Mycologia Iranica 2025, Vol. 12 (No. 1): 107–114 JIrMS

Short Article

Phytopythium montanum, a new species for Iran

Negin Ramezanzadeh, Khalil-Berdi Fotouhifar ✉

Department of Plant Protection, Faculty of Agriculture, College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran

https://doi.org/10.22092/mi.2025.368635.1307

ABSTRACT

To investigate Oomycete species in the aquatic habitats of Tehran Province, Iran, water samples were randomly collected from various aquatic ecosystems based on their geographical distribution from April to November 2021. Oomycete isolates were recovered by the baiting method with citrus (*Citrus limetta*) leaves and cultured on CMA+PARP semi-selective culture medium. Finally, two isolates (KAN0230 and KAN0218) obtained from the Kan River were identified as *Phytopythium montanum* based on the morphological features of the vegetative and reproductive organs as well as molecular data from the internal transcribed spacer (ITS-rDNA) sequences in a maximum likelihood phylogenetic analysis. Based on the available literature, *Phytopythium montanum* is reported for the first time as a new taxon for the Oomycete biota of Iran.

KEYWORDS

Morphology, Phylogeny, ITS-rDNA, *Oomycota*, aquatic ecosystem.

INTRODUCTION

Oomycota, a monophyletic group of filamentous fungal-like organisms (*Stramenopila*), is ubiquitous in the oceans, freshwater, and terrestrial environments throughout the world (Thines and Kamoun 2010, Jankowiak et al. 2015). The species belonging to the class *Oomycetes* are fungus-like organisms that are much closely related to diatoms and brown algae than to the kingdom of fungi (Beakes et al. 2012). Because they are related to aquatic organisms, their dependence on water is strong as all or some stages of their lifecycle are reliant on water (Walker and van West 2007). Some of these species are saprophytes, however, others can colonize plant tissues and thus be pathogenic and capable of causing severe diseases (Thines 2014). Two genera of *Oomycetes*, *Pythium* and *Phytopythium*, have a variety of nutritional modes and ecological niches. They are well established as soil-borne plant pathogens or saprophytes but are also distributed widely in freshwater ecosystems (Nechwatal et al. 2008). Species of *Pythium* are categorized into 11 clades (A-K), according to their phylogenetic relationships, morphological characteristics, and host preferences. Members of the genus *Phytopythium* were originally classified in clade K of the genus *Pythium* according to the molecular phylogenetic subdivision of *Pythium sensu lato* by Levesque and de Cock (2004). They are similar to the *Pythium* species based on the zoospore differentiation and release mechanism but produce globose to ovoid, papillate sporangia, often with internal proliferation similar to species of *Phytophthora* (Bala et al. 2010a). As a result, a new genus, *Phytopythium*, an intermediate between *Phytophthora* and *Pythium* was introduced to separate it from other groups in *Pythium* (de Cock et al. 2015).

Oomycete species are pathogens of many plants and they represent one of the biggest threats to global food security and natural ecosystems. Until 2015, only three *Phytopythium* species with previous generic name of *Pythium*, including *P. helicoides*, *P. ostracodes*, and *P. vexans*, have been reported from Iran (Babai-Ahary et al. 2004, Mostowfizadeh-Ghalamfarsa 2015), but subsequent studies using morphological and sequence

Received: 14 Feb. 2025 Revised: 22 Mar. 2025 Accepted: 11 Apr. 2025 Published online: 13 Apr. 2025

✉ Corresponding Author: Khalil-Berdi Fotouhifar; Email: fotowhi@ut.ac.ir

Published by Iranian Mycological Society (IrMS)—https://mij.areeo.ac.ir

data documented the presence of *P. carbonicum*, *P. litorale*, *P. boreale*, *P. mercuriale*, *P. oedochilum*, *P. babaiaharii*, *P. longitubum*, *P. palingenes* and *P. sterile* in different provinces of Iran, indicating that the most isolated *Phytopythium* species from Iran belong to clade 1 that have been recovered from agricultural soils (Chenari Bouket et al. 2016, Salmaninezhad and Mostowfizadeh-Ghalamfarsa 2017, Hosseini Badrbani et al. 2018, Rezaei et al. 2021, Salmaninezhad and Mostowfizadeh-Ghalamfarsa 2023).

Considering the importance of aquatic ecosystems in the transmission of plant pathogens, identifying these pathogens and determining their characteristics are very important. Before our study, information on *Phytopythium* was scarce and no species of this genus had been reported from Tehran Province, Iran. Therefore, the present study was conducted to identify the Oomycetous species in some aquatic ecosystems of the Tehran Province.

MATERIALS AND METHODS

Water samples were collected from some aquatic ecosystems (running waters, reservoirs, fountains, and lakes) of Tehran Province, Iran, between April to November of 2021. Isolates were obtained from water samples by baiting technique (van der Plaats-Niterink 1981), using sterile citrus (*Citrus limetta*) leaves. Baits embedded in water samples were incubated at room temperature for 24 h and then, the colonized baits were washed under running tap water to remove the excess contaminants, blotted dry on sterile filter paper and then plated on CMA+PARP agar culture medium (extract of 60 g ground maize, pimaricin 0.01 g, ampicillin 0.25 g, rifampin 0.01 g, PCNB 0.1 g, agar 15 g, distilled water 1l) (Mostowfizadeh-Ghalamfarsa and Banihashemi 2005). The grown mycelia on the culture medium were sub-cultured on 2% water agar (WA) culture medium (agar 20 g, distilled water 1 liter) and the isolates were purified by transferring the hyphal tips onto Petri dishes containing handmade potato-dextrose-agar (PDA; extract of 200 g cooked peeled potato, agar 20 g, dextrose 15 g, distilled water 1l).

Table 1. ITS-rDNA sequences used for phylogeny. The newly generated sequence is in boldface.

Taxon	Origin	Isolate ID	GenBank no.	Reference
Phytopythium montanum	**Iran**	**IRAN 4844C**	**OQ825978**	**Present study**
	Japan	CBS111349	AB725883	Baten et al. (2014)
	Germany	ADC9762	HQ643391	Robideau et al. (2011)
	Germany	CBS111349	HQ643389	Robideau et al. (2011)
	Germany	ADC9766	HQ643390	Robideau et al. (2011)
Phytopythium aichiense	Japan	MAB-2014	AB948197	Baten et al. (2014)
Phytopythium babaiaharii	Iran	Iran-Ppy1	PP892678	Rezaei et al. (2021)
Phytopythium boreale	China	CBS55188	HQ643372	Robideau et al. (2011)
Phytopythium carbonicum	France	CBS112544	HQ643373	Robideau et al. (2011)
Phytopythium citrinum	Netherlands	ADC9442	HQ643380	Robideau et al. (2011)
Phytopythium chamaehyphon	Japan	CBS259.30	AB690609	Baten et al. (2014)
Phytopythium cucurbitacearum	Canada	CBS 748.96	AY598667	Levesque and de Cock (2004)
Phytopythium delawarense	Japan	382B	AB725875	Baten et al. (2014)
Phytopythium dogmae	Philippines	USTCMS 4101	MF353170	Unpublished
Phytopythium helicoides	Japan	CBS286.31	AB725878	Baten et al. (2014)
Phytopythium iriomotense	Japan	CBS292.37	AB690624	Baten et al. (2014)
Phytopythium fagopyri	Japan	FP1	AB690625	Baten et al. (2014)
Phytopythium kandeliae	Taiwan	CBS11191	HQ643134	Robideau et al. (2011)
Phytopythium litorale	France	CBS122662	HQ643385	Robideau et al. (2011)
Phytopythium megacarpum	South Korea	Pet-Stol-SW7	AB725588	Unpublished
Phytopythium mercuriale	Japan	CBS122443	AB690614	Baten et al. (2014)
Phytopythium mirpurense	Pakistan	CBS124524	KJ831614	Unpublished
Phytopythium nanjingens	China	Chen 218	MF459636	Unpublished
Phytopythium oedochilum	Japan	CBS292.37	AB108020	Baten et al. (2014)
Phytopythium ostracodes	Spain	CBS76873	HQ643395	Robideau et al. (2011)
Phytopythium palingenes	Vietnam	VN429	MN872742	Jung et al. (2020)
Phytopythium paucipapillatum	South Africa	STE-U7843	KX372749	Unpublished
Phytopythium sindhum	Pakistan	CBS:124522	HM244828	Bala et al. (2010b)
Phytopythium sterile	Iran	KH1-2	KX228096	Salmaninezhad and Mostowfizadeh-Ghalamfarsa (2017)
Phytopythium sterilum	Spain	PE101	DQ217603	Belbahri et al. (2006)
Phytopythium vexans	South Africa	CBS119.80	GU133572	Spies et al. (2011)
Achlya sparrowii	Canada	CBS10249	HQ643108	Robideau et al. (2011)

To induce the formation of sporangia, mycelial plugs from the actively growing colony margins of the isolates grown on PDA culture medium were transferred into Petri dishes containing sterile distilled

water or soil extract (10 g/L), and boiled hemp seed (Banihashemi et al. 1992). Petri dishes were incubated at 25°C under the cool white fluorescent light and were examined daily and the shape and size of the asexual structures were determined for each isolate by preparing microscopic slide mounts. To induce the formation of oospores, isolates were grown on hemp seed agar (HSA; ground hemp seed extract 60 g/L; agar 15 g/L) (Salmaninezhad and Mostowfizadeh-Ghalamfarsa 2019) culture medium and the inoculated Petri dishes were incubated at 25°C in continuous darkness. Colony pattern and average daily growth rate at 25°C were measured in three replicates growing on PDA and corn meal agar (CMA) culture media. The living culture of the investigated taxon has been deposited in the Fungal Collection of the Iranian Research Institute of Plant Protection, Tehran, Iran (IRAN).

For molecular study, isolates were grown in handmade Potato Dextrose Broth (PDB; extract of 200 g cooked peeled potato, dextrose 15 g, distilled water 1l) at 25°C for seven days on a rotary shaker and total genomic DNA was extracted from obtained mycelium using the method described by Zhong and Steffenson (2001). The primer pair ITS4 (TCCTCCGCTTATTGATATGC) (White et al. 1990) and ITS6 (GAAGGTGAAGTCGTAACAAGG) (Cooke et al. 2000) were used to amplify the internal transcript spacer (ITS) region from nuclear rDNA of the isolates. The PCR cycling parameters were: initial denaturation at 94°C for 2 min followed by 30 cycles of denaturation at 94°C for 2 s, annealing at 62°C for 25 s, extension at 72°C for 1 min and final extension at 72°C for 10 min. The PCR product was analyzed using 1% agarose gel electrophoresis, stained with ethidium bromide (0.5 µg/ml), and visualized under UV light, and then sent to the Codon Genetic Research Center (IRAN) for sequencing. The generated sequence was manually edited with Chromas 2.6.6 software (Technelysium Pty Ltd, Australia) and the edited sequence was saved in FASTA format. The resulting sequence was subjected to BLAST search (Altschul et al. 1997) in the National Center of Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov) to find the most similar and relevant sequences. Sequences of the reference isolates were obtained from GeneBank and *Achlya sparrowii* (HQ643108.1) was used as an outgroup taxon. All obtained sequences (Table 1) were aligned together with the sequence of our isolate (IRAN 4844C) using the Clustal W (Thompson et al. 1994) algorithm implemented in MEGA 11.0 (Tamura et al. 2021). Phylogenetic analysis using the maximum likelihood method (Felsenstein 1973) with default options (nucleotide substitution model: Tamura-Nei model; rates among sites: uniform rates; gaps/missing data treatment: use all sites; tree inference options: ML heuristic method, with nearest-neighbor-interchange, NNI) was conducted in MEGA 11.0. The generated tree was tested using the bootstrap method with 1000 replicates. The newly generated ITS-rDNA sequence of the present study (IRAN 4844C) was submitted to GenBank with accession number of OQ825978.

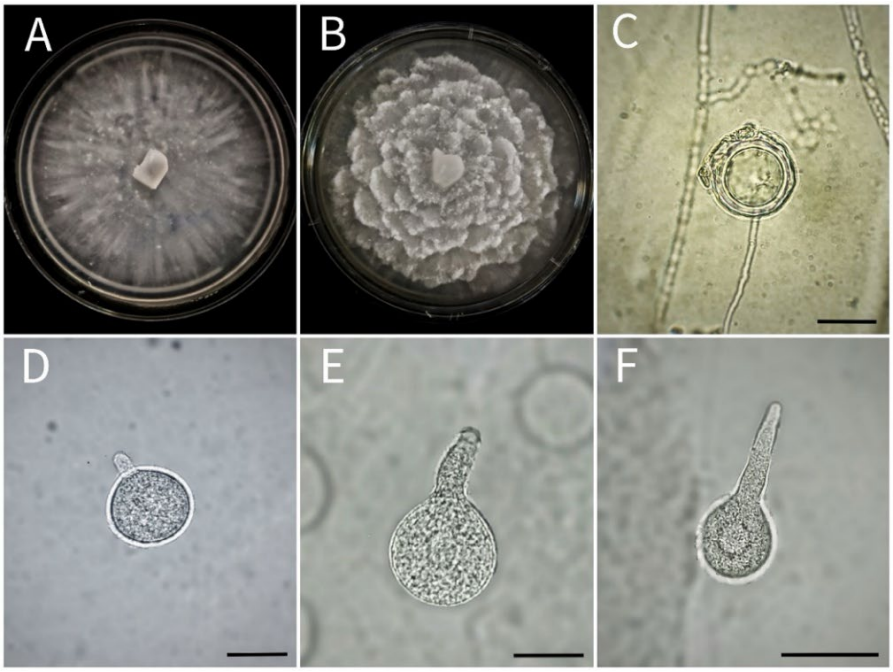

Fig. 1. *Phytopythium montanum*, isolate IRAN 4844C: (A) Colony pattern on CMA, (B) Colony pattern on PDA after 10 days in continuous darkness at 25°C, (C) Oospore, (D-F) Sporangia showing various degrees of apical elongation (Bars = 20µm).

RESULTS AND DISCUSSION

Two Oomycete isolates [KAN0230 (IRAN 4844C) and KAN0218] with similar cultural and morphological features were obtained from samples collected from the Kan River and were identified as *Phytopythium*

montanum (Nechw.) Abad, de Cock, Bala, Robideau, Lodhi & Levesque, based on the morphological and molecular data of the ITS-rDNA sequence. Colonies on agar culture media (PDA, CMA and HSA) were submerged, showing a petaloid pattern on PDA and stellate to chrysanthemum pattern on CMA. The average daily growth rate at 25°C ranged from 5.5 mm/day on PDA to 6 mm/day on CMA. The width of the main hyphae was up to 5 µm. Hyphal swelling or chlamydospores were not observed. Sporangia formed in water were terminal, globose, ovoid or ob-pyriform. Mature sporangia with apical or lateral papilla and papilla either giving rise to a short discharge tube with 2-8 µm width, subsequent release of sporangium contents for zoospore development, or developing into a large rostrum up to 20 µm. After zoospore release, new sporangia developed by internal proliferation, either within or outside of the empty sporangium. Oogonia were spherical, smooth-walled and mostly terminal, measuring 22-27 µm (av. 23) in diameter. Antheridia were monoclinous and extremely variable in shape. Oospore was aplerotic, 16-21 µm in diameter (av. 18.5) and oospore walls 1.6-2 µm thick (Fig. 1).

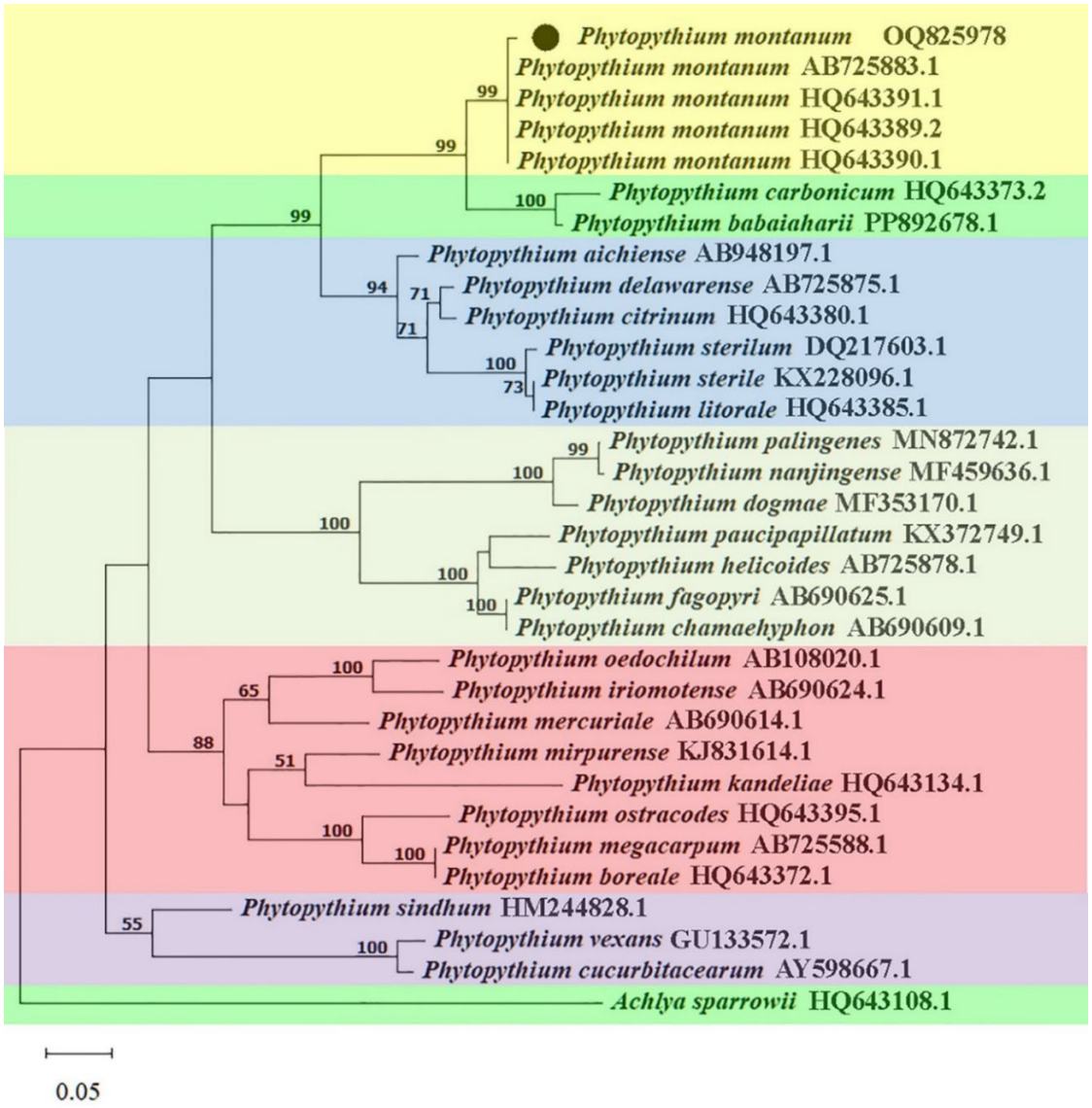

Fig. 2. Phylogenetic tree inferred using the maximum likelihood (ML) method based on the nucleotide sequences of ITS-rDNA region in 31 isolates of *Phytopythium* species. The solid circle indicates the isolate obtained in the present study. Numbers on the branches represent the percentage of bootstrap values from1000 replicates. *Achlya sparrowii* (HQ643108.1) was used as an out-group taxon.

Morphological features of the investigated isolates were similar to those of *Pythium montanum* as described by Nechwatal and Osswald (2003). *Pythium montanum* was first introduced by Nechwatal and Osswald (2003) having a unique combination of sporangial and gametangial characters as well as ITS-rDNA sequence data that could not be assigned to any other known species of

the genus *Pythium*. The species has relatively low growth rate, internally proliferating sporangia and extremely variable, monoclinous, sessile or shortly stalked antheridia with frequently direct germination of sporangia in water culture. de Cock et al. (2015) described the new genus *Phytopythium* to accommodate the members of *Pythium* clade K, as described by Lévesque and de Cock (2004), and transferred *Pythium montanum* to the genus *Phytopythium,* establishing the new combination *Phytopythium montanum*.

Phytopythium montanum is phylogenetically and morphologically related to but distinct from *P. babaiaharii*. *Phytopythium babaiaharii* has recently been reported from the soil of sugar beet fields in West Azarbaijan as a new species. Morphologically, *P. babaiaharii* is distinguished from *P. montanum* by the production of lateral oogonia and having both plerotic and aplerotic oospores (Rezaei et al. 2021). *Phytopythium montanum* as *Pythium montanum* has been isolated from the rhizosphere soil of Norway spruce [*Picea abies* (L.) H. Karst] in Bavarian Alps at an altitude of 1000 m above sea level. In experimental conditions, the weak aggressiveness of this species on lupine (*Lupinus angustifolius* L.) and Norway spruce has been demonstrated (Nechwatal and Oßwald, 2003). In the present study, the ITS-rDNA sequence of the *Phytopythium montanum* (IRAN 4844C) showed more than 98% similarity with valid sequences such as HQ643389, HQ643390, HQ643391, (Robideau et al. 2011), and AB725883 (Baten et al. 2014) of previously identified and deposited taxa in the GenBank. The maximum likelihood phylogenetic tree constructed based on ITS region sequences indicated that the Iranian specimen is placed in the same clade with *P. montanum* isolates reported by other authors with 99% bootstrap support (Fig. 2). Based on the results of morphological and phylogenetic investigations, *P. montanum* is reported for the first time as a new taxon for the Oomycete biota of Iran. The living culture of the isolate Kan0230 has been deposited in the Fungal Collection of the Iranian Research Institute of Plant Protection, Tehran, Iran (IRAN), with accession number IRAN 4844C.

ACKNOWLEDGMENT

The present research was supported by the University of Tehran. The authors would like to express their appreciation to the University of Tehran.

AUTHOR CONTRIBUTION

The individual contributions of authors to the manuscript are as follows. Negin Ramezanzadeh performed the research and wrote the primary manuscript, Khalil-Berdi Fotouhifar designed and supervised the research and reviewed the primary manuscript. In addition, Kh. -B. Fotouhifar is corresponding author.

DATA AVAILABILITY

All generated datasets during the current study are available in the manuscript. The newly generated ITS sequence was deposited in the NCBI with accession number of OQ825978.

DECLARATION

The authors declare that there is no conflict of interest.

FUNDING

There is no fund for this research to be declared.

ETHICS APPROVAL

Not applicable.

REFERENCES

Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z et al. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Research 25(17): 3389-3402. https://doi.org/10.1093/nar/25.17.3389.

Babai-Ahary A, Abrinnia M, Majidi Heravan I. 2004. Identification and pathogenicity of *Pythium* species causing damping-off in sugarbeet in northwest Iran. Australasian Plant Pathology 33: 343-347. https://doi.org/10.1071/AP04038.

Bala K, Robideau GP, Desaulniers N, de Cock AWAM, Lévesque CA. 2010a. Taxonomy, DNA barcoding and phylogeny of three new species of *Pythium* from Canada. Persoonia 25: 22-31. https://doi.org/10.3767/003158510X524754.

Bala K, Robideau GP, Lévesque CA, Lodhi AM, Shahzad S, De Cock AWAM. 2010b. *Phytopythium* Abad, de Cock, Bala, Robideau, Lodhi & Lévesque, gen. nov. and *Phytopythium sindhum* Lodhi, Shahzad & Lévesque, sp. nov. Fungal Planet 49. Persoonia 24: 136-137.

Belbahri L, Calmin G, Sanchez-Hernandez E, Oszako T, Lefort F. 2006. *Pythium sterilum* sp. nov. isolated from Poland, Spain and France: its morphology and molecular phylogenetic position. FEMS Microbiology Letters 255(2): 209-214. https://doi.org/10.1111/j.1574-6968.2006. 000 59 .x.

Banihashemi Z, MacDonald JD, Stite J. 1992. Combine baiting and ELISA to detect and quantify *Phytophthora* spp. in container media. Phytopathology 82: 1101.

Baten MA, Asano T, Motohashi K, Ishiguro Y, Rahman MZ, Inaba S, Suga H, Kageyama K. 2014. Phylogenetic relationships among *Phytopythium* species, and re-evaluation of *Phytopythium fagopyri* comb. nov., recovered from damped-off buckwheat seedling in Japan. Mycological Progress 13:1145-1156. https://doi.org/ 10.1007/s11557-014-1003-1.

Beakes GW, Glockling SL, Sekimoto S. 2012. The evolutionary phylogeny of the oomycete “fungi”.

Protoplasma 249(1):3–19. https://doi.org/ 10.1007/ s00709-011-0269-2.

Chenari Bouket A, Babai-Ahari A, Arzanlou M, Tojo M. 2016. Morphological and molecular characterization of *Phytopythium litorale* and *Pp. oedochilum* from Iran. Nova Hedwigia 102(1-2): 257-270. https://doi.org/10.1127/nova_hedwigia /2015/ 0307.

Cooke DE, Drenth A, Duncan JM, Wagels G, Brasier CM. 2000. A molecular phylogeny of *Phytophthora* and related Oomycetes. Fungal Genetics and Biology 30(1): 17-32. https://doi.org/10.1006/fgbi.2000.1202.

de Cock AWAM, Lodhi AM, Rintoul TL, Bala K, Robideau GP, Abad ZG, Coffey MD, Shahzad S, Lévesque CA. 2015. *Phytopythium*: molecular phylogeny and systematics. Persoonia 34: 25-39. https://doi.org/10.3767/003158515X685382.

Felsenstein J. 1973. Maximum likelihood and minimum-steps methods for estimating evolutionary trees from data on discrete characters. Systematic Zoology 22(3): 240-249. https://doi.org/10.2307/2412304.

Jankowiak R, Stepniewska H, Bilanski P. 2015. Notes on some *Phytopythium* and *Pythium* species occurring in oak forests in southern Poland. Acta Mycologica 50(1): 1052. https://doi.org/10.5586/ am.1052.

Jung T, Scanu B, Brasier CM. et al. 2020. A survey in natural forest ecosystems of Vietnam reveals high diversity of both new and described *Phytophthora* taxa including *P. ramorum*. Forests 11(93): 1-20. https://doi.org/10.3390/f11010093.

Hosseini Badrbani A, Bolboli Z, Jamali S, Sharifi R. 2018. Morphological and molecular characterization of Oomycetes associated with root and crown rot of cucurbits in Kermanshah province, Iran. Mycologia Iranica 5(1): 15-27. https://doi.org/10.22043/mi.2019.118409.

Levesque CA, de Cock AWAM. 2004. Molecular phylogeny and taxonomy of the genus *Pythium*. Mycological Research 108(12): 1363-1383. https://doi.org/10.1017/S0953756204001431.

Mostowfizadeh-Ghalamfarsa R. 2015. The current status of *Pythium* species in Iran: challenges in taxonomy. Mycologia Iranica 2(2): 79-87. https://doi.org/10.22043/mi.2015.19901.

Mostowfizadeh-Ghalamfarsa R, Banihashemi Z. 2005. Identification of soil *Pythium* species in Fars Province of Iran. Iranian Journal of Science & Technology, Transaction 29(1): .79-87.

Nechwatal J, Osswald WF. 2003. *Pythium montanum* sp. nov., a new species from a spruce stand in the Bavarian Alps. Mycological Progress 2: 73–80. https://doi.org/10.1007/s11557-006-0046-3.

Nechwatal J, Wielgoss A, Mendgen K. 2008. Diversity, host, and habitat specificity of oomycete communities in declining reed stands (*Phragmites australis*) of a large freshwater lake. Mycological Research 112(6): 689-696. https://doi.org/10.1016/j.mycres.2007.11.015.

Rezaei S, Abrinbana M, Ghosta Y. 2021. Taxonomic and pathogenic characterization of *Phytopythium* species from West Azarbaijan, Iran, and description of two new species. Mycologia 113(3): 612-628. https://doi.org/10.1080/ 00275514. 2020.1853986.

Robideau GP, de Cock AWAM, Coffey MD, Voglmayr H, Brouwer H, Bala K, et al. 2011. DNA barcoding of oomycetes with cytochrome c oxidase subunit I and internal transcribed spacer. Molecular Ecology Resources 11: 1002-1011. https://doi.org/10.1111/j.17550998.2011.03041. x.

Salmaninezhad F, Mostowfizadeh-Ghalamfarsa R. 2017. Taxonomy, phylogeny and pathogenicity of *Pythium* species in rice paddy fields of Fars province. Iranian Journal of Plant Pathology 53(1): 31-53.

Salmaninezhad F, Mostowfizadeh-Ghalamfarsa R. 2019. Phenotypic plasticity of the isolates assigned to *Pythium plurisporium*. Mycologia Iranica 6(2): 59-71. https://doi.org/10.22043/ mi.2020.121377.

Salmaninezhad F, Mostowfizadeh-Ghalamfarsa R. 2023. The current status of *Phytopythium* species in Iran: Challenges in identification of an intermediate taxon. Mycologia Iranica, 10(1): 1-12. https://doi.org/10.22092/MI.2022.360305.1237.

Spies CFJ, Mazzola M, Botha WJ, Van Der Rijst M, Mostert L, Mcleod A. 2011. Oogonial biometry and phylogenetic analyses of the *Pythium vexans* species group from woody agricultural hosts in South Africa reveal distinct groups within this taxon. Fungal Biology 115(2): 157-168. https://doi.org/10.1016/j.funbio.2010.11.005.

Tamura K, Stecher G, Kumar S. 2021. MEGA11: Molecular Evolutionary Genetics Analysis version 11. Molecular Biology and Evolution 38: 3022-3027. https://doi.org/10.1093/molbev/msab120.

Thompson JD, Higgins DG, Gibson TJ. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22: 4673-4680. https://doi.org/10.1093/nar/22.22.4673.

Thines M. 2014. Phylogeny and evolution of plant pathogenic oomycetes—a global overview. European Journal of Plant Pathology 138: 431-447. https://doi.org/10.1007/s10658-013-0366-5.

Thines M, Kamoun S. 2010. Oomycete-plant coevolution: recent advances and future prospects. Current Opinion in Plant Biology 13: 427-433. https://doi.org/10.1016/j.pbi.2010.04.001.

van der Plaats-Niterink J. 1981. Monograph of the genus *Pythium*. Studies in Mycology 21: 1-244.

Walker CA, van West P. 2007. Zoospore development in the oomycetes. Fungal Biology Reviews 21: 10-8. https://doi.org/10.1016/j.fbr.2007.02.001.

White TJ, Bruns TD, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: PCR protocols: a guide to the methods and applications. (Innis MA, Gelfand JJ, Sninsky DH and White TJ, eds): 315-322. Academic Press, USA.

Zhong S, Steffenson BJ. 2001. Virulence and molecular diversity in *Cochliobolus sativus*. Phytopathology 91(5): 469-476. https://doi.org/ 10.1094/ PHYTO.2001.91.5.469.

Phytopythium montanum، گونه جدیدی برای ایران

نگین رمضان زاده، خلیل‌بِردی فتوحی‌فر ✉

گروه گیاه‌پزشکی، دانشکده کشاورزی، دانشکدگان کشاورزی و منابع طبیعی، دانشگاه تهران، کرج، ایران

چکیده

در طی اردیبهشت تا آذر سال ۱۴۰۰، برای بررسی تنوع گونه‌های اُمیستی در برخی از زیست بوم‌های آبی استان تهران، نمونه‌های آب از برخی آب‌های جاری، راکد، ذخیره‌ای، چشمه و چاه به صورت تصادفی و با رعایت پراکنش جغرافیایی جمع‌آوری شدند. به منظور جداسازی گونه های اُمیستی، قطعات برگ لیمو شیرین (*Citrus limetta*) به ظروف حاوی هر نمونه آب قرار داده شدند و به مدت ۲۴ ساعت در ۲۵ درجه سلسیوس نگهداری گردیدند. سپس برگ‌ها روی محیط کشت نیمه اختصاصی CMA-PARP قرار داده شدند و از میسلیوم‌های رشد کرده در اطراف برگ لیمو شیرین، پرگنه‌های خالص تهیه شدند. از بین جدایه های به دست آمده، بر اساس ویژگی های ریخت شناختی اندام های رویشی و زایشی و همچنین داده های مولکولی مبتنی بر توالی نوکلئوتیدی نواحی ITS-rDNA، دو جدایه (KAN0230 و KAN0218) حاصل از رودخانه کَن به گونه *Phytopythium montanum* (Nechw.) Abad, de Cock, Bala, Robideau, Lodhi & Levesque تعلق داشتند. بر اساس منابع موجود، این نخستین گزارش از گونه *Phytopythium montanum* در ایران می‌باشد و آرایه جدیدی برای زیواگان اُمیستی ایران است.

کلمات کلیدی

ریخت‌شناسی، تبارزایی، ITS-rDNA، اُمیکوتا، زیست بوم آبی.

مکاتبه کننده: خلیل‌بِردی فتوحی‌فر fotowhi@ut.ac.ir

تاریخ دریافت: ۱۴۰۳/۱۱/۲۶، تاریخ بازنگری: ۱۴۰۴/۰۱/۰۲، تاریخ پذیرش: ۱۴۰۴/۰۱/۲۲، تاریخ انتشار برخط: ۱۴۰۴/۰۱/۲۴