As we know, about 400 species of Perlidae in the world, most species are widely distributed in the northern part of the earth, and a few are extended to the southern part of Africa and South America (DeWalt et al. 2019). But, there are only three species have been reported in the genus *Etrocorema* of the family Perlidae in the world. The earliest discovered species *E. ahenobarba* was found in Southeast Asian mainland, Sumatra, Borneo in 1909 (Sivec et al. 1988). Subsequently, the second species *E. Hochii* was reported but the species was originally named in genus *Tetropina* by Wu (1938) but tentatively placed in genus *Etrocorema* by Zwick (1984). And, the *E. Hochii* was a special species which only distribute in Hainan, China. The last species *E. belumensis* was discovered in Malaya and presented by Wan Nur Asiah and Che Salmah (Wan Nur Asiah 2009). Although eight species in Perlidae have been sequenced and published, the genus *Etrocorema* has not yet been involved (Qian et al. 2014; Elbrecht et al. 2015; Huang et al. 2015; Wang, Ding, et al. 2016; Wang, Wang, et al. 2016; Cao, Li, et al. 2019, Cao, Wang, et al. 2019; Li et al. 2019). In this paper, the complete mitochondrial genome sequences of *E. Hochii* were determined using illumina sequencing for the first time which represent the genome *Etrocorema* to facilitate future studies on the identification, population genetics, and evolution of the Perlidae. The specimens of *E. hochii* was collected in Yinggeling National Nature Reserve (19.06°N, 109.57°E), Hainan Province, China in April 2016. Samples and voucher specimens (No. Voh-0068) were deposited in the museum of Henan Institute of Technology, Henan Province, China.

The complete mitogenome of *E. Hochii* is 15,854 bp in length with the GenBank accession number MK905888, which contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and one control region. The nucleotide composition of this genome is A (36.0%), T (31.4%), C (20.9%), and G (11.7%). All PCGs use the typical start codon ATN, except ND1, ND2, and COI, which start with TTG, GTG, and ACC, respectively. Only the ND5 genes terminated with single T—>, and the rest use the stop codon TAA/TAG. We used this new nucleotide information under Bayesian and maximum-likelihood analyses to explore the relationships of Perlidae. Phylogenetic analyses showed that *E. hochii* is closely related to the clade (*Togoperla + Kamimuria*), which is widely accepted view.
widely accepted view. We hope our data will be useful for further study.

Disclosure statement
No potential conflict of interest was reported by the authors.

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