# بررسی تنوع میزبانی گیاهان علفی و ارتباطات فیلوژنتیکی در میان جدایههای Phytophthora parsiana

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چکیدہ

محاضر در یک آزمایش مقدماتی، دامنه میزبانی بیمارگر روی گونه های مختلف گیاهان علفی با استفاده از شش جدایهی معرفی بی سامل حاضر در یک آزمایش مقدماتی، دامنه میزبانی بیمارگر روی گونه های مختلف گیاهان علفی با استفاده از شش جدایهی معامل کدوبیان، فلفل، جدایههای تیپ این گونه از منابع مختلف، در شرایط گل خانه بررسی شد. دو جدایه قارچ، از میان گیاهان علفی شامل کدوبیان، فلفل، حبوبات و گیاهان روغنی، تنها روی فلفل بیماریزا بودند. سپس به منظور بررسی واکنش ارقام مختلف فلفل به بیمارگر، بیماریزا بی د. حبوبات و گیاهان روی فلفل زمان معاریزا بودند. سپس به منظور بررسی واکنش ارقام مختلف فلفل به بیمارگر، بیماریزا بی جدایه معان و گیاهان علفی شامل کدوبیان، فلفل، حبوبات و گیاهان روغنی، تنها روی فلفل بیماریزا بودند. سپس به منظور بررسی واکنش ارقام مختلف فلفل به بیمارگر، بیماریزا بود. جدایه معان از و گیاهان کروی معان قرمز و نه فلفل دلمه می بیماریزا بود. این اولین گزارش از میزبان علفی برای Parsiana است. بین جدایههای Parsiana بیماریزا روی فلفل قرمز و دو جدایه دیگر از ایسن اولین گزارش از میزبان علفی برای Parsiana است. بین جدایههای Parsiana بیماریزا روی فلفل قرمز و دو جدایه دیگر از ایسن اولین گزارش از میزبان علفی برای Parsiana است. بین جدایههای Parsiana بیماریزا روی فلفل قرمز و دو جدایه دیگر از ایسن اولین گزارش از میزبان علفی برای Parsiana است. بین جدایه می میارگر نبودند، ار تباطات فیلوژنتیکی مورد بررسی قرار گرفت. بر اساس توالی سنجی ناحیه ی فلمای ترانویسی شده دو روی فلفل قرمز بیمارگر روی فلفل و جدایه رفتیکی مورد بررسی قرار گرفت. بر اساس توالی سنجی ناحیه ی فلمای ترانویسی شده داخلی (ITS)، جدایه یی بیمارگر روی فلفل و جدایه رفتیکی مراه با دیگر جدایه می می و مراه با دیگر به می مراه با دیگر بیمار گرونتیکی مراه با دیگر جدایه اساس توالی سنجی باه مراه با دامه مراه با دیگر بودند، ار تباطات فیلوژنتیکی مواره با دیگر جدایه اساس توالی سنجی ناحیه ی فلمای ترانویسی شده ی در حران گروه بی مراه با دیگر به مراه با میه و در تبار مراه تر شنه و در تبار قرمن و در تبار شن در حصال موان می می مراه با میه مراه با میه و در به مراه با دیگر و بندی و فلما و در تبار مانه و در تبار مراه تر شراه با مامه می مراه با مراه با مراه می مراه با مامه مراه با مامه مره می مرونتیکی مدی مراه م

كليدواژه: پسته، Phytophthora taxon Walnut، ايران، فلفل

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# Herbaceous host plants diversity and phylogenetic relationship among isolates of *Phytophthora parsiana*

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# Abstract

The high temperature-tolerant oomycete *Phytophthora parsiana* was considered to be limited to woody plants. In the preliminary study, the host range of the pathogen on annual herbaceous plant species using six isolates of *P. parsiana* including type strains from different sources was examined under greenhouse conditions. Among herbaceous species including cucurbits, pepper, pulse and oil crops, two isolates were pathogenic to pepper. Then three cultivars of pepper were used to discriminate pepper cultivars to sixteen isolates of *P. parsiana*. Results showed *P. parsiana* were pathogenic to red pepper ('Anheim' and 'Casabel' cultivars) but not bell pepper. This is the first report of an herbaceous host of *P. parsiana (sensu lato)*. Phylogenetic relationships of the pathogenic isolates of *P. parsiana* from pistachio to pepper and two isolates of the species from pistachio from Rafsanjan and Yazd were not pathogenic to pepper were examined. Based on sequences of the internal transcribed spacer (ITS) region of the ribosomal RNA, isolates pathogenic to pepper and one from Rafsanjan were in a group of *P. parsiana* belonging to clade 10 but the Yazd isolate had no genetic similarity to *P. parsiana*, being placed in clade 6 of the ITS tree, closely matching that of *Phytophthora* taxon Walnut from pistachio in Iran.

Keywords: Pistachio, Phytophthora taxon walnut, Iran, pepper

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# Introduction

*Phytophthora parsiana* was originally isolated from the crown of a fig tree in southern Iran (Shabankareh in Bushehr province) and reported as a high temperature *P. cryptogea* (Banihashemi and Ghaisi, 1992). Upon phylogenetic studies using different genes it was subsequently described as a new species in clade 10 as *P. parsiana* (Mostowfizadeh-Ghalamfarsa *et al.*, 2008). The host range of this new species was further studied and it was found to be limited to woody hosts (Hajebrahimi and Banihashemi, 2011; Rafiee and Banihashemi, 2013). Among woody plants almond and apricot were the most susceptible hosts (Rafiee and Banihashemi, 2013).

Six isolates of *P. parsiana* from fig and pistachio were inoculated to various hosts by Hajebrahimi and Banihashemi (2011). Fig isolate (PH21-5-90) and an isolate from a pistachio trunk in California, USA (PH21-3-92) were genetically identical but the other isolates from pistachio from Rafsanjan in Kerman province showed genetic variations. The physiological characteristics of identification of *P. parsiana* were high temperature tolerance and formation of botryose hyphal swellings (Banihashemi, unpublished 1992). Further studies then showed that isolates of *P. parsiana* (*sensu lato*) selected according to these criteria were phylogenetically related (Mostowfizadeh-Ghalamfarsa *et al.*, 2008).

Among six original isolates of *P. parsiana* used, almond isolate from Greece was basal to other isolates. Pistachio isolates from Iran including isolates PH21-6-92, PH21-7-92 and PH21-4-92 showed a recent common ancestor, while PH21-3-92 (pistachio trunk isolate from USA) and PH21-5-90 (fig trunk from southern Iran) to be sister taxa and considered to be *P. parsiana* (Mostowfizadeh-Ghalmfarsa *et al.*, 2008).

The objective of the present study was using more isolates of *P. parsiana* to study their diversity in respect to host range and phylogenetic traits.

## **Materials and Methods**

#### Sources of isolates

In the preliminary study six isolates tentatively identified as *P. parsiana* (PH21-2-05, PH21-3-92, PH21-4-92, PH21-5-90, PH21-6-92, PH21-7-92)

study.			
Year	Location	Host	Isolate code
1976	Greece	Almond	PH21.2.05
1992	USA	Pistachio	PH21.3.92
1992	Iran (Kerman)	Pistachio	PH21.4.92
1991	Iran (Bushehr)	Fig	PH21.5.90
1993	Iran (Kerman)	Pistachio	PH21.6.92
1993	Iran (Kerman)	Pistachio	PH21.7.92
2008	Iran (Kerman)	Pistachio	PH21.13.08
2009	Iran (Kerman)	Pistachio	PH21.21.10
2009	Iran (Kerman)	Pistachio	PH21.22.10
2010	Iran (Kerman)	Pistachio	PH21.24.10
2010	Iran (Yazd)	Pistachio	PH21.27.10
2010	Iran (Yazd)	Pistachio	PH21.30.10
2012	Iran (Kerman)	Pistachio	PH21.33.12
2012	Iran (Kerman)	Pistachio	PH21.34.12
2012	Iran (Kerman)	Pistachio	PH21.35.12
2012	Iran (Kerman)	Pistachio	PH21.36.12

and then sixteen isolates were used (Table 1).

#### Inoculum production

Hyphal tip isolates were grown on corn meal agar (CMA) for 3-4 days at 25°C and few blocks were transferred to vermiculate amended with hemp seed extract (Banihashemi, 2004) and incubated at room temperature for 4-5 weeks.

#### Herbaceous host range study

Seeds of herbaceous plants from different families including sunflower (*Helianthus annuus*), broad bean (*Faba vulgaris*), chickpea (*Cicer arietinum*), pumpkin (*Cucurbita moschata*), long melon (*Cucumis melo cv. inodorus*) common bean (*Phaseolus vulgaris*), red ('Anheim' and 'Casabel'cultivars) and bell pepper (*Capsicum annuum*), soybean (*Glycine max*) and safflower (*Carthamus tinctorius*) were surface-disinfested in 0.5% sodium hypochlorite for 5 min, washed several times in sterile distilled water and incubated between sterile moist paper towels at 25°C to induce germination.

Ten to 12 germinated seeds were sown in 15 cm plastic pot containing sterilized soil and sand (2/1 ratio) and incubated in a greenhouse  $(20-25^{\circ}\text{C})$  and irrigated as needed. After two weeks, the number of seedlings in each pot was reduced to 4–5.

#### Inoculation

In the preliminary study, ten ml of vermiculate inoculum of selected isolates of *P. parsiana* (PH21-2-05, PH21-3-92, PH21-4-92, PH21-5-90, PH21-6-92, PH21-7-92) was placed around seedlings in the pot and flooded overnight with the drainage hole closed. To monitor the activities of the isolates, the drainage holes were opened the next day and drained water was collected and baited with citrus leaf disc (Banihashemi, 2004). Controls received vermiculite hempseed extract. The flooding and drainage baiting were repeated every other week.

#### Reaction of pepper cultivars to P. parsiana isolates

Based on the preliminary results of herbaceous plants, three cultivars of pepper were used to discriminate pepper cultivars to 16 isolates (Table 1) of *P. parsiana* using red ('Anheim' and 'Casabel') and bell pepper. They were inoculated with 4-week-old vermiculite inoculums of 16 isolates of *P. parsiana* and the activity of the isolates was monitored as described. Isolates PH21-4-92 and PH21-7-92 caused mortality of 33 and 22% in cultivar Anheim and 44 and 22% in cultivar Casabel respectively but could not infect bell pepper. Other isolates of *P. parsiana* failed to infect peppers.

#### DNA extraction and sequencing

Fungal isolates (PH21-30-10 from Harat in Yazd province and PH21-34-12 from Kerman province) were grown in 50 ml culture of potato broth (extract of 300 gL<sup>-1</sup> potato) at 20°C for 7 days. After vacuum filtration, the mycelia were harvested and freeze-dried. DNA was extracted from freeze-dried fungal mycelium as described by Mirsoleimani and Mostowfizadeh-Ghalamfarsa (2013). The internal transcribed spacer (ITS) region of the ribosomal RNA genome was amplified by polymerase chain reaction using the universal primers ITS 6 (5' GAA GGT GAA GTC GTA ACA AGG 3') and ITS 4 (5'- TCC TCC GCT TAT TGA TAT GC-3') (White et al., 1990; Cooke et al., 2000). The PCR reaction mixture, PCR conditions and visualization were as described by Mirsoleimani and Mostowfizadeh-Ghalamfarsa (2013). The amplification products of all isolates were purified through purification columns (GeneJet<sup>TM</sup>

PCR Purification Kit; Fermentas) to remove extra primers and nucleotides. PCR products were sequenced in forward and reverse orientation using the primers used for amplification by means of dye terminator cycle sequencing kits (BigDye sequencing kit, Applied Biosystems, Foster City, California, USA) on an AB1377-96 automated sequencer (Applied Biosystems) according to the manufacturer's instructions.

#### DNA analysis

Sequences were edited using Bioedit software (Hall, 1999) and aligned with ClustaX1.8 (Larkin et al., 2007). Manual adjustment of sequence alignments was performed to accommodate insertions/deletions. The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model (Kimura, 1980). The tree with the highest log likelihood (-4439.4317) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.4140). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 632 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013). The sequence of *Pythium aphanidermatum* AF271227 (obtained from GenBank) was used as outgroup. The GenBank accession numbers of Phytophthora species used for phylogenetic studies are listed in Table 2.

# Results

#### Herbaceous plants

From annual herbaceous plants inoculated with isolates of *P. parsiana* only two isolates (PH21-4-92 and PH21-7-92), showed disease symptoms on red peppers after 20 days. Isolate PH21-4-92 was

Table 2. GenBank accession numbers of isolates of Phytphthora spp. used for phylogenetic studies.

Isolate	Species	Accession number
PH21-30-10 <sup>a</sup>	Phytophthora taxon Walnut	KU577517 <sup>1</sup>
PH21-34-12 <sup>a</sup>	Phytophthora parsiana	KU577518 <sup>1</sup>
PIS15	Phytophthora pistaciae	AF403506 <sup>2</sup>
32F6	Phytophthora melonis	EU088256 <sup>3</sup>
23J6	Phytophthora drechsleri	EU423315 <sup>4</sup>
UQ881	Phytophthora cinnamomi	AF266764 <sup>5</sup>
IMI296829	Phytophthora syringae	AF266803 <sup>5</sup>
IMI180616	Phytophthora heveae	AF266770 <sup>5</sup>
MD 9/2	Phytophthora quercetorum	DQ313223 <sup>6</sup>
CBS678.85	Phytophthora mirabilis	AF266777 <sup>5</sup>
IMI158964	Phytophthora iranica	AJ131987 <sup>5</sup>
IMI133317	Phytophthora megasperma	AF266794 <sup>5</sup>
P246b	Phytophthora inundata	AF266791 <sup>5</sup>
IMI302303	Phytophthora humicola	AF266792 <sup>5</sup>
52	Phytophthora rosacearum	EU925376 <sup>7</sup>
JP-08-328	Phytophthora taxon Walnut	KJ405953 <sup>8</sup>
P532	Phytophthora sp.	AF541910 <sup>9</sup>
B164	Phytophthora taxon Walnut	KC291550 <sup>10</sup>
NZFS310L	Phytophthora fallax	DQ297391 <sup>11</sup>
NZFS310C	Phytophthora captiosa	DQ297402 <sup>11</sup>
IMI288805	Phytophthora insolita	AF271222 <sup>5</sup>
UASWS0198	Phytophthora polonica	DQ396410 <sup>12</sup>
SUC7 (PH21-3-92 <sup>a</sup> )	Phytophthora parsiana	AY659737 <sup>13</sup>
SUC25 (PH21-5-90 <sup>a</sup> )	Phytophthora parsiana	AY659739 <sup>13</sup>
SUC19 (PH21-4-92 <sup>a</sup> )	Phytophthora parsiana	AY659738 <sup>13</sup>
Rf17 (PH21-7-92 <sup>a</sup> )	Phytophthora parsiana	AY659741 <sup>13</sup>
SURf6 (PH21-6-92 <sup>a</sup> )	Phytophthora parsiana	AY659740 <sup>13</sup>
SCRP237(PH21-2-05 <sup>a</sup> )	Phytophthora parsiana	AY659736 <sup>13</sup>
P21282	Phytophthora parsiana	GU594784 <sup>14</sup>
1D12	Phytophthora hydropathica	EU583797 <sup>15</sup>
44A9	Phytophthora hydropathica	EU583796 <sup>15</sup>
44J1	Phytophthora hydropathica	EU583794 <sup>15</sup>
GAL	Phytophthora gallica	DQ286726 <sup>16</sup>
UQ2071	Pythium aphanidermatum	AF271227 <sup>5</sup>

<sup>1</sup>Submitted in this study. <sup>2</sup>Mirabolfathy *et al.*, 2001. <sup>3</sup>Ho *et al.*, 2007. <sup>4</sup>Gallegly and Hong.,2008. <sup>5</sup>Cooke *et al.*, 2000. <sup>6</sup>Balci *et al.*,2008 <sup>7</sup>Hansen *et al.*,2009. <sup>8</sup>Parke *et al.*, 2014. <sup>9</sup>Brasier *et al.*,2003. <sup>10</sup>Ginetti *et al.*, 2014. <sup>11</sup>Dick *et al.*,2006. <sup>12</sup>Belbahri *et al.*,2006. <sup>13</sup>Mostowfizadeh–Ghalamfarsa *et al.*, 2008. <sup>14</sup>Unpubl. data (Coffey,M.D., Brar,A.K., Xu,E. and Zhang,Y.H.). <sup>15</sup>Hong *et al.*, 2010. <sup>16</sup>Jung *et al.*,2008. <sup>a</sup> Plant Protection Department of Shiraz University code.

more aggressive than the other isolate. Other isolates were not pathogenic to herbaceous plants. The pathogen was re-isolated from symptomatic tissue. All isolates in the pot monitored during the experiment were active with the presence of zoospores. To discriminate isolates of *P. parsiana*, sixteen isolates were inoculated to red and bell peppers cultivars. Isolates PH21-4-92 and PH21-7-92 caused mortality of 33 and 22% in cultivar Anheim and 44 and 22% in cultivar Casabel respectively but could not infect bell pepper. Other isolates of *P. parsiana* failed to infect peppers.

#### Molecular assays

Two isolates of *Phytophthora* (PH21-30-10 and PH21-34-12) were amplified using the primers ITS6 and ITS4. An amplicon of about 700 bp was obtained for two isolates of *Phytophthora*. BIASTn searches in GenBank showed that ITS sequences of PH21-30-10 and PH21-34-12 isolates had 99-100% identity with isolates of *Phytophthora* taxon Walnut (GenBank KJ405953, AF541910, KC291550) and *Phytophthora parsiana* (GenBank AY659738, GU594784), respectively (Figure 1).

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Figure 1. Phylogram of maximum likelihood analysis of the *Phytophthora parsiana* and *Phytophthora* taxon Walnut isolates examined in this study (indicated in bold), together with 20 *Phytophthora* species based on the rDNA ITS region. The numbers at the branch points indicate the percentages of the bootstrap values ( $\geq$ 70%).

## Discussion

Among annual herbaceous plants only two isolates of *P. parsiana* from pistachio in Rafsanjan (PH21-4-92 and PH21-7-92) infected red pepper plants and PH21-4-92 was more aggressive. This is the first indication of an herbaceous plant as host for *P. parsiana*.

The two type cultures of *P. parsiana* from Bushehr in fig and stem canker of pistachio in USA along with the rest of the isolates used failed to infect red pepper and were limited to woody plants. An isolate of the pathogen from pistachio recovered from Kerman province (PH21-34-12), although related to PH21-4-92 and PH21-7-92 based on ITS sequencing (Figure 1), was not pathogenic to peppers. Hong *et al.* (2010) assumed the two latter isolates to represent new species.

An isolate of the pathogen from pistachio in Harat (PH21-30-10) in Yazd province morphologically similar to *P. parsiana* with high temperature tolerance, was different from *P. parsiana*; based on ITS sequencing, it belongs to clade 6 close to *P.* taxon Walnut (Figure 1) (Anvari, 2014; Anvari *et al.*, 2014). This is the first report of *P.* taxon Walnut in pistachio in Iran.

Clade 6 comprised five taxa, among them found

in riparian ecosystem such as ponds, river and flooded situation with high temperature growth requirement. Among them few are pathogenic on plants such as Salix and Olea (Brasier et al., 2003). Most of these species require high temperature for growth, and are sexually sterile. Some of the clade 6 isolates still need to be described. Taxon Walnut isolated from walnut in California belongs to clade 6, grows at 38°C, and is sexually sterile (Brasier et al., 2003). Phytophthora isolates from walnut with dieback symptoms in Italy were high temperaturetolerant and, based on ITS sequencing, are also identified as taxon Walnut with 94% similarity. The pathogenic behavior of taxon Walnut in Italy is considered to be due to recent global warming for a taxon that otherwise behaved saprophytically (Ginett et al., 2014).

The present study shows that the Harat isolate (PH21-30-10), although morphologically similar to *P. parsiana*, belonged to clade six close to *P.* taxon Walnut (Figure 1). With the limited number of isolates available from pistachio orchards in Iran it appears that under *P. parsiana* some different species are hidden. More detailed phylogenetic studies using more isolates are required to describe new species.

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