Huanglongbing Pandemic: Current Challenges and Emerging Management Strategies

Subjects: Microbiology
Contributor: Dilip Ghosh , Sunil Kokane , Brajesh Kumar Savita , Pranav Kumar , Ashwani Kumar Sharma , Ali Ozcan , Amol Kokane , Swadeshmukul Santra

Huanglongbing (HLB, aka citrus greening), one of the most devastating diseases of citrus, has wreaked havoc on the global citrus industry in recent decades. The culprit behind such a gloomy scenario is the phloem-limited bacteria "*Candidatus* Liberibacter asiaticus" (*C*Las), which are transmitted via psyllid. To date, there are no effective long-termcommercialized control measures for HLB, making it increasingly difficult to prevent the disease spread. To combat HLB effectively, introduction of multipronged management strategies towards controlling *C*Las population within the phloem system is deemed necessary. This entry presents a comprehensive review of up-to-date scientific information about HLB, including currently available management practices and unprecedented challenges associated with the disease control. Additionally, a triangular disease management approach has been introduced targeting pathogen, host, and vector. Pathogen-targeting approaches include (i) inhibition of important proteins of *C*Las, (ii) use of the most efficient antimicrobial or immunity-inducing compounds to suppress the growth of *C*Las, and (iii) use of tools to suppress or kill the *C*Las. Approaches for targeting the host include (i) improvement of the host immune system, (ii) effective use of transgenic variety to build the host's resistance against *C*Las, and (iii) induction of systemic acquired resistance. Strategies for targeting the vector include (i) chemical and biological control and (ii) eradication of HLB-affected trees. Finally, a hypothetical model for integrated disease management has been discussed to mitigate the HLB pandemic.

HLB pandemic | citrus greening | Candidatus Liberibacter asiaticus

1. Introduction

Citrus is the most widely grown specialty fruit crop in the world, containing a variety of health-promoting compounds, including vitamin C. The crop is highly vulnerable to various fungal, bacterial, and viral diseases, owing to its narrow genetic diversity [1]. Huanglongbing (HLB, aka citrus greening) is one of the most devastating diseases, which has affected the global citrus industry during last few decades [2][3]. The disease was first reported in southern China [4]. The discovery of HLB in India was attributed to a citrus dieback in the 1700s [5][6], resulting in a hypothesis that the disease was established in India before spreading to China [3][7]. A similar malady was observed in South Africa in 1929 and named "citrus greening disease" based on the poor color development of the stylar end of affected fruit [8]. The disease was also confirmed in South America, in the state of Sao Paulo in Brazil in 2004 [9], and in the state of Florida in the USA [10]. It has seriously impacted the US citrus industry, with an approximate loss of USD 3.6 billion per year [11]. In the USA, the disease was also detected in other states, including two significant citrus-producing states, Texas [12] and California [13], as well as in South Carolina, Georgia, and Louisiana [14]. The disease had also become established in several Caribbean countries such as Cuba [15], Jamaica [16], Belize [17], and Mexico [18]. Other major citrus-growing areas of the Mediterranean Basin and Australia are under threat. The disease also has moved west from Pakistan into Iran [19] and is threatening the neighboring areas. Presently, the disease is distributed in over 58 countries of Asia, America, Africa, Oceania, and the Caribbean. Reports are based on symptomatology, DNA-DNA hybridization with specific probe, PCR followed by *XbaI* restriction digestion of the amplified DNA, electron microscopy, and real-time PCR (**Figure 1**, **Table 1**) [20].

Figure 1. The world map represents geographical distribution of HLB based on DNA-DNA hybridization with probe, PCR followed by *XbaI* restriction digestion of the amplified DNA, electron microscopy, and symptomatology.

Table 1. Worldwide distribution of HLB disease.

Sr. No	Continent/Country/Region	Distribution of HLB	Causal Organism	Reference
	Asia			
1	Bangladesh	Present	*Ca*. Liberibacter asiaticus	[21]
2	Bhutan	Present	*Ca*. Liberibacter asiaticus	[22]
3	Cambodia	Present	*Ca*. Liberibacter asiaticus	[23]
4	China	Present	*Ca*. Liberibacter asiaticus	[22]

Sr. No	Continent/Country/Region	Distribution of HLB	Causal Organism	Reference
5	India	Present, Widespread	*Ca*. Liberibacter asiaticus	[24]
6	Indonesia	Present	*Ca*. Liberibacter asiaticus	[25]
7	Iran	Present, Localized	*Ca*. Liberibacter asiaticus	[26]
8	Japan	Present	*Ca*. Liberibacter asiaticus	[27]
9	Laos	Present	*Ca*. Liberibacter asiaticus	[23]
10	Malaysia	Present, Localized	*Ca*. Liberibacter asiaticus	[24]
11	Myanmar	Present	*Ca*. Liberibacter asiaticus	[23]
12	Nepal	Present, Widespread	*Ca*. Liberibacter asiaticus	[28]
13	Oman	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
14	Pakistan	Present	*Ca*. Liberibacter asiaticus	[29]
15	Philippines	Present, Widespread	*Ca*. Liberibacter asiaticus	[29]
16	Saudi Arabia	Present, Localized	*Ca*. Liberibacter asiaticus	[30]
17	Sri Lanka	Present	*Ca*. Liberibacter asiaticus	[22]
18	Taiwan	Present, Widespread	*Ca*. Liberibacter asiaticus	[22]
19	Thailand	Present	*Ca*. Liberibacter asiaticus	[31]
20	Vietnam	Present, Localized	*Ca*. Liberibacter asiaticus	[32]
21	Yemen	Present, Localized	*Ca*. Liberibacter asiaticus	[30]
	North America		*Ca*. Liberibacter asiaticus	
22	Barbados	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
23	Belize	Present, Localized	*Ca*. Liberibacter asiaticus	[17]
24	Costa Rica	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
25	Cuba	Present, Widespread	*Ca*. Liberibacter asiaticus	[22]

Sr. No	Continent/Country/Region	Distribution of HLB	Causal Organism	Reference
26	Dominica	Present, Few occurrences	*Ca*. Liberibacter asiaticus	[22]
27	Dominican Republic	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
28	El Salvador	Present	Unknown	[33]
29	Guadeloupe	Present, Localized	Unknown	[34]
30	Guatemala	Present	*Ca*. Liberibacter asiaticus	[22]
31	Honduras	Present	*Ca*. Liberibacter asiaticus	[22]
32	Jamaica	Present, Widespread	*Ca*. Liberibacter asiaticus	[22]
33	Martinique	Present, Localized	*Ca*. Liberibacter asiaticus	[34]
34	Mexico	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
35	Nicaragua	Present	*Ca*. Liberibacter asiaticus	[22]
36	Panama	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
37	Puerto Rico	Present	*Ca*. Liberibacter asiaticus	[22]
38	Trinidad and Tobago	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
39	U.S. Virgin Islands	Present, Few occurrences	*Ca*. Liberibacter asiaticus	[22]
40	United States	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
	South America			
41	Argentina	Present, Localized	*Ca*. Liberibacter asiaticus	[22]
42	Brazil	Present, Localized	*Ca*. Liberibacter americanus and Ca. Liberibacter asiaticus	[9]
43	Colombia	Present, Few occurrences	*Ca.*Liberibacter asiaticus	[22]
44	Paraguay	Present, Localized	*Ca*. Liberibacter asiaticus	[35]
45	Venezuela	Present	*Ca*. Liberibacter asiaticus	[36]
	Africa			

Sr. No	Continent/Country/Region	Distribution of HLB	Causal Organism	Reference
46	Burundi	Present	*Ca*. Liberibacter africanus	[37]
47	Cameroon	Present	*Ca*. Liberibacter africanus	[37]
48	Central African Republic	Present	*Ca*. Liberibacter africanus	[37]
49	Comoros	Present	*Ca*. Liberibacter africanus	[22]
50	Eswatini	Present	*Ca*. Liberibacter africanus	[38]
51	Ethiopia	Present	*Ca*. Liberibacter africanus and *Ca*. Liberibacter asiaticus	[37]
52	Kenya	Present	*Ca*. Liberibacter africanus	[29]
53	Madagascar	Present	*Ca*. Liberibacter africanus	[38]
54	Malawi	Present	*Ca*. Liberibacter africanus	[37]
55	Mauritius	Present	*Ca*. Liberibacter africanus and *Ca*. Liberibacter asiaticus	[22]
56	Rwanda	Present	*Ca*. Liberibacter africanus	[37]
57	Somalia	Present	*Ca*. Liberibacter africanus	[22]
58	South Africa	Present, Localized	*Ca*. Liberibacter africanus	[39]
59	Tanzania	Present, Localized	*Ca*. Liberibacter africanus	[38]
60	Uganda	Present	*Ca*. Liberibacter africanus	[40]
61	Zimbabwe	Present, Localized	*Ca*. Liberibacter africanus	[29]

een, with [41][42] localized back [43]. s such as [44][45][46] cted trees leveloped [47] e of their the most efruit (*C.* [2] no known t is more re initially [2][48]

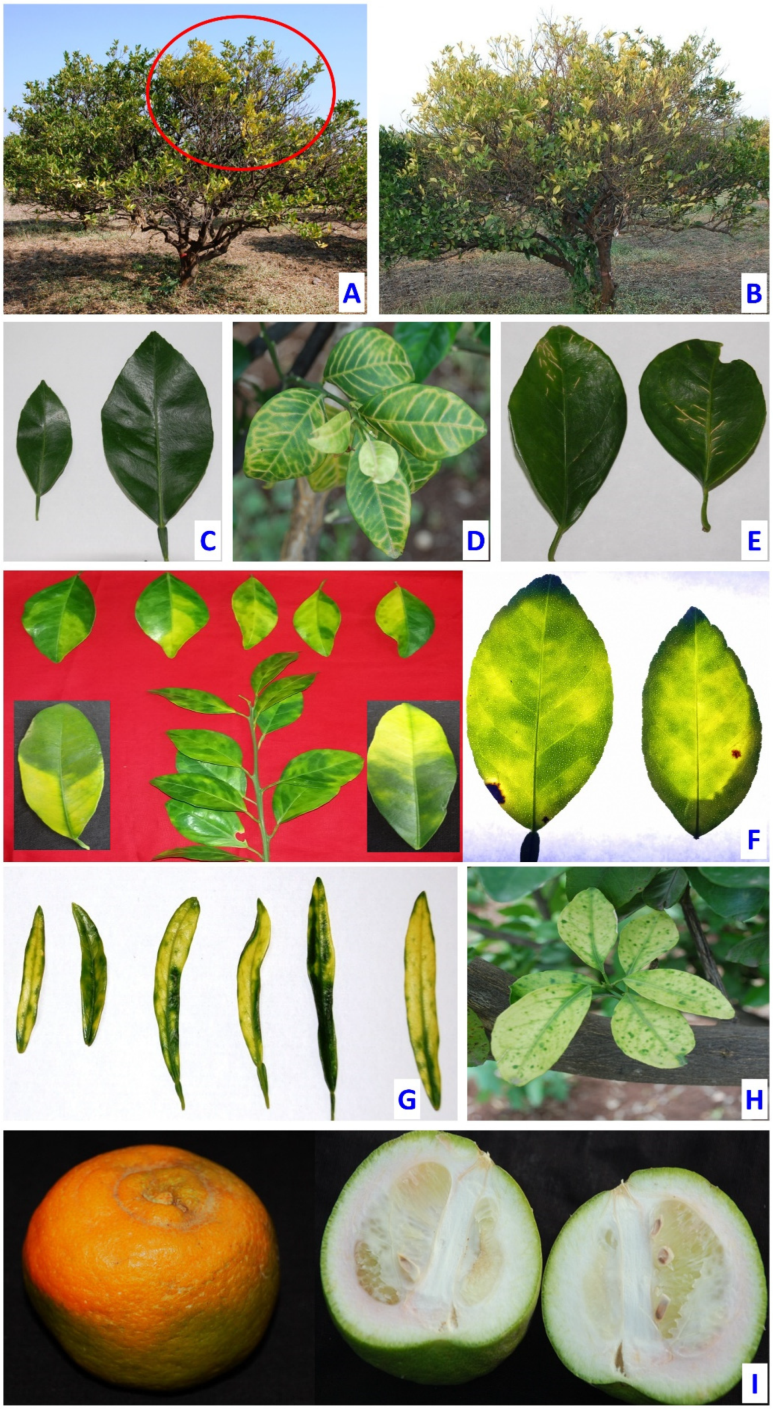

Figure 2. (**A**) HLB-infected sweet orange plant in the field showing characteristic yellow shoot symptoms at initial stage. (**B**) HLB-infected sweet orange in the field at severe stage. (**C**) Healthy leaf. (**D**) Vein yellowing and corking. (**E**) Vein corking. (**F**) Blotchy mottle (a random pattern of chlorosis). (**G**) Narrow leaf with blotchy mottle. (**H**) Green island. (**I**) HLB-affected with color inversion and misshapen sweet orange fruit (lopsided) with aborted seeds.

2. Causative Agent, Genomics, and Pathogenesis Mechanism

The pathogen associated with HLB was initially thought to be a mycoplasma-like organism. Subsequent electron microscopic studies confirmed that the causative organism is a bacterium. The fastidious nature of the pathogen was an impediment in traditional taxonomical classification like the study of morphology and growth characteristics. The phloem-limited causal agent was classified based on the 16S rRNA gene sequence and grouped under the α-subdivision of proteobacteria, genus *Candidatus* Liberibacter in the family *Rhizobiaceae* [49][50]. So far, three species of bacterium are known to be associated with citrus greening disease: '*Candidatus* Liberibacter asiaticus' (*C*Las), '*Candidatus* Liberibacter africanus' (*C*Laf), and '*Candidatus* Liberibacter americanus' (*C*Lam). To date, no successful attempts have been made to grow these bacteria in culture.

Among them, *C*Las is the most destructive, widely prevalent, highly divergent, and has caused significant economic loss in citrus production globally [51]. *C*Lam and *C*Laf are only present in Brazil and Africa, respectively. *C*Lam, originally identified in Brazil, was the major species, but later *C*Las became the most prevalent species [52]. This intracellular plant pathogen acts as an insect symbiont and is transmitted by two sap-sucking insect species, *Diaphorinacitri* and *Triozaerytreae*. *D. citri* isalso known as the Asian citrus psyllid (ACP) (**Figure 3**). The ACP is responsible for the spread of *C*Las and *C*Lam in Asia as well as in the Americas [53]. The ACP is heat-tolerant and can withstand high temperatures (up to 45 °C) but is sensitive to high humidity (above 90%) [54]. On the other hand, *T. erytreae,* African citrus psyllid (AfCP), the vector for spread of *C*Laf in Africa [29], is heat-sensitive. The adult and juvenile forms grow in a cool, moist environment and cannot withstand temperatures above 32 °C [55]. The rapid spread of HLB throughout the globe sparked research interest in understanding the genomics, transcriptomics, and proteomics of the host/vector/pathogen virulence and diversity.

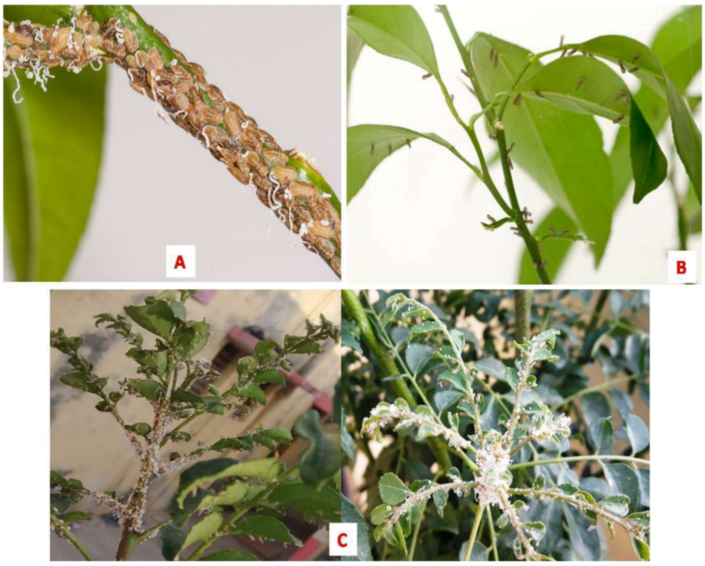

Figure 3. (**A**) ACP nymph on a citrus plant in the field. (**B**) ACP adults feeding on the leaf. (**C**) Infestation of ACP nymph and adults on curry leaf plants.

Despite the unculturable nature of *C*Las, the complete circular genome sequence was generated from *C*Las-infected psyllid by metagenomics, which became the foundation platform for further research in functional genomics [56]. Presently, 42 complete isolate sequences of *C*Las are available in GenBank.Ten genomes are fully assembled in a single scaffold: psy62 [56], gxpsy [57], Ishi-1 [58], A4 [59], JXGC [60], AHCA1 [61], JRPAMB1 [62], TaiYZ2 [63], CoFLP1 [64], and ReuSP1 [65] (**Table 2**). A total of 4.5% and 8% of genes are involved in cell motility and active transport mechanism, respectively, and they might contribute to its virulence activity in the citrus plant phloem system [56]. Bacterial plant pathogens use the secreted proteins (effectors) in their defense mechanism to suppress plant immunity and create a favorable environment for colonization and proliferation [66][67]. The *C*Las genome consists of all Type I secretion system genes that encode proteins involved in multidrug efflux and toxin effectors: HlyD (membrane fusion protein, CLIBASIA_01355), PrtD (ABC transporter, CLIBASIA_1350), and TolC (outer membrane export protein, CLIBASIA_04145). However, *C*Las lacks type III, type IV, and type VI secretion systems and typical degradative enzymes, which are required for its free-living state [67][68][69].

*C*Las also possesses the general Sec secretion system/Sectransloconcapable of pathogenicity to the host plants by secreting effectors directly outside bacterial cells. *C*Las secretory proteins CLIBASIA 05315, CLIBASIA 03875, CLIBASIA 00460, and CLIBASIA 04025 have been reported as Sec-dependent secretory proteins engaged in starch accumulation, cell death, and host plant infections [67][68][69][70][71]. Different peroxidase enzymes, such as SC2_gp095 and CLIBASIA_RS00445, have been identified as non-classical secretory proteins in *C*Las, which counter the reactive-oxygen-species (ROS)-mediated defense-signaling response, including H_2O_2, used by plants to combat disease progression [69]. This indicates that *C*Las may have developed a non-classical secretion pathway to release virulence proteins to combat the host. According to secretome analysis, the *C*Las genome contains a total of 27 non-classically secreted proteins (ncSecPs), the majority of which are involved in suppressing early plant defense mechanisms by diminishing the hypersensitive response [69]. The peroxiredoxin (Prx) superfamily proteins are ubiquitous cysteine-based non-heme peroxidases present in *C*Las. For example, bacterioferritin comigratory protein (BCP) is involved in the oxidative stress defense system of *C*Las due to its ROS scavenging activity [72]. Lipopolysaccharides (LPS), the most important outer membrane module of *C*Las encoded by 21 genes, not only play a critical role in maintaining the robust structural integrity to the bacterial cell, but also play a role in the virulence mechanism. However, there are some differences between *C*Las, *C*Laf, and *C*Lam for type I secretion system, and LPS production has been reported [67][73].

Quorum sensing is a cell-to-cell signaling cascade where chemical-based regulatory communications occur among bacterial populations for their motility, biofilm formation, and virulence mechanism [11]. The mechanism of quorum sensing is regulated by two genes: *luxI* and *luxR*. The *luxI* gene encodes different quorum-sensing molecules, acyl-homoserine lactone (AHL), which induce biofilm formation by activation of *luxR* genes [68]. As *C*Las has a solo LuxR system but lacks LuxI [56], there is currently no evidence on how the *C*Las pathogen employs a quorum-sensing-based mechanism to cause the pathogenicity in citrus plants, although it is speculated that the disease is established like other phytopathogens [74][75]. It has been hypothesized that the communication among the *C*Las, endosymbiont, and psyllid is based on luxR and luxI genes [74]. *C*Las potentially communicates with the endosymbiont (*Wolbachia* spp.) and psyllid after adhering in the saliva sheath. Proteins like Mucin-5AC protein (23.46 kDa) were identified in *D. citri* saliva in a proteome study, which might be involved in the formation of the salivary sheath. Studies have shown that the down-regulation of Mucin 5AC results in reduced bacterial pathogen acquisition by inhibiting bacterial adhesion to the insect gut [76]. It has been reported that some proteins of psyllid (haemocyanin protein and myosin protein) and *C*Las (phosphopantothenoylcysteine synthetase and pantothenate kinase) interact with each other after the acquisition of *C*Las [76]. Therefore, a comprehensive understanding of the quorum-sensing system in *C*Las and the interaction with the citrus and the vector with respect to co-evolved protein interaction networksmay provide a target for combating HLB by hampering acquisition, growth, and biofilm formation of *C*Las.

Table 2. Details of sequenced genomes of *C*Las, *C*Lam, and *C*Laf.

Sr. No	***Candidatus* Liberibacter spp.**	Strain	Host	Sample Origin	Genome Size (Mb)	Number CDS Present in the Genome	Reference
1	*Candidatus* Liberibacter asiaticus	A4 (CP010804.1)	*Citrus reticulata*	China: Guangdong	1.23025	1067	[59]
2	*Candidatus* Liberibacter asiaticus	Gxpsy (CP004005.1)	*Diaphorinacitri*	China: Guangxi	1.26824	1094	[57]
3	*Candidatus* Liberibacter asiaticus	JRPAMB1 (CP040636.1)	*Diaphorinacitri*	USA: Florida	1.23716	1072	[62]
4	*Candidatus* Liberibacter asiaticus	TaiYZ2 (CP041385.1)	*Citrus maxima*	Thailand: Songkhla	1.23062	1067	[77]
5	*Candidatus* Liberibacter asiaticus	psy62 (CP001677.5)	-	USA: Florida	1.22732	1049	[56]
6	*Candidatus* Liberibacter asiaticus	JXGC (CP019958.1)	Citrus	China: Jiangxi	1.22516	1033	[60]
7	*Candidatus* Liberibacter asiaticus	Ishi-1 (AP014595.1)	*Diaphorinacitri*	Japan: Ishigaki	1.19085	1001	[58]
8	*Candidatus* Liberibacter asiaticus	AHCA1 (CP029348.1)	*Diaphorinacitri*	USA: California	1.23375	1056	[61]
9	*Candidatus* Liberibacter asiaticus	FL17 (JWHA00000000.1)	Citrus	USA: Florida	1.22725	1019	[78]
10	*Candidatus* Liberibacter	YNJS7C (QXDO00000000)	Citrus	China: Yunnan	1.25898	1102	[79]

Sr. No	*Candidatus* Liberibacter spp.	Strain	Host	Sample Origin	Genome Size (Mb)	Number CDS Present in the Genome	Reference
	asiaticus						
11	*Candidatus* Liberibacter asiaticus	YCPsy LIIM00000000)	*Diaphorinacitri*	China: Guangdong	1.233647	1037	[80]
12	*Candidatus* Liberibacter asiaticus	LBR19TX2 (VTMA00000000	-	USA: Texas	1.20275	1008	[67]
13	*Candidatus* Liberibacter asiaticus	LBR23TX5 (VTMB00000000)	-	USA: Texas	1.20347	1009	[67]
14	*Candidatus* Liberibacter asiaticus	AHCA17 (VNFL00000000)	Citrus maxima	USA: California	1.20862	1036	[81]
15	*Candidatus* Liberibacter asiaticus	YNXP-1 (VIGA00000000)	Cuscuta	China: Yunnan	1.20707	1031	-
16	*Candidatus* Liberibacter asiaticus	SGCA16 (VTLZ00000000)	-	USA: San Gabriel	1.20994	1015	[67]
17	*Candidatus* Liberibacter asiaticus	JXGZ-1 (VIQL00000000)	Cuscuta	China: JiangXi	1.21799	1040	-
18	*Candidatus* Liberibacter asiaticus	DUR1TX1 VTLT00000000.1)	-	USA: Texas	1.20629	1011	[67]
19	*Candidatus* Liberibacter asiaticus	Mex8 (VTLU00000000.1)	-	Mexico: Mexicali	1.24313	1042	[67]
20	*Candidatus* Liberibacter asiaticus	SGCA5 (LMTO00000000.1)	Orange citrus	USA: San Gabriel	1.20138	1001	[80]
21	*Candidatus* Liberibacter asiaticus	CHUC (VTLV00000000)	-	China	1.20845	1032	[67]

Sr. No	*Candidatus* Liberibacter spp.	Strain	Host	Sample Origin	Genome Size (Mb)	Number CDS Present in the Genome	Reference
22	*Candidatus* Liberibacter asiaticus	TX2351 (MTIM00000000)	Asian citrus psyllid	USA: Texas	1.252	1129	[82]
23	*Candidatus* Liberibacter asiaticus	GFR3TX3 (VTLR00000000)	-	USA: Texas	1.20932	1013	[67]
24	*Candidatus* Liberibacter asiaticus	HHCA16 (VTLY00000000)	-	USA: Hacienda Heights	1.20705	1012	[67]
25	*Candidatus* Liberibacter asiaticus	MFL16 (VTLX00000000)	-	USA: Florida	1.19922	1012	[67]
26	*Candidatus* Liberibacter asiaticus	DUR2TX1 (VTLS00000000)	-	USA: Texas	1.21232	1009	[67]
27	*Candidatus* Liberibacter asiaticus	CRCFL16 (VTLW00000000)	-	USA: Florida	1.20828	1028	[67]
28	*Candidatus* Liberibacter asiaticus	HHCA (JMIL00000000.2)	*Citrus* sp.	USA: Hacienda Heights	1.15062	867	[59]
29	*Candidatus* Liberibacter asiaticus	TX1712 (QEWL00000000)	*Citrus sinensis*	USA: Texas	1.20333	0	[83]
30	*Candidatus* Liberibacter asiaticus	SGpsy (QFZJ00000000.1)	*Diaphorinacitri*	USA: San Gabriel	0.769888	0	[61]
31	*Candidatus* Liberibacter asiaticus	SGCA1 (QFZT00000000.1)		USA: San Gabriel	0.233414	557	[61]
32	*Candidatus* Liberibacter asiaticus	YCPsy (LIIM00000000)	*Diaphorinacitri*	Guangdong, China	1.233647	-	[80]
33	*Candidatus* Liberibacter	PA19 (WOXD01000000)	Kinnow mandarin	Pakistan	1.224156	1059	[84]

Sr. No	*Candidatus* Liberibacter spp.	Strain	Host	Sample Origin	Genome Size (Mb)	Number CDS Present in the Genome	Reference
	asiaticus						
34	*Candidatus* Liberibacter asiaticus	PA20 (WOUN01000000)	Kinnow mandarin	Pakistan	1.226225	1062	[84]
35	*Candidatus* Liberibacter asiaticus	CoFLP1 (CP054558.1)	*Diaphorinacitri*	Colombia: Municipio Dibulla	1.231639	1048	[64]
36	*Candidatus* Liberibacter asiaticus	9PA (JABDRZ000000000.1)	*Citrus sinensis*	Brazil (South America)	1.231881	-	[85]
37	*Candidatus* Liberibacter asiaticus	MFL16 (VTLX00000000)	Citrus	USA: Florida	1,199,225 bp	-	[67]
38	*Candidatus* Liberibacter asiaticus	CRCFL16 (VTLW00000000)	Citrus	USA: Florida	1,208,280 bp	-	[67]
39	*Candidatus* Liberibacter asiaticus	ReuSP1 (CP061535.1)	*Diaphorinacitri*	France: La Reunion	1.230064	1043	[65]
40	*Candidatus* Liberibacter asiaticus	Tabriz.3(JAKQYA000000000.1)	*Elaeagnus angustifolia*	Iran: East Azerbaijan, Tabriz	1.22409	589	-
41	*Candidatus* Liberibacter asiaticus	YNHK-2 (WUUB01000000.1)	Citrus	China: Yunnan	1.08957	-	[86]
42	*Candidatus* Liberibacter asiaticus	A-SBCA19 (JADBIB010000000.1)	*Diaphorinacitri*	USA: California, San Bernardino County	1.18688	1067	[87]
43	*Candidatus* Liberibacter americanus	Sao Paulo (NC_022793)	*Citrus sinensis*	Brazil	1.1952	945	[73]
44	*Candidatus* Liberibacter americanus	PW_SP	Catharanthus roseus	Brazil: Sao Paulo	1.17607	924	-

ost. The
orted [88].
ently, the
), based
reported
particles
and, is a
encodes
ved that
[88][90]. The
onse by
minating
ains [92].
ophages.
species
virulence
protease,
believed
nce, the
defense
ctors [94].
ns using
ating the

response to exogenous SA [95]. The secretion and transport of the effector proteins in the host plant cells is one of the most important virulence factors of the bacterial pathogen [66]. Thevirulence factor CaLas5315 (Sec-delivered effector 1) hinders the papain-like cysteine protease's activity to suppress the defense mechanism of citrus. It also induces the callose deposition inside the vascular tissue, starch formation, chlorosis, and plant cell death after localization in the chloroplast of *Nicotiana benthamiana* [69][71][96]. Ying et al. (2019) have assessed 60 total putative virulence factors of *C*Las and identified four candidates (detrimental virulence factors) which are responsible for

50 and [97]

Sr. No	*Candidatus* Liberibacter spp.	Strain	Host	Sample Origin	Genome Size (Mb)	Number CDS Present in the Genome	Reference
45	*Candidatus* Liberibacter africanus	PTSAPSY	Psyllid	South Africa: Pretoria	1.19223	1036	-

1. Wu, G.A.; Prochnik, S.; Jenkins, J.; Salse, J.; Hellsten, U.; Murat, F.; Perrier, X.; Ruiz, M.; Scalabrin, S.; Terol, J.; et al. Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nat. Biotechnol. 2014, 32, 656–662.
2. Bové, J.M. Huanglongbing: A destructive, newly-emerging, century-old disease of citrus. J. Plant Pathol. 2006, 88, 7–37.
3. Gottwald, T.R. Current epidemiological understanding of citrus huanglongbing. Annu. Rev. Phytopathol. 2010, 48, 119–139.
4. Reinking, O.A. Diseases of economic plants in Southern China. Philipp. Agric. 1919, 8, 109–135.
5. Husain, M.A.; Nath, D. The citrus psylla (Diaphorinacitri, Kuw.) . Mem. Dept. Agric. India Entomol. Ser. 1927, 10, 5–27.
6. Capoor, S.P. Decline of citrus in India. Bull. Natl. Inst. Sci. 1963, 24, 48–64.
7. Beattie, G.A.C.; Holford, P.; Mabberley, D.J.; Haigh, A.M.; Bayer, R. Aspects and insights of Australia-Asia collaborative research on huanglongbing. In Proceedings of the International Workshop for the Prevention of Citrus Greening Disease in Severely Infected Areas, Ishigaki, Japan, 6–7 December 2006; Japanese Ministry of Agriculture, Forestry and Fisheries: Tokyo, Japan, 2006; pp. 47–64.
8. Merwe, A.J.; Anderssen, F.G. Chromium and manganese toxicity. Is it important in Transvaal citrus greening. Farming S. Afr. 1937, 12, 439–440.
9. Coletta-Filho, H.D.; Targon, M.; Takita, M.A.; De Negri, J.D.; Pompeu, J.; Machado, M.A.; do Amaral, A.M.; Muller, G.W. First report of the causal agent of Huanglongbing (Candidatus Liberibacter asiaticus) in Brazil. Plant Dis. 2004, 88, 1382.
10. Halbert, S.E. The discovery of huanglongbing in Florida. In Proceedings of the Second International Citrus Canker and Huanglongbing Research Workshop, Orlando, FL, USA, 7–11 November 2005; p. H-3.
11. Molki, B.; Call, D.R.; Ha, P.T.; Omsland, A.; Gang, D.R.; Lindemann, S.R.; Killiny, N.; Beyenal, H. Growth of ‘Candidatus Liberibacter asiaticus’ in a host-free microbial culture is associated with microbial community composition. Enzym. Microb. Technol. 2020, 142, 109691.

12. da Graca, J.V.; Kunta, M.; Setamou, M.; Rascoe, J.; Li, W.; Nakhla, M.K.; Salas, B.; Bartels, D.W. Huanglongbing in Texas: Report on the first detections in commercial citrus. J. Citrus Pathol. 2015, 2, 27939.
13. Kumagai, L.B.; LeVesque, C.S.; Blomquist, C.L.; Madishetty, K.; Guo, Y.; Woods, P.W.; Rooney-Latham, S.; Rascoe, J.; Gallindo, T.; Schnabel, D.; et al. First report of Candidatus Liberibacter asiaticus associated with citrus huanglongbing in California. Plant Dis. 2013, 97, 283.
14. Halbert, S.E.; Manjunath, K.L.; Ramadugu, C.; Brodie, M.W.; Webb, S.E.; Lee, R.F. Trailers transporting organges to processing plants move asian citrus psyllids. Florida Entomol. 2010, 93, 33–38.
15. Luis, M.; Collazo, C.; Llauger, R.; Blanco, E.; Pena, I.; López, D.; González, C.; Casín, J.C.; Batista, L.; Kitajima, E.; et al. Occurrence of citrus Huanglongbing in Cuba and association of the disease with Candidatus Liberibacter asciaticus. J. Plant Pathol. 2009, 91, 709–712.
16. Oberheim, A.P.; Brown, S.E.; McLaughlin, W.A. The identification and distribution of citrus greening disease in Jamaica. In Proceedings of the 2nd International Research Conference on Huanglongbing, Orlando, FL, USA, 10–14 January 2011; p. 114.
17. Manjunath, K.L.; Ramadugu, C.; Majil, V.M.; Williams, S.; Irey, M.; Lee, R.F. First report of the citrus huanglongbing associated bacterium ‘Candidatus Liberibacter asiaticus’ from sweet orange, mexican lime, and asian citrus psyllid in Belize. Plant Dis. 2010, 94, 781.
18. Trujillo-Arriaga, J.; Sanchez, A.H.; Robles, G.P.; de la Rosa, A.A.; Delgadillo, V.I.; Márquez, S.M. Antecedantes y situacion actual de Huanglongbing de loscıtricosen Mexico. In Proceedings of the 1er Simposio Nacional Sobre Investigacion para el Manejo del Psılido Asiatico de losCıtricos y el HLB en Mexico, Monterrey, Mexico, 8–9 December 2010; pp. 1–7.
19. Faghihi, M.M.; Salehi, M.; Bagheri, A.; Izadpanah, K. First report of citrus huanglongbing disease on orange in Iran. Plant Pathol. 2009, 58, 793.
20. CABI. Citrus Huanglongbing (Greening) Disease (Citrus Greening). In Invasive Species Compendium; CABI International: Wallingford, UK, 2020.
21. Catling, H.D.; Garnier, M.; Bove, J.M. Presence of citrus greening disease in Bangladesh and a new method for rapid diagnosis. FAO Plant Prot. Bull. 1978, 26, 16–18.
22. EPPO (European and Mediterranean Plant Protection Organization). ‘Candidatus Liberibacter asiaticus’. EPPO Datasheets on Pests Recommended for Regulation. 2022. Available online: https://gd.eppo.int (accessed on 25 November 2022).
23. Garnier, M.; Bové, J.M. Huanglongbing in Cambodia, Laos and Myanmar. In Proceedings of the 14th Conference of the International Organization of Citrus Virologists, Riverside, CA, USA, 2000; da Graça, J.V., Lee, R.F., Yokomi, R.K., Eds.; IOCV: Concordia, Argentina, 2000; Volume 14, pp. 378–380.

24. Bové, J.M.; Garnier, M.; Ahlawat, Y.S.; Chakraborty, N.K.; Varma, A. Detection of the Asian strains of the greening BLO by DNA-DNA hybridization in Indian orchard trees and Malaysian Diaphorina Citri Psyllids. Int. Organ. Citrus Virol. Conf. Proc. 1993, 12, 1957–2010.
25. Aubert, B.; Garnier, M.; Guillaumin, D.; Herbagyandono, B.; Setiobudi, L.; Nurhadi, F. Greening, a serious threat for the citrus productions of the Indonesian archipelago. Future prospects of integrated control. Fruits 1985, 40, 549–563.
26. Salehi, M.; Faghihi, M.M.; Khanchezar, A.; Bagheree, A.; Izadpanah, K. Distributioin of citrus Huanglongbing disease and its vector in southern Iran. Iranian J. Plant Pathol. 2012, 48, 195–208.
27. Miyakawa, T.; Tsuno, K. Occurrence of citrus greening disease in the southern islands of Japan. Jpn. J. Phytopathol. 1989, 55, 667–670.
28. Regmi, C.; Garnier, M.; Bové, J.M. Detection of the Asian Huanglongbing (Greening) Liberobacter in Nepal by DNA-DNA hybridization. Int. Organ. Citrus Virol. Conf. Proc. 1996, 13, 267–270.
29. Garnier, M.; Bové, J.M. Distribution of the huanglongbing (greening) Liberobacter species in fifteen African and Asian countries. Int. Organ. Citrus Virol. Conf. Proc. 1996, 13, 1957–2010.
30. Bové, J.M.; Garnier, M. Citrus greening and psylla vectors of the disease in the Arabian Peninsula. Int. Organ. Citrus Virol. Conf. Proc. 1984, 9, 1957–2010.
31. Promintara, M. Simultaneous infection of mandarin (Citrus reticulata Bl.) with tristeza virus and greening organism in Thailand. In Proceedings of the 4th International Asia Pacific Conference on Citrus Rehabilitation, Chiang Mai, Thailand, 4–10 February 1990; FAO-UNDP RAS/86/022 Regional Project. pp. 96–99.
32. Bové, J.M.; Navarro, L.; Bonnet, P.; Zreik, L.; Garnier, M. Reaction of citrus cultivars to graft-inoculation of Phytoplasma aurantifolia-infected lime shoots. Int. Organ. Citrus Virol. Conf. Proc. (1957–2010) 1996, 13, 13.
33. MAG. Declaraemergenciafitosanitarianacionalporpresencia de HLB, Enfermedad de Loscítricos, El Salvador, Ministerio de Agricultura y Ganadería. 2020. Available online: http://www.mag.gob.sv/mag-declara-emergencia-fitosanitaria-nacional-por-presencia-de-hlb-enfermedad-de-los-citricos/ (accessed on 25 November 2022).
34. Cellier, G.; Moreau, A.; Cassam, N.; Hostachy, B.; Ryckewaert, P.; Aurela, L.; Picard, R.; Lombion, K.; Rioualec, A.L. First report of ‘Candidatus Liberibacter asiaticus’ associated with huanglongbing on Citrus latifolia in Martinique and Guadeloupe, French West Indies. Plant Dis. 2014, 98, 683.
35. Leite, R., Jr.; Cordeiro, A.B.; Meneguim, L. Primera deteccion de la enfermedadHuanglongbing (HLB) enasociacion con la bacteria Candidatus Liberibacter asiaticus en Paraguay. In Proceedings of the VII Congresso Argentino de Citricultura, Puerto Iguazu, Missiones, Argentina, 15–17 May 2013.

36. Marys, E.; Rodríguez-Román, E.; Mejías, R.; Mejías, A.; Mago, M.; Hernández, Y. First report on molecular evidence of Candidatus Liberibacter asiaticus associated with citrus Huanglongbing in Venezuela. J. Plant Pathol. 2020, 102, 1333.
37. Aubert, B.; Garnier, M.; Cassin, J.E.; Bertin, Y. Citrus greening disease survey in East and West African countries South of Sahara. Int. Organ. Citrus Virol. Conf. Proc. (1957–2010) 1988, 10, 231–237.
38. Garnier, M.; Jagoueix-Eveillard, S.; Cronje, P.R.; Le Roux, H.F.; Bove, J.M. Genomic characterization of a liberibacter present in an ornamental rutaceous tree, Calodendrumcapense, in the Western Cape Province of South Africa. Proposal of 'Candidatus Liberibacter africanus subsp. capensis'. Int. J. Syst. Evol. Microbiol. 2000, 50, 2119–2125.
39. Korsten, L.; Jagoueix, S.; Bové, J.M.; Garnier, M. Huanglongbing (greening) detection in South Africa. Int. Organ. Citrus Virol. Conf. Proc. (1957–2010) 1996, 13.
40. Kalyebi, A.; Aisu, G.; Ramathani, I.; Ogwang, J.; McOwen, N.; Russell, P. Detection and identification of etiological agents (Liberibacter spp.) associated with citrus greening disease in Uganda. Uganda J. Agric. Sci. 2015, 16, 43–54.
41. Ghosh, D.; Bhose, S.; Mukherjee, K.; Baranwal, V.K. Sequence and evolutionary analysis of ribosomal DNA from Huanglongbing (HLB) isolates of western India. Phytoparasitica 2013, 41, 295–305.
42. Nageswara-Rao, M.; Miyata, S.I.; Ghosh, D.; Irey, M.; Garnsey, S.M.; Gowda, S. Development of rapid, sensitive and non-radioactive tissue-blot diagnostic method for the detection of citrus greening. Mol. Cell. Probes 2013, 27, 176–183.
43. Hu, W.Z.; Wang, X.F.; Zhou, Y.; Li, Z.A.; Tang, K.Z.; Zhou, C. Diversity of the OMP gene in 'Candidatus Liberibacter asiaticus' in China. J. Plant Pathol. 2011, 93, 211–214.
44. Kokane, S.B.; Bhose, S.; Kokane, A.; Gubyad, M.; Ghosh, D.K. Molecular detection, identification, and sequence analysis of Candidatus Liberibacter asiaticus associated with Huanglongbing disease of citrus in North India. 3Biotech 2020, 10, 341.
45. Kokane, S.B.; Misra, P.; Kokane, A.D.; Gubyad, M.G.; Warghane, A.J.; Surwase, D.; Reddy, M.K.; Ghosh, D.K. Development of a real-time RT-PCR method for the detection of Citrus tristeza virus (CTV) and its implication in studying virus distribution in planta. 3Biotech 2021, 11, 431.
46. Ghosh, D.K.; Kokane, A.; Kokane, S.B.; Tenzin, J.; Gubyad, M.G.; Wangdi, P.; Murkute, A.A.; Sharma, A.K.; Gowda, S. Detection and molecular characterization of Candidatus Liberibacter asiaticus and Citrus tristeza virus associated with citrus decline in Bhutan. Phytopathology 2021, 111, 870–881.
47. Brlansky, R.H. Blight. In Compendium of Citrus Disease, 2nd ed.; Timmer, L.W., Garnsey, S.M., Graham, J.H., Eds.; APS Press: St. Paul, MN, USA, 2000; pp. 65–66.

48. Tsai, J.H.; Liu, Y.H. Biology of Diaphorinacitri (Homoptera: Psyllidae) on four host plants. J. Econ. Entomol. 2000, 93, 1721–1725.

49. Jagoueix, S.; Bové, J.M.; Garnier, M. The phloem-limited bacterium of greening disease of citrus is a member of the alpha subdivision of the proteobacteria. Int. J. Syst. Evol. Microbiol. 1994, 44, 379–386.

50. Kokane, S.B.; Kokane, A.D.; Misra, P.; Warghane, A.; Kumar, P.; Gubyad, M.G.; Sharma, A.K.; Biswas, K.K.; Ghosh, D.K. In-silico characterization and RNA-binding protein based polyclonal antibodies production for detection of Citrus tristeza virus. Mol. Cell. Probes. 2020, 54, 101654.

51. Ghosh, D.K.; Motghare, M.; Kokane, A.; Kokane, S.; Warghane, A.; Bhose, S.; Surwase, D.; Ladaniya, M.S. First report of a ‘Candidatus phytoplasma cynodontis’-related strain (group 16SrXIV) associated with Huanglongbing disease on Citrus grandis in India. Aus. Plant Dis. Notes 2019, 14, 9.

52. Wang, N. A perspective of citrus Huanglongbing in the context of the mediterranean Basin. J. Plant Pathol. 2020, 102, 635–640.

53. Pelz-Stelinski, K.S.; Brlansky, R.H.; Ebert, T.A.; Rogers, M.E. Transmission parameters for ‘Candidatus Liberibacter asiaticus’ by Asian citrus psyllid (Hemiptera: Psyllidae). J. Econ. Entomol. 2010, 103, 1531–1541.

54. El-Shesheny, I.; Hijaz, F.; El-Hawary, I.; Mesbah, I.; Killiny, N. Impact of different temperatures on survival and energy metabolism in the Asian citrus psyllid, Diaphorina citri Kuwayama. Comp. Biochem. Physiol. Part A Mol. Integr. Physiol. 2016, 192, 28–37.

55. Mann, R.S.; Pelz-Stelinski, K.; Hermann, S.L.; Tiwari, S.; Stelinski, L.L. Sexual transmission of a plant pathogenic bacterium, ‘Candidatus Liberibacter asiaticus’, between conspecific insect vectors during mating. PLoS ONE 2011, 6, e29197.

56. Duan, Y.; Zhou, L.; Hall, D.G.; Li, W.; Doddapaneni, H.; Lin, H.; Liu, L.; Vahling, C.M.; Gabriel, D.W.; Kelly, P.; et al. Complete genome sequence of citrus huanglongbing bacterium, ‘Candidatus Liberibacter asiaticus’ obtained through metagenomics. Mol. Plant-Microbe Interact. 2009, 22, 1011–1020.

57. Lin, H.; Han, C.S.; Liu, B.; Lou, B.; Bai, X.; Deng, C.; Civerolo, E.L.; Gupta, G. Complete genome sequence of a chinese strain of “Candidatus Liberibacter asiaticus. ” Genome Announc. 2013, 1, e00184-13.

58. Katoh, H.; Miyata, S.; Inoue, H.; Iwanami, T. Unique features of a Japanese ‘Candidatus Liberibacter asiaticus’ strain revealed by whole genome sequencing. PLoS ONE 2014, 9, e106109.

59. Zheng, Z.; Deng, X.; Chen, J. Whole-genome sequence of ‘Candidatus Liberibacter asiaticus’ from Guangdong, China. Genome Announc. 2014, 2, e00273-14.

60. Zheng, Z.; Bao, M.; Wu, F.; Van Horn, C.; Chen, J.; Deng, X. A Type 3 Prophage of ‘Candidatus Liberibacter asiaticus’ carrying a restriction-modification system. Phytopathology 2018, 108, 454–461.

61. Dai, Z.; Wu, F.; Zheng, Z.; Yokomi, R.; Kumagai, L.; Cai, W.; Rascoe, J.; Polek, M.; Chen, J.; Deng, X. Prophage diversity of ‘Candidatus Liberibacter asiaticus’ strains in california. Phytopathology 2019, 109, 551–559.

62. Petrone, J.R.; Muñoz-Beristain, A.; Glusberger, P.R.; Russell, J.T.; Triplett, E.W. Unamplified, Long-Read Metagenomic Sequencing Approach to Close Endosymbiont Genomes of Low-Biomass Insect Populations. Microorganisms 2022, 10, 513.

63. Li, S.; Wu, F.; Duan, Y.; Singerman, A.; Guan, Z. Citrus Greening: Management strategies and their economic impact. Hort. Sci. 2020, 55, 604.

64. Wang, Y.; Kondo, T.; He, Y.; Zhou, Z.; Lu, J. Genome Sequence Resource of ‘Candidatus Liberibacter asiaticus’ from Diaphorinacitri Kuwayama (Hemiptera: Liviidae) in Colombia. Plant Dis. 2021, 105, 193–195.

65. Lu, J.; Delatte, H.; Reynaud, B.; Beattie, G.A.; Holford, P.; Cen, Y.; Wang, Y. Genome sequence resource of ‘Candidatus Liberibacter asiaticus’ from Diaphorinacitri Kuwayama (Hemiptera: Liviidae) from La Réunion. Plant Dis. 2021, 105, 1171–1173.

66. Toruno, T.Y.; Stergiopoulos, I.; Coaker, G. Plant-pathogen effectors: Cellular probes interfering with plant defenses in spatial and temporal manners. Annu. Rev. Phytopathol. 2016, 54, 419–441.

67. Thapa, S.P.; De Francesco, A.; Trinh, J.; Gurung, F.B.; Pang, Z.; Vidalakis, G.; Wang, N.; Ancona, V.; Ma, W.; Coaker, G. Genome-wide analyses of Liberibacter species provides insights into evolution, phylogenetic relationships, and virulence factors. Mol. Plant Pathol. 2020, 21, 716–731.

68. Kruse, A.; Fleites, L.A.; Heck, M. Lessons from one fastidious bacterium to another: What can we learn about liberibacter species from Xylella fastidiosa. Insects 2019, 10, 300.

69. Du, P.; Zhang, C.; Zou, X.; Zhu, Z.; Yan, H.; Wuriyanghan, H.; Li, W. “Candidatus Liberibacter asiaticus” secretes nonclassically secreted proteins that suppress host hypersensitive cell death and induce expression of plant pathogenesis-related proteins. Appl. Environ. Microbiol. 2021, 87, e00019-21.

70. Pitino, M.; Armstrong, C.M.; Cano, L.M.; Duan, Y. Transient expression of Candidatus Liberibacter asiaticus effector induces cell death in Nicotiana benthamiana. Front. Plant Sci. 2016, 7, 982.

71. Pitino, M.; Allen, V.; Duan, Y. LasΔ5315 effector induces extreme starch accumulation and chlorosis as Candidatus Liberibacter asiaticus infection in Nicotiana benthamiana. Front. Plant Sci. 2018, 9, 113.

72. Singh, A.; Kumar, N.; Tomar, P.P.; Bhose, S.; Ghosh, D.K.; Roy, P.; Sharma, A.K. Characterization of a bacterioferritin comigratory protein family 1-Cys peroxiredoxin from Candidatus Liberibacter asiaticus. Protoplasma 2017, 254, 1675–1691.
73. Wulff, N.A.; Zhang, S.; Setubal, J.C.; Almeida, N.F.; Martins, E.C.; Harakava, R.; Kumar, D.; Rangel, L.T.; Foissac, X.; Bové, J.M.; et al. The complete genome sequence of ‘Candidatus Liberibacter americanus’, associated with citrus huanglongbing. Mol. Plant Microbe Interact. 2014, 27, 163–176.
74. Killiny, N. Quorum sensing controls Candidatus Liberibacter asiaticus interactions with host plant and insect vector. APS Annu. Meet. 2015, 105, 72.
75. Shahzad, F.M.; Kadyampakeni, D.; Vashisth, T. Effect of Growing Media pH on Performance of Huanglongbing-Affected Young Citrus Trees. Agronomy 2021, 11, 439.
76. Ramsey, J.S.; Chavez, J.D.; Johnson, R.; Hosseinzadeh, S.; Mahoney, J.E.; Mohr, J.P.; Robison, F.; Zhong, X.; Hall, D.G.; MacCoss, M.; et al. Protein interaction networks at the host-microbe interface in Diaphorinacitri, the insect vector of the citrus greening pathogen. Royal Soc. Open Sci. 2017, 4, 160545.
77. Li, T.; Thaochan, N.; Huang, J.; Chen, J.; Deng, X.; Zheng, Z. Genome sequence resource of ‘Candidatus Liberibacter asiaticus’ from Thailand. Plant Dis. 2020, 104, 624–626.
78. Zheng, Z.; Sun, X.; Deng, X.; Chen, J. Whole-genome sequence of “Candidatus Liberibacter asiaticus” from a huanglongbing-affected citrus tree in central Florida. Genome Announc. 2015, 3, e00169-15.
79. Chen, Y.; Li, T.; Zheng, Z.; Xu, M.; Deng, X. Draft whole-genome sequence of a “Candidatus Liberibacter asiaticus” strain from Yunnan, China. Microbiol. Res. Announc. 2019, 8, e01413-18.
80. Wu, F.; Zheng, Z.; Deng, X.; Cen, Y.; Liang, G.; Chen, J. Draft genome sequence of “Candidatus Liberibacter asiaticus” from Diaphorinacitri in Guangdong, China. Genome Announc. 2015, 3, e01316-15.
81. Cai, W.; Nunziata, S.; Costanzo, S.; Kumagai, L.; Rascoe, J.; Stulberg, M.J. Genome resource for the huanglongbing causal agent ‘Candidatus Liberibacter asiaticus’ strain AHCA17 from citrus root tissue in California, USA. Plant Dis. 2020, 104, 627–629.
82. Kunta, M.; Zheng, Z.; Wu, F.; da Graca, J.V.; Park, J.W.; Deng, X.; Chen, J. Draft whole-genome sequence of “Candidatus Liberibacter asiaticus” strain TX2351 isolated from Asian citrus psyllids in Texas, USA. Genome Announc. 2017, 5, e00170-17.
83. Cai, W.; Yan, Z.; Rascoe, J.; Stulberg, M.J. Draft whole-genome sequence of “Candidatus Liberibacter asiaticus” strain TX1712 from citrus in texas. Genome Announc. 2018, 6, e00554-18.

84. Liu, K.; Atta, S.; Cui, X.; Zeng, C.; Chen, J.; Zhou, C.; Wang, X. Genome sequence resources of two 'Candidatus Liberibacter asiaticus' strains from Pakistan. Plant Dis. 2020, 104, 2048–2050.
85. Silva, P.A.; Huang, J.; Wulff, N.A.; Zheng, Z.; Krugner, R.; Chen, J. Genome sequence resource of 'Candidatus Liberibacter asiaticus' strain 9PA from Brazil. Plant Dis. 2021, 105, 199–201.
86. Cui, X.J.; Zeng, C.H.; Liu, K.H.; Teng, C.L.; Zhou, C.Y.; Wang, X.F. Decreasing detection frequency of MITE (MCLas-A) in the population of 'Candidatus Liberibacter asiaticus' recently collected in southern China. J. Integr. Agric. 2020, 19, 2597–2601.
87. Huang, J.; Dai, Z.; Zheng, Z.; Silvia, P. Metagenomic Analyses of ACP and Citrus Samples Infected with "Candidatus Liberibacter asiaticus" in California. In American Phytopathological Society Abstracts; USDA: Washington, DC, USA, 2020. Available online: https://www.ars.usda.gov/research/publications/publication/?seqNo115=373141 (accessed on 25 November 2022).
88. Jain, M.; Fleites, L.; Gabriel, D.W. Prophage encoded peroxidase in "Candidatus Liberibacter asiaticus" is a secreted effector that suppresses plant defenses. Mol. Plant-Microbe Interac. 2015, 28, 1330–1337.
89. Dominguez-Mirazo, M.; Jin, R.; Weitz, J.S. Functional and comparative genomic analysis of integrated prophage-like sequences in "Candidatus Liberibacter asiaticus". mSphere 2019, 4, e00409-19.
90. Zhang, S.; Flores-Cruz, Z.; Zhou, L.; Kang, B.H.; Fleites, L.A.; Gooch, M.D.; Wulff, N.A.; Davis, M.J.; Duan, Y.P.; Gabriel, D.W. 'Ca. Liberibacter asiaticus' carries an excision plasmid prophage and a chromosomally integrated prophage that becomes lytic in plant infections. Mol. Plant-Microbe Interact. 2011, 24, 458–468.
91. Fu, S.M.; Hartung, J.; Zhou, C.Y.; Su, H.N.; Tan, J.; Li, Z.A. Ultrastructural changes and putative phage particles observed in sweet orange leaves infected with 'Candidatus Liberibacter asiaticus'. Plant Dis. 2015, 99, 320–324.
92. Zheng, Z.; Bao, M.; Wu, F.; Chen, J.; Deng, X. Predominance of single prophage carrying a CRISPR/cas system in "Candidatus Liberibacter asiaticus" strains in Southern China. PLoS ONE 2016, 11, e0146422.
93. Castro, M.S.; Fontes, W. Plant defense and antimicrobial peptides. Protein Pept. Lett. 2005, 12, 11–16.
94. Casteel, C.L.; Hansen, A.K.; Walling, L.L.; Paine, T.D. Manipulation of plant defense responses by the Tomato psyllid (Bactericercacockerelli) and its associated endosymbiont Candidatus Liberibacterpsyllaurous. PLoS ONE 2012, 7, e35191.
95. Li, J.; Pang, Z.; Trivedi, P.; Zhou, X.; Ying, X.; Jia, H.; Wang, N. "Candidatus Liberibacter asiaticus" encodes a functional salicylic acid (SA) hydroxylase that degrades SA to suppress plant

defenses. Mol. Plant-Microbe Interac. 2017, 30, 620–630.

96. Clark, K.; Franco, J.Y.; Schwizer, S.; Pang, Z.Q.; Hawara, E.; Thomas, W.H.; Pagliaccia, D.; Zeng, L.; Gurung, F.B.; Wang, P.; et al. An effector from the Huanglongbing-associated pathogen targets citrus proteases. Nat. Commun. 2018, 9, 1718.

97. Ying, X.; Wan, M.; Hu, L.; Zhang, J.; Li, H.; Dianqiu, L. Identification of the virulence factors of Candidatus Liberibacter asiaticus via heterologous expression in Nicotiana benthamiana using Tobacco mosaic virus. Int. J. Mol. Sci. 2019, 20, 5575.

Retrieved from https://encyclopedia.pub/entry/history/show/90365