Research Article

Detection and molecular characterization of tomato big bud disease in Qazvin province

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Abstract: Some samples were collected from tomato fields in Qazvin from tomato plants with big bud symptoms such as plant droop and purplish vein under the leaf, enlarged and sac-like pistils and malformed buds. DNA was extracted from the veins and vascular tissues of the plant with CTAB-based methods. In symptomatic plants, DNA fragments of 1800 and 1200bp were amplified by PCR using P1/P7, R16F2n/R16R2 primers. Restriction fragment length polymorphism (RFLP) analysis of nested R16F2n/R16R2 primed PCR product (1200bp) showed that the tomato big bud phytoplasma from Qazvin (TOM-Qazvin) is a member of clover proliferation (16SrVI). Phylogenetic analysis of 16SrRNA was performed by putting restriction site analysis of the R16F2n/R16R2 primed sequence classified TOM phytoplasma in clover proliferation (16SrVI) group and belonged to subgroup 16SrVI-A. Virtual RFLP by using 1200bp sequencing of 16SrRNA and 17 restriction enzymes confirmed that TOM-Qazvin belonged to the subgroup 16SrVI-A and16SrVI group. To our knowledge, this is the first report of tomato big bud disease in Qazvin province.

Keywords: big bud, iphyclasifer, RFLP, tomato, phytoplasma

Introduction

Phytoplasmas are plant pathogenic (previously called MLOs) un-culturale and wall-less bacteria, they are associated with a wide variety of economically important plants (McCoy et al., 1989; Seemuller et al., 2002). Tomato big bud is a phytoplasma diseases reported from some countries in the world (Shaw et al., 1993; Dale and Smith, 1975; Del Serrone et al., 2001; Anfoka et al., 2003; Ciccarone, 1951; Zimmermann-Gries and Klein, 1978; Vibio et al., 1996). Affected tomato plants reveal stunting, purpling, dwarfed, enlargement and elongation of stems and pedicels and enlarged, malformed buds accompanied by enlarged, malformed sepals and virescence petals (Ghandi et al., 2003). Detection and identification of phytoplasmas is necessary for proper management of these diseases (Maixner, 2010). Unfortunately, phytoplasma diseases are increasing (Baghaee et al., 2016). Significant progress has been made by the use of DNA-based methods for detection, identification and classification of phytoplasmas (Ghandi et al., 2003). In particular, by restriction site and sequence analysis of 16SrDNA many phytoplasmas have been identified and phylogenetically classified (Anfoka et al., 2003; Lee et al., 2000; Schneider et al., 1993). The introduction of the polymerase chain reaction

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(PCR) to amplify conserved genes has greatly improved the detection and identification of a broad range of phytoplasmas (Gunderson and Lee, 1996). Phytoplasmas are present in low titer in plant tissues, so the nested PCR method is used to improve phytoplasma detection (Olmos et al., 1999). Symptoms of tomato big bud have been previously reported from different provinces of Iran: Fars (Salehi and Izadpanah, 1992), Isfahan, Ardabil, Western Azarbaijan (Rashidi et al., 2006), Khorasan (Jamshidi et al., 2010), Lorestan (Dehghani and Salehi, 2011) and Karaj (Moslemkhani et al., 2014) but there is a little information about phytoplasma group in Iran. This study was performed for detection and characterization of big bud disease of tomato from naturally symptomatic plants in Qazvin province by using PCR and RFLP assay with specific primer.

Materials and Methods

Plant sample
Tomoato plants that showed big bud symptoms such as shoot proliferation and swollen, virescent buds were collected from tomato fields in Qazvin province. Samples were placed in a plastic bag with a moist towel and stored at 4 °C.

Nucleic acid extraction
DNA was extracted from 300 grams of fresh veins tissues of naturally symptomatic plants, using CTAB methods (Doyle et al., 1990). Total DNA of healthy tomato plants were used as negative controls.

PCR analysis
Detection and characterization of phytoplasma contamination was performed using direct PCR by two primer pairs P1/P7 to amplify 1800bp ribosomal operon. It consists part of the 16SrRNA gene, the 16S-23S spacer region and a portion of the 5′ region of 23SrRNA gene. A 1:40 dilution of the direct PCR product amplified by P1/P7 primer pair were used as template for nested PCR, using primer pair R16F2n/R2, which amplifies an internal DNA fragment of 1200bp from the 16SrRNA gene based on Gunderson and Lee method (Gunderson and Lee, 1996). PCR was conducted in 20 μl using 2 μl of extracted DNA, 0.5 μM of each primer P1/P7, 200 mM of each dNTP, 1 unit of Taq DNA polymerase (CinnaGen, Iran) and IX PCR buffer and 2 mM MgCl2. PCR of performed in a thermal cycler (Eppendorf, Germany) using denaturation step at 94 °C for 5 min and the second step, 35 cycles containing denaturation at 94 °C for 1 min. Annealing at 57 °C and at 72 °C for 1.5 min, the third step, at 72 °C for 10 min. Nested PCR were performed in a thermal cycler using a denaturation step at 94 °C for 5 min and the second step, 35 cycles containing denaturation at 94 °C for 1 min annealing at 57 °C and at 72 °C for 1.5 min. The third step, at 72 °C for 10 min. PCR products were analyzed by electrophoresis in a 1% agarose gel in 1X TBE buffer (67 mM Tris-HCl, 22 mM boric acid, 10 mM EDTA, pH 8.0) together with 100bp DNA markers. DNA band were stained with ethidium-bromide and visualized with a UV transilluminator.

Restriction fragment length polymorphism and Virtual RFLP
Nested-PCR products (1200bp) of phytoplasma were separately digested with 8 restriction endonucleases: Rsal, Msel, TaqI, Alul, CfoI, HinfI, HaeIII and HpaII (Lee et al., 1998) in restriction fragment length polymorphism (RFLP) analysis. The RFLP products were conducted by electrophoresis of digested DNA through 2% agarose gel, staining with ethidium-bromide and visualization with a UV transilluminator (Lee et al.1998). Virtual RFLP analysis of 16SrDNA fragment was carried out using the software iPhyClassifier to determine subgroup association of big bud in tomato and selected phytoplasmas (Zhao et al., 2009a,b). The 1200bp R16F2n/R16R2 fragment of 16SrRNA gene from phytoplasma isolate were separately digested with 17 restriction enzymes Rsal, Msel, TaqI, Alul, CfoI, HinfI, HaeIII, HpaII, BamHI, BfaI, BsrUI, DraI, EcoRI, Hhal,
KpnI, RsaI, Sspi and Sau3AI. Then the putative restriction site maps were compared with the patterns of isolates that were deposited in GenBank (Lee et al., 1998). Digested fragments of nested-PCR products were separated on 1% agarose gel and visualized under UV transilluminator.

**DNA sequencing and phylogenetic analyses**
Based on the Tamura et al. method after comparing the RFLP patterns, direct sequence was performed and the intended isolate was selected to determine its nucleotide sequence (Macrogen Biosystems, South Korea) (Tamura et al. 2007). Each selected sequence was deposited in the GenBank database and compared with other sequences (Table 1) by CLUSTALW program. A phylogenetic tree was constructed by the neighbour-joining method (Saitou and Nei, 1987). *Acholeplasma laidlawii*, a culturable mollicute phylogenetically related to phytoplasmas was used as outgroup to root the tree. The resulted phylogram was printed using TREEVIEW.

**Table 1** Phytoplasma group designations and GenBank accession numbers of 1200bp of 16SrRNA gene sequences examined in this study.

<table>
<thead>
<tr>
<th>Phytoplasma/disease common name</th>
<th>GenBank (Acc. No.)</th>
<th>16SrDNA (group-subgroup)</th>
</tr>
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<tr>
<td>Tomato big bud phytoplasma</td>
<td>JF508507</td>
<td>16SrI</td>
</tr>
<tr>
<td>Willow proliferation phytoplasma</td>
<td>JX123321</td>
<td>16SrVI-A</td>
</tr>
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<td>JF508511</td>
<td>16SrVI-A</td>
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<td>JF508512</td>
<td>16SrVI-A</td>
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<tr>
<td>Tomato big bud phytoplasma</td>
<td>JF508509</td>
<td>16SrVI</td>
</tr>
<tr>
<td>Tomato big bud phytoplasma Yazd</td>
<td>MG788318</td>
<td>16SrII</td>
</tr>
<tr>
<td>Behshahr periwinkle</td>
<td>KC661072</td>
<td>16SrVI</td>
</tr>
<tr>
<td>Tomato big bud phytoplasma</td>
<td>KR150879</td>
<td>16SrVI</td>
</tr>
<tr>
<td>Candidatus phytoplasma</td>
<td>KY321932</td>
<td>16SrVI</td>
</tr>
<tr>
<td>Tomato big bud phytoplasma Yazd</td>
<td>MG788318</td>
<td>16SrII</td>
</tr>
<tr>
<td>Iranian cabbage</td>
<td>EF592606</td>
<td>16SrVI-A</td>
</tr>
<tr>
<td>Candidatus phytoplasma</td>
<td>AY390261</td>
<td>16srVI</td>
</tr>
<tr>
<td>Elm phytoplasma</td>
<td>AF268895</td>
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<td>Potato purple top</td>
<td>GU004369</td>
<td>16srVI</td>
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<td>Ash yellow phytoplasma</td>
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<td>16srVI</td>
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<td>Stolbur phytoplasma</td>
<td>AF248959</td>
<td>16SrXII-A</td>
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<tr>
<td>Oenthera phytoplasma</td>
<td>M30790</td>
<td>16SrI</td>
</tr>
</tbody>
</table>

**Results**

**Plant sample**
Tomato plants collected from Qazvin province showed disease symptoms similar to tomato big bud phytoplasma such as swollen green buds that fail to develop normally and do not set fruit and had purple veins, proliferated leaves of lateral shoots, hypertrophic calyxes and greening of flower petals (Fig. 1).

**PCR analysis**
Target DNA fragments of approximately 1800 and 1200bp were amplified using two universal primer pairs P1/P7 and R16f2n/R16R2, respectively (Fig. 2). No DNA band observed from similarly processed sample of healthy plant. Nested-PCR assays with the primer pair R16F2/R2 showed the strong band and of approximately 1200bp (Fig. 2).
Actual and in silico RFLP analysis
Digestion of nested PCR products of TOM phytoplasma showed bands of approximately 1200bp that amplified by using primer pair R16F2n/R2 with Rsal, Msel, TaqI, AluI, CfoI, HinfI, Haell and HpaII restriction enzymes (Fig. 3). Digestion with VIII restriction enzymes were shown in a considerably similar RFLP profile of 16SrDNA with each enzyme (Fig. 3). TOM- Qazvin phytoplasma identified in this study was identical with patterns previously published for subgroup 16SrVIA members of 16SrVI group (Shaw et al., 1993). Virtual RFLP patterns using iPhyclassifire program after digestion with 17 different endonucleases (Fig. 4) confirmed actual RFLP were most similar to members of 16SrVI group. Virtual RFLP pattern of TOM-Qazvin and Kermanshah tomato big bud (KTBB) (JF508507) that related to sub-group A in 16SrVI group was identical (Jamshidi et al., 2014).

Figure 1 Big bud symptoms in naturally infected tomato. Respectively left to Right: (1) Purplish leaves in infected plants. (2) Floral phyllody on infected tomato plants. (3) Big bud symptom in infected tomato plants.

Figure 2 A- Electrophoresis pattern of 1200bp of 16SrRNA operon amplified by nested-PCR using primer pairs P1/P7 and R16F2n/R16R2n. B- Electrophoresis pattern of 1800bp of rRNA operon amplified by direct PCR using primer pairs P1/P7, Lane M: DNA ladder (100 bp). C (-), Healthy plant. C (+) Candidatus Phytoplasma asteris.
Figure 3  Restriction fragment length polymorphism of 16S rDNA amplified by nested-PCR using P1/P7 followed by R16F2n/R2 primer pairs from infected tomato plant. Lane M, DNA ladder. DNA products digested using HpaII, TaqI, Rsal, HinfI, AluI, Rsal, CfoI, MseI separated through a 1% agarose gel.

Figure 4 Virtual restriction fragment length polymorphism (RFLP) pattern of R16F2n/R2 PCR product sequence recognition sites for the following 17 restriction enzymes were used in the simulated digestions: Rsal, MseI, TaqI, AluI, CfoI, HinfI, HaeIII, HpaII, BamHI, BfiI, BstUI, DraI, EcoRI, HhaI, KpnI, Rsal, SspI and Sau3AI.

Sequence analyses
A phylogenetic tree was created by neighbour-joining analyses of nearly identical lengths of 16SrRNA gene from 23 isolates and Acholeplasma laidlawii as outgroup (Fig. 5). Based on the results of blast searches by using P1/P7 primed sequence of 23 TBB phytoplasma isolates showed that TOM-Qazvin was closely related to Clover proliferation (16SrVI) group (GenBank No. JF508507) with 99% identity. This isolate also was closely related to the phytoplasmas that infect willows trees in China (Zhang et al., 2012).
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Figure 5 A neighbour-joining tree created of the 16SrRNA inter-genic spacer region of 23 phytoplasma strains associated with tomato big bud disease from GenBank and Acholeplasma laidlawii as an out-group and position of TOM-Qazvin was showed in phylogram. Numbers above the branches bootstrap support (100 replicates).

Discussion

Tomato is a very important crop grown in Iran for fresh eating, industry, seed production and export. Disease symptom of tomato plants in Qazvin province from different area were similar to tomato big bud symptoms that have been reported from different areas in the world (Anfoka et al., 2003; Serrone et al., 2001). Phytoplasma disease of tomato plant was reported previously in different countries such as China (Xu et al., 2013), Mexico (Tapia-Tusell et al., 2012), Egypt (EL-Banna et al., 2007), Brazil (Amaral Mello et al., 2008). In previous studies data showed that phytoplasma belonged to groups I, II, III, V, VI and XII of 16SrRNA, indicating phytoplasma disease of the tomato is genetically diverse (Santos-Cervantes et al., 2008). besides, tomato big bud was associated with phytoplasma group 16SrI in the USA (Lee et al. 1993, 1998), with phytoplasma group 16SrI, 16SrV, 16SrXII in Italy (Serrone et al., 2001) also 16SrVI group was associated with tomato plants with symptoms of big bud disease in Jordan (Anfoka et al., 2003). In Australia, 16SrII group belonging to phytoplasma was associated with tomato big bud (Davis et al. 1997). Shaw et al. (1993) showed the beet leafhopper transmitted virescence agent (BLTVA) that caused tomato big bud in California which belonged to group 16SrVI. Del Serrone et al. showed that tomato plants in central Italy showing big bud-like disease symptoms were infected with phytoplasmas belonging to four different groups (I, III, V and XII) (Del Serrone et al., 2001). It was also reported that the tomato big bud phytoplasma from Arkansas was affiliated with genetic subgroup 16SrI-A (Lee et al., 1993). Different phytoplasmas associated with tomato diseases from 16SrDNA groups have been characterized all over the world using
DNA-based techniques and sequence analysis (Anfoka et al., 2003; Santos-Cervantes et al., 2007, 2008). Presence of tomato big bud previously reported in provinces of Iran (Dehghani and Salehi, 2011). Symptom of tomato big bud in region of Iran is different. Tomato big bud disease was reported from provinces such as Khorasan, Western Azerbaijan, Eastern Azerbaijan, Kermanshah, Kurdistan and Fars for the first time, with except of Fars (Salehi et al. 2005) and Western Azerbaijan (Rashidi et al., 2006). Association of a 16SrII group related phytoplasma with big bud disease had been previously reported from Fars and Yazd provinces (Salehi et al. 2005). Actual and putative RFLP and sequence analyses of AGTB (JF508509), KETBB (JF508507), KRTBB (JF508509), FTBB (JF508508) and ASTBB (JF508511) isolates were almost identical and related to the 16SrVI group. Also KTBB (JF508509) and KSTBB (JF508513) isolates were similar and belonged to the 16SrIX group. Based on the same analyses, clover proliferation group related TBB phytoplasma that belonged to 16SrVI-A subgroup, and pigeon pea witches’ broom phytoplasma group related to TBB phytoplasma belongs to 16SrVI-E subgroup (Jamshidi et al., 2014). Another study in Karaj vicinity on different cultivars of tomato indicated that 89% of phytoplasmas present in tomato samples belonged to 16SrVI; but less than 11% belonged to 16SrI group which were observed only in the Pardis and Mateen cultivars (Moslemkhani et al. 2014). In Iran, cabbage Brassica oleraceavar. capitata and safflower Carthamus tinctorius L. were reported as hosts for 16SrVI group (Salehi et al., 2007, 2009). In this study, based on the results of RFLP and sequence analyses TOM-Qazvin phytoplasma belongs to 16SrVI-A subgroup and it is the first report of tomato plant as a host for 16SrVI in Qazvin province.

References


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J. Crop Prot.


شناسایی و ردیابی مولکولی عامل بیماری تورم جوانه گوجه فرنگی در استان قزوین

عباس داودی، ناصر پنجه، کیرو مسلم خانی و عبدالحسین ظاهری

چکیده: در بررسی‌های انجام شده از مزارع گوجه فرنگی استان قزوین از بونه‌های گیاهی تورم جوانه شامل کوتولگی ارغوانی، رگیدسی و سطح زیرین پرگ، تبدیل کننده بال که یک جسم کیسه‌مانند و جوانه‌های بدنک و رشدی نمونه برداری صورت گرفت. برای شناسایی عامل بیماری از نمونه‌های شناسایی‌کننده CTAB استخراج شد. ردیابی احتمالی آلودگی فیتولاسیمی با آزمون PCR مستقیم با استفاده از جفت آغازگرهای P1/P7 آزمون PCR انجام شد و با اتصال R16F2n/R16R2 و P1/P7 مرحله پنجم با استفاده از جفت آغازگرهای ۱۶SrVI و P1/P7 مرحله پنجم با استفاده از جفت آغازگرهای ۱۶SrVI ریفرنژ سنجیده شد. میزان نشان داده که عامل بیماری تورم جوانه گوجه فرنگی iphyclassifier متعلق به زیرگروه ۱۶SrVI-A از گروه اسپیتالاسیمی RFLP متعلق به زیرگروه ۱۶SrVI-A است.

واژگان کلیدی: تورم جوانه، گوجه فرنگی، فیتولاسیمی، RFLP، iphyclassifier.