

The analysis of variance (ANOVA) of the potato yield traits and its components showed highly significant differences among genotypes, growing seasons and the interaction between genotypes and growing seasons for all the studied traits (Table 4).

Some traits showed better performances during the growing season of 2015 such as tuber weight in grams, tuber
yield/plant in grams and the percentage of tuber size (35-55 and 55-70 mm in diameter traits); while the other parameters (e.g. total yield/Feddan and percentage of tuber size <35 and >70 mm in diameter) were better in the growing season of 2014 (Table 5).

The NAP genotype gave the highest significant values for the yield parameters (yield/plant 960 g and total yield/Feddan 16107 Kg) overall the other genotypes and the NIZ genotype gave the highest significant value (146.5 g) for the tuber weight trait. On the other hand, OH, Cleopatra and Sophie potato genotypes showed the least significant values for tuber weight (50.9 g), yield/plant (550 g) and total yield/Feddan (8663 Kg), respectively (Table 6). These results are in good harmony with those reported by Bekhit et al. (2005) and Danilchenko et al. (2005). Similar results were recorded by Kate et al. (2005), Levy and Tai (2013), Khan et al. (2013) and Habib et al. (2014). They found highly significant differences among potato genotypes concerning potato yield and its components.

Tuber size traits

LSD values of the tuber size traits showed that the highest percentage of the tuber size with more than 70 mm in diameter was obtained from the NAP; (60.2%); and the lowest percentage of both sizes less than 35 mm (6.6%) and 35-55 mm in diameter (12.8%) were also obtained from the same genotype (Table 6). On the other hand, the highest percentage of the small size; <35 mm in diameter (55.2%); and the least percentage of the big size; >70 mm in diameter (0.7%); were obtained from the OH genotype. The highest significant percentages of the medium tuber size were recorded for the genotypes Vr808 for the size 35-55 mm (35.2%) and Cleopatra for the size 55-70 mm in diameter (49.7%); while the lowest significant percentage of the size 55-70 mm in diameter (15.9%) was noted for the Mondia genotype (Table 6). Such differences in the total yield and its components among the tested cultivars may be related to the differences in their vegetative growth vigor and to their response to fertilizers and suitable weathering to growth characteristics. These results are in agreement with those reported by Arafa (2004), Alva et al. (2008) and Alva et al. (2012). Khan et al. (2013), on the contrary, reported that pyramid height for Desiree cultivar indicated that maximum tuber yield, size and weight traits among all potato cultivars which contributed to its high yield.

Morphological Two-way Hierarchical Cluster Analysis

A two-way hierarchical cluster analysis was carried out using JMP IN 7 software for the twenty-six potato genotypes among the seven morphological traits. According to this analysis, the potato genotypes were separated into three main cluster groups. The first cluster was included the ALF, Liseta, Mozart, NIZ, Red Sun, Safari, Spunta, LYS, Adora, Mondial, RAF and NAP genotypes. The second group was included the
Red Scarlett, Desiree, MEM, FIS, RAF, Fortus, Vr808, EIB, Colomba, Dynamica, Astrix and Cleopatra genotypes. The third cluster was included the OH and Sophie genotypes (Fig. 1).

In the second way of the hierarchical clustering (traits clustering), the morphological traits were separated into two clusters. The first cluster included four morphological traits (tuber weight, tuber size >70 mm in diameter, yield/plant and total yield/Feddan) while the second cluster contained three morphological traits (tuber sizes of <35 mm and from 35-55 and 55-70 mm in diameter) (Fig. 1). This result means that the yield traits and its component were clustered together along with the trait of tuber size >70 mm in diameter. Therefore, the tuber size >70 mm in diameter trait may be strongly correlated with the yield traits in potato plants.

Similar results were reported by Haydar et al. (2007), who studied the genetic diversity of tuber yield traits and its components of 30 potato genotypes and they reported that the genotypes were grouped into six clusters and the maximum diversity was contributed by tuber weight/plant.

**Molecular analysis**

Ten RAPD and ten ISSR primers were used for PCR amplification of the 26 potato genotypes. The amplification of fragments was in different sizes depending upon the genotype (Fig. 2). All RAPD and the half of the ISSR primers produced polymorphic fragments (Table 3). The total amplified fragments generated from each RAPD primer were ranged from 14 fragments for the OPW07 primer to 32 fragments for the OPB10 primer, while they were ranged from six to 13 fragments for the ISSR UBC818 and UBC811 primers, respectively. The polymorphic fragments percentage of the RAPD primers was ranged from 76.19% for the OPR02 primer to 88.46% for the OPA09 primer; and from 72.72% to 90.9% for the ISSR UBC817 and UBC810 primers, respectively (Table 3). Comparable results were reported by Abbas et al. (2008), who obtained amplification of 26.3 alleles per potato genotype using RAPD primers. They mentioned that the size of score able fragments were ranged from approximately 250 to >1000 bp. Similarly, Gauchan et al. (2012) produced 29 different marker fragments of which 69.0% were polymorphic. The same result was recorded for ISSR markers, whereas, Nováková et al. (2010) reported that both SSR and ISSR markers afford sufficient polymorphism for variety identification in Czech potato variety. Torabi-Giglou et al. (2015) studied the genetic diversity of wild and cultivated potato and they found that the average numbers of score able fragments which produced per primer using ISSRs were eight polymorphic fragments for all genotypes and the UBC826, UBC820 and UBC824 primers gave the best results for all attributes.

**RAPD cluster analysis**

Dendrogram was established depending upon the RAPD data (Fig. 3).
According to the cluster analysis, the Mondial genotype was separated at the uppermost of the dendrogram apart of the other genotypes and the Red Sun genotype was separated at the lowermost of the dendrogram. The other 24 potato genotypes were separated into five clusters. The first cluster was located at the uppermost part of the dendrogram and contained the NAP, Safari, Adora, RAF, Cleopatra, RAF and Mozart genotypes. The second cluster was included the EIB, ALF, Spunta, NIZ, OH and FIS genotypes. The third cluster was involved the Desiree, Dynamica, MEM, LYS, Asterix and Sophie genotypes. The fourth cluster was contained the Fortus and Vr808 genotypes while the last cluster included the Liseta, Red Scarlett and Colomba genotypes (Fig. 3). Genetic diversities among potato genotypes were identified by several researchers (Abbas et al., 2008; Rocha et al., 2010; Gauchan et al., 2012; Hoque et al., 2013). All of them found a high level of genetic diversity among potato genotypes using cluster analysis.

**ISSR cluster analysis**

According to the ISSR analysis, the Mozart and ALF genotypes were separated apart of all other genotypes at the lower most of the dendrogram while the Mondial, Sophie, Liseta, NAP and Red Sun genotypes were distributed separately throughout the dendrogram (Fig. 4). The other genotypes were separated into four clusters. The first cluster included the Cleopatra, EIB, OH, Adora, FIS and Vr808 genotypes. The second cluster contained RAF, Spunta, Fortus, Dynamica and Safari genotypes. The third cluster contained the Bartina and Asterix genotypes. The fourth cluster included the NIZ, Desiree, LYS, MEM, Red Scarlett and Colomba genotypes (Fig. 4). Nováková et al. (2010) discriminated genetic relationships among twenty potato varieties using cluster analysis and they reported that the similarity values among these varieties were ranged between 65-80%. On the other hand, Torabi-Giglouet al. (2015) mentioned that pairwise species matrix of Neigenetic distance were varied from 0.058 to 0.645 among some potato genotypes based on ISSR marker.

Thus, it can be concluded that both morphological and molecular markers could be efficiently used to study genetic diversity in potato genotypes. Although the morphological characteristics are affected with the environment, their results could be supported by the molecular markers results.

**SUMMARY**

Twenty-six potato genotypes including seventeen cultivars were used to investigate the genetic diversity of potato plants (*Solanum tuberosum* L.) grown in Egyptian sandy soil using both morphological characteristics and molecular markers. The analysis of variance (ANOVA) of the potato yield traits and its components showed highly significant differences among the genotypes, the growing seasons and the interaction between genotypes and the growing seasons for all the studied traits. The NAP geno-
type gave the highest significant values for the yield traits and the highest percentage of the tuber size more than 70 mm in diameter trait. The NIZ genotype gave the highest significant value (146.5 g) for the tuber weight trait. On the other hand, OH, Cleopatra and Sophie potato genotypes showed the least significant values for tuber weight and tuber size traits. According to the two-way hierarchical cluster analysis, the potato genotypes were separated into three main cluster groups, while in the second way of the hierarchical clustering (traits clustering), the morphological traits were separated into two clusters. According to RAPD cluster analysis, the Mondial genotype was separated at the uppermost of the dendrogram apart of the other genotypes and the Red Sun genotype was separated at the lowermost of the dendrogram. The other 24 potato genotypes were separated into five clusters. Depending upon ISSR cluster analysis; the Mozart and ALF genotypes were separated apart of all other genotypes at the lowermost of the dendrogram, while the Mondial, Sophie, Liseta, NAP and Red Sun genotypes were distributed separately throughout the dendrogram. The other genotypes were separated into four clusters. Thus, it can be concluded that both morphological and molecular markers could be efficiently used to study the genetic diversity among potato genotypes. Although the morphological characteristics are affected with the environment, their results could be supported by the molecular markers results.

REFERENCES


MOLECULAR AND MORPHOLOGICAL EVALUATION OF POTATO

British Biotechnology J., 3: 2231-2927.


Table (1): Sources and some morphological characteristics of potato genotypes that used in this study.

<table>
<thead>
<tr>
<th>No.</th>
<th>Genotypes</th>
<th>Skin Color</th>
<th>Source</th>
<th>Cross breeding</th>
<th>Maturity</th>
<th>Flesh color</th>
<th>Shape</th>
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<tbody>
<tr>
<td>1</td>
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<td>Y</td>
<td>HZPC</td>
<td>SPUNTA x VE 66-295</td>
<td>L</td>
<td>LY</td>
<td>LO</td>
</tr>
<tr>
<td>2</td>
<td>NAP</td>
<td>Y</td>
<td>HZPC</td>
<td>Unknown</td>
<td>L</td>
<td>LY</td>
<td>O</td>
</tr>
<tr>
<td>3</td>
<td>Cleopatra</td>
<td>R</td>
<td>HZPC</td>
<td>ZPC 50 35 x DESIREE</td>
<td>E</td>
<td>LY</td>
<td>ROO</td>
</tr>
<tr>
<td>4</td>
<td>Mozart</td>
<td>R</td>
<td>HZPC</td>
<td>REDSTAR x CAESAR</td>
<td>ME</td>
<td>Y</td>
<td>O</td>
</tr>
<tr>
<td>5</td>
<td>RAF</td>
<td>Y</td>
<td>HZPC</td>
<td>Unknown</td>
<td>ME</td>
<td>LY</td>
<td>OLO</td>
</tr>
<tr>
<td>6</td>
<td>EIB</td>
<td>Y</td>
<td>HZPC</td>
<td>Unknown</td>
<td>ME</td>
<td>LY</td>
<td>OLO</td>
</tr>
<tr>
<td>7</td>
<td>ALF</td>
<td>DR</td>
<td>HZPC</td>
<td>Unknown</td>
<td>ME</td>
<td>W</td>
<td>RLO</td>
</tr>
<tr>
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<td>NIZ</td>
<td>DR</td>
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<td>ME</td>
<td>Y</td>
<td>RLO</td>
</tr>
<tr>
<td>9</td>
<td>Spunta</td>
<td>Y</td>
<td>DE NIJS</td>
<td>Bea x USDA 96-56</td>
<td>Medium E</td>
<td>Light Y</td>
<td>Long O/long</td>
</tr>
<tr>
<td>10</td>
<td>OH</td>
<td>DR</td>
<td>HZPC</td>
<td>Unknown</td>
<td>ME</td>
<td>LY</td>
<td>ROO</td>
</tr>
<tr>
<td>11</td>
<td>FIS</td>
<td>Y</td>
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<td>L</td>
<td>CREM</td>
<td>RO</td>
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<tr>
<td>12</td>
<td>Adora</td>
<td>Y</td>
<td>HZPC</td>
<td>PRIMURA x ALCMARIA</td>
<td>VE</td>
<td>LY</td>
<td>O</td>
</tr>
<tr>
<td>13</td>
<td>Bartina</td>
<td>R</td>
<td>HZPC</td>
<td>SATURNA x ZPC 62- 75</td>
<td>L</td>
<td>Y</td>
<td>ROO</td>
</tr>
<tr>
<td>14</td>
<td>VR 808</td>
<td>DY</td>
<td>HZPC</td>
<td>LADY CLAIRE x ATLANTIC</td>
<td>E</td>
<td>Y</td>
<td>RO</td>
</tr>
<tr>
<td>15</td>
<td>Fortus</td>
<td>Y</td>
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<td>ME</td>
<td>Y</td>
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<td>HZPC</td>
<td>CARRERA x AGATA</td>
<td>E</td>
<td>Y</td>
<td>ROO</td>
</tr>
<tr>
<td>18</td>
<td>Red Scarlett</td>
<td>R</td>
<td>HZPC</td>
<td>ZPC 80 O239 x MANS.MGB78-286</td>
<td>ME</td>
<td>Y</td>
<td>OLO</td>
</tr>
<tr>
<td>19</td>
<td>Desiree</td>
<td>R</td>
<td>DE NIJS</td>
<td>Urgenta x Depesche</td>
<td>Medium L</td>
<td>Light Y</td>
<td>OLO</td>
</tr>
<tr>
<td>20</td>
<td>Dynamica</td>
<td>R</td>
<td>HZPC</td>
<td>CORNADO x RZ- 86-2918</td>
<td>M</td>
<td>LY</td>
<td>OLO</td>
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<tr>
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<td>MEM</td>
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<td>ME</td>
<td>Y</td>
<td>ROO</td>
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<td>Asterix</td>
<td>R</td>
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<td>L</td>
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<td>24</td>
<td>Sophie</td>
<td>Y</td>
<td>DE NIJS</td>
<td>TE 93-26-02 x Lady Claire</td>
<td>Medium L</td>
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<td>Round</td>
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<td>25</td>
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<td>R</td>
<td>DE NIJS</td>
<td>Inova x Amadeus</td>
<td>Medium E</td>
<td>Y</td>
<td>O</td>
</tr>
<tr>
<td>26</td>
<td>Safari</td>
<td>Y</td>
<td>Greenvale AP</td>
<td>Obelix x Amadeus</td>
<td>Medium E</td>
<td>Y</td>
<td>RO</td>
</tr>
</tbody>
</table>

Y: Yellow, R: Red, DR: Dark red, E: Early, L: Late, O: Oval, VE: very early, LY: Late Yellow, ROO: Round Oval/ Oval, OLO: Oval Long/Oval and LO: Long Oval
Table (2): Some physical and chemical characteristics of the soil and nutrients of Bentoniet in Sadat City.

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<tr>
<th>PH (KCl)</th>
<th>EC Mg/l</th>
<th>% OM</th>
<th>% CaCO₃</th>
<th>Ceccmol. K g⁻¹</th>
<th>% Sand</th>
<th>% Silt</th>
<th>% Clay</th>
<th>Texture</th>
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<tr>
<td>7.72</td>
<td>8.23</td>
<td>0.116</td>
<td>1.45</td>
<td>13.90</td>
<td>69.90</td>
<td>20.50</td>
<td>7.66</td>
<td>Sandy loam</td>
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<tr>
<td>7.39</td>
<td>0.37</td>
<td>13.10</td>
<td>7.85</td>
<td>300</td>
<td>14.98</td>
<td>3.01</td>
<td>1.82</td>
<td></td>
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Table (3): RAPD and ISSR primer sequences and their polymorphisms percentage.

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<th>RAPD markers</th>
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<td>Primer</td>
<td>Sequence</td>
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<td>OPA07</td>
<td>GAAACGGGTG</td>
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<td>CTTGACGCA</td>
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<td>OPW07</td>
<td>CTGGACGTCA</td>
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Table (4): Analysis of variance of seven morphological traits calculated from two growing seasons of the 26 potato genotypes.

<table>
<thead>
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<th>Source</th>
<th>DF</th>
<th>Mean of squares</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>Tuber weight (g)</td>
</tr>
<tr>
<td>Genotypes</td>
<td>25</td>
<td>51127.6**</td>
</tr>
<tr>
<td>Years</td>
<td>1</td>
<td>2070.2**</td>
</tr>
<tr>
<td>Genotypes x Years</td>
<td>25</td>
<td>17903.9**</td>
</tr>
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</table>
Table (5): LSD differences between the two growing seasons (2014 and 2015) of seven morphological traits. $\alpha = 0.050$, $t = 2.00758$.

<table>
<thead>
<tr>
<th>Years</th>
<th>Tuber weight (g)</th>
<th>Yield/plant (g)</th>
<th>Total yield/Fed. (Kg)</th>
<th>% tuber size &lt;35</th>
<th>% tuber size (35-55)</th>
<th>% tuber size (55-70)</th>
<th>% tuber size &gt;70</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015</td>
<td>109.4 A</td>
<td>734.1 A</td>
<td>11533.2 B</td>
<td>17.3 B</td>
<td>23.863 A</td>
<td>28.2 A</td>
<td>30.6 B</td>
</tr>
<tr>
<td>2014</td>
<td>100.5 B</td>
<td>680.7 B</td>
<td>12115.2 A</td>
<td>17.7 A</td>
<td>23.861 B</td>
<td>27.6 B</td>
<td>30.8 A</td>
</tr>
</tbody>
</table>

Levels not connected by same letter are significantly different.

Table (6): LSD differences among the 26 potato genotypes between of seven morphological traits recorded during the two growing seasons (2014 and 2015). $\alpha = 0.050$, $t = 2.00758$.

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Tuber weight (g)</th>
<th>Yield/plant (g)</th>
<th>Total yield/Fed. (Kg)</th>
<th>% of tuber size (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>&lt;35</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>35-55</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>55-70</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>&gt;70</td>
</tr>
<tr>
<td>Mondial</td>
<td>100.5 Q</td>
<td>718.5 M</td>
<td>11993.5 M</td>
<td>18.8 J</td>
</tr>
<tr>
<td>NAP</td>
<td>133.1 C</td>
<td>950.0 A</td>
<td>16107.0 A</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Cleopatra</td>
<td>91.7 T</td>
<td>550.0 Z</td>
<td>9999.5 Y</td>
<td>19.1 H</td>
</tr>
<tr>
<td>Mozart</td>
<td>121.6 G</td>
<td>775.5 E</td>
<td>13016.0 N</td>
<td>15.9 Z</td>
</tr>
<tr>
<td>RAF</td>
<td>108.8 L</td>
<td>767.0 G</td>
<td>12857.0 H</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>EIB</td>
<td>102.9 O</td>
<td>814.5 C</td>
<td>13697.5 C</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>ALF</td>
<td>109.3 J</td>
<td>708.0 O</td>
<td>11816.0 N</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>NIZ</td>
<td>146.5 A</td>
<td>805.5 D</td>
<td>13546.0 D</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Spunta</td>
<td>128.7 D</td>
<td>640.5 U</td>
<td>11110.5 R</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>OH</td>
<td>50.9 Z</td>
<td>558.5 Y</td>
<td>9155.0 X</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>FIS</td>
<td>88.7 W</td>
<td>715.0 N</td>
<td>11435.5 P</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Adora</td>
<td>121.9 F</td>
<td>734.0 K</td>
<td>12274.5 K</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Bartina</td>
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<td>729.0 L</td>
<td>12188.0 L</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Vr 808</td>
<td>89.8 U</td>
<td>648.0 S</td>
<td>10744.0 T</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Fortus</td>
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<td>578.5 W</td>
<td>9510.5 W</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Liseta</td>
<td>115.2 H</td>
<td>820.0 B</td>
<td>13799.0 B</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Colomba</td>
<td>93.9 S</td>
<td>743.0 I</td>
<td>12435.0 J</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Red Scarlett</td>
<td>107.9 M</td>
<td>646.0 T</td>
<td>10705.0 U</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Desiree</td>
<td>102.6 P</td>
<td>698.0 P</td>
<td>11638.0 O</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Dynamica</td>
<td>89.3 V</td>
<td>770.0 F</td>
<td>12918.5 G</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>MEM</td>
<td>109.2 K</td>
<td>680.0 Q</td>
<td>11316.0 Q</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>LYS</td>
<td>114.5 I</td>
<td>656.5 R</td>
<td>10898.0 S</td>
<td>6.6 Y</td>
</tr>
<tr>
<td>Asterix</td>
<td>74.9 X</td>
<td>759.0 H</td>
<td>12718.5 I</td>
<td>6.6 Y</td>
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<tr>
<td>Sophie</td>
<td>57.0 Y</td>
<td>559.0 X</td>
<td>8663.0 Z</td>
<td>6.6 Y</td>
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<tr>
<td>Red Sun</td>
<td>138.8 B</td>
<td>736.5 J</td>
<td>13321.5 E</td>
<td>6.6 Y</td>
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<tr>
<td>Safari</td>
<td>127.4 E</td>
<td>631.5 V</td>
<td>10566.0 V</td>
<td>6.6 Y</td>
</tr>
</tbody>
</table>

Levels not connected by same letter are significantly different.
Fig. (1): Two-way hierarchical cluster analysis of the 26 potato genotypes and the seven morphological traits collected from the two growing seasons.

Fig. (2): DNA polymorphasim of potato genotypes based on RAPD-PCR using OPA07 primer and ISSR-PCR using UPC817 primer.
Fig. (3): Cluster analysis using the UPGMA method for the 26 imported potato genotypes based on RAPD-PCR, according to the similarity index of Jaccard.

Fig. (4): Dendrogram generated using UPGMA analysis, showing relationships among potato genotypes, using ISSR data.