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Review of the genus *Ceratovacuna* (Hemiptera: Aphididae) with descriptions of five new species from China

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Abstract

The genus *Ceratovacuna* Zehntner, 1897 (Hemiptera: Aphididae: Hormaphidinae) is reviewed for the first time in China, with the descriptions of five new species, *C. angusticorna* Qiao **sp. n.**, *C. beijingensis* Qiao **sp. n.**, *C. imperata* Qiao **sp. n.**, *C. multiglandula* Qiao **sp. n.**, *C. separata* Qiao **sp. n.** and four new records for China, *C. graminum* (van der Goot, 1917), *C. keduensis* Noordam, 1991, *C. panici* (van der Goot, 1917) and *C. uscare* (Tao, 1964). The molecular analyses based on COI and Cytb sequences both supported the status of these new species.

Key words: *Ceratovacuna*, *C. angusticorna*, *C. beijingensis*, *C. imperata*, *C. multiglandula*, *C. separata*, new species, COI, Cytb

Introduction

Ceratovacuna Zehntner, 1897 is a relatively large genus in Hormaphidinae. It is a typical group in the subfamily, having developed frontal horns, some of 1st instar nymphs developed as soldiers, bearing white wax powders or tufts in life. These aphids can induce galls on the leaves of their primary hosts, *Styrax* spp. and sometimes cause serious damages on their secondary hosts, such as sugar canes, cogongrass, bamboos and other weeds. The species of this genus are mainly restricted to Southeast Asia, including China, Japan, Korea, Vietnam, Nepal, India, Sri Lanka, Thailand, Malaysia, Indonesia and Philippines.

During the survey of the Chinese Hormaphidinae species, many specimens of *Ceratovacuna* were checked and reviewed. Among them, five new species and four new records from China are reported here. In total, 18 out of the 25 known species worldwide (Remaudière & Remaudière, 1997; Chakrabarti & Debnath, 2011; Favret, 2015) have been recorded in China.

Material and methods

Morphological description. Aphid terminology and the measurements in this paper generally follow Blackman & Eastop (2006) and Aoki *et al.* (2013). The unit of measurement in this paper is millimeters (mm).

Molecular analyses. Forty-eight samples belonging to 12 *Ceratovacuna* species were included. The standard molecular barcode, mitochondrial cytochrome *c* oxidase subunit I (COI), and a faster-evolving gene, cytochrome *b* (Cytb), were used. All sequences were taken from Foottit *et al*. (2008) and Zhang *et al*. (2013). Voucher information and GenBank accession numbers for all samples are listed (Table 2). Multiple alignments were conducted with ClustalX 2.0.12 (Larkin *et al*., 2007) and then verified manually. Neighbor-joining (NJ) trees and genetic distances were estimated for both COI and Cytb sequences with MEGA 6.06 (Tamura *et al*., 2013), using Kimura's two-parameter (K2P) model (Kimura, 1980). Bootstrap analyses were performed with 1000 replications.

The holotypes and some paratypes of the 5 new species and the studied specimens of the other 11 known species were deposited in the National Zoological Museum of China, Institute of Zoology, Chinese Academy of

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