Research Article

Molecular characterization of a 16SrIX phytoplasma associated with Convolvulus glomeratus witches' broom and with an insect vector in Iran

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Abstract: During a survey in 2016, Convolvulus glomeratus showing symptoms resembling those caused by phytoplasmas were observed in Bandar Abbas, Hormozgan province, Iran. These plants were examined for phytoplasma presence by nested-PCR assays using universal primer pair P1/P7 followed by R16F2n/R16R2. All the infected plants indicated positive results using universal primer pairs of P1/P7 followed by R16F2n/R16R2. Results of phylogenetic and virtual RFLP analyses of the 16S rRNA gene sequences revealed that the phytoplasma associated with Convolvulus glomeratus witches' broom (CgWB) was a strain of 'Candidatus Phytoplasma phoenicium'. The phytoplasma was successfully transmitted to healthy plants by leafhopper, Orosius albicinctus (Distant) which account as a vector of this phytoplasma. This is the first report on the presence of 'Candidatus Phytoplasma phoenicium' (phytoplasma group 16SrIX-J) in C. glomeratus and its insect vector in Iran.

Keywords: 16SrIX, Convolvulus glomeratus, Orosius albicinctus, Bandar Abbas, witches' broom

Introduction

Phytoplasmas are pleomorphic, cell wall-less phytopathogenic bacteria, falling under the class Mollicutes (Firrao et al., 2005) that can cause significant yield loss in diverse, high value crops worldwide including food, vegetable, and fruit crops; ornamental plants, trees and medicinal and aromatic plants (Du Toit, 2014). Phytoplasmas can also infect many wild plant species (Mori et al., 2015). Phytoplasmas associated with these diseases, can be transmitted via dodder and grafting in laboratory conditions and by phloem-feeding insects like leafhoppers and planthoppers (Hemiptera) in nature (Weintraub and Beanland, 2006), especially those classified in Opsini tribe. In addition, the phytoplasmas have a persistent and propagative relationship with insects, similar to other symbiotic prokaryotes found in Hemiptera (Weintraub, 2008).

Convolvulus is a genus of about 200 to 250 species of flowering plants in the bindweed family Convolvulaceae, with a cosmopolitan distribution. They are annual or perennial climbing or creeping herbaceous plants and a few species of woody shrubs. Many of the species are problematic weeds, which can smother other more valuable plants by climbing over them, but some are also cultivated for their attractive flowers (Carin and Robba, 2010).

In July 2016, typical symptoms of phytoplasma diseases, including witches' broom and little leaf

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were observed in *Convolvulus glomeratus* in Bandar Abbas, Hormozgan province, Iran (Fig. 1A). Accordingly, they were suspected of phytotplasma infection. So, this study was carried out to identify the phytotplasma associated with *C. glomeratus* and the insect vector in Iran.

**Figure 1** (A) Symptoms of witches’ broom, little leaf and yellowing (B) in comparison with healthy *Convovulus glomeratus*.

**Materials and Methods**

Samples of both symptomatic and asymptomatic *Convolvulus glomeratus* were collected from Bandar Abbas growing as weeds in municipal lands and parks in Bandar Abbas (N27°11'40"; E56°19'58"), Hormozgan province, Iran. Total DNA was extracted from leaves of the three symptomless and five symptomatic samples using cetyltrimethylammonium bromide (CTAB) extraction procedure described by Doyle and Doyle (1990). A nested polymerase chain reaction (PCR) was employed for the detection of phytotplasmas using the universal primers P1/P7 (Deng and Hiruki 1991) followed by R16F2n/R16R2 (Gundersen and Lee, 1996) which amplify a phytotplasma 16S rRNA fragment (approximately 1.25kbp). The PCR was performed in 20μl of reaction mixture containing 10μl PCR Master Mix (Amplicon), 1μl of each primer (10μM), 2μl of template DNA and 6μl sterile distilled water. The thermocycling program was done as described by Hemmati and Nikooei (2017). The P1/P7 primed PCR product was diluted at 1: 10 ratio in sterile water and 2μl was used in nested-PCR as a template. The nested-PCR cycles were the same as for the first round PCR. *Candidatus Phytoplasma aurantifolia*’ and DNA template free were used as positive and negative controls, respectively.
Insects feeding on the symptomatic *C. glomeratus* were collected using a D-Vac aspirator (Echo-ES210; Japan). Insects were separated and specimens preserved in acetone (Fukatsu, 1999) and stored at -20 ºC. The nucleic acids from individual leafhoppers were extracted using a cetyltrimethyl-ammonium-bromide (CTAB) method in accordance with the protocol of Reineke et al. (1998) with some modifications. The primers and PCR conditions used for phytoplasma detection in insects were the same as above. 

To confirm the presence of phytoplasma and for phylogenetic analysis, two fragments (one plant, one insect) were randomly selected from the nested PCR round and sequenced bidirectionally by primer P1/P7 and R16F2a/R16R2 by Macrogen Sequencing Service (Republic of Korea). Sequences received in this study were assembled and aligned using software: DNAsStar and ClustalX. Phylogenetic analyses were conducted by neighbor joining (NJ) method using MEGA 6.0 software (Tamura et al., 2013) with 10,000 replicates for bootstrap analysis. *Acholeplasma laidlawii* was used as out-group to root the tree. The sequences of 16S rRNA of different phytoplasma groups used in comprehensive phylogenetic analyses were downloaded from GenBank database.

*Catharanthus roseus* was used for transmission trials. Before transmission trials, all plants were tested for phytoplasma presence by Nested-PCR using the same primer pairs. For transmission trial, insects were collected from infected plants using a D-Vac aspirator and *Orosius albicinctus* (Distant, 1908) were separated. The leafhoppers (5-7 individuals per plants) were released under the insect-proof net where five healthy *C. roseus* (5-6 week old) were maintained. The plants with leafhoppers were maintained in the growth chamber (25 ºC, 16: 8 L: D and 70 ± 5 %RH) for monitoring disease symptoms development and sampling for PCR assays. After 8-10 weeks after inoculation, plants were molecularly tested for phytoplasma presence. Symptoms of disease development also were observed weekly. Five individual plants, that had no contact with insects, kept in the same conditions, of the growth chamber, were used as control.

**Results**

A correct size PCR product was detected in all five symptomatic plants tested by nested PCR assays. Two of the obtained PCR products was directly sequenced by P1/P7 and R16F2a/R16R2 primers. Similarly, correct amplificions were obtained from positive control samples but not from non-symptomatic plant samples and negative control. BLAST analysis revealed that the phytoplasma associated with *Convolvulus glomeratus* witches' broom (CgWB) was a phytoplasma belonging to group 16SrIX, ‘*Candidatus Phytoplasma phoenicium*’ with the highest identity (99%) to the Eggplant big bud phytoplasma (accession no. JX483702), *Lactuca serriola* phytoplasma (DQ889749) and ‘*Candidatus Phytoplasma phoenicium*’ (JX857827). The representative nucleotide sequence of the detected phytoplasma was deposited in the GenBank database (accession no. MG569789). A phylogenetic tree constructed was in accordance with the outcome of BLAST analysis and the sequence from present study was clustered in group 16SrIX (Fig. 2). This result was further confirmed by the analysis using the iPhyClassifier online tool (http://plant pathology.ba.ars.usda.gov/cgi-bin/resource/iphy classifier.cgi) (Zhao et al., 2009) where it was determined that the *C. glomeratus* phytoplasma was related to 16SrIX group, subgroup J.

Insects collected on the symptomatic plants were morphologically identified (according to the phytoplasma (accession no. JX483702), *Lactuca serriola* phytoplasma (DQ889749) and ‘*Candidatus Phytoplasma phoenicium*’ (JX857827). The representative nucleotide sequence of the detected phytoplasma was deposited in the GenBank database (accession no. MG569789). A phylogenetic tree constructed was in accordance with the outcome of BLAST analysis and the sequence from present study was clustered in group 16SrIX (Fig. 2). This result was further confirmed by the analysis using the iPhyClassifier online tool (http://plant pathology.ba.ars.usda.gov/cgi-bin/resource/iphy classifier.cgi) (Zhao et al., 2009) where it was determined that the *C. glomeratus* phytoplasma was related to 16SrIX group, subgroup J.
obtained from insect was aligned in Clustal omega with that obtained from symptomatic plants and showed 100% similarity. The sequence obtained from *O. albicinctus* was also deposited in GenBank database (Acc. No. MG570468).

**Figure 2** Phylogenetic tree of partial 16S rRNA gene sequences from *Convolvulus glomeratus* witches’ broom phytoplasma isolates (marked by boldface type) and phytoplasma reference sequences belonging to different 16Sr groups. GenBank accession numbers shown in brackets and 16Sr groups are annotated to the right. *Acholeplasma laidlawii* was used as out-group to root the tree. The tree was constructed by the neighbour-joining method using MEGA 6 software. The bar indicates the number of nucleotides substitution per site. Bootstrap values are shown at nodes with 50% support.
In transmission trial, after 2-4 months of inoculation, four out of five C. roseus plants fed on by the O. albicinctus showed phytoplasma disease symptoms such as yellowing, little leaf, stunting, phyllody and witches' broom (data not shown). Infection of symptomatic insect-inoculated plants were verified by Nested-PCR and sequences were deposited in GneBank under acc. No. MH999453. The plants that were not exposed to O. albicinctus were grown normally. Based on these results, O. albicinctus is a vector of the phytoplasma 16SrIX-J subgroup, causing disease of Convolvulus glomeratus in Bandar Abbas. As reported by other researchers (Esmailzadeh-Hosseini et al., 2007; Omidi et al., 2010; Ikten et al., 2014; Salehi et al., 2015), O. albicinctus can vector many diverse phytoplastmas to diverse plants.

Discussion

In Iran, group 16SrIX phytoplasmas have often been identified in some hosts including, grapevine (Salehi et al. 2016), eggplant (Tohidi et al., 2015), Chrysanthemum (Bayat et al., 2013), sainfoin (Esmailzadeh-Hosseini et al., 2007). C. glomeratus is a widespread weed of crop fields in Iran, occurring in association with economically important species, including some of those listed previously, as well as citrus which are widely planted in southern parts of Iran. In nature, in the absence of preferential host(s), leafhoppers may feed on alternative host and transmit pathogens to new plants expanding the host range of a phytoplasma to cultivated crops. This phenomenon can be a potential threat to agriculture. For instance, O. albicinctus has been reported as the experimental vector of cucumber phyllody (Azadvar et al., 2005), a disease which is suspected to have originated from sesame. It is believed that during the autumn, when sesame, the preferential host of the insect, has already been harvested, O. albicinctus may have been forced to feed on alternative plants, such as greenhouse cucumbers and has transmitted the disease.

Our findings implicate that C. glomeratus can be a reservoir for a relevant group of phytoplasmas that occur in diverse Iranian crops. In addition, we could indicate that O. albicinctus is an insect vector of the 16SrIX-J phytoplasma. In summary, the availability of the diverse phytoplasma 16SrIX host plants in Hormozgan province and wide distribution of O. albicinctus in this region, together with warm and humid climate, suitable for the insect to be active in all seasons, this pathogen can be a new threat to all plants planted in the region. In addition, to the best of our knowledge, our results reveal for the first time that C. glomeratus is a host of phytoplasmas in Iran or worldwide.

Statement of conflicting interest

The authors state that there is no conflict of interest.

Author contribution

All authors contribute equally in this research.

References


Molecular characterization of a 16SrIX phytoplasma


خصوصيات مولکولی فیتوپلاسمای Convululus glomeratus 16SrIX مرتب به بیماری جاروک پیچک و ناقل آن در ایران

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چکیده: طی پژوهشی به عمل آمده در سال 1395 از فضای سبز شهری بندرعباس، علاوه بر گیاهان بیماری Convululus glomeratus مشاهده شد. به همین منظور پژوهش حاضر به منصوب شدن فیتوپلاسمای همراه بیماری و شناسایی ناقل آن انجام شد. از نمونه‌ها در تکثیر و جفت آغازه‌های تکثیری از روشهای PCR و جفت آغازه‌های عمومی P1/P7 (دور اول) و R16F2n/R16R2 (دور دوم) استفاده شد. نتایج تجزیه و تحلیل پروتئن‌فیل و آغازه‌های آشیانه‌ای 16S rRNA محضی که توانایی زنجرک Orosius albicinctus از نقده و ناقل بیماری جاروک Convululus glomeratus (CgWB) را می‌باشد در آزمون‌های کارایی نشان داد. 

ویژگی‌کلیدی: فیتوپلاسمای Convululus glomeratus 16SrIX و گیاه Convululus glomeratus كان به بیماری جاروک Convululus glomeratus.