



Citation: Fodor, A., Palkovics, L. & Végh, A. (2025). First report of *Xanthomonas arboricola* on oleander. *Phytopathologia Mediterranea* 64(1): 101-108. doi: 10.36253/phyto-15575

Accepted: April 28, 2025

Published: May 15, 2025

©2025 Author(s). This is an open access, peer-reviewed article published by Firenze University Press (<https://www.fupress.com>) and distributed, except where otherwise noted, under the terms of the CC BY 4.0 License for content and CC0 1.0 Universal for metadata.

Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Competing Interests: The Author(s) declare(s) no conflict of interest.

Editor: Joel L. Vanneste, Plant and Food Research, Sandringham, New Zealand.

ORCID:

AF: 0000-0003-3399-4585

LP: 0000-0002-1850-6750

VA: 0000-0002-5942-038X

Research Papers

First report of *Xanthomonas arboricola* on oleander

ATTILA FODOR¹, LÁSZLÓ PALKOVICS², ANITA VÉGH^{1*}

¹ Hungarian University of Agriculture and Life Sciences, Buda Campus, Institute of Plant Protection, H-1118, Budapest Ménesi Road 44, Hungary

² Széchenyi István University, Department of Plant Sciences, Albert Kázmér Faculty of Mosonmagyaróvár, 2. Vár square, Mosonmagyaróvár; Hungary; ELKH-SZE PhotoPlant-Lab, Széchenyi István University, 2. H-9200, Mosonmagyaróvár Vár square, Hungary

*Corresponding author E-mail: karacs.vegh.anita@uni-mate.hu

Summary. *Nerium oleander* L is a long-lasting flowering vegetatively propagated ornamental plant of the Mediterranean region, where it is a major imported flowering pot plant. Only a few bacteria can infect it such as *Pseudomonas savastanoi* pv. *nerii*, *Agrobacterium tumefaciens* and *Xylella fastidiosa*. Between 2018 and 2022 we collected several infected plant parts in our country. In 2020 we observed atypical symptoms on the leaves and stems, which were not clearly similar to the known bacterial infection of oleander. In our work, we aimed to identify the pathogen. The isolates formed yellow-coloured bacterial colonies on King-B and on YDC agar, were Gram-negative, oxidase negative and induced hypersensitive reaction on tobacco leaves. The biochemical properties were determined by API 20E and API 50CH tests. Brown necrosis was observed on oleander leaves in a pathogenicity test. Multilocus sequence analysis was used for molecular identification of the pathogen. Three housekeeping genes (*gyrB*, *fyuA* and *rpoD*) were amplified. According to symptoms, colony morphology, biochemical features, pathogenicity and molecular methods, the pathogen was identified as *Xanthomonas arboricola*. This is the first report of the plant pathogenic *Xanthomonas* spp. on oleander.

Keywords. *Nerium oleander*, *Xanthomonas*, bacterial disease, Hungary.

INTRODUCTION

Nerium oleander L. is an evergreen tropical and subtropical plant of the *Apocynaceae* family. It is a vegetatively propagated ornamental plant. The plant is appreciated for its striking flower of different colours. Only a few bacteria can infect oleander during cultivation, but only *Pseudomonas savastanoi* pv. *nerii* (Janse) Young, Dye & Wilkie causes significant damage. The typical symptoms are knots or galls on stems, twigs, leaves and seedcases. The knots are few millimetres, soft and green in the early stages of infection. Then it grows to a few centimetres, turns brown (Smith, 1906) and decays as the periderm blocks the source of water and nutrients. The severity of symptoms is influenced by phytohormone production (Themsah *et*

al., 2010). *Xanthomonas* (Dowson 1939) is a large genus of plant pathogenic Gram-negative bacteria, which are obligate aerobes and generally rod shaped with a single polar flagellum (Bradbury, 1984). Many members of this genus are yellow-pigmented because of xanthan production (Kennedy and Bradshaw, 1984). The *Xanthomonas* genus comprises 45 species (Parte *et al.*, 2020) which show a high degree of host plant specificity. The range of host plants is mostly a single plant or a few plants from the same botanical family (Ryan *et al.*, 2011). However, it is difficult to define the exact range of host plants, as pathogenicity tests are only carried out on a few cultivated plants (Bull and Koike, 2015). The symptoms are ranging from water-soaked spots, wilting to cankers (Rudolph, 1993). *Xanthomonas* spp. cause serious diseases on important crops such as rice, citrus, banana, cabbage, tomato and walnut (Kennedy and Bradshaw, 1984; Ryan *et al.*, 2011). Additionally, *Xanthomonas* produces a polysaccharide called xanthan gum, which is used in industry as a thickener and emulsifier (Backer *et al.*, 1998).

MATERIALS AND METHODS

We have been investigating oleander knot in Hungary since 2018. Only a few cases of atypical symptoms were observed during the nationwide sampling of approximately 300 samples. In 2020 two infected plant samples, one from Southern Great Plain (Kecskemét) and one from Northern Great Plain (Nyírbátor) were collected from hobby gardeners. Symptoms of brown, necrosis on the leaf, and untypical canker on the stem were observed. The symptomatic plant parts were delivered to the laboratory of the Department of Plant Pathology, Hungarian University of Agriculture and Life Sciences. The samples were surface-sterilized, homogenized and streaked onto King's B agar (King *et al.*, 1954). The agar plates were incubated at room temperature (RT) for 48 to 72 h, and pure cultures of bacterial isolates were obtained by colony subculturing. Hypersensitive reaction (HR) was tested on tobacco leaves (*Nicotiana tabacum* L. Xanthi) using pure bacterial suspension of 5×10^7 cells mL⁻¹. The suspension was determined with a spectrophotometer set at $\lambda = 560$ nm. Leaves were assessed at 24 and 48 h post-inoculation. Gram feature was determined by the KOH test (Powers, 1995). Biochemical analysis was performed using the API 20E and API 50CH kit (BioMérieux). Colony morphology was observed on Yeast Extract-Dextrose-Calcium Carbonate agar (YDC). For pathogenicity test 1 year old oleander plants were used. Stem internodes,

between the first and the second leaves were injected using sterile syringes containing bacterial suspension of 5×10^7 cells mL⁻¹ and 2 leaves of each plant were also lacerated with the inoculant syringe needle. Sterilized distilled water was used for injection as a negative control. 3 plants were used for each replicate. The inoculated plants were maintained at RT with a relative humidity greater than 90% for 1 week. Symptoms were observed daily for 3-week post-inoculation. To determine host plants specificity of isolates detached leaves of apricot (*Prunus armeniaca* L.), walnut (*Juglans regia* L.), pepper (*Capsicum annum* L.), kohlrabi (*Brassica oleracea* L. convar. *acephala* var. *gongylodes*), cabbage (*B. oleracea* convar. *capitata*), geranium (*Pelargonium zonale* L'Hér ex Aiton), poplars (*Populus alba* L., *P. nigra*) and willow (*Salix alba* L.) were used. The surface-sterilized leaves were infected in two ways: inoculated with bacterial colonies using sterilised toothpicks and transferred with bacterial suspension of 5×10^7 cells mL⁻¹ using a sterilized paintbrush. Positive control leaves were infected with bacteria from Gene Bank of Institute of Plant Protection. Negative control leaves were inoculated with sterilized distilled water. The leaves were incubated at high relative humidity. 5 leaves were used for replicates. The cabbage and the kohlrabi were bought in a supermarket and the leaves of apricot, walnut, pepper and geranium were collected in a hobby garden. Symptoms were observed daily for 2 weeks after inoculation.

Multilocus sequence analysis (MLSA) was conducted using three housekeeping genes (*fyuA*, *rpoD*, *gyrB*) and forty strains (Table 1). The polymerase chain reaction (PCR) cycling conditions for *fyuA* and *rpoD* genes were 3 min at 94°C, then 30 s at 94°C, 30 s at 54°C, 1 min at 72°C for 30 cycles, then 10 min at 72°C (Young *et al.*, 2008). The PCR cycling conditions for *gyrB* were 2.5 min at 94°C, then 30 s at 94°C, 45 s at 50°C, 1 min at 68°C for 34 cycles, then 7 min at 68°C (Parkinson *et al.*, 2007). The re-isolated bacteria were confirmed by 16S rDNA PCR using 63F and 1389R primers. The PCR cycling conditions were 5 min at 94°C, then 15 s at 95°C, 30 s 55°C, 90 s 72°C for 30 cycles, then 10 min at 72°C (Osborn *et al.*, 2000). Primers for partial sequences of *fyuA*, *rpoD* *gyrB* and 16S rDNA are listed in Table 2. The amplification was visualised on a 1% (w/v) agarose gel in 1 × TBE buffer with ECOSafe (Biocenter). The PCR products were cleaned with the High Pure PCR Product Purification Kit (Roche Diagnostics GmbH). The nucleotide sequence of the PCR amplified DNA fragment was determined and compared with sequences from the National Center for Biotechnology Information (NCBI) database, using the Basic Local Alignment Search Tool (BLAST) program. Homologous sequences from other

Table 1. *Xanthomonas* strains referred to in this study with collection numbers (CFBP: French Collection for Plant-associated Bacteria, ICMP: International Collection of Microorganisms, LMG: Belgian Coordinated Collections of Microorganisms, NCPPB: National Collection of Plant Pathogenic Bacteria Fera (UK)) or isolate codes (X1, X2, Xp10, KBNS163, KBNS165) and NCBI GenBank database accession numbers.

Strain	<i>Xanthomonas</i> spp.	NCBI Accession Numbers		
		<i>gyrB</i>	<i>fyuA</i>	<i>rpoD</i>
X1	<i>arboricola</i>	PQ094467	PQ094469	PQ094471
X2	<i>arboricola</i>	PQ094468	PQ094470	PQ094472
CFBP 1159	<i>arboricola</i> pv. <i>corylina</i>	EU499002	EU498895	EU499121
CFBP 2528	<i>arboricola</i> pv. <i>juglandis</i>	EU498951	EU498852	EU499070
CFBP 2535	<i>arboricola</i> pv. <i>pruni</i>	EU498853	EU498854	EU499072
Xp10	<i>arboricola</i> pv. <i>pruni</i>	MN520634	MN520626	MN520630
CFBP 4924	<i>axonopodis</i> pv. <i>axonopodis</i>	EU498952	EU498853	EU499071
LMG 982	<i>axonopodis</i> pv. <i>axonopodis</i>	EU498981	EU498914	EU499100
CFBP 3836	<i>axonopodis</i> subsp. <i>alfalfae</i>	EU499001	EU498894	EU499120
CFBP 2524	<i>axonopodis</i> pv. <i>begoniae</i>	EU498962	EU498909	EU499081
ICMP 7493	<i>axonopodis</i> pv. <i>citri</i>	EU499024	EU498910	EU499143
ICMP 10022	<i>axonopodis</i> pv. <i>citri</i>	EU499045	EU498930	EU499165
CFBP 2526	<i>axonopodis</i> pv. <i>glycines</i>	EU499003	EU498896	EU499122
CFBP 7153	<i>axonopodis</i> pv. <i>manihotis</i>	EU499006	EU498898	EU499125
CFBP 6546	<i>axonopodis</i> pv. <i>phaseoli</i>	EU499015	EU498904	EU499134
CFBP 7663	<i>axonopodis</i> pv. <i>phaseoli</i>	EU498968	EU498864	EU499087
ICMP 7462	<i>axonopodis</i> pv. <i>ricini</i>	EU499023	EU498771	EU499142
LMG 8122	<i>campestris</i> pv. <i>campestris</i>	EU499018	EU498907	EU499137
CFBP 2350	<i>campestris</i> pv. <i>campestris</i>	EU498948	EU498849	EU499067
CFBP 5828	<i>campestris</i> pv. <i>raphani</i>	EU498982	EU498877	EU499101
CFBP 7270	<i>dyei</i>	GQ183103	GQ183117	GQ183090
CFBP 7261	<i>dyei</i> pv. <i>eucalypti</i>	GQ183102	GQ183115	GQ183088
CFBP 2157	<i>fragariae</i>	EU499000	EU498893	EU499119
NCPPB 2949	<i>fragariae</i>	EU499012	EU498901	EU499131
ICMP 6646	<i>fragariae</i>	EU499019	EU498908	EU499138
ICMP 1661	<i>hortorum</i> pv. <i>hederae</i>	EU498987	EU498880	EU499106
CFBP 4925	<i>hortorum</i> pv. <i>hederae</i>	KY984200	KYP984167	KYP984233
KBNS163	<i>hortorum</i> pv. <i>pelargoni</i>	KP900004	KP899987	KP899953
KBNS165	<i>hortorum</i> pv. <i>pelargoni</i>	KP900006	KP899889	KP899955
ICMP 12013	<i>oryzae</i> pv. <i>oryzicola</i>	EU499050	EU498935	EU499170
CFBP 2286	<i>oryzae</i> pv. <i>oryzicola</i>	EU499007	EU498899	EU499126
ICMP 16690	<i>euvesicatoria</i> pv. <i>perforans</i>	EU499059	EU498944	EU499179
NCPPB 762	<i>psi</i>	EU498976	EU498872	EU499095
CFBP 3123	<i>populi</i>	EU499035	EU498919	EU499155
NCPPB 989	<i>vasicola</i>	EU498974	EU498870	EU499093
CFBP 2543	<i>vasicola</i>	EU498992	EU498885	EU499111
ICMP 3490	<i>vasicola</i>	EU498994	EU498887	EU499113
NCPPB 422	<i>vesicatoria</i>	EU498954	EU498855	EU499073
ICMP 696	<i>vesicatoria</i>	EU498980	EU498876	EU499099
ICMP 115	<i>vesicatoria</i>	EU498956	EU498857	EU499075

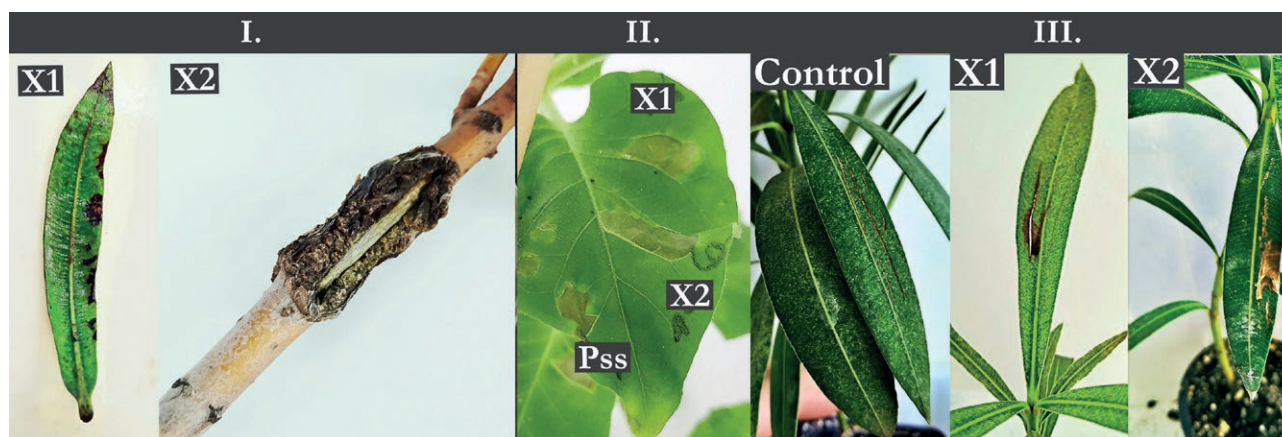
members of the *Xanthomonas* spp. were included in the phylogenetic analysis for comparisons. For phylogenetic analysis Mega 11.1 was used (Tamura and Nei, 1993; Tamura *et al.*, 2021).

RESULTS AND DISCUSSION

Between 2018 and 2022 we collected several infected oleander plant parts in Hungary. First of all, we brought

Table 2. Primers used in this study (Parkinson *et al.*, 2007; Young *et al.*, 2008).

Sequence	Forward	Reverse
<i>fyuA</i>	XfyuA1F AGCTACGAYGTGCGYTACGA	XfyuA1R GTTTCACGCCRAACTGGTAG
<i>rpoD</i>	XrpoD1F TGGAACAGGGCTATCTGACC	XrpoD1R CATTCYAGGTTGGTCTGRTT
<i>gyrB</i>	XgyrPCR2F AAGCAGGGCAAGAGCGAGCTGTA	Xgyrrsp1 CAAGGTGCTGAAGATCTGGTC
16S rDNA	63F CAGGCCTAACACATGCAAGTC	1389R ACGGGCGGTGTGTACAAG

**Figure 1.** I. The symptoms of the plant parts used for isolation, II. Hypersensitive reactions from infiltration of tobacco leaves 36 h post-inoculation with negative control (*Pseudomonas syringae* pv. *syringae*-Pss) and III. Necrosis on oleander leaves around the points of injections 2 weeks post-inoculation.

into focus *Pseudomonas savastanoi* pv. *nerii*, however other pathogens (among others *Botrytis cinerea*, *Cercospora* spp.) were also investigated. In 2020 we observed two atypical symptoms, one from Southern Great Plain (Kecskemét) and one from Northern Great Plain (Nyírbátor). On the stem splitting of the canker bark were observed, which was not typical symptoms of oleander canker. In addition, there was no isolation of *Pseudomonas* spp. from the sample. On the leaf margins and main stem of the leaf scattered brown spots and watery necrosis were observed (Figure 1). It was assumed that the symptoms were caused by bacteria, which are unknown pathogens of oleander. Our previous research confirmed this hypothesis, as we isolated for the first time the pathogen *Serratia marcescens* bacteria on oleander leaf and seedcase (Fodor *et al.*, 2022). The colonies of both isolates (X1, X2) were yellow-colored, smooth-edged, slightly convex on King-B and on YDC agar. The KOH tests were positive, so both isolates were Gram-negative. The isolates induced HR on tobacco leaves 24 h post-inoculation (Kennedy and Bradshaw, 1984; Trébaol, *et al.*, 2000; Vicente and Holub, 2013) (Figure 1).

There was little variation in the biochemical properties of the isolates. The API 20NE test gave a positive reaction during sixteen reactions (NO₃, GLU, ESC, GEL, PNPG, GLU, ARA, MNE, MAN, NAG, MAL, GNT, CAP, ADI, MLT, CIT). Only the production of arginine dihydrolase (ADH) showed differences (X1-negative, X2-positive) (Table 3). On the API 50CH kit the isolates differed in eight tests (DXYL, ARB, SAL, CEL, MEL, TRE, GLGY, XLT). The X2 isolate showed positive results on D- Xylose, arbutin, cellobiose melibiose, trehalose, glycogen, xylitol, while the X1 isolate showed negative results. On salicin and xylitol tests of the isolate X2 showed a positive reaction, while X1 showed a negative reaction (Table 4). Vauterin and co-authors (1995) studied the biochemical properties of two *X. populi* strains. Our isolates show difference from their isolates in arabinose (ARA) utilization (positive), while in 11 reaction (NAG, CEL, GAL, MAN, TRE, SOR, TUR, XLT, GLY) our isolates were differed their isolates by half and half. The result *X. populi* of López and co-authors (2018) showed differences only in mannitol (MAN) assimilation.

Table 3. Result of API 20NE test (NO₃: nitrate reduction, TRP: tryptophan deaminase, GLU: glucose acidification, ADH: arginine dihydrolase, URE: urease, ESC: esculin ferric citrate, GEL: gelatinase, PNPG: β -galactosidase, ARA: arabinose, MNE: mannose utilization, MAN: mannitol utilization, NAG: N-acetyl glucosamine utilization, MAL: maltose utilization, GNT: gluconic acid utilization, CAP: capric acid utilization, ADI: adipic acid utilization, MLT: malic acid utilization, CIT: citric acid utilization, PAC: phenylacetic acid utilization).

	NO ₃	TRP	GLU	ADH	URE	ESC	GEL	PNPG	GLU	ARA
X1	+	-	+	+	-	+	+	+	+	+
X2	+	-	+	-	-	+	+	+	+	+
	MNE	MAN	NAG	MAL	GNT	CAP	ADI	MLT	CIT	PAC
X1	+	+	+	+	+	+	+	+	+	-
X2	+	+	+	+	+	+	+	+	+	-

Two weeks after inoculation, necrosis was observed on the oleander leaves around the injection points. Control showed no symptoms. Although the isolated bacteria did not cause knots. It is assumed that the X2 isolate did not produce tumour. The pathogen of interest was the only microorganism re-isolated from lesions on the different inoculated plants, which was confirmed by colony morphology and PCR. The Koch's postulates were fulfilled only in the case of X1 isolate. The X2 isolate were

also pathogen of oleander, however the symptoms experienced during isolation were not observed during pathogenicity test (Figure 1). Leaves of apricot, walnut, pepper, kohlrabi, cabbage, geranium, poplars and willow did not show symptoms. There was no difference between infected and negative control leaves. However, the positive control isolates caused necrosis around the inoculation points (Figure 2).

The phylogenetic tree was constructed using *fyuA*, *rpoD*, *gyrB* housekeeping genes, which was separated two branches. On one branch *X. oryzae*, *X. pisi*, *X. dey*, *X. vesicatoria*, *X. fragariae* and pathotypes of *X. axonopodis* were separated. On the other branch, *X. arboricola* and the pathotypes of *X. campestris*, *X. hortorum* and *X. populi* were found. The X1 and X2 isolate were on a separate branch with pathotype of *X. arboricola* (*X. arboricola* pv. *corylina*, *X. arboricola* pv. *juglandis*, *X. arboricola* pv. *pruni*) and *X. populi*. Both isolates were similar and related to a *Xanthomonas arboricola* pv. *pruni* isolate from Montenegro (Xp10). They were on the same branch with *X. populi* (CFBP 3123). However, our isolates were different. They did not cause symptoms on *Populus* spp. and *Salix* spp. leaves, which plants are the only host of *X. populi* (De Kam, 1984). This indicates that our isolates may belong to a different pathotype, which needs to be confirmed by further studies- e.g. molecular test-

Table 4. Result of API 20NE test (0: Control, GLY: Glycerol, ERY: Erythritol, DARA: D-Arabinose, LARA: L-Arabinose, RIB: Ribose, DXYL: D- Xylose, LXYL: L-Xylose, ADO: Adonithol, MDX: Methyl xyloside, GAL: Galactose, GLU: D-Glucose, FRU: D-Fructose, MNE: D-mannose, SBE: Sorbose, RHA: Rhamnose, DUL: Dulcitol, INO: Inositol, MAN: Mannitol, SOR: Sorbitol, MDM: Methyl-D-mannoside, MDG: Methyl-D-glucoside, NAG: N-acetyl-glucosamine, AMY: Amygdalin, ARB: Arbutin, ESC: Esculine, SAL: Salicin, CEL: Cellobiose, MAL: Maltose, LAC: Lactose, MEL: Melibiose, SAC: Sucrose, TRE: Trehalose, INU: Inulin, MLZ: Melizitose, RAF: D-raffinose, AMD: Starch, GLGY: Glycogen, XLT: Xylitol, GEN: Gentibiose, TUR: Turanose, LYX: Lyxose, TAG: Tagatose, DFUC: D-fucose, LFUC: L-fucose, DARL: D-Arabitol, LARL: L-Arabitol, GNT: Gluconate, 2KG :2, Keto-gluconate, 5KG :5, keto-gluconate).

	0	GLY	ERY	DARA	LARA	RIB	DXYL	LXYL	ADO	MDX	GAL
X1	-	-	-	-	-	-	-	-	-	-	+
X2	-	-	-	-	-	-	+	-	-	-	+
	GLU	FRU	MNE	SBE	RHA	DUL	INO	MAN	SOR	MDM	MDG
X1	+	+	+	-	-	-	-	-	-	-	-
X2	+	+	+	-	-	-	-	-	-	-	-
	NAG	AMY	ARB	ESC	SAL	CEL	MAL	LAC	MEL	SAC	TRE
X1	+	+	-	-	+	-	+	-	-	+	-
X2	+	+	+	-	-	+	+	-	+	+	+
	INU	MLZ	RAF	AMD	GLGY	XLT	GEN	TUR	LYX	TAG	DFUC
X1	-	-	-	+	-	+	-	-	-	-	+
X2	-	-	-	+	+	-	-	-	-	-	+
	LFUC	DARL	LARL	GNT	2KG	5KG					
X1	+	-	-	-	-	-					
X2	+	-	-	-	-	-					



Figure 2. Results from host plant specificity tests: positive controls (I.), negative control (II), inoculated with two *Xanthomonas arboricola* isolates (X2-III., X1-IV.). The first column shows cabbage, the second column kohlrabi, the third column apricot, the fourth column walnut, the fifth column pepper, the sixth column geranium, the seventh and eighth column poplars, the ninth column willow leaves at 7 days post-inoculation.

ing, DNS-DNS hybridization, fatty acid analysis. To the best of our knowledge, this is the first report of the *Xanthomonas* as a pathogen of oleander. Additionally, a *Xanthomonas* spp. have been identified from olive (*Olea europaea* L), which caused brown necrosis and canker on the stem (Taylor *et al.*, 2001; Young *et al.*, 2010). Our isolates caused only on the oleander leaves necrosis in the pathogenicity test. They did not induce canker, although they may play a role in the evolve of on oleander knot symptoms.

ACKNOWLEDGEMENT

This work was supported by the ELKH TKI (project number: 3200107). The research was funded by the “VP4-10.2.2.-20.Ex situ conservation of genetic resources of rare and endangered plant species and microorganisms”.

REFERENCES

- Backer A., Katzen F., Puhler L., Ielpi L., 1998. Xanthan gum biosynthesis and application: a biochemical/genetic perspective. *Applied Microbiology and Biotechnology* 50: 145–152. <https://doi.org/10.1007/s002530051269>
- Bradbury J.F., 1984. Genus II *Xanthomonas* (Dowson 1939). In: Bergey's Manual of Systematic Bacteriology (Krieg, N.R., Holt, J.G. ed) vol. 1. The Williams & Wilkins Co., Baltimore, 199-210.
- Bull C.T., Koike S.T., 2015. Practical benefits of knowing the enemy: modern molecular tools for diagnosing the etiology of bacterial diseases and understanding the taxonomy and diversity of plant-pathogenic bacteria. *Annual Review of Phytopathology* 53: 157–180. <https://doi.org/10.1146/annurev-phyto-080614-120122>
- De Kam M., 1984. *Xanthomonas campestris* pv. *populi*, the causal agent of bark necrosis in poplar. *Nether-*

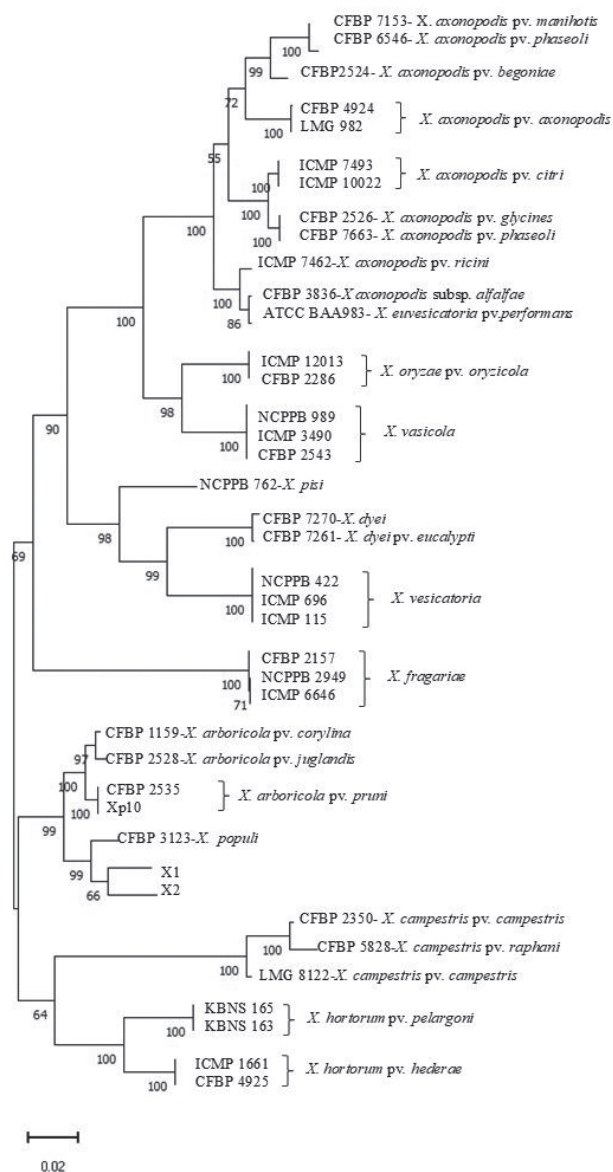


Figure 3. Maximum likelihood tree of concatenated *Xanthomonas* spp. nucleotide sequences for partial *fyuA*, *gyrB* and *rpoD* gene with identifier numbers. Tamura-Nei G5 model was used. The bootstrap values were 1000 samplings. The percentage of trees in which the associated taxa clustered together is shown below the branches. There were a total of 2109 positions in the final dataset (Tamura and Nei, 1993; Tamura *et al.*, 2021).

lands Journal of Plant Pathology 90: 13–22. <https://doi.org/10.1007/BF02014178>

Fodor A., Palkovics L., Végh A., 2022. First report of *Serratia marcescens* from oleander in Hungary. *Phytopathologia Mediterranea* 61: 311–317. <https://doi.org/10.36253/phyto-13354>

Kennedy J.F., Bradshaw I.J. 1984. Production, properties and applications of xanthan. *Progress in Industrial Microbiology* 19, 319–371.

King E.O., Ward M.K., Raney D.E., 1954. Two simple media for the demonstration of pyocyanin and fluorescein. *Journal of Laboratory and Clinical Medicine* 44: 301–307.

López M.M., Lopez-Soriano P., Garita-Cambronero J., Beltrán C., Taghouti G., ... Marco-Noales E., 2018. *Xanthomonas prunicola* sp. nov., a novel pathogen that affects nectarine (*Prunus persica* var. *nectarina*) trees. *International Journal of Systematic and Evolutionary Microbiology* 68(6): 1857–1866. <https://doi.org/10.1099/ijsem.0.002743>

Osborn A.M., Moore E.R., Timmis K.N., 2000. An evaluation of terminal-restriction fragment length polymorphism (T-RFLP) analysis for the study of microbial community structure and dynamics. *Environmental Microbiology* 2: 39–50. <https://doi.org/10.1046/j.14622920.2000.00081.x>

Parkinson N., Aritua V., Heeney J., Cowie C., Bew J., Stead D., 2007. Phylogenetic analysis of *Xanthomonas* species by comparison of partial gyrase B gene sequences. *International Journal of Systematic and Evolutionary Microbiology* 57(12): 2881–2887. <https://doi.org/10.1099/ijse.0.65220-0>

Parte A.C., Carbasse S.J., Meier-Kolthoff J.P., Reimer L.C., Göker M., 2020. List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. *International Journal of Systematic and Evolutionary Microbiology* 70(11): 5607–5612. <https://doi.org/10.1099/ijsem.0.004332>

Powers E.M., 1995. Efficacy of the Ryu nonstaining KOH technique for rapidly determining gram reactions of food-borne and waterborne bacteria and yeasts. *Applied and Environmental Microbiology* 61: 3756–3758. <https://doi.org/10.1128/aem.61.10.3756-3758.1995>

Rudolph K., 1993. Infection of the plant by *Xanthomonas*. In: *Xanthomonas* (Swings J. G., Civerolo E. L. ed) Chapman and Hall, London. 193–264.

Ryan R.P., Vorhölter F.J., Potnis N., Jones J.B., Van Sluys M.A., ... Dow, J.M. 2011. Pathogenomics of *Xanthomonas*: understanding bacterium-plant interactions. *Nature Reviews Microbiology* 9(5): 344–355. <https://doi.org/10.1038/nrmicro2558>

Smith C.O., 1906. A Bacterial disease of oleander. *Bacillus oleae* (Arcang.) Trev. *Botanical Gazette*, 42(4): 301–310.

Tamura K., Nei M., 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* 10(3): 512–526. <https://doi.org/10.1093/oxfordjournals.molbev.a040023>

- Tamura K., Stecher G., Kumar S., 2021. MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution*. 38(7): 3022–3027. <https://doi.org/10.1093/molbev/msab120>
- Taylor R.K., Hale C.N., Hartill, W.F.T., 2001. A stem cancer disease of olive (*Olea europaea*) in New Zealand. *New Zealand Journal of Crop and Horticultural Science* 29(3): 219–228. <https://doi.org/10.1080/01140671.2001.9514181>
- Temsah M., Hanna L., Saad A.T., 2010. Histological pathogenesis of *Pseudomonas savastanoi* on *Nerium oleander*. *Journal of Plant Pathology* 92(2): 407–413.
- Trébaol G., Gardan L., Manceau C., Tanguy J. L., Tirilly Y., Boury S., 2000. Genomic and phenotypic characterization of *Xanthomonas cynarae* sp. nov., a new species that causes bacterial bract spot of artichoke (*Cynara scolymus* L.). *International Journal of Systematic and Evolutionary Microbiology* 50(4): 1471–1478.
- Vauterin L., Hoste B., Kersters K., Swings J., 1995. Reclassification of *Xanthomonas*. *International Journal of Systematic and Evolutionary Microbiology* 45(3): 472–489. <https://doi.org/10.1099/00207713-45-3-472>
- Vicente J.G., Holub E.B., 2013. *Xanthomonas campestris* pv. *campestris* (cause of black rot of crucifers) in the genomic era is still a worldwide threat to brassica crops. *Molecular Plant Pathology* 14(1): 2–18. <https://doi.org/10.1111/j.1364-3703.2012.00833.x>
- Young J.M., Park, D.C., Shearman H.M., Fargier E., 2008. A multilocus sequence analysis of the genus *Xanthomonas*. *Systematic and Applied Microbiology* 31(5): 366–377. <https://doi.org/10.1016/j.syapm.2008.06.004>
- Young J.M., Wilkie J.P., Park D.C., Watson D.R.W., 2010. New Zealand strains of plant pathogenic bacteria classified by multi-locus sequence analysis; proposal of *Xanthomonas dyei* sp. nov. *Plant Pathology* 59(2): 270–281. <https://doi.org/10.1111/j.1365-3059.2009.02210.x>