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# Plant Pathology



An International Journal edited by  
the British Society for Plant Pathology  
**Senior Editor Matt Dickinson**

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# Plant Pathology

An international journal edited by the British Society for Plant Pathology

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## Detection of ‘*Candidatus Liberibacter asiaticus*’ in citrus by concurrent tissue print-based qPCR and immunoassay

S. M. Fu<sup>ab</sup>, H. W. Liu<sup>b</sup>, Q. H. Liu<sup>a</sup>, C. Y. Zhou<sup>a</sup> and J. S. Hartung<sup>b\*</sup>

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‘*Candidatus Liberibacter asiaticus*’ (CLAs) is associated with the most destructive disease of citrus, huanglongbing (HLB). The most widely used methods for detection of CLAs are PCR-based and require purification of DNA from plant samples. Elution of DNA from tissue prints made on nitrocellulose membranes followed by qPCR (TPE-qPCR) was compared to DNA extraction of plant tissue followed by PCR (X-PCR) by testing the same tissue samples. The former estimated a higher CLAs population in tissue prints than the latter (*t*-test; *P* = 0.009). All extracts prepared for TPE-qPCR throughout the experiment were also tested by conventional PCR and 80.8% were identified as positive. A similar set of stem and petiole tissue samples was tested by TPE-qPCR and immunoassay. Although the detection rate by TPE-qPCR was higher than by immunoassay, about 6% of tissue prints were positive by immunoassay but not by TPE-qPCR. Thus, a higher detection rate would be achieved by combining TPE-qPCR with immunoassay. Significant differences were observed in the performance of nitrocellulose membranes from different manufacturers in these assays. Immunotissue prints showed that the spatial distribution pattern of CLAs infection varied widely from one sample to another, but the patterns were highly correlated among serial sections from the same sample, suggesting that CLAs preferentially colonizes adjacent phloem cells in a vertical rather than horizontal direction.

**Keywords:** ‘*Candidatus Liberibacter asiaticus*’, citrus greening, huanglongbing, immunotissue printing, qPCR, tissue prints

### Introduction

Huanglongbing (HLB), also known as citrus greening, is the most destructive citrus disease. HLB was first found in Chaoshan, China in 1919 (Bové, 2006) and shortly thereafter was described in India (Nath & Husain, 1927). HLB is now widely distributed in more than 40 countries in Asia, Africa and the Americas (Gottwald *et al.*, 1989; Coletta-Filho *et al.*, 2004; Bové, 2006). Since HLB was reported in Florida in 2005 (Chung & Brlansky, 2005), production of sweet orange and grapefruit has been reduced by 80% or more and production of frozen orange-juice concentrate has been dramatically reduced. ‘*Candidatus Liberibacter asiaticus*’ (CLAs), a nonculturable member of the  $\alpha$ -proteobacteria, is one of three ‘*Ca. Liberibacter*’ species associated with HLB, but CLAs is the only globally important species.

Symptoms of HLB are variable and may be affected by citrus variety and environmental and seasonal effects. Symptoms of HLB that are commonly and easily observed include newly emerged shoots with upright and pale yellow leaves, malformed fruits with colour

inversion and aborted seeds (Bové, 2006) and root decline (Graham *et al.*, 2013; Johnson *et al.*, 2014). Collapse and blockage of phloem cells can also be observed microscopically (Folimonova & Achor, 2010). A distinct ‘blotchy mottle’ of mature leaves is often used for presumptive diagnosis of HLB (Bové, 2006).

A variety of methods have been developed for confirmatory diagnosis of HLB by detection of CLAs or by biological indexing. These include graft transmission assays (Garnier & Bové, 1983; Roistacher, 1991), DNA probes (Villeanoux *et al.*, 1992), microscopic examination (Garnier *et al.*, 1984; Folimonova & Achor, 2010), conventional polymerase chain reaction (PCR; Jagoueix *et al.*, 1996; Ding *et al.*, 2005), quantitative PCR (qPCR; Li *et al.*, 2006, 2008; Morgan *et al.*, 2012), loop-mediated isothermal amplification (LAMP; Okuda *et al.*, 2005) and immunoassays (Ding *et al.*, 2015; Pagliaccia *et al.*, 2017).

PCR-based methods are the most commonly used methods for detection of CLAs. PCR requires DNA extraction and, generally, purification with organic solvent-based protocols. CLAs is restricted to phloem cells, typically sampled from leaf midribs or bark, and, because these tissues are very difficult to grind to homogeneity for optimal recovery of CLAs, DNA preparation is time-consuming, costly and problematic; this severely limits the number of samples that can be processed. In addition, the distribution of CLAs within the tree is notoriously difficult to predict,

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and extensive sampling is required to have confidence in the results of the testing of a given tree (Tatineni *et al.*, 2008; Li *et al.*, 2009; Ding *et al.*, 2015).

In contrast, immunotissue printing is a simple and inexpensive technique and also preserves the cellular locations of macromolecules, such as proteins, enzymes, soluble metabolites and nucleic acids (Cassab & Varner, 1987; Taylor *et al.*, 1993). The method is widely used in both field and laboratory for the detection of other important phloem-limited pathogens of citrus such as citrus tristeza virus (CTV; Garnsey *et al.*, 1993) and *Spiroplasma citri* (Shi *et al.*, 2014). Immunotissue printing has been developed to detect CLAs with an anti-OmpA polyclonal antibody (Ding *et al.*, 2015, 2016). Others have demonstrated the amplification by PCR of plum pox virus RNA from nitrocellulose membranes (Olmos *et al.*, 1996; Bertolini *et al.*, 2014). In addition, elution of DNA captured on nitrocellulose membranes in glycine buffer was shown to be useful for the detection of CLAs by PCR (Bertolini *et al.*, 2014).

In this study, immuno- and PCR-based methods to detect CLAs on nitrocellulose membranes were compared. Tissue prints were processed for immunodetection as described previously in published protocols, or used for sample preparation by simple elution into glycine buffer without tissue grinding or other DNA purification (Bertolini *et al.*, 2014). The eluted DNA was subjected to both conventional PCR and probe hydrolysis-based qPCR. The results of these tests were also compared with PCR and qPCR tests on the same plant samples after conventional tissue homogenization and DNA purification (Li *et al.*, 2006). The results of tissue print elution (TPE)-qPCR were compared with those of immunotissue prints prepared simultaneously from the same samples. The effect of the source of nitrocellulose membranes on the results and the distribution pattern of CLAs phloem cells of stem and leaf petioles were also investigated.

## Materials and methods

### Plant materials and pathogens

Plants used throughout the experiments were from either the Exotic Pathogens of Citrus Collection (EPCC) at the USDA Beltsville Agricultural Research Center (BARC) in Beltsville, USA or from the Citrus Research Institute in Chongqing, China. In the USA, trees infected with CLAs were maintained and propagated by bud inoculation of sweet orange seedlings (*Citrus sinensis*) as described previously (Li *et al.*, 2009). In China, trees infected with CLAs were propagated by bud inoculation of sweet orange cv. Madame Vinous seedlings and maintained as previously described (Fu *et al.*, 2015).

Field-grown plants were also used, including mandarin (*Citrus reticulata* 'Bing-tang') and sweet orange cv. Navel from groves in Hunan, Guangxi and Sichuan, China.

### Sample preparation for TPE-qPCR and X-qPCR

Tissue printing was performed based on a published protocol (Ding *et al.*, 2015). Plants from the greenhouse or field were

tested by conventional PCR after DNA extraction (Jagoueix *et al.*, 1996) and confirmed to be infected by CLAs; control plants from the greenhouse were also confirmed to be healthy by the same method. For each tissue print, transverse sections, approximately 0.5 mm thick, of petioles or stems were cut and the freshly cut surfaces were pressed onto nitrocellulose membranes (Whatman, 0.45 µm pore size; cat. no. 88018) to give five partially overlapping prints, after which the cut plant tissue disks (*c.* 100 mg) were collected (Fig. 1a,b). The membranes were air dried for 10 min at room temperature and the five partially overlapping prints were cut into pieces and soaked in 20 µL glycine buffer (0.1 M glycine, 0.05 M NaCl, 1 mM EDTA). The five tissue disks collected were pooled for DNA extraction with the DNeasy kit (QIAGEN) and eluted with 20 µL TE buffer (Fig. 1c) for testing by qPCR (X-qPCR) following the published protocol, using a 16S rDNA-based primer probe set (Li *et al.*, 2006). Extracts used to compare TPE-qPCR and X-qPCR were assayed on the same 96-well plates.

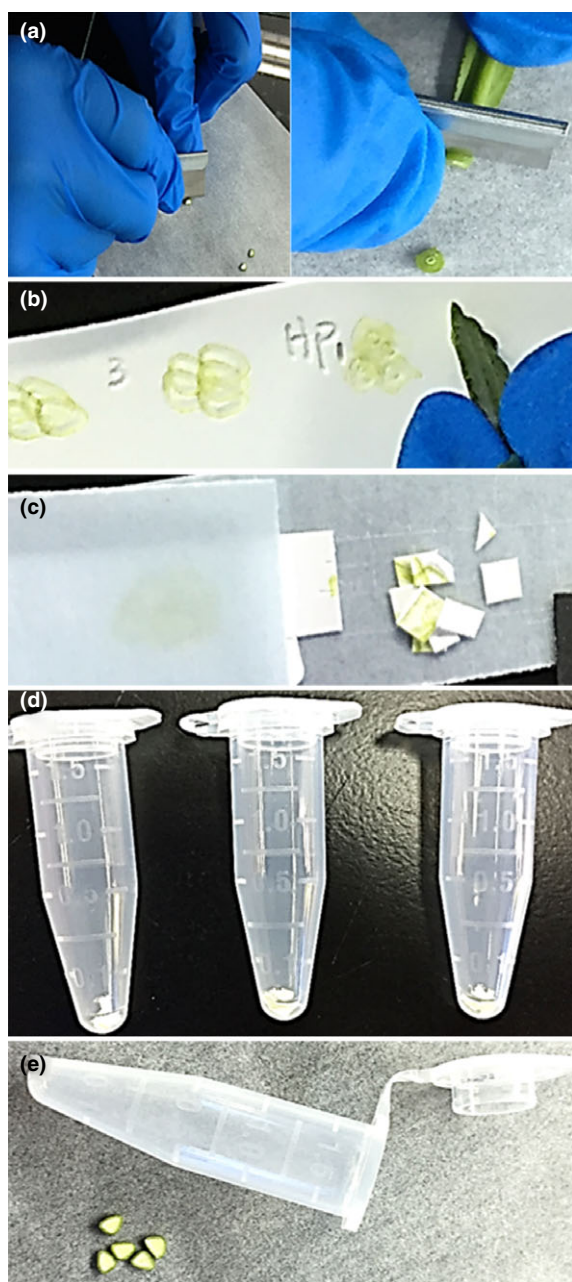
To determine the sensitivity of TPE-qPCR to detect a CLAs-infected sample among a large number of pooled samples, tissue prints prepared from trees known to be positive for CLAs by qPCR were mixed with tissue prints prepared from healthy trees in ratios of 5:0, 4:1, 2:3 and 1:4. Student's *t*-test with unequal variance was used to compare the C<sub>q</sub> values after qPCR. Chi-square tests were applied to compare the proportion of samples declared positive for CLAs using a cut-off for the 16S rDNA qPCR of quantification cycle (C<sub>q</sub>) <38.0. Likewise, a cut-off of C<sub>q</sub> <38.0 for the positive internal control of the mitochondrial cytochrome oxidase (COX) gene was used to confirm the presence of plant DNA in the extracts throughout. Statistical analyses were carried out with SPSS v. 16.0.

### Sample preparation for TPE-qPCR with membranes from different manufacturers

A test was conducted with three different brands of nitrocellulose membranes to determine whether they were equally suitable for TPE-qPCR. Field-grown plants were identified as CLAs-positive or -negative by conventional PCR after extraction of DNA (Jagoueix *et al.*, 1996) and used to prepare tissue prints using stems and leaf petioles. Fifteen serial sections were prepared, and sequential tissue prints were made on nitrocellulose membranes obtained from three suppliers, manufacturers X, Y and Whatman. Each tissue print assayed was made from five serial sections, pressed alternately onto each of the three membranes (Fig. 1). DNA was eluted directly from the tissue prints on the three different nitrocellulose membranes with 20 µL glycine buffer (Bertolini *et al.*, 2014; Fig. 1d,e). qPCR was performed according to Li *et al.* (2006) using 3 µL of template from each sample. A set of 32 samples eluted from each of the three membranes was run on each 96-well plate. qPCR was performed on the eluted extracts in three plates in all, making a total of 96 samples tested for each membrane, of which 86 were from trees known to be positive and 10 from trees known to be negative. A one-way ANOVA analysis was applied for qPCR results from both the 16S rDNA and COX genes with SPSS v. 16.0.

### Preparation of TPE-qPCR and immunoassay

In order to directly compare TPE-qPCR and tissue print immunoassay for detection of CLAs, samples taken from greenhouse and field-grown trees were identified as CLAs positive or CLAs negative in advance by conventional PCR with primers OI1/OIc2 (Jagoueix *et al.*, 1996). Tissue prints, consisting of



**Figure 1** Preparation of samples for tissue print elution (TPE)-qPCR and DNA extraction-qPCR (DNA X-qPCR). (a) Either stem (left) or petiole (right) can be chosen for tissue prints. The freshly cut end of the tissue is pressed to the nitrocellulose membrane and held for 5 s. After each imprint is made, a fresh surface is exposed by removing a 0.5 mm slice. Tissue sections are saved. (b) Five serial imprints are overlapped to create one test sample. (c) The membrane with the tissue print samples is cut and placed in a 1.5 mL centrifuge tube, to which 20  $\mu$ L glycine buffer (0.1 M glycine, 0.05 M NaCl, 1 mM EDTA; pH 9) is added. (d) Tubes are incubated at room temperature for 30 min or at 4 °C overnight; 3  $\mu$ L of eluate is used for qPCR testing. (e) The five tissue sections are collected in a tube and total DNA is extracted with a QIAGEN DNeasy kit. DNA is eluted in 20  $\mu$ L TE and 3  $\mu$ L is used per qPCR.

one to five sections from known CLas-positive or from CLas-negative field trees and healthy greenhouse trees, were prepared as described above, but alternate sections were pressed onto two different Whatman membranes to make matched tissue imprints (Fig. S1). One set of prints was eluted into 20  $\mu$ L glycine buffer for TPE-qPCR (Li *et al.*, 2006) and the other was used for immunoassay (Ding *et al.*, 2015).

### Detection of CLas by conventional PCR from samples eluted from tissue prints

All samples prepared for TPE-qPCR throughout the experiments were also tested by conventional PCR (Jagoueix *et al.*, 1996) as follows: reaction mixes (12  $\mu$ L) were preheated at 95 °C for 3 min; followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 64 °C for 35 s and extension at 72 °C for 80 s; with a final extension at 72 °C for 10 min. Amplification products were evaluated by electrophoresis on 1.5% agarose gels and stained with ethidium bromide.

## Results

### TPE-qPCR and X-qPCR

When the data from the four sets of tissue prints (taken from diseased and healthy samples in ratios of 5:0, 4:1, 2:3 and 1:4) were pooled, the mean C<sub>q</sub> of 16S rDNA was  $30.8 \pm 4.4$  ( $n = 186$  positive samples) for TPE-qPCR and  $31.5 \pm 6.4$  ( $n = 191$  positive samples) for X-qPCR ( $P = 0.009$ ; Table 1; Data S1). The mean C<sub>q</sub> of the COX assay was  $22.2 \pm 2.2$  for TPE-qPCR and  $24.1 \pm 6.4$  for X-qPCR ( $P = 0.000$ ; Table 1; Data S1). Thus, the means of both 16S rDNA (CLas) and COX (plant mitochondrial control) assays were significantly different and the TPE-qPCR estimated higher populations of CLas in the samples than the X-qPCR tests. This is probably because the TPE-qPCR directly detects CLas DNA on the cut surface of the sample, whereas a portion of the CLas DNA to be tested by X-qPCR from corresponding tissues is diluted and not recovered during the extraction process. However, the magnitude of the difference was not sufficient to change significantly the proportion of tests declared to be positive (76–77% for both assays;  $P = 0.651$ ; Table 1; Data S2).

### Comparison of different membranes for use in TPE-qPCR

The detection rates of CLas from matched samples were 20.9%, 19.8% and 81.4% for membranes manufactured by companies X, Y and Whatman, respectively (Table 2). The  $P$ -values of one-way ANOVA tests were 1.000, 0.056 and 0.001 between manufacturers X and Y, Whatman and manufacturer Y, and between Whatman and manufacturer X for the 16S rDNA gene (Data S3 & Data S4). Thus, in the tests presented here, the Whatman membranes produced better results than comparable membranes from manufacturers X and Y for TPE-qPCR. All other data in this report were taken from Whatman membranes.

**Table 1** Comparison of TPE-qPCR and X-qPCR for detection of '*Candidatus Liberibacter asiaticus*' (CLas).

No. prints	TPE-qPCR <sup>a</sup>				X-qPCR <sup>b</sup>			
	Cq <sup>c</sup>		CLas positive		Cq		CLas positive	
	16S rDNA	COX	No./tested <sup>d</sup>	%	16S rDNA	COX	No./tested	%
5D + 0H <sup>e</sup>	30.9 ± 5.2	22.6 ± 3.4	88/118	74.6	30.7 ± 8.7	23.8 ± 9.6	81/118	68.6
4D + 1H	29.5 ± 0.9	21.8 ± 0.4	35/35	100.0	30.7 ± 12.3	22.7 ± 3.5	17/35	48.6
2D + 3H	30.8 ± 4.4	21.5 ± 0.3	47/47	100.0	32.1 ± 2.2	25.6 ± 1.6	47/47	100.0
1D + 4H	33.0 ± 0.2	22.4 ± 1.3	16/45	35.6	32.5 ± 1.9	24.2 ± 1.8	46/46	100.0
Combined	30.8 ± 4.4	22.2 ± 2.2	186/245	75.6	31.5 ± 6.4	24.1 ± 6.4	191/246	77.6

<sup>a</sup>TPE-qPCR, tissue prints on nitrocellulose membrane were eluted into glycine buffer and used for qPCR.

<sup>b</sup>X-qPCR, DNA was extracted from tissue pieces used to make tissue prints with a QIAGEN kit and used for qPCR.

<sup>c</sup>Cq, quantification cycle.

<sup>d</sup>The number of samples declared CLas positive/the total number of samples tested. Statistical analyses of the data are presented in Data S1 and Data S2.

<sup>e</sup>D, the number of tissue prints tested from diseased samples; H, the number of tissue prints tested from healthy samples.

### Comparison of TPE-qPCR and TPE-PCR

Five datasets with 916 tests in total were compiled based on both qPCR and conventional PCR after DNA was eluted from tissue prints. Each test consisted of one to five tissue prints. Among these, 82.6% and 80.8% of the tests detected CLas by qPCR or PCR, respectively, and 77.4% of tests resulted in the detection of CLas by both (Table 3). The results also showed that there was neither

gain nor loss of sensitivity from pooling individual tissue prints prior to elution of DNA (Table 3).

### Comparison of TPE-qPCR and immunoassay

Citrus trees previously identified as CLas positive by X-PCR were sampled to prepare tissue prints for both TPE-qPCR and immunodetection with anti-OmpA polyclonal antibody. Among 786 tests, 81.2% and 52.9% were declared CLas positive by TPE-qPCR and immuno-detection, respectively (Table 4). Among the 416 tissue samples declared positive by immunodetection, 48 samples were identified as positive by immunodetection but not by TPE-qPCR on the prints made from matched sections (Table 4).

### Visualization of CLas in plant samples

As expected following immunodetection, a dark purple colour was observed in phloem cells of tissue prints prepared from samples collected from trees that had tested positive for CLas by qPCR, but not in tissue prints prepared from healthy plants. CLas showed uneven distribution within the vascular rings observed in prints from individual sections but the distribution patterns were very consistent among tissue prints from serial sections of single stem samples (Fig. 2). The leaves on this stem

**Table 2** Comparison of different brands of nitrocellulose membranes for use in TPE-qPCR.

Brand	Average Cq <sup>a</sup>		Detection rate <sup>b</sup>	
	16S rRNA	COX	No./tested	%
X	33.6 ± 3.1	31.0 ± 3.1	18/86	20.9
Y	32.5 ± 3.2	30.7 ± 3.4	17/86	19.8
Whatman	30.2 ± 3.7	22.0 ± 1.5	70/86	81.4

<sup>a</sup>Cq, quantification cycle.

<sup>b</sup>The number of samples testing positive/the total number of samples tested. Statistical analyses are presented in Data S3 and Data S4.

**Table 3** Detection of '*Candidatus Liberibacter asiaticus*' (CLas) by tissue print-based qPCR and PCR.

No. prints <sup>a</sup>	qPCR		PCR		qPCR & PCR	
	No./tested <sup>b</sup>	%	No./tested	%	No./tested	%
1P	134/160	83.8	134/160	83.8	130/160	81.3
2P	134/173	77.5	140/173	80.9	126/173	72.8
3P	161/174	92.5	156/174	89.7	155/174	89.1
4P	113/141	80.1	110/141	78.0	107/141	75.9
5P	215/268	80.2	200/268	74.6	191/268	71.3
Combined	757/916	82.6	740/916	80.8	709/916	77.4

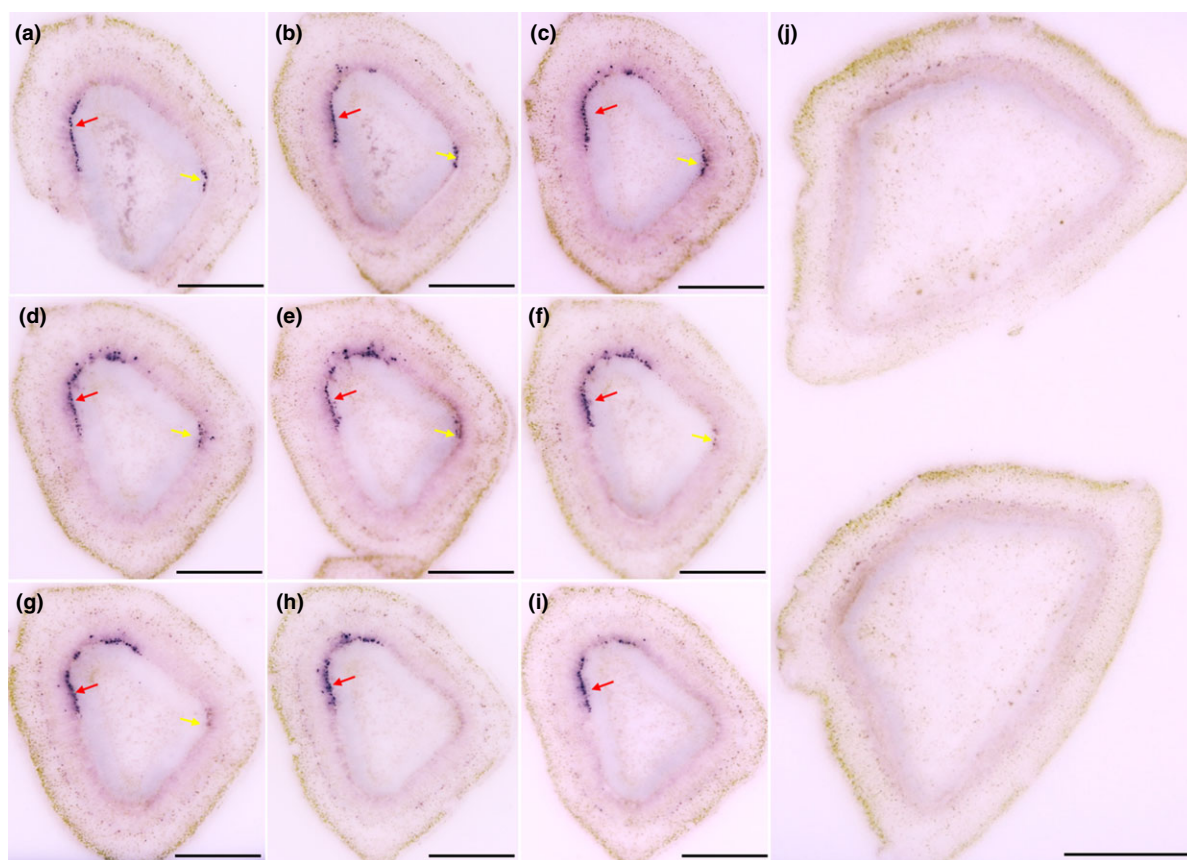
<sup>a</sup>Number of tissue prints pooled prior to elution of DNA.

<sup>b</sup>The number of samples declared CLas positive/the total number of tested samples.

**Table 4** Detection of '*Candidatus Liberibacter asiaticus*' by tissue print elution (TPE)-qPCR and immunoassay with anti-OmpA antibody.

Method	Detection rate	
	No./tested	%
TPE-qPCR	638/786	81.2
OmpA	416/786	52.9
TPE-qPCR & OmpA	368/786	46.8
ΔN <sup>a</sup>	48/786	6.1

<sup>a</sup>ΔN, samples declared positive by immunoassay with anti-OmpA polyclonal antibody but not by TPE-qPCR.



**Figure 2** Uneven distribution pattern of '*Candidatus Liberibacter asiaticus*' (CLas) in phloem sieve cells of consecutive stem tissue prints, visualized by immunotissue printing using the anti-OmpA antibody. (a–i) Consecutive stem tissue prints of diseased sweet orange from the greenhouse, without symptoms; (j), stem tissue prints of healthy plant. Red and yellow arrows point to distinct CLas infection foci that were maintained in consecutive serial tissue prints; bars = 1 mm.

did not show any symptoms of HLB, demonstrating the difficulty of diagnosis of HLB and the potential power of immunotissue printing. Similar patterns were also observed in the tissue prints from serial sections of petioles (Fig. 3). DNA eluted from the matched prints made from the same tissues was also positive by TPE-qPCR.

## Discussion

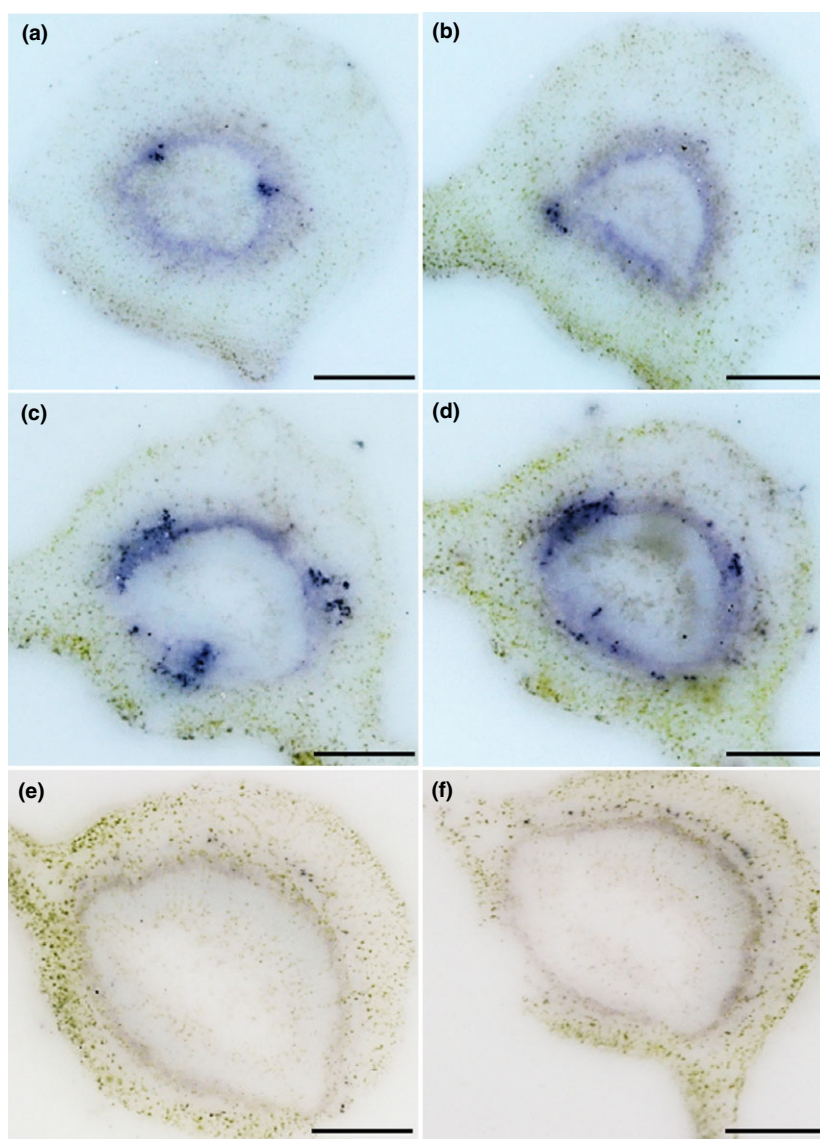
For detection of a high-consequence pathogen like CLas, at least two independent methods should be used to provide mutually confirmatory results. Tissue prints are therefore ideal, because they can be assayed for CLas by both immuno- (Ding *et al.*, 2015, 2016) and PCR-based methods (Bertolini *et al.*, 2014).

In preliminary experiments, positive tissue prints were identified by immunoassay and then the same prints were tested by TPE-qPCR (data not shown). The TPE-qPCR tests were negative, presumably because the CLas DNA was eluted from the nitrocellulose membrane during the development of the immunotissue prints, and subsequently was not available for TPE-qPCR. Based on this observation it was decided to test alternate

tissue prints from samples by either immuno- or TPE-qPCR methods.

In the course of these experiments, the supplier of nitrocellulose membranes was changed and it was noticed that results were not comparable. This prompted a systematic comparison of different suppliers of membranes, as described. In this investigation, the Whatman nitrocellulose membrane provided better and more consistent results in both TPE-qPCR and immunoassays, indicating all nitrocellulose membranes may not be equivalent for CLas detection. For this reason, Whatman nitrocellulose membranes were used throughout this study.

The uneven distribution of CLas in citrus plants has been reported in many studies by symptom observation (Bové, 2006) or PCR-based detection (Tatineni *et al.*, 2008; Li *et al.*, 2009). Here, immunodetection with anti-Omp-A antibody has demonstrated that the radially nonuniform distribution of CLas within a vascular ring in cross-section is maintained vertically over substantial distances. CLas showed consistent radial distribution patterns within two to nine consecutive tissue prints with 0.5 mm spacing. In other words, CLas distribution



**Figure 3** Uneven distribution pattern of '*Candidatus Liberibacter asiaticus*' (CLAs) in phloem sieve cells of consecutive tissue prints of petiole, visualized by immunotissue printing using the anti-OmpA antibody. (a–d) Consecutive leaf petiole tissue prints of diseased samples of sweet orange from the greenhouse, without symptoms; (e, f), tissue prints from healthy plants; black bars = 0.5 mm.

among serial sections is correlated within 1–4.5 mm. This enables confirmatory testing by independent methods on consecutive serial sections of samples. The size of CLAs is approximately  $0.2 \times 2 \mu\text{m}$  but varies substantially (Bové, 2006). The average diameter of phloem sieve pores is approximately  $0.411 \mu\text{m}$  in soybean and  $5 \mu\text{m}$  in cucurbits (Mullendore *et al.*, 2010), while the diameter of plasmodesmata is much smaller, usually less than  $0.1 \mu\text{m}$ . Thus, CLAs can move with relative ease with phloem flow in the vertical direction through sieve pores but with much more difficulty through plasmodesmata in the horizontal direction. This would explain why CLAs tends to maintain a presence in a vertical column of cells rather than spreading radially. The concentration of CLAs changes along the phloem section, as evidenced by a stronger or weaker colour signal during immunodetection. The direct visualization of the uneven distribution patterns of CLAs in phloem tissues provides

compelling evidence that sampling of trees for PCR-based testing will always be problematic, and the uneven distribution pattern of CLAs in different tissues will contribute to false negative results by PCR-based methods, particularly for large trees. Therefore, extensive sampling is minimally required for each tree for field HLB screening. This is very difficult to implement at an adequate level using conventional methods due to expensive and laborious tissue extraction and DNA purification procedures.

TPE-qPCR offers several advantages for detection of CLAs. Tissue prints can be prepared with fresh tissue in the field with only razor blades, gloves, nitrocellulose membranes and a cutting surface. This is a particularly good option to preserve DNA and proteins for shipment of samples between distant locations. The elution of DNA directly from nitrocellulose membranes in simple glycine buffer eliminates the need for, and expense of,

DNA purification kits. TPE-qPCR is thus a simple and inexpensive technique and can easily be scaled to large numbers of samples of any plant tissue, including peduncle, petioles, leaf midrib and stem. Peduncle is the best tissue to sample for *S. citri* (Wang *et al.*, 2015) and also produced excellent results by immunotissue printing (Ding *et al.*, 2015) and TPE-qPCR (data not shown), suggesting that peduncles are a good tissue for HLB screening if available. Tissue prints from one to five serial sections combined with probe hydrolysis qPCR works well to determine whether a given sample is positive or negative for CLAs, with a large majority identified by conventional PCR as well. As with immunotissue printing, CLAs can be detected from a single print by TPE-qPCR. This successful detection of CLAs on nitrocellulose membranes by either immuno- or PCR-based methods may be because the concentration of CLAs in single phloem cells is higher than an average concentration sampled by DNA extraction of a larger volume of tissue (some of which may be uninfected). qPCR assays in the probe hydrolysis format are less susceptible to the nonspecific amplification seen in the SYBR Green format. In the present study, the cut-off C<sub>q</sub> value was conservatively set at 38.0. The results showed that the proportion of samples declared positive for CLAs with the rapid and simple TPE-qPCR was not significantly different from the much more laborious and expensive X-qPCR. Although the overall rate of detection was not different, the TPE-qPCR estimated higher CLAs populations than X-qPCR for equivalent samples in the study; this is in contrast to the results of Bertolini *et al.* (2014). In addition, the proportion of samples from symptomless leaves that tested positive for CLAs in the present study was higher than found by Bertolini *et al.* (2014). Both TPE-qPCR and immunotissue printing detected CLAs in symptomless tissues, although the proportion was lower than from leaves with symptoms.

The simplicity of TPE-qPCR also greatly reduces the cost of the assay, the possibility of cross-contamination among samples, and reduces the environmental impact of testing by eliminating hazardous laboratory waste. Of particular interest, sampling by TPE-qPCR can be effectively and rapidly scaled and applied to extensive HLB screening or to exhaustive sampling of individual suspect trees. This could be especially useful if an HLB-suspect tree is identified in an area previously free of the disease and pathogen. The tissue sections cut to expose fresh tissue surfaces for TPE-qPCR can be saved for later DNA extraction for confirmatory testing, limiting laborious extraction to samples with a very high likelihood of being positive.

Although the overall detection rate for CLAs by TPE-qPCR was higher than by immunoassay on the same sample set, the results were highly correlated. The immunoassay requires an intact CLAs membrane to properly display the OmpA antigen. In contrast, PCR-based methods detect DNA, which is present in HLB-affected trees in both living and dead cells (Hu *et al.*, 2014). This effect may contribute to a higher detection rate for

TPE-qPCR than for the immunoassay in these experiments. However, there were about 6% of samples declared positive by immunodetection but not TPE-qPCR, which was probably due to the sporadic distribution of CLAs and the fact that the immunoassay performs very well in symptomless tissues (Ding *et al.*, 2017). The results of this study indicate that greater success in detection of CLAs will be achieved by using PCR-based and serological methods together.

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## Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's web-site.

**Figure S1.** Preparation of samples for tissue print elution (TPE)-qPCR and immunoassay. (a) Either stem (left) or petiole (right) can be chosen for tissue prints. The freshly cut end of the tissue is pressed to the nitrocellulose membrane and held for 5 s. After each imprint is made, a fresh surface is exposed by removing a 0.5 mm slice. Tissue sections are saved. (b) Ten tissue prints are made alternately onto two membranes. On one membrane, the prints are overlapping and used for TPE-qPCR and on the other membrane, the prints are made separately for immunoassay. (c) Tissue prints for TPE-qPCR are cut and placed in a 1.5 mL centrifuge tube and 20 µL glycine buffer (0.1 M glycine, 0.05 M NaCl, 1 mM EDTA; pH 9) is added. (d) Separate prints on the other membrane are processed with anti-OmpA antibody. (e) The 10 tissue sections are collected in a tube and total DNA is extracted with a QIAGEN DNeasy kit. DNA is eluted in 20 µL TE and 3 µL is used per qPCR.

**Data S1.** Statistical analysis of qPCR assay for ‘*Candidatus Liberibacter asiaticus*’ and plant mitochondrial DNA.

**Data S2.** Chi-square analysis of results of TPE-qPCR and X-qPCR for the detection of ‘*Candidatus Liberibacter asiaticus*’ in infected citrus.

**Data S3.** ANOVA of results of the comparison of different brands of nitrocellulose membranes for the detection of ‘*Candidatus Liberibacter asiaticus*’ by TPE-qPCR in infected citrus.

**Data S4.** ANOVA of results of the comparison of different brands of nitrocellulose membranes for the detection of plant cytochrome oxidase (COX1) DNA by TPE-qPCR in infected citrus.