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## Journal of Citrus Pathology

### Title

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### Permalink

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### Journal

Journal of Citrus Pathology, 1(1)

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### Publication Date

2014

### DOI

10.5070/C411025218

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**9.13 P****First Report of ‘Candidatus Liberibacter asiaticus’ associated with huanglongbing in the weeds *Cleome ruidosperma*, *Pisonia aculeata* and *Trichostigma octandrum* in Jamaica**Brown, S.E.<sup>1\*</sup>, Oberheim, A.P.<sup>1</sup>, Barrett, A.<sup>2</sup>, and McLaughlin, W.A.<sup>1</sup><sup>1</sup>Department of Basic Medical Sciences, University of the West Indies Mona, Kingston 7, Jamaica<sup>2</sup>Jamaica Citrus Protection Agency, Bog Walk, St Catherine, Jamaica

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Additional key words: citrus greening, alternative host plants

Citrus huanglongbing (HLB) also known as citrus greening is the most destructive disease of citrus worldwide. Three species of the causal organism have been identified. These are ‘Candidatus Liberibacter asiaticus’, ‘Ca. L. africanus’ and ‘Ca. L. americanus’ (Bové, 2006). In 2010 a survey of non-citrus plants was conducted on two major citrus producing farms in Clarendon and St Catherine in Jamaica. This was to determine the possibility of the existence of non-citrus hosts of HLB. A total of 120 plants belonging to 10 different species and nine families were collected over a period of two months. The plants collected included weeds as well as non-citrus trees. None of the plants collected exhibited any symptoms of HLB and at the time of sample collection, no citrus psyllids was observed on the plants. DNA was extracted from plant samples using the method of Dellaporta et al. (1983) and analysed by PCR using the primer pair OI1 (5` GCGCGTATGCAATACGAGCGGCA3`) and OI2c (5`GCCTCGCGACTTCGCAACCCAT 3`). DNA obtained from a confirmed HLB infected citrus plant from Florida served as the positive control whereas DNA from a citrus plant uninfected by HLB was used as the negative control.

Amplification of a 16S rDNA product of the expected size (1200 bp) confirmed the presence of HLB infection in three of the weed species that were tested. These included *Cleome ruidosperma* (Family Capparaceae) (1/9), *Pisonia aculeata* (Nyctaginaceae) (3/3) and *Trichostigma octandrum* (Phytolaccaceae) (2/8). No amplification was obtained for the following species: *Bidens pilosa* (0/17), *Parthenium hysterophorus* (0/18) (both Asteraceae), *Sida jamaicensis* (Malvaceae) (0/11), *Waltheria indica* (Sterculiaceae) (0/27), *Priva lappulacea* (Verbenaceae) (0/7), *Psidium guajava* (Myrtaceae) (0/12), *Hyptis capitata* (Lamiaceae) (0/8). Positive PCR products from the above mentioned weeds were digested with XbaI, and restriction fragments of approximately 530 bp and 650 bp were obtained which corresponded to the fragments expected for ‘Ca. L. asiaticus’ as well as the positive control that was used. PCR products from each of the weed species were cloned and sequenced (in both directions) and the sequences were deposited in GenBank (Accession Nos. JN245977, JN245976, and JN245973). Blast analysis determined the consensus sequence to be most similar (98%) to ‘Ca. L. asiaticus’ found in Florida (EU265646), Belize (GQ502291) and Brazil (AY919311). Weeds have been known to act as reservoir hosts of many pathogens. However, to our knowledge this is the first report of ‘Ca. L. asiaticus’ in the weeds, *C. ruidosperma*, *P. aculeata* and *T. octandrum*. The presence of ‘Ca. L. asiaticus’ in weeds has very serious implications for the control of HLB in

Jamaica. The current practices by farmers include the removal of infected citrus trees and control of the vector through the spraying of insecticides. The presence of the HLB pathogen in weeds would now imply that weed removal must be part of the HLB management program in Jamaica as they can serve as reservoirs for the disease as well as source of breeding for the vector.

#### Acknowledgements

This work was made possible through the Research and Publication Fund provided by the University of the West Indies (Mona).

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