

Fig. S1

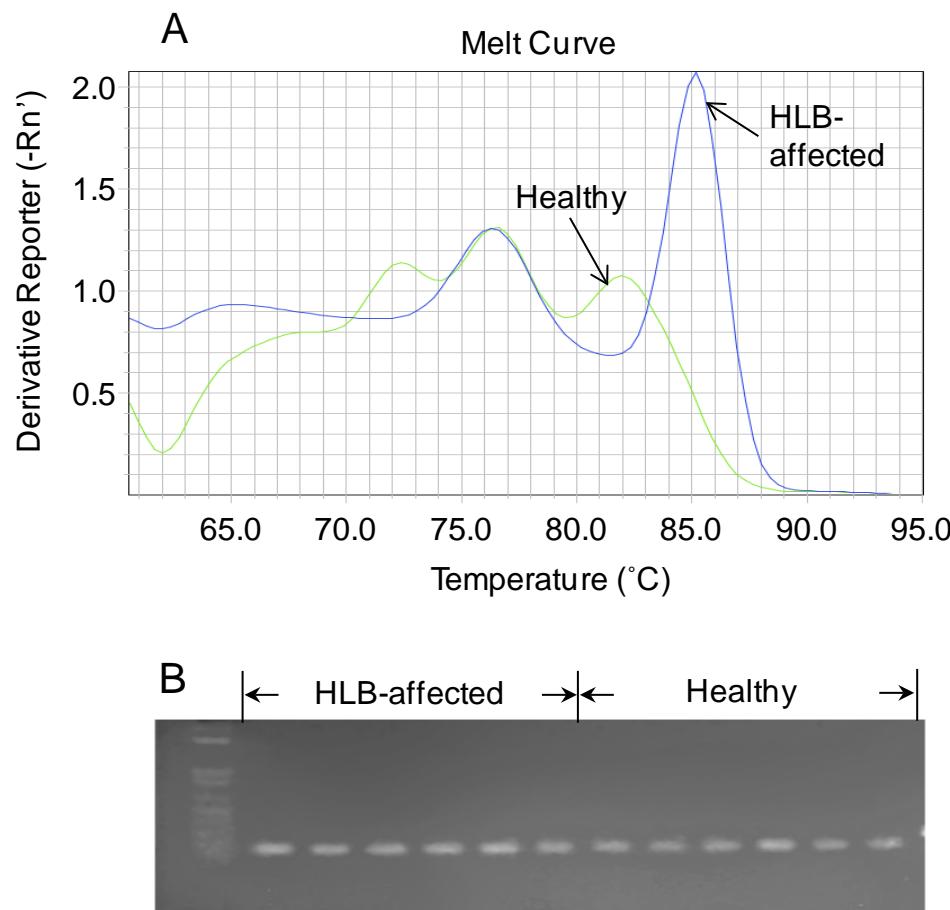


Fig. S1 Melt curves for PCR products from healthy (CLas negative) and HLB-affected (CLas positive) orange juice by a set of universal fungal primers (A); and 1.5% agarose gel image of the PCR products (B). (CLas=*Candidatus Liberibacter asiaticus*, HLB=huanglongbing)

Fig. S2

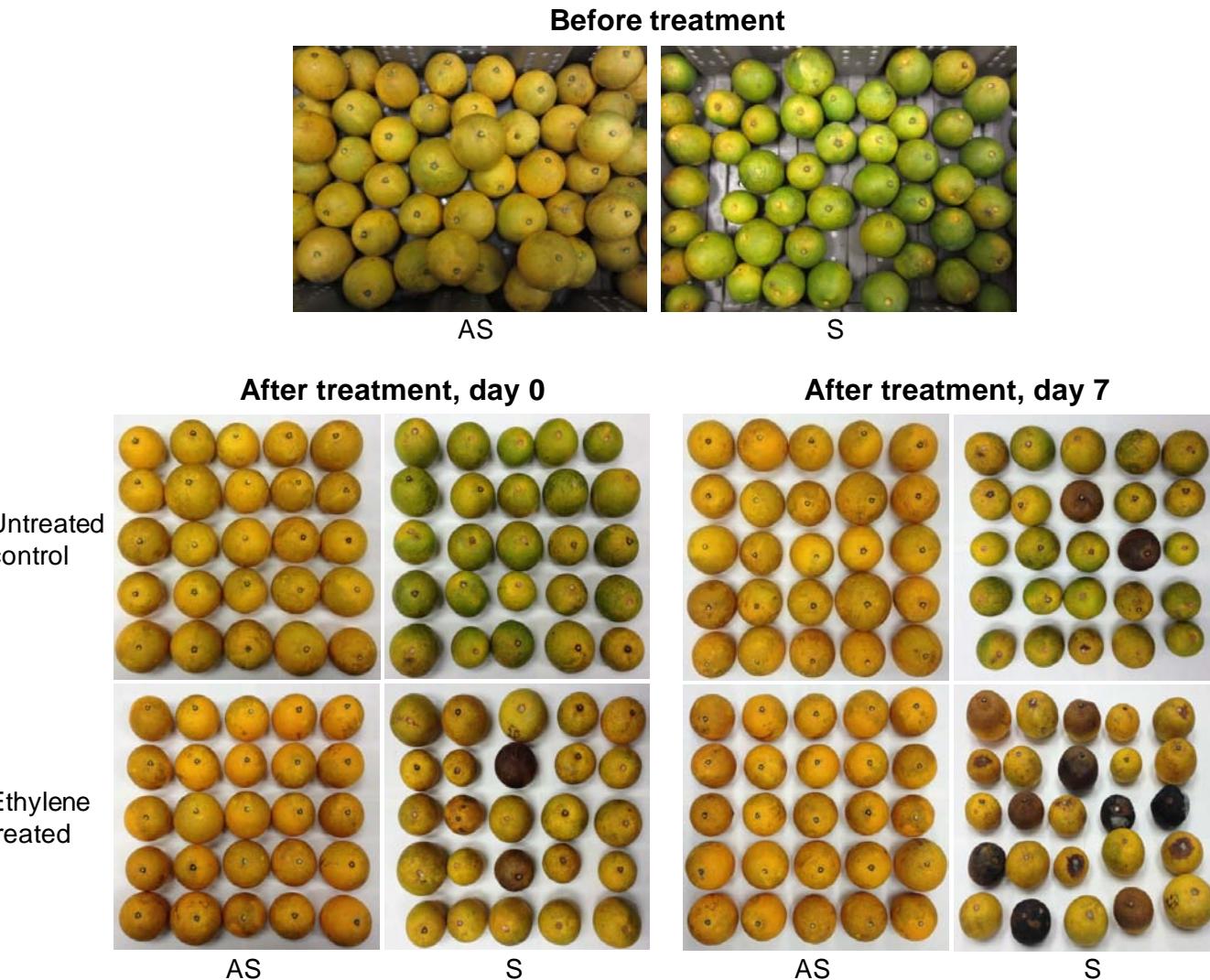


Fig.S2 One of the batches of Hamlin fruit used in the decay assay (AS=asymptomatic, S=huanglongbing-symptomatic)

Fig.S3

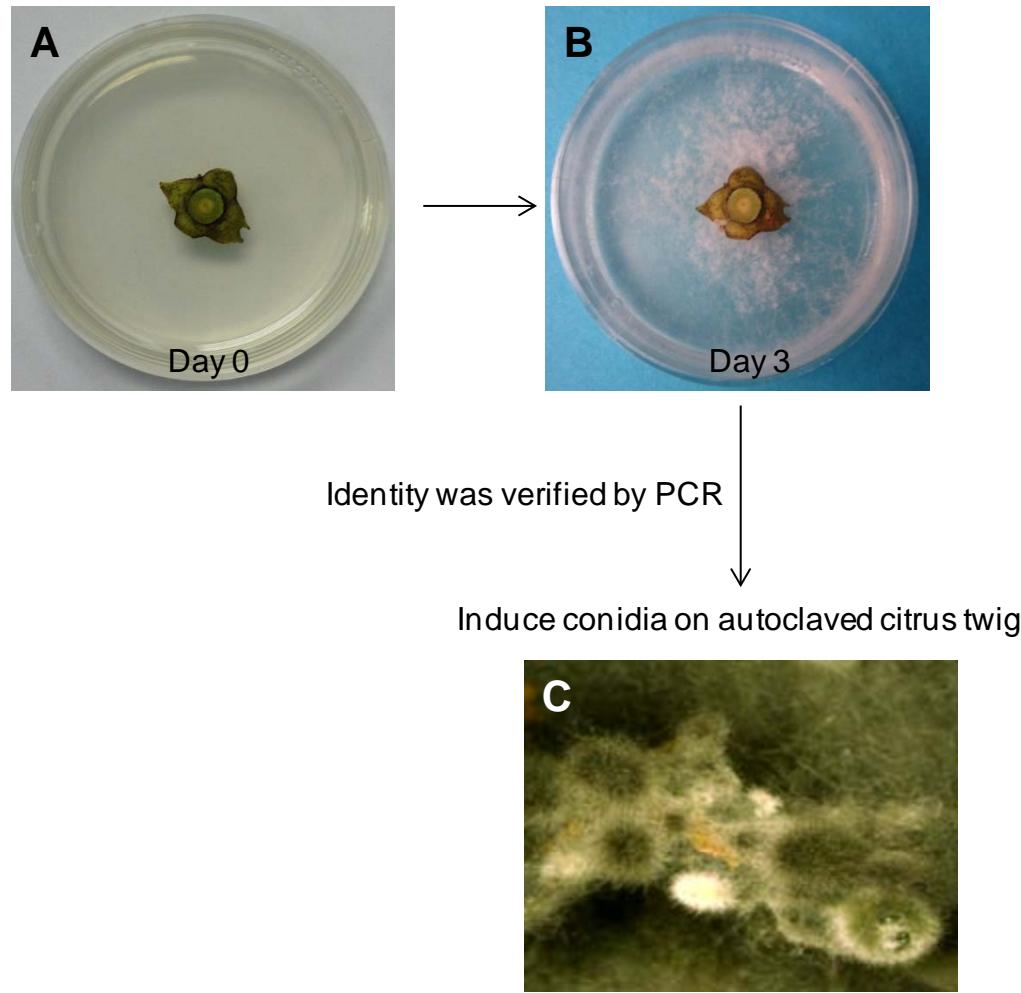


Fig.S3. Isolation of *Diplodia* from plant calyx abscission zone (AZ-C) on potato-dextrose agar media (A and B); Sub-culture of *Diplodia* on autoclaved citrus twigs (C).

Fig. S4



Fig. S4. Pre-harvest stem-end rot occurred on fruit attached to a huanglongbing-symptomatic tree.

Table S1 Sequences amplified from 6 HLB (CLas positive) and 6 healthy (CLas negative) juice samples. The highlighted 4 samples are those from which the *Diplodia* was identified with 100% identity; the DNA sequences highlighted in red are the universal fungal primer sequences (CLas = *Candidatus Liberibacter asiaticus*).

OJ	sequence cloned	top match in gene bank	identity	accession #	priming miss match (nt)
HLB-1	<b>CTCGTAGTTGAAACCTTGGGCCTGGCTGGCCGGTCTGCCCTCACCGCATGTAC</b> TGGTTCGGCCGGTCTTCCTCCTGGGGATCCGATGCCCTCACTGGGT GTGTTGGGAACCAGGACTTTACTTGAAAAAATT <b>AGAGTGTCAAAGCAG</b> <b>GC</b>	<i>Botryosphaeria rhodina</i> , <i>Lasiodiplodia theobromae</i> 18S rRNA gene	100%	U42476.1, EU673195.1, KC442314.1, etc.	0
HLB-2	<b>CTCGTAGTTGAAACCTTGGGCCTGGCTGGCCGGTCTGCCCTCACCGCATGTAC</b> TGGTTCGGCCGGTCTTCCTCCTGGGGATCCGATGCCCTCACTGGGT GTGTTGGGAACCAGGACTTTACTTGAAAAAATT <b>AGAGTGTCAAAGCAG</b> <b>GC</b>	<i>Botryosphaeria rhodina</i> , <i>Lasiodiplodia theobromae</i> 18S rRNA gene	100%	U42476.1, EU673195.1, KC442314.1, etc.	0
HLB-3	<b>CTCGTAGTTGAAACCTTGGGCCTGGCTGGCCGGTCTGCCCTCACCGCATGTAC</b> TGGTTCGGCCGGTCTTCCTCCTGGGGATCCGATGCCCTCACTGGGT GTGTTGGGAACCAGGACTTTACTTGAAAAAATT <b>AGAGTGTCAAAGCAG</b> <b>GC</b>	<i>Botryosphaeria rhodina</i> , <i>Lasiodiplodia theobromae</i> 18S rRNA gene	100%	U42476.1, EU673195.1, KC442314.1, etc.	0
HLB-4	<b>CTCGTAGTTGAAACCTTGGGACGAGGGTCCGGTCCGCTTTTGCAGTACT</b> GGCCACTCTTCCCCACGGACCGCTCTCTGGAGTGGCCGAATTACTT TGAGTAAATG <b>AGAGTGTCAAAGCAGC</b>	<i>Clavispora reshetoviae?</i> (a soil yeast) 18S rRNA gene	79%	FN433522.1	0
HLB-5	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGTCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Citrus maxima</i> 18S rRNA gene	99%	FJ866629.1	2
HLB-6	<b>CTCGTAGTTGAAACCTTGGGCCTGGCTGGCCGGTCTGCCCTCACCGCATGTAC</b> TGGTTGGCCGGTCTTCCTCCTGGGGATCCGATGCCCTCACTGGGT GTGTTGGGAACCAGGACTTTACTTGAAAAAATT <b>AGAGTGTCAAAGCAG</b> <b>GC</b>	<i>Botryosphaeria rhodina</i> , <i>Lasiodiplodia theobromae</i> 18S rRNA gene	100%	U42476.1, EU673195.1, KC442314.1, etc.	0
Healthy-1	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGTCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Citrus maxima</i> 18S rRNA gene	99%	FJ866629.1	2
Healthy-2	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGTCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Citrus maxima</i> 18S rRNA gene	99%	FJ866629.1	2
Healthy-3	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGTCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Citrus maxima</i> 18S rRNA gene	99%	FJ866629.1	2
Healthy-4	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGTCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Citrus maxima</i> 18S rRNA gene	99%	FJ866629.1	2
Healthy-5	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGGCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Poncirus trifoliata</i> , and a uncultured fungus 18S rRNA gene	99%	AF206997.1, JQ350757.1	2
Healthy-6	<b>CTCGTAGTTGAAACCTTGGTTGGTCGGCCGGTCCGCCCTCGCGGTGTGCA</b> CCGGCCGGCTCGTCCCTCTGCCGGCGATGCGCTCTGGCCTTAATTGGC CGGGTCGTGCCACCGCGCTTACTTGAAAGAAATT <b>AGAGTGTCAAAGC</b> <b>AGGC</b>	<i>Poncirus trifoliata</i> , and a uncultured fungus 18S rRNA gene	99%	AF206997.1, JQ350757.1	2