

Comparison of *P. syringae* pv. *syringae* from Different Hosts Based on Pathogenicity and BOX-PCR in Iran

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ABSTRACT

During 2007-2008, 58 strains of *P. syringae* pv. *syringae* (*Pss*) were isolated from various *Prunus* species and other hosts such as sugar beet, pear, quince, oat, millet, wheat, barley, and rice in Fars, Isfahan, Kohgiluyeh and Boyer-Ahmad, Chaharmahal-o-Bakhtiari provinces of Iran. The strains were tested for pathogenicity, the presence of the *syrB* gene and BOX-PCR (BOX A1R primer). All tested *Pss* strains were pathogenic on peach seedlings regardless of their original hosts. A total of 58 isolates of the *Pss* and *Pss* IVIA 773-1 amplified a 752-bp fragment with the *syrB* primers. The results of analysis of the BOX fingerprints from *P. syringae* pv. *syringae* strains showed that the strains isolated from stone fruits, graminous hosts and pome fruits formed a relatively distinct cluster, which were separable from the strains isolated from the other hosts. Results of this study indicate the existence of a relative degree of host specialization within the heterogeneous pathovar *Pss*.

Keywords: BOX-PCR, Pathogenicity, *P. syringae* pv. *syringae*, Stone fruit, *syrB* gene.

INTRODUCTION

P. syringae pv. *syringae* (*Pss*), the causal agent of bacterial canker and blast of stone fruit trees, is one of the most important plant pathogens in the world. *Pss* is a particular bacterium among *P. syringae* pathovars due to its capacity to cause disease in many species of plants (Little *et al.*, 1998). Traditionally, strains of *Pss* are recognized based on biochemical, nutritional, and physiological characteristics and ability of pathogenicity on lilac and peach seedling (Little *et al.*, 1998; Scortichini *et al.*, 2003; Vicente and Roberts, 2003; Vicente and Roberts, 2007; Gilbert *et al.*, 2009; 2010). *P. syringae* strains that are found infecting a host and are similar to *Pss* strains based on biochemical and nutritional characteristics have been assigned in this pathovar. In many cases, biochemical and nutritional tests are not the best methods to

differentiate strains at or below the pathovar level and pathogenicity test in greenhouse is not a suitable index of natural host preference (Little *et al.*, 1998). The analysis of DNA based on nucleic acid hybridization revealed that *P. syringae* is a heterogeneous species (Pecknold and Grogan, 1973). Nine genomic species were described within *P. syringae* on the basis of the results of DNA studies. Strains belonging to several pathovars of *P. syringae* include *P. s.* pv. *syringae*, *P. s.* pv. *aptata*, *P. s.* pv. *pisi*, *P. s.* pv. *papulans* were clustered in genomic species I (Gardan *et al.*, 1999). The *Pss* host specificity among the strains that infect different hosts such as beans, grasses, and *Prunus* species were reported on the basis of pathogenicity tests (Little *et al.*, 1998). Many researchers have found that peach seedlings are sensitive to *Pss* strains from different hosts (Otta and English, 1971; Vicente and Roberts, 2007; Gilbert *et al.*, 2010). Similarly, Lai and Hass (1973) showed that cowpea leaves have different

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susceptibility to *Pss* strains isolated from different hosts.

Genomic fingerprinting methods based on the polymerase chain reaction (PCR) have been applied for identification and classification of plant associated bacteria to the subspecies level (Louws *et al.*, 1995 and 1999). Rep-PCR technique is a useful method to differentiate and classify bacterial strains below the level of species (Versalovic *et al.*, 1991). Rep-PCR is based on DNA primers corresponding to naturally occurring repetitive elements in bacteria, such as the REP, ERIC and BOX elements (Versalovic *et al.*, 1994). In this method, the prior knowledge of target DNA sequence is not necessary (Louws *et al.*, 1999). Several *Pseudomonas syringae* pathovars including *phaseolicola*, *glycinae*, *tabaci*, *lachrymans* and *mori* that were studied based on ERIC- and REP-PCR showed that, in many cases, differences among strains within a pathovar were small. The researchers concluded that these methods could be used to identify and classify strains of the *Pseudomonas syringae* pathovars (Weingart and Volksch, 1997). The Australian isolates of *Pseudomonas syringae* pv. *pisi* and *Pss* were compared with rep-PCR. Using DNA fingerprinting, it was possible to distinguish these two pathovars and races 2 and 6 of *Pseudomonas syringae* pv. *pisi* (Hollaway *et al.*, 1997). Rep-PCR methods, particularly BOX-PCR, proved to be useful for identifying the *Psm* race 1 and *Psm* race 2 isolates (Gilbert *et al.*, 2009). In the same study, combined genetic results using rep-PCR and IS50-PCR confirmed high diversity in the pv. *syringae*, in which homogeneous genetic groups were found on the same hosts (pear, cherry, and plum). Analysis of the ERIC fingerprints of *Pss* strains isolated from stone fruits in California showed that these strains formed a distinct cluster that could be separated from the strains isolated from the other hosts (Little *et al.*, 1998). Another study revealed that different strains within *P.s. pv. pisi* could be separated in two distinct groups using Rep-PCR method (Suzuki *et al.*, 2003).

Analysis of *Pss* and *P. syringae* pv. *morsprunorum*, isolated from cherry in UK

using rep-PCR, showed that this method can easily distinguish these two major pathovars (Vicente and Roberts, 2007). Moreover, researchers found that nine genomic groups, proposed by Gardan *et al.* (1999) could be distinguished using BOX-PCR. They showed that the results corresponded with Gardan's results (Marques *et al.*, 2008).

In Iran, *Pss* strains were isolated from various plants of different areas and characterized (Bahar *et al.*, 1982; Bana pour *et al.*, 1990; Al-e-Yasine and Banihashemi, 1993; Elahi nia and Rahimian, 1996; Afionian *et al.*, 1996; Afionian and Sahragard, 1996; Shams bakhsh and Rahimian, 1997; Ghasemi *et al.*, 1998; Mohammadi *et al.*, 2001; Taghavi and Ziaee, 2003; Ashorpour *et al.*, 2008). In many cases, they emphasized phenotypic and nutritional characteristics of the pathogen and showed differences between isolates from various hosts, whereas genotypic features of this important plant pathogen have not been studied yet. Recently, using ERIC- and BOX-PCR primers, it was shown that the fingerprints of the strains isolated from sugarcane were distinct from those of the strains isolated from stone fruits and wheat. The results indicated that the *Pss* strains isolated from sugarcane with red streak symptom constitute a group genotypically distinct from those inciting canker on stone fruit trees and blight of wheat (Mosivand *et al.*, 2009).

The aim of this study was to compare and differentiate strains of *Pss* isolated from various *Prunus* species and other hosts such as sugar beet, pear, quince, oat, millet, wheat, barley, and rice by using pathogenicity test and BOX-PCR analyses.

MATERIALS AND METHODS

Isolation

During 2007 to 2008, samples of both healthy and diseased tissues of stone fruit trees such as apricot, peach, cherry, almond, wild almond, sugar beet, pear, quince, oat, millet, wheat, barley, rice, rose, pelargonium

and *Malva* sp were collected from different orchards in Fars, Isfahan, Kohgiluyeh and Boyer-Ahmad, Chaharmahal-o-Bakhtiari provinces of Iran. The tissues were surface sterilized in 1% sodium hypochlorite for 1 minute, rinsed in sterile water, ground in a small amount of phosphate buffer (PB) and 2 ml of liquid suspension was spread on King's B medium. After incubation for 4 days, the fluorescent colonies were purified and tested for LOPAT tests (oxidase reaction, the ability to rot potato slices, presence of arginine dihydrolase, levan production, and tobacco hypersensitivity) (Lelliot *et al.*, 1966; Schaad *et al.*, 2001). Characteristics of bacterial isolates used in this study are listed in Table 1. The *Pss* (IVIA773-1) and *P. savastanoi* pv. *savastanoi* (IVIA 2558-IT), from Instituto Valenciano de Investigaciones Agrarias (IVIA) Spain, were used as reference strains in this study.

Pathogenicity Test

Bacterial strains were grown for 48 hours on KB medium at 25°C and were suspended in Phosphate Buffer (PB) to a concentration of 10⁷ CFU (OD₆₀₀= 1). One ml of bacterial suspensions was injected into the green stems of peach seedlings by using a needle (Little *et al.*, 1998). Each plant was inoculated in five places with one strain and was covered with parafilm at the injection site. One isolate of *P. savastanoi* pv. *savastanoi*, was also injected into the stem of peach seedling. PB was injected as a control to peach seedlings. Peach seedlings were maintained in a greenhouse at 28°C and rated after 2 weeks for symptoms development.

DNA Preparation

All strains were grown on KB medium at 25°C for 3 days. A loopful of colony from each strain was suspended in sterile distilled

water to a concentration of 10⁷ CFU (OD₆₀₀= 1). The suspensions were boiled for 8-10 minutes and after cooling in the room temperature, were used as template DNA for pathovar-specific PCR and BOX-PCR (Clerc *et al.*, 1998).

Identification of *Pss* with Specific Primers

Two 21-mer oligonucleotides from *syrB* gene [primer B1 (5'-CTTCCGTGGTCTTGATGAGG-3') and primer B2 (5'-TCGATTTTGCCGTGATGAGTC-3')] were selected for PCR and were purchased from Metabion Co., Germany. The primers B1 and B2 locate into the open reading frame of the *syrB* gene and yield a 752-bp product (Sorensen *et al.*, 1998). The PCR reactions were performed in Bio-Rad I-cycler (USA) in 26 µl PCR mixture: 2 µl of DNA template was transferred to 24 µl of a PCR mixture containing 50 pmol of each primer, 0.2 mM dNTP mix, 2 U of *Taq* DNA polymerase (Metabion Co., Germany), and 1.6 mM magnesium chloride. The PCR reaction was carried out for 35 cycles using the following procedure: template denaturation at 94°C for 1.5 minutes, primer annealing at 60°C for 1.5 minutes, DNA extension for 3.0 minutes at 72°C and final extension at 72°C for 10 minutes. The PCR products were electrophoresed on 1% TBE agarose gel at room temperature at 90 V cm⁻¹ for 1 hour. Following staining with ethidium bromide, the gels were viewed and photographed under UV illumination.

BOX-PCR Conditions

The BOX-PCR was carried out with BOX A1R primer (Versalovic *et al.*, 1991). BOX A1R primer [5'-CTACggCAAggCgACgCTgACg-3'] was purchased from Metabion Co., Germany. The PCR reactions were performed in

**Table 1.** Characteristics of bacterial strains used in this study.

| Strain | Host | Location |
|--|---------------|---|
| <i>P. syringae</i> pv. <i>syringae</i> | | |
| 1. | Almond | Fars |
| 2. | Barley | Fars |
| 3. | Rice | Fars |
| 4. | Oat | Kohgiloye and Boyer Ahmad |
| 5. | Peach | Fars |
| 6. | Rose | Fars |
| 7. | Cherry | Fars |
| 8. | Healthy Peach | Chahar Mahal-o-Bakhtiari |
| 9. | Peach | Isfahan |
| 10. | Almond | Kohgiloye and Boyer Ahmad |
| 11. | Rose | Fars |
| 12. | Unknown | <i>P. savastanoi</i> pv. <i>savastanoi</i> IVIA 2558-IT |
| 13. | Apricot | Kohgiloye and Boyer Ahmad |
| 14. | Peach | Fars |
| 15. | Cherry | Chahar Mahal-o-Bakhtiari |
| 16. | Beet | Fars |
| 17. | Apricot | Fars |
| 18. | Cherry | Fars |
| 19. | Peach | Chahar Mahal-o-Bakhtiari |
| 20. | Cherry | Fars |
| 21. | Peach | Chahar Mahal-o-Bakhtiari |
| 22. | Pelargonium | Fars |
| 23. | Pear | Fars |
| 24. | Peach | Isfahan |
| 25. | <i>Malva</i> | Fars |
| 26. | Wild Almond | Fars |
| 27. | Peach | Isfahan |
| 28. | Almond | Kohgiloye and Boyer Ahmad |
| 29. | Wheat | Chahar Mahal-o-Bakhtiari |
| 30. | Wild Almond | Fars |
| 31. | Almond | Kohgiloye and Boyer Ahmad |
| 32. | Peach | Chahar Mahal-o-Bakhtiari |
| 33. | Peach | Isfahan |
| 34. | Almond | Kohgiloye and Boyer Ahmad |
| 35. | Peach | Fars |
| 36. | Quince | Fars |
| 37. | Peach | Chahar Mahal-o-Bakhtiari |
| 38. | Peach | Isfahan |
| 39. | Wild Almond | Fars |
| 40. | Cherry | Chahar Mahal-o-Bakhtiari |
| 41. | Peach | Fars |
| 42. | Wheat | Chahar Mahal-o-Bakhtiari |
| 43. | Wild Almond | Fars |
| 44. | Almond | Kohgiloye and Boyer Ahmad |
| 45. | Cherry | Fars |
| 46. | Apricot | Kohgiloye and Boyer Ahmad |
| 47. | Almond | Fars |
| 48. | Pelargonium | Fars |
| 49. | Pear | Fars |
| 50. | Almond | Chahar Mahal-o-Bakhtiari |
| 51. | Apricot | Fars |

Table 1. continued

| Strain | Host | Location |
|--|-------------|---|
| <i>P. syringae</i> pv. <i>Syringae</i> | | |
| 52. | Wild Almond | Fars |
| 53. | Cherry | Chahar Mahal- o –Bakhtiari |
| 54. | Cherry | Fars |
| 55. | Wheat | Fars |
| 56. | Unknown | <i>Pss</i> IVIA 773-1(Standard isolate) |
| 57. | Wild Almond | Fars |
| 58. | Cherry | Fars |
| 59. | Almond | Isfahan |
| 60. | Millet | Fars |

Bio-Rad I-cycler (USA) in 26 μ l PCR mixture: 2 μ l of DNA template was transferred to 24 μ l of a PCR mixture containing 45 pmol BOX A1R primer, 0.2 mM dNTP mix, 2 U of *Taq* DNA polymerase, 1.6 mM magnesium chloride. PCR was performed under the following conditions: 1 cycle at 95°C for 2 minutes; 35 cycles at 94°C for 1 minute, 52°C for 1 minute, and 65°C for 8 minutes; and a final extension cycle at 68°C for 16 minutes (Opgenorth *et al.*, 1996; Versalovic, *et al.*, 1991). The PCR products were electrophoresed on 1 % TBE agarose gel at room temperature at 80 V cm^{-1} for 3 hours. The DNA fragments were visualized by staining with ethidium bromide and photographed under UV illumination.

Data Analysis

The amplified fragments of each strain were detected, using Total Lab (v.1.1) program and were scored as 1 (present) or 0 (absent) and pair wise comparisons were made of each unique pattern by using the SM similarity coefficient of the NTSYSpc Software (Exeter Software, New York) (Rademaker *et al.*, 1998). A similarity matrix was generated by using the unweighted pair-group method (UPGMA) with averages. Phenograms were constructed with the Tree Display Option (Rolph, 2000).

RESULTS

Fifty-eight strains of *Pss* were isolated from almond, wild almond, peach, apricot, cherry, beet, pear, quince, oat, millet, wheat, barley, rice, pelargonium, *Malva* sp. and rose in Fars, Isfahan, Kohgiloye and Boyer Ahmad and Chahar Mahal-e-Bakhtiari provinces. The bacterium was detected in diseased samples and, as an epiphyte, on several apparently healthy plants. All *P. syringae* pv. *syringae* strains used in this study were negative for oxidase, potato rot, and arginine dihydrolase, but, positive for levan production and the hypersensitive response on tobacco.

Pathogenicity Tests

Twenty five strains of *Pss* isolated from different plants and one strain of *P. savastanoi* pv. *savastanoi*, were tested for pathogenicity on peach seedlings. All of the *Pss* strains were pathogenic on peach and produced progressive necrotic symptom on the inoculated site of the stem (Figure 1), but, *P. savastanoi* pv. *savastanoi* isolate was not.

Identification of *Pss* with Specific Primer

A total of 60 strains, including 58 strains of *Pss*, *Pss* IVIA 773-1 and *P. savastanoi*



Figure 1. Necrotic symptom on stem of peach seedling inoculated with *Pss* strain.

pv. savastanoi (IVIA 2558-IT), were tested for the presence of the *syrB* gene. All 58 isolates of the *Pss* and *Pss* IVIA 773-1, amplified a 752-bp fragment with the *syrB* primers as expected (Figure 2), whereas *P. savastanoi pv. savastanoi* did not.

BOX Analysis

The DNA fingerprints of 59 strains of *Pss* from different hosts (Table 1) were determined by BOX-PCR. Genomic fingerprints were generated for the isolates. More than 16 DNA fragments, ranging from 200 to 2500 bp in size, were amplified with

BOX-PCR primer. The fingerprint patterns of strains of *Pss* are shown in Figure 3. The occurrence of a particular BOX fingerprint pattern clearly differentiated strains isolated from different hosts. Based on genomic fingerprints using BOX A1R primer, the strains formed three clusters. Cluster one contained the strains of stone fruit, healthy peach, *Malva sp.*, two strains of rose, and one strain from pelargonium. The second cluster contained the strains isolated from quince and pear, one isolate from pelargonium, two isolates from peach, and the standard isolate (*Pss* IVIA 773-1). The third cluster consisted of graminous strains, one peach isolate and one isolate from beet.

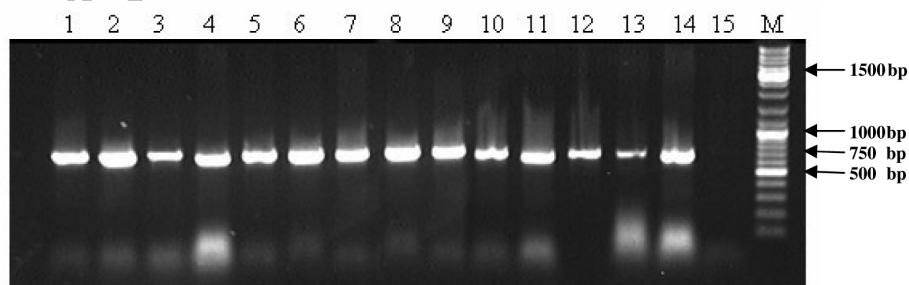


Figure 2. Agarose gel electrophoresis of PCR-products of *Pss* strains with primers B1 and B2. Left to right: 1-14: *Pss* strains; 15: Negative control, M: 100bp DNA molecular marker.

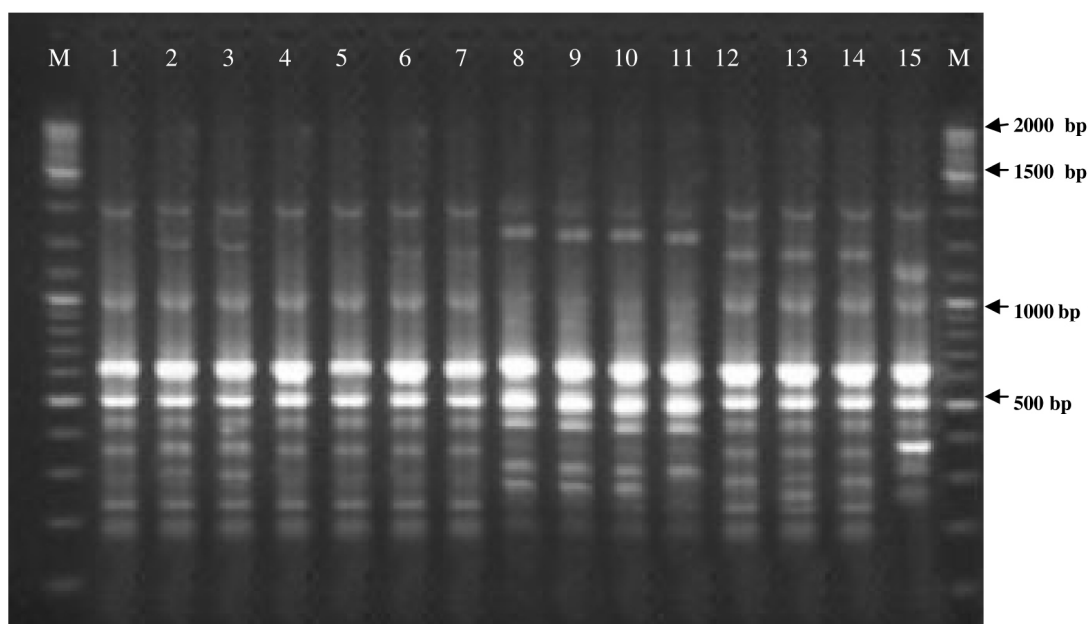


Figure 3. BOX-PCR fingerprint patterns of *Pss* strains isolated from different hosts. M: 100bp DNA molecular marker; 1: Healthy peach isolate; 2: Rose isolate; 3: Apricot isolate; 4: Cherry isolate; 5: Pelargonium isolate; 6: Wild almond isolate; 7: Almond isolate; 8: Wheat isolate; 9: Beet isolate; 10: Oat isolate; 11: Millet isolate; 12: Standard isolate (*Pss* IVIA 773-1); 13: Quince isolate; 14: Pear isolate; 15: *P. savastanoi* (IVIA2558IT).

Furthermore, *P. savastanoi* strain fell into a distinct cluster.

DISCUSSION

A total of 59 strains, including 58 strains of *Pss* and *Pss* IVIA 773 -1, amplified a 752-bp fragment with the *syrB* primers, whereas *P. savastanoi* pv. *savastanoi* did not. These results show that all of the isolates could synthesize syringomycine, which is very important toxin for pathogenicity induction in plant. *P. s.* pv. *savastanoi*, that can not produce this toxin, didn't amplify the *syrB* gene.

In this study, the *Pss* strains isolated from various hosts in Fars, Isfahan, Kohgiluyeh and Boyer-Ahmad, and Chaharmahal-e-Bakhtiari provinces generated several genetic profiles in BOX-PCR. For example, almost all prunus isolates produced similar patterns. Similarly, graminous isolates and pome fruit isolates produced special

patterns, which could be used for their differentiation from each other. The resulting dendrogram suggests a host specialization of several *Pss* strains within the heterogeneous pathovar *syringae*. The host specialization of *Pss* strains in a special host has been reported in prior studies. For example, bean pod pathogenicity assay have revealed that strains of *Pss* isolated from beans caused pathogenic reaction on bean pods, whereas strains isolated from other hosts did not show this reaction (Saad and Hagedorn, 1972). Similar results have been reported in other studies of the strains isolated from beans (Cheng *et al.*, 1989; Ercolani *et al.*, 1974; Rudolph, 1979) and, therefore, a new pathovar has been proposed for bean strains as *P. syringae* pv. *phaseolicola* (Rudolph, 1979). Grass strains of *Pss* have been reported to be more virulent on inoculated maize plants than strains isolated from non grass hosts (Gross and DeVay, 1977). Moreover, analysis of 13 *Pss* strains isolated from sugarcane, wheat

bacterial canker in susceptible tissues. These results are in agreement with previous studies (Little *et al.*, 1998).

Louws *et al.* (1995) found that rep-PCR methods are low cost, rapid, and reliable procedures to discriminate plant-pathogenic bacteria at the pathovar level. In this study, the results of comparison of *Pss* strains isolated from stone fruits, graminous plants and pome fruits showed that BOX-PCR can differentiate those isolates from each other. This result supports the hypothesis that, within the heterogeneous pathovar *syringae*, the strains infecting stone fruit, pome fruit, and graminous plant have adapted genetically to a particular host. Previously, a close relationship was reported between strains that infect pome fruits, such as pear, and stone fruits (Gross and DeVay, 1977; Roos and Hattingh, 1987). These findings are similar to the results of our study. REP-PCR analysis of 100 *Pss* strains from pear trees together with six strains from other hosts such as peach, wheat, tomato, and maize, showed that all of the pear strains clustered into one of the two nearly related groups, while the strains from other hosts did not have any similarities to the pear strains or to each other (Sundin, *et al.*, 1994). On the other hand, few similarities were found in the ERIC patterns of five strains of *Pss* isolated from pear, apple, and cherry trees in Germany (Weingart and Völksch, 1997).

Our results suggest that strains of *Pss*, at least those isolated from stone fruits, graminous hosts, and pome fruit were relatively adapted to a special host. Likely, this adaptation resulted from a long lasting life of a population of genetically heterogeneous *Pss* strains on a special host.

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مقایسه جدایه‌های *P. syringae* pv. *syringae* از میزبان‌های مختلف، بر اساس آزمون بیماری‌زایی و BOX-PCR در ایران

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چکیده

طی سال‌های ۱۳۸۶ و ۱۳۸۷، پنجاه و هشت جدایه *Pseudomonas syringae* pv. *syringae* (*Pss*) از میزبان‌های مختلف، نظیر هسته‌داران، چغندر قند، گل‌ابی، به، یولاف، ارزن، برنج، گندم و جو در استان‌های فارس، کهگیلویه و بویراحمد، چهارمحال و بختیاری و اصفهان جداسازی گردید. جدایه‌ها بر اساس آزمون بیماری‌زایی، وجود ژن *syrB* و BOX-PCR مورد ارزیابی قرار گرفتند. کلیه جدایه‌ها، صرف‌نظر از نوع میزبان روی نهال‌های هلو بیماری‌زا بودند. تعداد ۵۸ جدایه *Pss* به همراه جدایه *Pss* 773-1 IVIA، قطعه ۷۵۲ جفت بازی با آغازگر *syrB* را تکثیر نمودند. تجزیه و تحلیل انگشت نگاری ژنتیکی جدایه‌های *Pss* با استفاده از آغازگر BOXAIR نشان داد که جدایه‌های هسته‌داران، غلات و دانه‌داران گروه‌های نسبتاً متمایزی را تشکیل داده و از سایرین قابل تفکیک می‌باشند. این نتایج نشان‌دهنده وجود ترجیح میزبانی نسبی در میان جدایه‌های مختلف *Pss* می‌باشد.