

ON THE SYNONYMY OF *TRICTENOTOMA FORMOSANA* KRIESCHE,
1919 (COLEOPTERA: TRICTENOTOMIDAE)

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Summary. The taxonomic status of *Trictenotoma formosana* Kriesche, 1919 is re-examined. Based on morphological and molecular evidence, it is recognized as a junior synonym of *T. davidi* Deyrolle, 1875.

Key words: beetles, *Trictenotoma davidi*, *Trictenotoma formosana*, morphology, COI, new synonymy.

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Резюме. Пересмотрен таксономический статус *Trictenotoma formosana* Kriesche, 1919. На основании морфологических и молекулярных данных он признан младшим синонимом *T. davidi* Deyrolle, 1875.

INTRODUCTION

Trictenotomidae Blanchard, 1845 is a small beetle family within the superfamily Tenebrionoidea, currently comprising 19 described species in two genera: *Autocrates* Thomson, 1860 (seven species) and *Trictenotoma* Gray, 1832 (twelve species) (Cho & Kim, 2024). The family is mainly distributed in the Oriental Region and extends into the Palearctic Region, including parts of China and South Korea. Members of Trictenotomidae are notable for their large body size and enlarged mandibles.

Trictenotoma davidi formosana Kriesche, 1919 was originally described from Taiwan as a subspecies of *T. davidi* Deyrolle, 1875, based on differences in body vestiture coloration and pronotal shape, and was later elevated to species rank by Kriesche (1921). More recently, *T. formosana* was redescribed and compared with *T. davidi* using characters of the male genitalia and terminal abdominal segments (Telnov *et al.*, 2020). However, differences in male genitalia between the two taxa appear to be subtle, whereas other species of *Trictenotoma* show distinct differences in male genital morphology (Telnov & Drumont, 2020).

Recent studies have shown that Trictenotomidae is suitable for species delimitation using DNA barcoding (Cho & Kim, 2024). In that study, interspecific COI divergences were relatively high, with values of 8.2–17.5% in *Autocrates* and 11.7% between two species of *Trictenotoma*.

In this study, we reassess the taxonomic status of *T. formosana* based on external morphology, male genitalia, and COI sequences, and evaluate its relationship with *T. davidi*.

MATERIAL AND METHODS

Specimens were examined under a Leica S8APO stereomicroscope. Dry specimens were softened in a plastic container (LocknLock) with moist tissue paper for 6–8 h; the abdomen was dissected along the lateroapical margin and the genitalia were extracted. Photographs of the habitus were taken with a Nikon D7500 digital camera, and genitalia were imaged using a Nikon D750 attached to the microscope. Images were stacked with Helicon Focus software.

Genomic DNA was extracted from abdominal tissues using the DNeasy Blood and Tissue Kit (QIAGEN). The mitochondrial COI gene was amplified using the universal primers LCO1490 and HCO2198 following Folmer et al. (1994). Genetic distances were calculated using the Kimura two-parameter (K2P) model in MEGA, and a maximum-likelihood tree was reconstructed with 1,000 bootstrap replicates. Comparative sequences were obtained from GenBank; accession numbers and collection localities are indicated in the figure. The examined specimens are deposited in the private collection of H.-W. Cho (HWC), and DNA samples are stored in the Nakdonggang National Institute of Biological Resources, South Korea (NNIBR).

TAXONOMY

Trictenotoma davidi Deyrolle, 1875

Figs 1–3

Trictenotoma davidi Deyrolle, 1875: 68 (type locality: China).

Trictenotoma davidi formosana Kriesche, 1919: 150 (type locality: Taiwan, Taihorin), elevated to species rank as *Trictenotoma formosana* by Kriesche (1921); **syn. n.**

For the complete taxonomic history, see Telnov & Drumont (2020) and Telnov *et al.* (2020).

MATERIAL EXAMINED. **China:** Fujian, Longyan, Mt. Meihuashan, VI 2021, 2♂ [HWC]; Guizhou, Qiandongnan, Leishan County, Mt. Leigongshan, VI 2022, 1♀ [HWC]; Yunnan, Funing, VII 2009, 1♂ [HWC]; **Taiwan:** Miaoli County, Yuanli, IX 2023, 4♂, 1♀ [HWC]; **Vietnam:** Ha Giang, VI 2022, 1♂ [HWC]; Ha Giang, VI 2023, 1♂ [HWC]; Ha Giang, VI 2025, 2♀ [HWC]; Nghe An, VI 2022, 1♂ [HWC]; Nghe An, V 2024, 1♂ [HWC]; Yen Bai, VII 2021, 1♂ [HWC]; Yen Bai, V 2022, 1♂ [HWC]; Yen Bai, VIII 2023, 1♂, 1♀ [HWC]; Yen Bai, VIII 2024, 2♂ [HWC].

DNA BARCODE. Partial mitochondrial COI sequences were generated and deposited in GenBank under the accession numbers PX797520–PX797527.

DISTRIBUTION. China (including Taiwan), Vietnam.

REMARKS. Individuals of *Trictenotoma davidi* are almost identical to those of *T. formosana* in external morphology, although Vietnamese specimens show greater variation in body size and coloration (Figs 1A–H). All examined specimens from Taiwan, China, and Vietnam share nearly identical male genital morphology, including the accessory lobes (Figs 2A–C), whereas other species of *Trictenotoma* have been reported to exhibit diagnostically informative differences in male genital characters (Telnov & Drumont, 2020). Taiwanese specimens tend to exhibit relatively paler body vestiture coloration; however, no clear morphological characters were found to reliably distinguish them from the Chinese and Vietnamese populations.

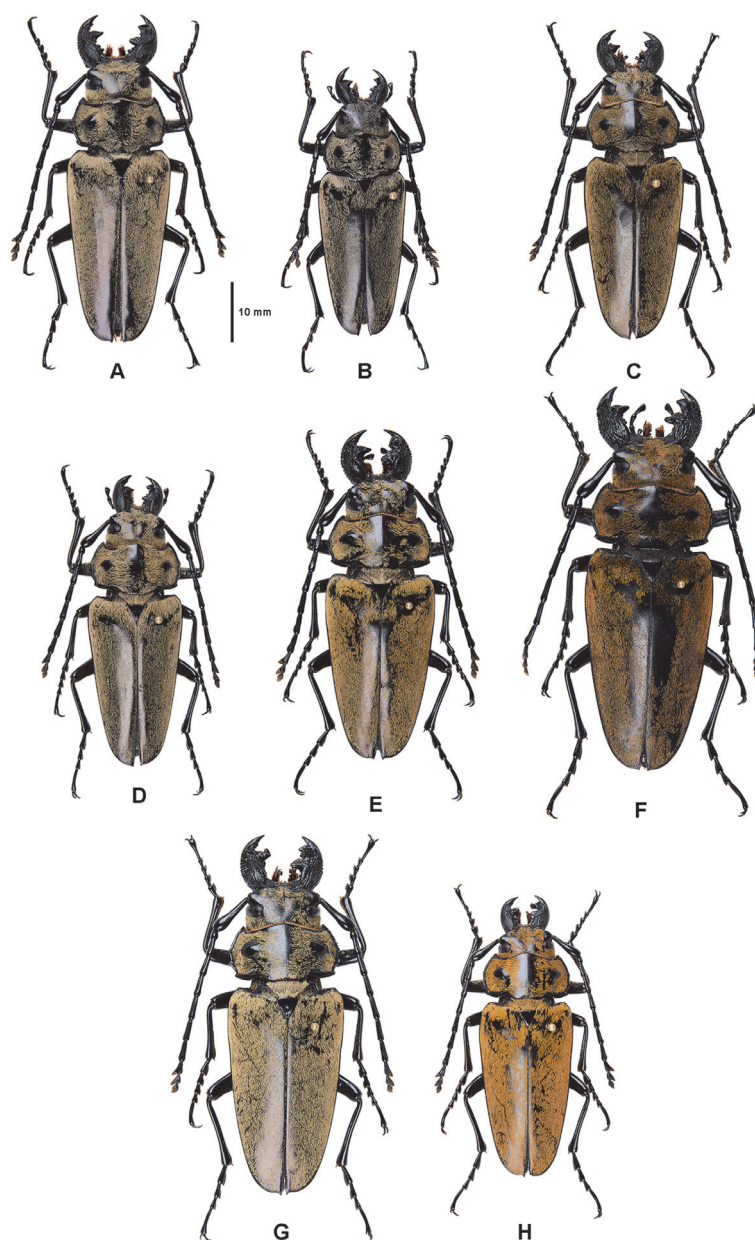


Fig. 1. Adult males of *Trictenotoma formosana* Kriesche (A–B) and *T. davidi* Deyrolle (C–H). A, B – Taiwan, Miaoli; C, D – China, Fujian; E – Vietnam, Nghe An; F – Vietnam, Ha Giang; G, H – Vietnam, Yen Bai.

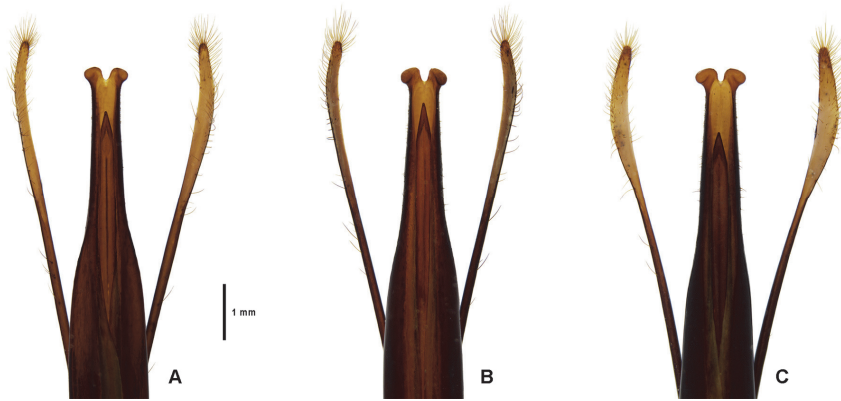


Fig. 2. Apical part of the aedeagus and accessory lobes of *Trictenotoma formosana* Kriesche (A) and *T. davidi* Deyrolle (B–C). A – Taiwan, Miaoli; B – China, Fujian; C – Vietnam, Ha Giang.

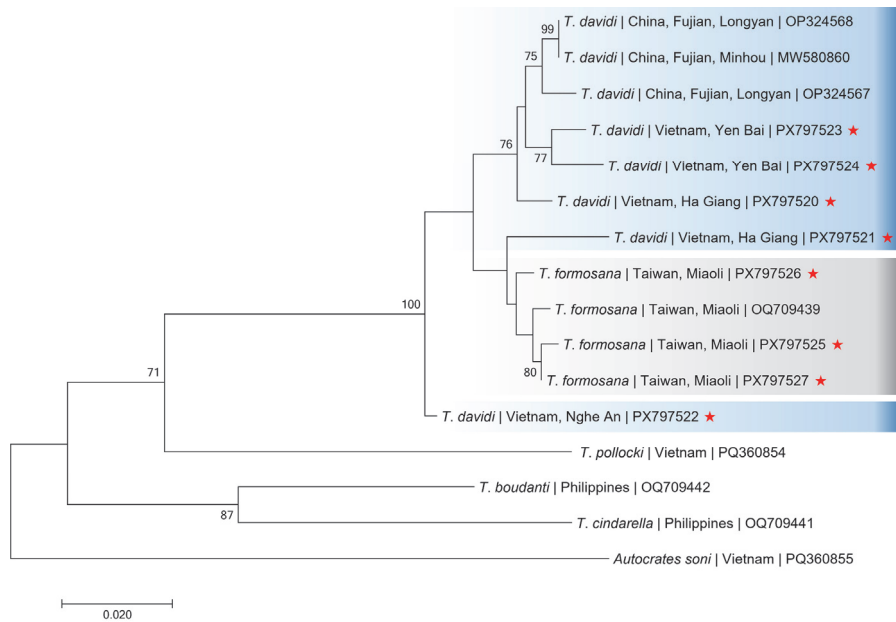


Fig. 3. Maximum-likelihood tree based on COI sequences of examined *Trictenotoma* species. Red stars indicate sequences newly obtained in this study.

Partial sequences of the mitochondrial COI gene were successfully obtained from five specimens of *T. davidi* and three specimens of *T. formosana*. Based on Kimura two-parameter (K2P) distances, genetic divergence between *T. formosana* and *T. davidi* ranged from 1.7–3.1% (mean 2.4%). In contrast, interspecific distances between *T. formosana*/*T. davidi* and

Table 1. Sequence divergence determined using K2P distance in MEGA.

	<i>T. boudanti</i>	<i>T. cindarella</i>	<i>T. davidi</i>	<i>T. formosana</i>	<i>T. pollocki</i>
<i>T. boudanti</i>	-				
<i>T. cindarella</i>	0.102	-			
<i>T. davidi</i>	0.128	0.144	-		
<i>T. formosana</i>	0.131	0.148	0.024	-	
<i>T. pollocki</i>	0.152	0.144	0.132	0.137	-

other congeners, each represented by a single specimen, were substantially higher, ranging from 10.2% to 15.2% (Table 1). The lowest interspecific divergence among these taxa was observed between *T. boudanti* and *T. cindarella* (10.2%), whereas the highest value was found between *T. boudanti* and *T. pollocki* (15.2%). In the maximum-likelihood tree based on COI sequences, specimens identified as *T. formosana* were not recovered as a distinct clade, but were intermingled with *T. davidi* from China and Vietnam within a strongly supported lineage (Fig. 3).

The lack of reciprocal monophyly between *Trictenotoma formosana* and *T. davidi*, together with low interspecific COI divergence and the absence of consistent morphological differences, supports the treatment of *T. formosana* as a junior synonym of *T. davidi*.

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