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## Title

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Author Zhou, Changyong

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#### **Review Article**



### **Graft-transmissible citrus diseases in P. R. China – research developments**

C Zhou<sup>1\*</sup>

<sup>1</sup>National Citrus Engineering Research Centre, Southwest University, Beibei, Chongqing 400715, P.R.China.

\*Correspondence to: zhoucy@cric.cn

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#### Abstract

In the P.R. China, ten graft-transmissible pathogens have been identified infecting citrus, including *Candidatus* Liberibacter asiaticus, *Citrus tristeza virus* (CTV), Citrus tatter-leaf virus (CTLV), *Citrus exocortis viroid* (CEVd), *Citrus yellow vein clearing virus* (CYVCV), *Satsuma dwarf virus* (SDV), *Citrus vein enation virus* (CVED), *Citrus psorosis virus* (CPsV), Citrus cachexia viroid (CCaVd), and *Citrus chlorotic dwarf virus* (CCDV). Of these pathogens, the first five cause damage in field citrus trees, whereas the latter five were occasionally detected from the imported citrus materials or field trees. Research progress on HLB, CTV, CYVCV etc. within recent three years are briefly reviewed.

In the P.R. China, ten graft-transmissible pathogens have been identified infecting citrus, including Candidatus Liberibacter asiaticus, Citrus tristeza virus (CTV), Citrus tatter-leaf virus (CTLV), Citrus exocortis viroid (CEVd), Citrus yellow vein clearing virus (CYVCV), Satsuma dwarf virus (SDV), Citrus vein enation virus (CVED), Citrus psorosis virus (CPsV), Citrus cachexia viroid (CCaVd) and Citrus chlorotic dwarf virus (CCDV) (Fu et al. 2015; Huang et al. 2015; Lin et al. 2013; Lin et al. 2015; Shang et al. 2016; Song, Kurth, et al. 2015; Song, Li, et al. 2015; Wang, Chen, et al. 2015; Wang, Su, et al. 2015; Wang et al. 2013; Wu et al. 2014; Yi and Zhou 2014; Zheng et al. 2014; Zheng and Zhou 2013; Zhou et al. 2017; Zhou et al. 2013). Of these pathogens, the first five cause damage in field citrus trees, whereas the latter five were occasionally detected from the imported citrus materials or field trees.

Since the 1980s, virus-free citrus propagation schemes have been executed in Hunan, Sichuan, and Chongqing at the provincial level. Although some progress has been made, they were all suspended due to a number of reasons. Before the 1980s, HLB-free propagation schemes were also conducted in Guangdong, Guangxi, and Fujian, respectively, but also were suspended.

Due to the fact that over 100 modern virus-free citrus nurseries have been established in 13 provinces through the implementation of a virus-free scheme since 2001, the loss caused by graft-transmissible citrus pathogens, especially for those that are non-vector transmissible such as CTLV, SDV, and CEVd has dramatically decreased. As a result, few research activities have been addressed on those non-vector transmissible pathogens within the last three years, although some damage still can be observed due to inappropriate budwood distribution and top-grafting larger trees carrying CTLV and/or CEVd.

Since 2012, however, the Huanglongbing (HLB) problem has increased in severity in some of the fast growing citrus provinces such as Guangdong, Jiangxi, and Hunan. For example, over 30 million citrus trees have been removed due to HLB in south Jiangxi within the last three years. So, a series of research projects have focused on the control of HLB. Some progress has been made: 1) putative prophage particles were observed in sweet orange (Fu et al. 2015); 2) the whole genomes of three Chinese isolates of the HLB bacterium were sequenced; bio-information is accumulating quickly, focusing on the prophage genomic region with high genetic variation and recombination events; two HLB origin centres were proposed in the P.R. China (Lin et al. 2013; Lin et al. 2015; Wang et al. 2013; Wang, Su, et al. 2015; Wang, Chen, et al. 2015; Zheng et al. 2014; Zheng and Zhou 2013); 3) transgenic citrus lines against HLB are in field trials for evaluation; 4) a few effective combinations of pesticides have been selected to control citrus psyllids (Diaphorina citri); 5) natural thermotherapy of the citrus tree canopy by covering with PVC mulch showed somewhat efficacy to reduce the disease symptoms.

Among the above listed citrus virus pathogens, a few vector-transmissible viruses such as CTV and CYVCV are topics of research due to the difficulty of their control in the field. Because severe stem-pitting isolates of CTV are widely distributed in P.R.China, a few mild isolates with potential cross-protective capability were obtained from screening of thousands of field isolates that are being applied in field trials for efficacy evaluation. Also, progress is being made in understanding the proteinprotein interactions between CTV isolates and their sensitive hosts and vector [brown citrus aphids (Toxoptera citricida)] (Shang et al. 2016; Yi and Zhou 2014; Zhou et al. 2013). CYVCV is a newly discovered virus causing severe damage in the lemon industry in the last few years (Huang et al. 2015; Song et al. 2015; Zhou et al. 2017). The citrus whitefly (Dialeurodes citri) has been experimentally proved to be the vector of this virus (unpublished data). All viruses above mentioned have been sequenced, and been subjected to phylogenetic analysis. Furthermore, a few types of infectious viral vectors have been constructed. Although viroids are of less importance than other pathogens for the citrus industry, a few new variants such as Citrus viroid V and Citrus viroid I-LSS were detected and the distribution of the above pathogens has been monitored.

As a lot of attempts have been made for improving the diagnostic methods for these ten pathogens, and some that showed higher efficacy have been being widely applied for quick diagnosis.

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### References

- Fu SM, Hartung JS, Zhou CY, Su HN, Tan J, Li ZA. 2015. Ultrastructural changes and putative phage particles observed in sweet orange leaves infected with '*Candidatus* Liberibacter asiaticus'. Plant Dis. 99(3):320-324.
- Huang AJ, Song Z, Cao MJ, Chen HM, Li ZA, Zhou CY. 2015. The complete genome sequence of Citrus vein enation virus from China. J Integr Agr. 14(3):598-601.
- Lin H, Han CS, Liu BH, Lou BH, Bai XJ, Deng CL, Civerolo EL, Gupta G. 2013. Complete genome sequence of a Chinese strain of '*Candidatus* Liberibacter asiaticus'. Genome Announce. 1(2):e00184-13.
- Lin H, Pietersen G, Han C, Read DA, Lou BH, Gupta G, Civerolo EL. 2015. Complete genome sequence of *Candidatus* Liberibacter africanus', a bacterium associated with citrus huanglongbing. Genome Announce. 3(4):e00733-15.
- Shang F, Xiong Y, Xia WK, Wei DD, Wei D, Wang JJ. 2016. Identification, characterization and functional analysis of a chitin synthase gene in the brown citrus aphid, *Toxoptera citricida* (Hemiptera, Aphididae). Insect Mol Biol. DOI: 10.1111/imb.12228.
- Song Z, Kurth EG, Peremyslov VV, Zhou CY, Dolja VV. 2015. Molecular characterization of a Citrus yellow vein clearing virus strain from China. Arch Virol. 160:1811–1813.
- Song Z, Li ZA, Liu KH, Zhou CY. 2015. Complete genome sequence analysis of two Citrus tatter leaf virus (CTLV) isolates from China. J Integr Agr. 14(5):984-987.

- Wang XF, Chen JY, Tan J, Duan S, Deng XL, Chen JC, Zhou CY. 2015. High genetic variation and recombination events in the vicinity of nonautonomous transposable elements from '*Candidatus* Liberibacter asiaticus'. J Integr Agr. 14(10):2002-2010.
- Wang XF, Su HN, Huang L, Deng XL, Chen JC, Zhou CY, Li ZA. 2015. Identification of a novel 1033nucleotide deletion polymorphism in the prophage region of '*Candidatus* Liberibacter asiaticus': potential applications for bacterial epidemiology. J Phytopathol. 163:681-685.
- Wang XF, Tan J, Bai ZQ, Su HN, Deng XL, Li ZA, Zhou CY, Chen JC. 2013. Detection and characterization of miniature inverted-repeat transposable elements in '*Candidatus* Liberibacter asiaticus'. J Bacteriol. 195(17):3979-3986.
- Wu Q, Cao MJ, Su HN, Atta S, Yang FY, Wang XF, Zhou CY. 2014. Molecular characterization and phylogenetic analysis of Citrus viroid I-LSS variants from citrus in Pakistan and China reveals their possible geographic origin. Eur J Plant Pathol. 139(1):13-17.
- Yi L, Zhou CY. 2014. Phylogenetic analysis of *Citrus tristeza virus* isolates of wild type citrus in China. Journal of Integrative Agriculture. 13(12):2669-2677.
- Zheng Z, Deng X, Chen J. 2014. Whole-genome sequence of *'Candidatus* Liberibacter asiaticus' from Guangdong, China. Genome Announce. 2.e00273-14.
- Zheng ZZ, Zhao YH. 2013. Transcriptome comparison and gene coexpression network analysis provide a systems view of citrus response to '*Candidatus* Liberibacter asiaticus' infection. BMC Genomics. 14(27):<u>https://doi.org/10.1186/1471-2164-14-27</u>.
- Zhou Y, Chen HM, Cao MJ, Wang XF, Jin X, Liu KH, Zhou CY. 2017. Occurrence, distribution, and molecular characterization of *Citrus yellow vein clearing virus* in China. Plant Dis. 101:137-143.
- Zhou Y, Li ZA, Wang XF, Liu KH, Li TS, Zhou CY. 2013. Variations of pathogenicity and composition of two *Citrus tristeza virus* isolates induced by host passage. J Plant Pathol. 95(2):265-273.