Genetic Diversity of Some Tomato *Lycopersicon esculentum* Mill Varieties in Iraq Using Random Amplified Polymorphic DNA (RAPD) Markers

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Abstract

This study was conducted to evaluate the genetic diversity among 19 tomato varieties (determinate and indeterminate) cultivated in Iraq using polymerase chain reaction based DNA markers (PCR based DNA markers) ; Random Amplified Polymorphic DNA (RAPDs). To achieve PCR reactions ,total genomic DNA was isolated from fresh leaves (2 weeks old). The average yields of DNA were in the range of 100-295 ng/μl with a purity ranging between 1.8-1.9. RAPDs amplifications were performed for varieties fingerprinting by testing 27 Operon primers. DNA polymorphisms among varieties were scored within detectable amplified fragments (their numbers and molecular weight) after agarose gel electrophoresis and staining by ethidium bromide. These 27 primers produced 442 of main bands ,out of which 312 were polymorphic bands (70.5%) and 70 were monomorphic (15.8%) across all tested varieties.

Each selected primer produced between 60 bands (OPA-14) to 290 bands (OPD-13). DNA amplification products ranged in their size from 250 bp ( OPA-01, OPU-14, OPX-15,OPX-19,OPT-08 ) to 2755 bp (OPX-18). The highest number of polymorphic bands (21 bands) was produced by primer OPU-03 while, the lowest number of polymorphic bands (3 band) was produced by both primers OPA-14 and OPB-17.

The primers varied in their capacity in producing polymorphic amplified profiles among studied tomato varieties which individually reflected variety specific DNA profiles (fingerprints). The most important primers for this purpose were primers that produced more variety specific DNA profiles, such as OPD-13, OPT-08, OPW-04, OPA-04, OPA-15, OPB-18, OPU-03, OPC-09. The highest value of discrimination among varieties in this study was obtained by primer OPC-09 while the lowest discrimination value was produced by both primers OPA-14 and OPB-17. The primer efficiency ranged from 0.13 in (primer OPC-09) to 0.02 in (primer OPB-17). The lowest genetic distance was (0.2294) between varieties Oula and Shadylady, while, the highest genetic distance was (0.9459) between varieties Fotton and Special pack. Cluster analysis (phylogenetic tree) by unweighted pair-group method of arithmetic means (UPGMA) based dendrogram revealed that they were two main genetic groups (major clusters). The first small major clusters included four (4 varieties) while the second large major cluster included (15 varieties). The overall analysis of the results show that RAPDs markers are powerful tool in fingerprinting and revealing the genetic relationships among tomato varieties. The relationship among varieties was not concern to their morphological characters and geographical origins.

Key words: Genetic diversity; *Lycopersicon esculentum*; RAPD markers; genetic distance.
Introduction

Tomato (Lycopersicon esculentum) is one of the most important vegetable crops grown throughout the world, it is second important vegetable after potato because of its wider adaptability, high yielding potential and multipurpose uses (Sekhar et al., 2008). It is a member of family Solanaceae and significant vegetable crop of special economic importance in the horticultural industry worldwide (Heet al., 2003; Wang et al., 2005).

Tomato also used as model plant species to study the physiology and biochemistry of seed development, germination and dormancy (Suhartanto, 2002). Therefore, tomato is an excellent tool to improve knowledge on horticultural crops (Taylor, 1986; Kinet and Peet, 1997).

Tomato breeding projects have improved characteristics such as disease resistance, fruit abscission, soluble solids, fruit size, texture, flavor, pigmentation, and storage ability, thus, the improvement in yield and quality in self-pollinated crops like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. The success of hybridization programme depends upon selection of suitable parents of diverse origin (Sekhar et al., 2008).

Among molecular markers, RAPDs were the first PCR-based molecular markers to be employed in genetic variation analyses (Welsh and McClelland, 1990). The standard RAPD utilizes short synthetic oligonucleotides decamer (10 bases long) (Miesfeld, 1999). This technique has been widely used in diversity studies because, in addition to its low cost, it allows polymorphism to be detected in a simple and rapid manner (Abu Ali et al., 2011).

As improvement of the tomato crop would enhance agricultural productivity and facilitate food security (Fehmida and Ahmad, 2007), furthermore, characterization of varieties and hybrids which are of wider acceptance by farming community need to be studied in order to regulate their genetic purity during their multiplication and seed evaluation (Vishwanath et al., 2010).
Materials and Methods

A collection of tomato varieties with different growth habit (determinate and indeterminate) and certified sources, such as: GSN, Sanam, Helam, Oula, Kenanh, Douna, Shady lady, Dalal, Bushra, Warda, Fotton, Super regina, Carioca, Special pack, Mongal, Super marimond, Super Queen, Shahirah, Tamara.

DNA Isolation:

The Genomic DNA Mini Kit (Geneaid Biotech. Ltd; Taiwan Company) provides a quick and easy method for purifying total DNA (including genomic DNA, mitochondrial and chloroplast DNA) from plant tissue. DNA was isolated from leaves according to the method protocol.

PCR Amplification of RAPD-Primers:

According to the Experimental Protocol of AccuPower® TLA PCR PreMix, the PCR reaction mixture was prepared as follows: 1. 5 µl template DNA and 2 µl of primer (10 pmole/µl), were added to each AccuPower® TLA PCR PreMix tube. 2. Sterilized deionized distilled water was added to AccuPower® TLA PCR PreMix tubes to the final volume of 20 µl. 3. The tubes were mixed with vortex to dissolve the lyophilized blue pellet, and briefly spine down (all these steps were done in ice). A sequence was amplified individually using oligonucleotide primer (listed in Table 1).

Amplification were performed in thermocycler programmed according to annealing temperatures as follows: 1. one cycle of 5 min at 94°C, for 40 cycle of each 1 min at 94°C, 2 min at 40°C and 2 min at 72°C, with a final extension for one cycle of 5 min at 72°C (OPA-03, OPC-19, OPD-13, OPT-08, OPX-04, OPX-01, OPX-03, PX-04, OPX-15, OPX-18, OPN-06, OPX-19). 2. one cycle of 3 min at 94°C, for 45 cycle of each 20 sec at 94°C, 20 min at 37°C and 40 sec at 72°C, with a final extension for one cycle of 10 min at 72°C (OPA-14, OPG-17, OPX-15, OPU-03, OPB-17, OPU-14, OPB-18, OPV-19, OPC-08, OPC-09).

Table 1: Operon primers and their sequences.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5'→3')</th>
<th>Primer</th>
<th>Sequence (5'→3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>OPA-01</td>
<td>CAGGCCCTTC</td>
<td>OPX-01</td>
<td>CTGGGCACGA</td>
</tr>
<tr>
<td>OPA-02</td>
<td>TGCCGAGCTG</td>
<td>OPX-03</td>
<td>TGCCGAGTGTG</td>
</tr>
<tr>
<td>OPA-04</td>
<td>AATCGGGGCTG</td>
<td>OPX-04</td>
<td>CCGCTACCGA</td>
</tr>
<tr>
<td>OPA-10</td>
<td>GTGATCGGCAG</td>
<td>OPX-15</td>
<td>CAGACAAGGCC</td>
</tr>
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<td>TCTGTGCTGG</td>
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<td>GACTAGGTTGG</td>
</tr>
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<td>OPX-19</td>
<td>TGGCAAGGCA</td>
</tr>
<tr>
<td>OPB-17</td>
<td>AGGGGAACGAG</td>
<td>OPA-03</td>
<td>AGTCAGCCAC</td>
</tr>
<tr>
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<td>CCACACGCAGT</td>
<td>OPC-19</td>
<td>GTGGCCAGGCC</td>
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<td>OPC-08</td>
<td>TGGACCGGTG</td>
<td>OPD-13</td>
<td>GGGTGGACGA</td>
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<td>CTCACCGGTCC</td>
<td>OPN-06</td>
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<td>OPG-17</td>
<td>ACCAACCGACA</td>
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<td>OPW-04</td>
<td>CAGAAGCGGA</td>
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<tr>
<td>OPV-19</td>
<td>GGGTGTCACAG</td>
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</table>

Then amplified DNA were separated by electrophoresis in 1.2% agarose gels (stained with ethidium bromide) (3-4 hr, 70V).

Scoring Data of RAPD Products:

Presence of a product was identified as (1) and absence was identified as (0). By this way, data were scored for all genotypes, their amplification product and primers. The data then entered into NTSYS-PC (Numerical Taxonomy and multivariate Analysis System), Version 1.8 (Applied Biostatistics) program (Rohlf, 1993) using the
program editor. The data were analyzed using SIMQUAL (Similarity for Qualitative Data) routine to generate genetic similarity index (Nei and Li, 1979): GS = 2Nij (Ni+Nj). Nij is the number of RAPD bands in common between genotypes i and j, and Ni and Nj are the total number of RAPD bands observed for genotypes i and j.

**Results and Discussion**

Across all genomes tested higher number of main bands was generated by both OPV-19 and OPU-03 and higher number of amplified bands obtained in primer OPD-13 while lower number of both main and amplified bands obtained by using primer OPA-14. Table 2. The results of both primers OPD-13 and OPU-03 indicate their usefulness in future since they give distinctive fingerprint for all nineteen tested tomato varieties (Figure 1 and 2).

**Figure 1:** The amplification results obtained with primer OPD-13, lane M: DNA ladder and lanes 1-19: tomato varieties.

**Figure 2:** The amplification results obtained with primer OPU-03, lane M: DNA ladder and lanes 1-19: tomato varieties.

Data in Table 2 show that the size of scored bands ranged from 250 bp to 2755 bp, this was nearly close to data obtained by (Huh et al., 2011). Across all genomes tested higher number of main bands was generated by both OPV-19 and OPU-03 and higher number of amplified bands obtained in primer OPD-13 while lower number of both main and amplified bands obtained by using primer OPA-14. These variation mainly due to that some primers recognize a high number of annealing site, which is more useful than primers recognizing lower number of annealing sites. In this case the
number of amplified bands will be higher, thus giving a better chance for detecting DNA polymorphisms among individuals (Williams et al., 1990).

Amplification profile show the presence of monomorphic bands 70 band out of 442 main band (15.8%) which reveal that genotypes that belong to one species share some genome sequences and differ in others (Russel, et al., 1997; Al-Judy, 2004 and Al-Badeiry, 2013). These identical sequences are constant in genome and commonly refer to as conserved sequence (Al-Judy, 2004).

The higher number of polymorphic bands generated in primers OPU-03, OPV-19 and OPC-19 they were higher than values obtained by other reports using the same primers (Abd El Hady et al., 2010 and Ezekiel et al., 2011). Study suggests that the primer which produces high polymorphic bands can be further used as polymorphic marker which will prove promising in identification and genetic purity testing in case of tomato (Pal and Singh, 2013). The lower values observed in both primers OPB-17 and OPA-14.

Data revealed the presence of unique bands up to 5-6 bands per primer, this indicate that every cultivar had one or more novel sequences which was not found in other cultivar. These bands can be successfully used as genetic markers for identification of these cultivars. (Vishwanath et al., 2010).

Data show that out of 4284 amplified bands 312 band were polymorphic while only 70 band were monomorphic. The low degree of similarity (monomorphic bands) indicated high divergence between the genotypes evaluated (Carelli et al., 2006). The level of polymorphism reaches 95% the value was higher than that obtained in other reports 63.8%, 85% and 83% in discrimination studies of tomato varieties (Archak et al., 2002; Abd El Hady et al., 2010; Ezekiel et al., 2011). In contrast polymorphism could reach 100% using another set of primers and varieties of diverse origin and wider genetic base (Vishwanath et al., 2010).

Evaluation of primer efficiency is of great important in reflecting ability of primer to produce high polymorphic bands according to total number of amplified bands this

Table 2: The fragment size range (bp), no. of main bands, no. of amplified bands, no. of monomorphic bands, no. of polymorphic bands, no. of unique bands, polymorphism, primer efficiency and discrimination value of each RAPD primer in this study.

<table>
<thead>
<tr>
<th>No.</th>
<th>Primer</th>
<th>Fragment size range (bp)</th>
<th>No. of main bands</th>
<th>No. of amplified bands</th>
<th>No. of monomorphic bands</th>
<th>No. of polymorphic bands</th>
<th>No. of unique bands</th>
<th>Polymorphism (%)</th>
<th>Primer efficiency</th>
<th>Discriminatory value (%)</th>
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<td>1</td>
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<td>80</td>
<td>0.88</td>
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</tbody>
</table>

Total no. of bands: 442, 40.64, 70, 31.2, 00. - - - -

Average bands per primer: 16.6, 1.8, 2.6, 2.6, 2.25

Average per primer %: 40.7, 0.7, 4.5.
indicate in high primer efficiency in both primers OPC-09 and OPU-03 compared to primer OPB-17 (AL-Badeiry, 2013).

The discriminatory power of primer which increases by increasing the number of identified varieties using the selected primers (Arif et al., 2010 and AL-Badeiry, 2013). The higher discriminatory power appear in primer OPU-03 which gave distinct fingerprint for all studied varieties while the lower discriminatory power shown by both primers OPB-17 and OPA-14 which failed to identify any variety.

Tomato cultivars well recognized using OPA-04, OPB-17 and OPD-13 by their ability to produce fragment specific for particular cultivar, this approach will be useful for developing marker-assisted selection tools for genetic enhancement of the tomato plant for desirable traits (Huh et al., 2011).

The genetic distance value provides a useful estimate of relationship between a specific pair and a small number of genotypes. Phylogenetic analysis, however, is more appropriate for the interpretation of all possible relationships among a large group of genotypes (Lang and Hang, 2007).

To achieve the calculation of genetic distance or dissimilarity using RAPD-PCR markers at least the results of 10 primers that produce complete and well defined amplification products should be used (Brummer et al., 1995).

The results in table (3) represent the genetic distance among tomato varieties. In order to calculate the genetic distances between tomato varieties, the positions of unequivocally scorable RAPD bands were transformed into a binary character matrix ("1" for the presence and "0" for the absence of a band at a particular position). Pair wise distance matrices were acompiled by the NTSYS-PC., version 1.8 software using the Dice's and Jacquard's coefficient of similarity to produce the most logical results (Rohlf, 1993; Maguire and Sedgley, 1997).

The lowest genetic distance was (0.2294) between varieties Oula and shadylady which means that the presence of similarity between these two varieties is high degree using RAPD markers, despite the fact they were introduced from different region of geographical origin (China and Holland respectively) and on the basis of morphological features and traits, it was found that these two varieties have diverse characters. Uddin and Boemer, (2008) found that the most closely related two varieties originated from different collection sites.

Ezekiel et al., (2011) reported that varieties may introduced from one locality to the other and assigned anew name.

The impression that the varieties of tomato from aparticular geographical zone are genetically similar may not be true; though, the phenotypic expressions and possible local trade names given by traders or may be the same. Thus, the phenotypic variations exhibited by closely related genotypes may be attributed to response to environmental influences (Falconer, 1989).

The highest genetic distance was (0.9459) between varieties Fotton and Special pack which means that the presence of similarity between them are very low. This concerned with their different geographical origins (China and Holland respectively) and diverse morphological characteristic.

The genetic similarity values ranging from (0.0541 to 0.7706) depending up on the genetic distance values ranging from (0.9459 to 0.2294), which indicate the substantial diversity (94% to 22%) among the varieties used for this study. The genetic distance that relies on nucleotides sequence of DNA giving an evidence for potential genetic similarity between two groups or among individuals within the same species or between species of same genus (Zaid et al., 1999).
Presence of some common morphological characters among varieties (inflorescence type, fruit shape and colour) increase the present of genetic similarity between studied varieties using RAPD marker (Huh et al., 2011) and this agrees with Bai et al., (1997) who found that the degree of genetic similarity between medical plant variety (ginseng) by applying RAPD marker is high when he selected long plants only compared with genetic similarity between random samples of the same species.

In previous studies Fan-juan et al., (2010) detected the lower genetic variation in the cultivated tomato species, the similarity coefficients detected by RAPD ranged from 0.72 to 1, with an average of 0.95, therefore, the cultivated tomato varieties had narrow genetic background, which was also reported by Hiroaki et al., (2000).

The study the genetic relationships among nineteen tomato genotypes varieties based on RAPD can be seen in dendrogram Figure 3, which shows how closely these varieties are related to each other. The aim of producing a dendrogram is to visualize the best representation of the phenetic (overall similarity) or phylogenetic (evolutionary history) relationships among a group varieties, individuals, cultivars, populations, or species. According to this dendrogram it was possible to distinguish two main genetic groups (major clusters). The first small major clusters included four varieties (Douna, GSN, Special pack, Tamara) originate from (Peru, France, and Holland respectively), the first three varieties run and meet at 0.3244, this refers to the genetic distance between them and the genetic similarity is 68%. (varieties that meet at the same genetic distance usually form independent group).

The second large major cluster included (15 varieties) divided in two sub groups.
The distribution of the tomato hybrid varieties into different sub clusters may be an indication of the diversity of the parental species used to generate these population. The phyllogram can be used in the formulation of breeding plans, for example, crosses between closely related genotypes are less likely to produce heterosis (Lang and Hang, 2007).

Genetic relationships will help plant breeders to prevent gene erosion within varieties by selecting a large number of different clones of each variety (Ruhl et al., 2000).

The importance of finding the genetic distance between varieties studied to help plant breeders in making the right decision by choosing appropriate parents to form new genetic consensus, especially when developing plants in terms of increasing resistance to pathogens and unfavorable environmental conditions (Weeden et al., 1992). Thus, the results of the present study have produced the first informative DNA-based markers for common tomato genotypes identification of Iraq and could have strong implications for breeding programs for development of tomato variety as a commercially important crop and would be helpful for future programs regarding tomato varieties genetic improvements, building a genetic map for the local tomato varieties.

References


Al-Judy, N. J. 2004 Detecting of DNA Fingerprints and Genetic Relationship Analysis in Local and Improved Rice (Oryza sativa L.) Varieties in Iraq Using RAPD Markers. Phd thesis, College of Science, Baghdad University, p 166.


