



## DNA barcoding and taxonomic review of the barklouse genus *Stenopsocus* (Psocoptera: Stenopsocidae) from Taiwan

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### Abstract

The barklouse genus *Stenopsocus* Hagen is the most diverse group of the family Stenopsocidae, with 139 described species recorded from China in a previous study. However, due to the considerably similar morphology, species identification in this genus is problematic. In the present study, we used DNA barcoding to delimit the six *Stenopsocus* species currently recorded in Taiwan. Our results show that *S. aphidiformis*, *S. niger*, *S. tibialis*, *S. makii*, and *S. formosanus* can be clearly distinguished based on COI sequences. Although genetic divergence between *S. formosanus* and *S. externus* was not detected, we tentatively consider that these two species are valid based on their remarkably different morphological features. Re-descriptions of these six valid species are provided. *Stenopsocus niger* is newly recorded from Taiwan, and *S. formosanus* newly recorded from Vietnam.

**Key words:** *Stenopsocus*, DNA barcoding, taxonomy, Taiwan

### Introduction

The barklouse genus *Stenopsocus* Hagen of the family Stenopsocidae has extraordinarily rich species diversity in Asia, especially in the Oriental realm, including 139 described species in China (including *Cubipilis* Li) (Li 2002, 2005; Mockford 2003). However, it is well known that species identification of *Stenopsocus* is difficult due to variable marking patterns on the head, and female gonapophyses that were reported to be unstable among conspecific individuals (Saville 2009). Moreover, male genitalia, particularly the phallosomes, have very similar characteristics among different species, providing limited information to distinguish species. The mitochondrial gene COI has been widely used for species identification in many animal groups as a standard DNA barcode. However, besides some studies on the DNA barcoding of important booklice pests (Li *et al.* 2012; Yang *et al.* 2012), the molecular identification of barklice is still rarely studied.

Previously, there are five species of *Stenopsocus* recorded in Taiwan, *S. aphidiformis*, *S. formosanus*, *S. tibialis*, *S. externus* and *S. makii* (see Lienhard & Smithers 2002). However, the genitalia of these species still remain poorly studied, and no subsequent revision of these species is available. In this study, we sequenced the standard barcoding region of COI of 34 specimens of *Stenopsocus*, representing six species currently known from Taiwan (*S. niger* as newly recorded species from Taiwan), as a case study to test the morphological criteria used for delimiting *Stenopsocus* species. Revised taxonomy and detailed re-description of the six *Stenopsocus* species from Taiwan are provided based on the present results.

### Material and methods

**Taxon sampling.** Specimens were stored in 95% ethanol after collection and all are deposited in the Entomological Museum of China Agricultural University, Beijing (CAU). The ingroup comprise 34 specimens of the six target species (Table 1). We selected *Graphypsocus cruciatus* (Linnaeus) as an outgroup because it belongs to a genus