



DNA barcoding and regional diversity of understudied Micropeplinae (Coleoptera: Staphylinidae) in Southwest China: phylogenetic implications and a new *Micropeplus* from Mount Emei

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Abstract

Extensive litter sampling at eight forested localities in Yunnan and Sichuan detected 381 specimens of Micropeplinae rove beetles. DNA barcoding data from 85 representative specimens were analysed to delimit species and infer their relationships. Statistical methods were implemented to assess regional species diversity of understudied Micropeplinae. The total number of sampled Micropeplinae species varied between 14 and 17, depending on a splitting versus lumping approach for allopatric populations. A single Micropeplinae species was sampled in six of eight studied localities, three species were found on Mount Gongga, while ten species were discovered on hyperdiverse Mount Emei in Sichuan. All Micropeplinae specimens from our samples belong either to the genus *Cerapeplus*, or to three other inclusive groups temporarily retained inside *Micropeplus sensu lato*. Each of the three groups potentially represents a separate genus: *tesserula* group, *sculptus* group and *Micropeplus sensu stricto*. A new species *Micropeplus jason* sp. n. from Mount Emei in Sichuan is described. Numerous illustrations introduce regional fauna and clarify the discussed morphological characters.

Key words: *Cerapeplus*, Yunnan, Sichuan, phylogeny, classification

Introduction

The mountains of Southwest China are noted for their exceptionally rich biota (Tang *et al.* 2006). This phenomenon is likely linked to the habitat diversification and fragmentation as a result of the accelerated orogeny caused by the collision of the Indian plate with Asia some 40–55 MY ago with the mountains reaching their approximate present day height by 5–15 MY (Favre *et al.* 2015). Additionally, regional species composition was extensively and repeatedly modified by the climate-induced fluctuations, including those which happened during the Pleistocene climatic cycles, fostering repeated colonisation events and promoting vicariant speciation. The resulting diverse and complex mosaic of life forms in mountains of Southwest China offers an intellectually stimulating phylogeographic sampling ground, particularly informative when one targets such stenotopic organisms as litter-inhabiting beetles (Grebennikov 2014a,b).

Here we attempt to shed light on the diversity and evolutionary history of Micropeplinae beetles richly represented in our forest leaf litter samples taken in two Southwest China provinces: Sichuan and Yunnan (Fig. 1). The Micropeplinae form an undoubtedly monophyletic group (Newton & Thayer 1995) of small and aberrant rove beetles with at least 82 species worldwide (Herman 2001). These species prefer relatively wet conditions and seem to be much restricted to such habitats. At least some species are wingless (personal observation) and seemingly narrowly distributed, suggesting accelerated vicariant speciation (Ikeda *et al.* 2011). Such characteristics would make wingless Micropeplinae a model group for unfolding the evolutionary past in the complex mountainous landscape of Southwest China, but for two significant limitations.

regions (Smetana 2004). It might be plausible to assume that all recognized species of this group other than *M. tesseraula*, like *M. dentatus* Zhao & Zhou, 2004 from Zhejiang province in China, are in fact only gradistic regional lineages rendering a more inclusive *M. tesseraula* paraphyletic (Ross 2014). In other words, the entire species group might be considered as a single and extremely widely distributed species. Unlike most *Micropeplus sensu lato* in Southwest China, specimens of the *tesseraula* species-group are fully winged and are likely capable of active flight, which fosters genetic exchange over large distributional area. Considering the above, the *tesseraula* species-group might be further characterized by an additional character of having a highly efficient mechanism to retain an abnormally high rate of genetic exchange efficiently preventing allopatric speciation. All these pieces of evidence corroborate a hypothesis that the Clade E represents a phylogenetically valid radiation worthy of formal generic status as *Arrhenoepplus* Koch.

Clades A, B and C: the genus *Micropeplus sensu stricto*. The assemblage of clades A, B and C in Fig. 2 was weakly recovered in ML analysis and collapsed in MP analysis. The present temporary delineation of this assemblage as the narrowly defined *Micropeplus* is adopted to stress the separation of both Clades E and G, which represent unrelated radiations possibly worthy of full generic status (see above). Not only monophyly, but also the naming of *Micropeplus sensu stricto* is controversial, since *M. porcatius*, the type species of the genus, was not represented in our DNA analyses. Assessment of its external morphology was inconclusive, since the species exhibits a conflicting mix of characters linking it with either *Micropeplus sensu stricto* (numerous small punctures forming two or three longitudinal lines on elytral intercostae, Fig. 8I), or with Clade G (seven elytral costae, Fig. 8L). Some other characteristics are intermediate (body length about 2.1 mm, weakly developed pronotal ridges, moderately separated metacoxae). The type species of *Micropeplus* has, therefore, approximately equal chances of belonging to either of these two groups: *Micropeplus sensu stricto* or Clade G, which, in turn, will determine the valid generic name of the lineage.

Clade D: the genus *Cerapeplus*. The relatively recently discovered genus *Cerapeplus* consists of two named species. The type species *C. siamensis* Löbl & Burckhardt is known from 15 specimens widely distributed in Southeast Asia (Thailand, Indonesia, possibly Malaysia: Sabah). *Cerapeplus sinensis* Löbl is restricted to the Qin Ling Mountain Range in China: Shaanxi and is known from three type specimens (Löbl & Burckhardt 1988, Löbl 1997). This genus was twice recorded in our samples: a single specimen #2875 from Mount Emei (Fig. 5J); a single specimen #4766 from the Tam Dao Mountain Range in Vietnam (Fig. 6H, a new generic record for the country) and about two dozen specimens of *C. sinensis* from the Qin Ling Mountain Range (Fig. 6G). Even if the first two specimens might represent unnamed species, we postpone their taxonomic assessment until more data become available. Overall, our *Cerapeplus* samples exceed in number of specimens and species all that was previously recorded for this genus and suggest a significantly higher diversity than previously known.

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