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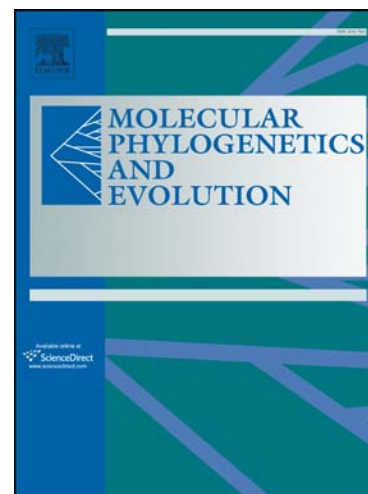
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Phylogenetic relationship and genetic diversity of citrus psyllid populations from China and Pakistan and their associated *Candidatus* bacterium

Muhammad Qasim^{1,2,3}, Wang Baohua¹, Huasong Zou^{1,4}, Yongwen Lin^{1,2,3}, Chandra Kanta Dash^{1,2,3}, Bamisope Steve Bamisile^{1,2,3}, Mubasher Hussain^{1,2,3}, Zhao Zhiwen^{1,4} and Liande Wang^{1,2,3*}

¹ State Key Laboratory of Ecological Pest Control for Fujian and Taiwan Crops, College of Plant Protection, Fujian Agriculture and Forestry University, Fuzhou 350002, China

² Key Laboratory of Biopesticide and Chemical Biology, Ministry of Education, Fuzhou-350002, China

³ Key Laboratory of Integrated Pest Management for Fujian-Taiwan Crops, Ministry of Agriculture, Fuzhou-350002, China

⁴ State Key Laboratory of Ecological Pest Control for Fujian and Taiwan Crops; Fujian University Key Laboratory for Plant-Microbe Interaction, Fujian Agriculture and Forestry University, Fuzhou, 350002, China

*Liande Wang; wang_liande@126.com

Abstract

Asian citrus psyllid (ACP), *Diaphorina citri* Kuwayama (Hemiptera: Liviidae), is a severely devastating pest of Rutaceae plants, mainly citrus, across the globe, and causal agent of Huanglongbing (HLB) disease. To find out the genetic relationship and diversity among the populations of ACP and associated *Candidatus* Liberibacter asiaticus (CLAs) from two countries (China and Pakistan), sequence data of three different genes, cytochrome oxidase subunit I (COI), Cu-transporting protein (ATOX1) and 16S rRNA, were used to characterize all populations. In the present study, MEGA-7 and statistical parsimony software (TCS-1.2) were used to depict the phylogenetic relationship among all populations under both genes, whereas diversity was calculated by DnaSP v5. All analyses were done for country wise and overall relationship among all populations. For ACP populations, both genes presented a significant strong intermingled relationship among all populations and put all population into a single haplotype (Dcit-2), which proved similarity between Chinese and Pakistani populations. Moreover, for CLAs strains, 16S gene also presented strong relationship for all sampled populations. All three genes of ACP and CLAs populations elucidated more than 95% resemblance to each other. On the other hand, a significant genetic variation was observed by

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