Taxonomic repositioning of twelve *Xanthomonas campestris*, seven *Xanthomonas axonopodis* and one *Pseudomonas cissicola* reference pathovars to *Xanthomonas citri*

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Abstract

Here on the basis of phylo-taxonogenomics criteria we present amended description of 20 pathovars to *Xanthomonas citri* majority (18/20) of which were first reported from India. 7/20 are currently classified as *X. axonopodis*, 12/20 as *X. campestris* and 1/20 as *Pseudomonas cissicola*. Here, we have generated genome sequence data for 4 pathovars and genomes of remaining 16 were used from the published data. Genome based investigation reveals that all these pathovars belong to *X. citri* and not to *X. axonopodis* or *X. campestris* as previously reported. Present proposal is to aid in resolving the taxonomic confusion of the *X. ctiri* pathovars and prevent future usage of invalid names.

Keywords: *Xanthomonas citri* pathovars, reference pathovars, taxonogenomics, phylogenomics

Xanthomonas sp. bears high degree of phenotypic and 16S rRNA similarity amongst diverse range of phytopathogens (Hayward 1993, Hauben, Vauterin et al. 1997, Moore, Krüger et al. 1997). Consequently, classical approach of taxonomy has resulted in various ambiguities in its classification and various revisions in the taxonomy of the constituent species (Vauterin, Rademaker et al. 2000, Naushad, Adeolu et al. 2015, Kumar, Bansal et al. 2019, Bansal, Kumar et al. 2020). *Citrus spp.* is associated with a vast range of *Xanthomonas* strains following pathogenic and non-pathogenic lifestyles (Hasse 1916, Vauterin, Yang et al. 1996, Bansal, Kumar et al. 2020). Genome-based approaches deciphered these non-pathogenic strains to be closely related to *X. sontii* which were earlier not resolved by classical taxonomy (Bansal, Kaur et al. 2019, Bansal, Midha et al. 2019). On the other hand, the pathogenic counterpart *X. citri* pv. citri is known over a century as the causal agent of citrus canker having a quarantine status (Raychaudhuri, Verma et al. 1972, Gottwald, Graham et al. 2002, Brunings and Gabriel 2003, Graham, Gottwald et al. 2004, Gottwald and Irey 2007). Earlier it was classified as *X. campestris* pv. citri (Group A) (ex Hasse, 1915) and then as *X. axonopodis* pv. citri based on classical approaches like: restriction fragment length polymorphism (RFLP), DNA-DNA hybridization etc. (Gabriel, Kingsley et al. 1989, Vauterin, Hoste et al. 1995). In the last two decades, numerous attempts were made to resolve the taxonomy and phylogeny of the strains belonging to *X. citri* (Schaad, Postnikova et al. 2006, Ah-You, Gagnevin et al. 2009) resulting in various revisions in taxonomy.

Detailed genomic investigation of the *X. axonopodis* species revealed that strains previously classified as *X. axonopodis* instead belong to four different species. These four species were namely, *X. citri, X. axonopodis, X. euvesicatoria* and *X. phaseoli* forming four distinct phylogroups (Constantin, Cleenwerck et al. 2016). Constantin and coworkers have identified fourteen different pathovars isolated form diverse host range constituting the *X. citri* species at the whole genome level. However, besides these pathovars of *X. citri* there are reports of twenty other reference pathovars majorly isolated from India over the century from diverse commercially important hosts (Parkinson, Aritua et al. 2007, Parkinson, Cowie et al. 2009). Due to limitations of classical taxonomic methods, these were classified as different species of *Xanthomonas* like *X. campestris, X. axonopodis* and one was even classified as *Pseudomonas cissicola* (Takimoto 1939). However, *gyrB* based phylogeny have revealed their phylogenetic relatedness with the *X. citri* (Parkinson, Aritua et al. 2007, Parkinson, Cowie et al. 2009). Further, whole genome level investigation of these reference pathovars also suggests the need of revisiting their taxonomy (Bansal, Midha et al. 2017).

These reference pathovars include *X. campestris* pv. durantae isolated from *Duranta repens* which is clonal to the *X. citri* pv. citri at the whole genome level (Bansal, Midha et al. 2017). Similarly, *X. campestris* pv. centellae isolated from *Centella asiatica* is clonal to *X. campestris* pv. mangiferaeindicae causing mango bacterial black spot leading substantial loss in fruit quality in Asia, Africa, Central America, Caribbean and Oceania (https://www.cabi.org/ISC/abstract/20123367489); (Pruvost 1993, Pruvost, Couteau et al. 1998). Additionally, 18 pathovars isolated from diverse hosts namely, *Cissus woodrowii, Bauhinia racemosa, Martynia diandra, Cayratia trifolia, Khaya senegalensis, Cayratia japonica, Tectona grandis, Aegle marmelos, Azadirachta indica, Cajanus cajan, Clitoria* sp., *Thespesia populnea* and *Leea asiatica, Sesbania aegyptiaca, Merremia gangetica, Triumfetta pilosa* and *Trichodesma zeylanicum* are included in the present study (table 1). Interestingly, all of these reference pathovars were first reported from India except for two pathogens i.e., *X. axonopodis* pv. khayae LMG 753 and *Pseudomonas cissicola* LMG 21719 reported from Sudan and Japan respectively (table 1). There is confusion surrounding the taxonomy of these reference pathovars. Genome-based investigation of these *X. citri* pathovars (XCPs) have revealed their phylogenetic relationship with the *X. ctiri* (Bansal, Midha et al. 2017).

For the present study, genomes of four pathovars namely, *X. axonopodis* pv. sesbaniae NCPPB 582, *X. campestris* pv. merremiae NCPPB 3114, *X. campestris* pv. thirumalacharii NCPPB 1452 and *X. campestris* pb. trichodesmae NCPPB 585 were obtained by Illumina MiSeq sequencing by following method as described by Bansal *et al* (Bansal, Midha et al. 2017) and genome statistics are provided in table 2. Here, genome size of the strains was around 5 MB with approximately 64.6% GC content (table 2).

To access their taxonomic status, various parameters of taxonogenomics like average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) were implemented. ANI and dDDH were calculated using orthoANI v1.2 (Yoon, Ha et al. 2017) and GGDC 2.1 (http://ggdc.dsmz.de/ggdc.php#) respectively. *X. citri* pv, citri LMG 9322 (T) and *X. citri* pv. fuscans LMG 826 (T) were having similar ANI and dDDH values with the reference pathovars i.e., >96% and >67% respectively (table 3). Whereas, reference pathovars were having minimum ANI values of 92%, 84% and dDDH values of 49%, 29% with the type strains *X. axonopodis* DSM 3585 (T) and *X. campestris* pv. campestris ATCC 33913 (T) respectively. Genome similarity assessment clearly demarcated reference pathovars under study (n=20) from *X. axonopodis* and *X. campestris.* Further, ANI values of >96% clearly indicates that all twenty reference pathovars belongs to *X. citri.* However, dDDH values among *X. citri* pv. citri LMG 9322 (T) and *X. citri* pv. fuscans LMG 826 (T) is 68.6% yet they belong to same species i.e. *X. citri* (Constantin, Cleenwerck et al. 2016). In the current study as well the dDDH values for *X. axonopodis* pv. sesbaniae NCPPB 582, *X. campestris* pv. merremiae NCPPB 3114, *X. campestris* pv. thirumalacharii NCPPB 1452 and *X. campestris* pv. trichodesmae NCPPB 585 were in the range of 67.2% - 68.3% and 88% - 89.7% for *X. citri* pv. citri LMG 9322 (T) and *X. citri* pv. fuscans LMG 826 (T) respectively. Hence, genome similarity values with the type strains of *X. citri*, *X. axonopodis* and *X. campestris* clearly depicted that all the twenty reference pathovars under study belong to *X. citri.*

In order to infer the phylogeny of reference pathovars with *X. citri*, *X. axonopodis* and *X. campestris* we have performed multi locus sequence type (MLST) and core genome-based phylogeny. For MLST six genes namely *fusA*, *gltA*, *gapA*, *gyrB*, *lacF*, *lepA* (http://www.pamdb.org) were used and their multiple sequence alignment was generated using clustalw (Thompson, Higgins et al. 1994). Mega7 was used to generate he phylogenetic based tree using neighbor joining (NJ) method with 500 bootstrap (figure 1 A). Further, core genome based phylogenetic tree was generated using roary v3.11.2 (Page, Cummins et al. 2015) with an identity cutoff of 95 (figure 1 B). MLST and whole genome-based phylogeny clearly depicted that the reference pathovars in the present study are related to *X. citri.*

Aim of the present study is to emend the taxonomic status of these pathovars and to formally transfer them to the *X. citri*. Owing to the quarantine status of the *X. citri* pv. citri along with other economically important pathovars in the XCPs, their correct taxonomy will aid in their correct identification and understanding the evolution of these closely related pathovars and also the species *X. citri*.

Emended description of *X. citri* (Hasse 1916) comb. nov.

The characteristics of the genus and species of *Xanthomonas citri* are as previously described (Vauterin, Hoste et al. 1995, Constantin, Cleenwerck et al. 2016). In addition to the pathovars previously described (Constantin, Cleenwerck et al. 2016) here we are providing MLSA, phylogenomic and taxonogenomic evidences for other pathovars to constitute *X. citri.*

Emended description of *X. citri* pv. vitiswoodrowii (Patel and Kulkarni 1951a) comb. nov.

= *X. campestris* pv. vitiswoodrowii (Patel and Kulkarni 1951a)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 954; ATCC 11636; Dye MW1; ICMP 3965; ICPB PV103; NCPPB 1014; Patel 19; PDDCC 3965; VdM 217

Emended description of *X. citri* pv. bauhiniae (Padhya, Patel et al. 1965a) comb. nov.

= *X. axonopodis* pv. bauhiniae (Padhya, Patel et al. 1965a)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 548; ICMP 5720; NCPPB 1335; PDDCC 5720; VdM 21 t1,t2

Emended description of *X. citri* pv. martyniicola (Moniz and Patel 1958) comb. nov.

= *X. axonopodis* pv. martyniicola (Moniz and Patel 1958)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9049; Dye XG1; ICMP 82; NCPPB 1148

Emended description of *X. citri* pv. vitiscarnosae (Moniz and Patel 1958) comb. nov.

= *X. campestris* pv. vitiscarnosae (Moniz and Patel 1958)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 939; Dye XH1; ICMP 90; NCPPB 1149; PDDCC 90; VdM 140

Emended description of *X. citri* pv. vitistrifoliae (Padhya, Patel et al. 1965b) comb. nov.

= *X. campestris* pv. vitistrifoliae (Padhya, Patel et al. 1965b)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 940; ICMP 5761; NCPPB 1451; PDDCC 5761; VdM 141

Emended description of *X. citri* pv. khayae (Sabet 1959) comb. nov.

= *X. axonopodis* pv. khayae (Sabet 1959)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 753; Dye XK1; ICMP 671; NCPPB 536; PDDCC 671; Sabet Kh1; VdM 81

Emended description of *X. citri* pv. cissicola (Takimoto 1939) comb. nov.

= *Pseudomonas cissicola* (Takimoto 1939)

Description as provided (Hu, Young et al. 1997) and extended genome-based evidences in the present study.

Pathotype strain: LMG 21719; ATCC 33616; CCM 2888; CCUG 18839; CFBP 2432; CIP 106723; Goto PC1; ICMP 4289; ICMP 8561; JCM 13362; LMG 2167; NCPPB 2982; PDDCC 4289

Emended description of *X. citri* pv. melhusii (Patel, Kulkarni et al. 1952b) comb. nov.

= *X. axonopodis* pv. melhusii (Patel, Kulkarni et al. 1952b)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9050; ATCC 11644; Dye XM1; ICMP 619; ICPB XM107; NCPPB 994; Patel 14

Emended description of *X. citri* pv. bilvae (Chakravarti, Sarma et al. 1984) comb. nov.

= *X. campestris* pv. bilvae (Chakravarti, Sarma et al. 1984)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: NCPPB 3213; ICMP 8918.

Emended description of *X. citri* pv. azadirachtae (Desai, Gandhi et al. 1966) comb. nov.

= *X. campestris* pv. azadirachtae (Desai, Gandhi et al. 1966)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 543; Dye NR1; ICMP 3102; NCPPB 2388; Patel PA; PDDCC 3102; VdM 18

Emended description of *X. citri* pv. durantae (Srinivasan and Patel 1957) comb. nov.

= *X. campestris* pv. durantae (Srinivasan and Patel 1957)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 696; ICMP 5728; NCPPB 1456; PDDCC 5728; VdM 50

Emended description of *X. citri* pv. cajani (Kulkarni 1950) comb. nov.

= *X. axonopodis* pv. cajani (Kulkarni 1950)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 558; ATCC 11639; Dye YR1; ICMP 444; ICPB XC111; NCPPB 573; Patel 5; PDDCC 444; VdM 27

Emended description of *X. citri* pv. clitoriae (Pandit and Kulkarni 1979) comb. nov.

= *X. axonopodis* pv. clitoriae (Pandit and Kulkarni 1979)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9045; Bradbury B7090; ICMP 6574; IMI B7090; ITCC 2237; NCPPB 3092

Emended description of *X. citri* pv. centellae (Basnyat and Kulkarni 1979) comb. nov.

= *X. campestris* pv. centellae (Basnyat and Kulkarni 1979)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9044; ICMP 6746; ITCC P32; NCPPB 3245

Emended description of *X. citri* pv. thespesiae (Patil and Kulkarni 1981) comb. nov.

= *X. campestris* pv. thespesiae (Patil and Kulkarni 1981)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9057; ICMP 7466; ITCC P33

Emended description of *X. citri* pv. leeana (Patel and Kotasthane 1969a) comb. nov.

= *X. campestris* pv. leeana (Patel and Kotasthane 1969a)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: LMG 9048; ICMP 5738; ICPB XL107; NCPPB 2229

Emended description of *X. citri* pv. sesbaniae (Patel, Kulkarni et al. 1952) comb. nov.

= *X. axonopodis* pv. sesbaniae (Patel, Kulkarni et al. 1952)

Description as provided in Vauterin *et al.* (1995), Constantin *et al.* (2016) and extended genome-based evidences in the present study.

Pathotype strain: NCPPB 582; ATCC 11675; ICMP 367; LMG 867

Emended description of *X. citri* pv. merremiae (Pant and Kulkarni 1978) comb. nov.

= *X. campestris* pv. merremiae (Pant and Kulkarni 1978)

Description as provided in (Pant and Kulkarni 1978) and extended genome-based evidences in the present study.

Pathotype strain: NCPPB 3114; ICMP 6747; LMG 9051

Emended description of *X. citri* pv. thirumalacharii (Padhya and Patel 1964) comb. nov.

= *X. campestris* pv. thirumalacharii (Padhya and Patel 1964)

Description as provided in Vauterin *et al.* (1995), Constantin *et al.* (2016) and extended genome-based evidences in the present study.

Pathotype strain: NCPPB 1452; ATCC 11675; ICMP 367; LMG 867

Emended description of *X. citri* pv. trichodesmae (Patel, Kulkarni et al. 1952b) comb. nov.

= *X. campestris* pv. trichodesmae (Patel, Kulkarni et al. 1952b)

Description as provided in Vauterin *et al.* (1995) and extended genome-based evidences in the present study.

Pathotype strain: NCPPB 585; ATCC 11678; ICMP 5754; LMG 874

Figure legend:

Figure 1: Phylogenetic tree. A). Phylogenetic tree obtained using concatenated MLST gene (*fusA*, *gltA*, *gapA*, *gyrB*, *lacF*, *lepA*). B). Phylogenetic tree obtained using the core gene obtained using roary.

Table 1: Metadata of the strains used in the present study. Strains sequenced in the preset study are highlighted in green color.

S. No.	**Pathovar**	**Accession no.**	**Isolation Year**	**Country**	**Host**	**Host Taxonomy**	**Reference**
1.	*X. campestris* pv. vitiswoodrowii LMG 954	LOKG00000000	1961	India	*Cissus woodrowii*	Vitaceae, Vitales, Rosids, Eudicots	(Patel and Kulkarni 1951a)
2.	*X. axonopodis* pv. bauhiniae LMG 548	LOKR00000000	1961	India	*Bauhinia racemosa*	Fabaceae, Fabales, Rosids, Eudicots	(Padhya, Patel et al. 1965a)
3.	*X. axonopodis* pv. martyniicola LMG 9049	LOJX00000000	1958	India	*Martynia diandra*	Martyniaceae, Lamiales, Asterids, Eudicots	(Moniz and Patel 1958)
4.	*X. campestris* pv. vitiscarnosae LMG 939	LOKI00000000	1962	India	*Cayratia trifolia*	Vitaceae, Vitales, Rosids, Eudicots	(Moniz and Patel 1958)
5.	*X. campestris* pv. vitistrifoliae LMG 940	LOKH00000000	1961	India	*Cayratia trifolia*	Vitaceae, Vitales, Rosids, Eudicots	(Padhya, Patel et al. 1965b)
6.	*X. axonopodis* pv. khayae LMG 753	LOKN00000000	1957	Sudan	*Khayasenegalensis*	Meliaceae, Sapindales, Rosids, Eudicots	(Sabet 1959)
7.	*Pseudomonas cissicola* LMG 21719	LOJT00000000	1974	Japan	*Cayratia japonica*	Vitaceae, Vitales, Rosids, Eudicots	(Takimoto 1939)
8.	*X. axonopodis* pv. melhusii LMG 9050	LOJW00000000	1961	India	*Tectonagrandis*	Lamiaceae, Lamiales, Asterids, Eudicots	(Patel, Kulkarni et al. 1952b)
9.	*X. campestris* pv. bilvae NCPPB 3213	CDHI01000000	1982	India	*Aegle marmelos*	Rutaceae, Sapindales, Rosids, Eudicots	(Chakravarti, Sarma et al. 1984)
10.	*X. campestris* pv. azadirachtae LMG 543	LOKS00000000	1971	India	*Azadirachtaindica*	Meliaceae, Sapindales, Rosids, Eudicots	(Desai, Gandhi et al. 1966
11.	*X. campestris* pv. durantae LMG 696	LOKP00000000	1956	India	*Durantarepens*	Verbenaceae, Lamiales, Asterids, Eudicots	(Srinivasan and Patel 1957)
12.	*X. citri* pv. citri LMG 9322	MDJT00000000	1915	United States	*Citrus aurantifolia*	Rutaceae, Sapindales, Rosids, Eudicots	(Hasse 1916)
13.	*X. axonopodis* pv. cajani LMG 558	LOKQ00000000	1950	India	*Cajanuscajan*	Fabaceae, Fabales, Rosids, Eudicots	(Kulkarni 1950)
14.	*X. axonopodis* pv. clitoriae LMG 9045	LOKA00000000	1974	India	*Clitoria sp.*	Fabaceae, Fabales, Rosids, Eudicots	(Pandit and Kulkarni 1979)
15.	*X. campestris* pv. centellae LMG 9044	LOJR00000000	1979	India	*Centella asiatica*	Apiaceae, Apiales, Asterids, Eudicots	(Basnyat and Kulkarni 1979)
16.	*X. campestris* pv. thespesiae LMG 9057	LOJU00000000	1978	India	*Thespesia populnea*	Malvaceae, Malvales, Rosids, Eudicots	(Patil and Kulkarni 1981)
17.	*X. campestris* pv. leeana LMG 9048	LOJY00000000	1967	India	*Leea asiatica*	Vitaceae, Vitales, Rosids, Eudicots	(Patel and Kotasthane 1969a)
18.	*X. axonopodis pv.* sesbaniae NCPPB 582	LOKL00000000	1958	India	*Sesbania aegyptiaca*	Fabaceae, Fabales, Rosids	(Patel, Kulkarni et al. 1952)
19.	*X. campestris* pv. merremiae NCPPB 3114	LOJV00000000	1976	India	*Merremia gangetica*	Convolvulaceae, Solanales, Asterids	(Pant and Kulkarni 1978)

20.	X. campestris pv. thirumalacharii NCPPB 1452	LOKK00000000	1961	India	*Triumfetta pilosa*	Malvaceae, Malvales, Rosids	(Padhya and Patel 1964)
21	*X. campestris* pv. trichodesmae NCPPB 585	LOKJ00000000	1953	India	*Trichodesma zeylanicum*	Boraginaceae, Boraginales, Asterids	(Patel, Kulkarni et al. 1952b)

Table 2: Genome statistics of the sequenced strains in the present study.

S. No.	**Pathovar**	**Genome size (bp)**	**No. of contigs**	**Coverage (X)**	**GC content (%)**	**N50 (bp)**	**No. of genes**	**No. of tRNAs+rRNA +ncRNA**	**NCBI accession no.**
1	*X. axonopodis* pv. sesbaniae NCPPB 582	54,04,710	190	140	64.52	1,04,268	4,703	52+2+1	LOKL00000000
2	*X. campestris* pv. merremiae NCPPB 3114	50,34,542	135	167	64.67	1,17,975	4,215	53+3+1	LOJV00000000
3	*X. campestris* pv. thirumalacharii NCPPB 1452	49,27,392	291	177	64.77	42,427	4,311	50+3+1	LOKK00000000
4	*X. campestris* pv. trichodesmae NCPPB 585	54,73,142	174	167	64.57	1,08,567	4,682	52+5+1	LOKJ00000000

Table 3: Digital DNA-DNA hybridization values of the reference pathovars with the *X. citri* pv. citri LMG 9322 (T), *X. axonopodis* DSM 3585 and *X. campestris* pv. campestris ATCC 33913 (T).

	***X. citri* pv. citri LMG 9322 (T)**		***X. axonopodis* DSM 3585 (T)**		***X. campestris* pv. campestris ATCC 33913 (T)**		***X. citri* pv. fuscan LMG 726 (T)**	
	dDDH	**ANI**	**dDDH**	**ANI**	**dDDH**	**ANI**	**dDDH**	**ANI**
X. citri pv. citri LMG 9322 (T)	100	100	50.3	93.1	30	85.1	68.6	96.3
X. campestris pv. durantae LMG 696	98.4	99.8	49.8	92.9	29.7	85.2	68	96.2
X. axonopodis pv. clitoriae LMG 9045	92.2	99.1	49.8	93	29.5	85	67.6	96.1
X. axonopodis pv. cajani LMG 558	92.2	99.1	49.6	92.9	29.7	85.1	68.3	96.3
X. campestris pv. centellae LMG 9044	90.8	98.8	49.6	93	29.7	85.1	68.4	96.3
X. campestris pv. bilvae NCPPB 3213	89.9	98.8	49.6	92.9	29.8	84.9	68.5	96.2
X. axonopodis pv. melhusii LMG 9050	89.6	98.8	49.6	92.9	29.6	85	68.7	96.3
X. campestris pv. azadirachtae LMG 543	89.1	98.8	49.4	92.9	29.4	84.9	67.8	96.3
X. axonopodis pv. bauhiniae LMG 548	89.1	98.8	49.5	92.9	29.6	85.0	68	96.2
X. campestris pv. leeana LMG 9048	88.7	98.7	49.5	92.9	29.4	84.9	68	96.3
X. campestris pv. thespesiae LMG 9057	88.7	98.8	49.5	92.8	29.4	85	67.9	96.3
X. campestris pv. vitiscarnosae LMG 939	88.7	98.7	49.5	92.9	29.4	84.7	68.2	96.3
X. campestris pv. vitistrifoliae LMG 940	88.6	98.6	49.4	92.9	29.4	84.9	67.7	96.3
X. axonopodis pv. martyniicola LMG 9049	88.6	98.8	49.5	93	29.4	84.8	68.2	96.3
X. campestris pv. vitiswoodrowii LMG 954	88.2	98.7	49.3	92.9	29.4	85	68.1	96.2
Pseudomonas cissicola LMG 21719	86.9	98.4	49.3	92.8	29.6	85.1	67.6	96.1
X. axonopodis pv. khayae LMG 753	86.3	98.5	49.6	92.9	29.5	84.9	68.8	96.4

X. campestris pv. trichodesmae NCPPB 585	68.3	96.1	49.7	93	29.5	84.9	89.7	98.8
X. campestris pv. merremiae NCPPB 3114	67.2	96.2	49.6	92.9	29.4	85.0	88.5	98.7
X. campestris pv. thirumalacharii NCPPB 1452	68.3	96.2	49.7	93	29.6	84.9	88	98.7
X. axonopodis pv. sesbaniae NCPPB 582	68.2	96.1	49.7	92.9	29.6	84.9	89.6	98.8
X. axonopodis DSM 3585 (T)	50.3	93.1	100	100	29.3	84.9	50.2	93.1
X. campestris pv. campestris ATCC 33913 (T)	30	85.1	29.3	84.9	100	100	29.9	85
X. citri pv. fuscan LMG 726 (T)	68.6	96.3	50.2	93.1	29.9	85	100	100

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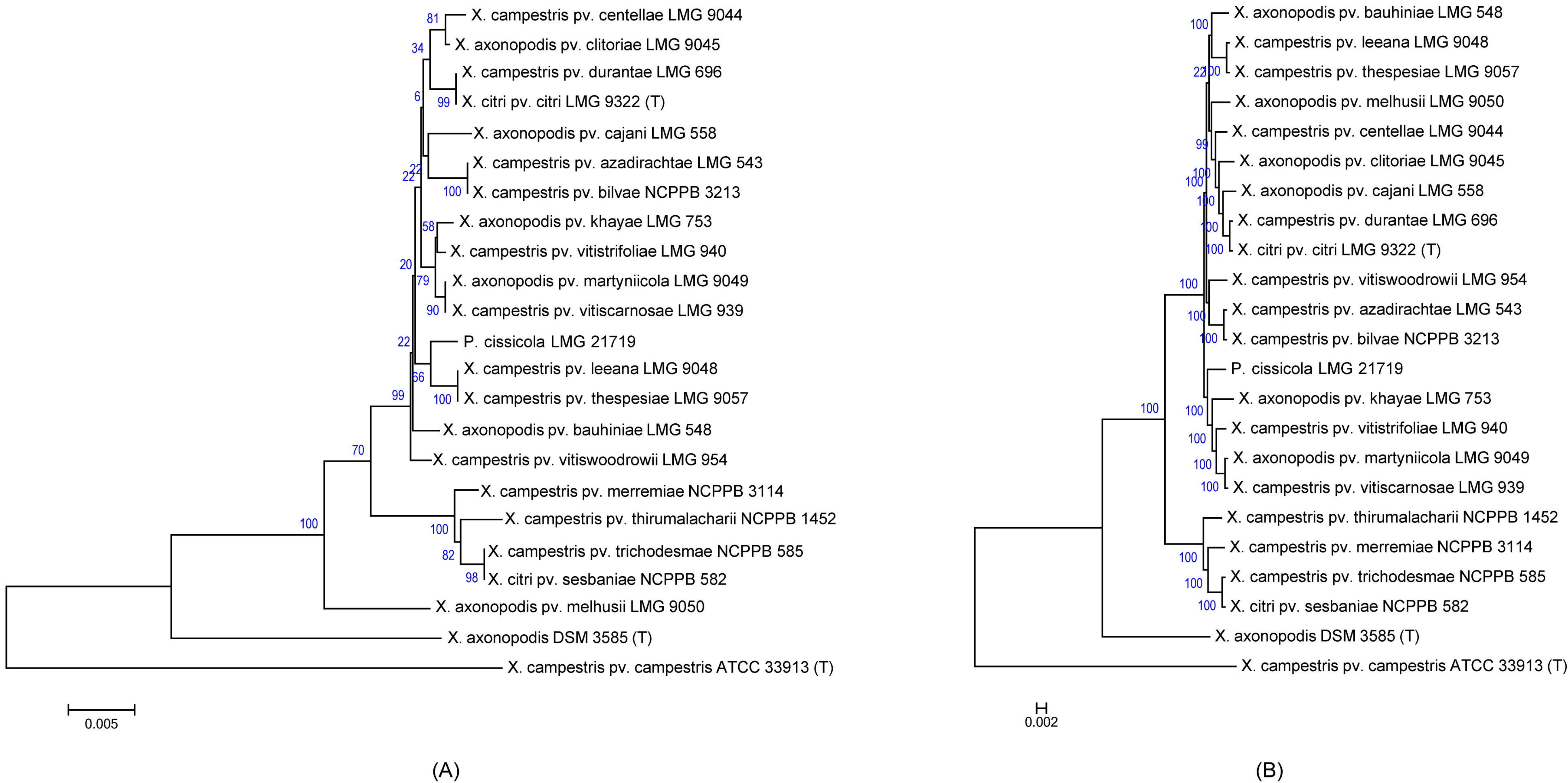
X. campestris pv. centellae LMG 9044
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X. citri pv. citri LMG 9322 (T)
X. axonopodis pv. cajani LMG 558
X. campestris pv. azadirachtae LMG 543
X. campestris pv. bilvae NCPPB 3213
X. axonopodis pv. khayae LMG 753
X. campestris pv. vitistrifoliae LMG 940
X. axonopodis pv. martyniicola LMG 9049
X. campestris pv. vitiscarnosae LMG 939
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X. campestris pv. leeana LMG 9048
X. campestris pv. thespesiae LMG 9057
X. axonopodis pv. bauhiniae LMG 548
X. campestris pv. vitiswoodrowii LMG 954
X. campestris pv. merremiae NCPPB 3114
X. campestris pv. thirumalacharii NCPPB 1452
X. campestris pv. trichodesmae NCPPB 585
X. citri pv. sesbaniae NCPPB 582
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