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## DNA barcode and phylogeography of six new high altitude wingless *Niphadomimus* (Coleoptera: Curculionidae: Molytinae) from Southwest China

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### Abstract

The genus *Niphadomimus* Zherikhin, 1987 is taxonomically revised herein. In addition to the two recorded Nepalese species, *N. nigriventris* Zherikhin and *N. niger* Zherikhin, known only from the holotypes, two additional specimens of *N. nigriventris* are reported and six new species from China represented by 96 specimens are described and illustrated. These are: *N. alcyone* sp. n. (Sichuan), *N. cелаeno* sp. n. (Yunnan), *N. electra* sp. n. (Yunnan), *N. maia* sp. n. (Yunnan), *N. merope* sp. n. (Shaanxi) and *N. sterope* sp. n. (Sichuan). All known *Niphadomimus* species are apterous inhabitants of the leaf litter in the upper *Rhododendron*-dominated forest zone between 2000 and 4114 m. Phylogenetic analyses using DNA barcodes of six new species and representatives of 13 other Molytinae genera with available DNA data (A.) corroborates *Niphadomimus* monophyly; (B.) strongly argues for the sister-group relationship between *N. merope* sp. n. from the Qinling Mt. Range and the rest of the species distributed in the Hengduan mountains; (C.) in two among four analyses weakly relates the genus with the East Palaearctic *Leiosoma*. The tribe Typoderini could not be shown as monophyletic, which may be due to insufficient signal content of the *cox1* marker at the tribal level. The detected phylogeographic pattern of *Niphadomimus* is compared with that of similarly distributed or closely related clades. Temporal DNA analysis estimates the *N. merope* sp. n. split at 6–11 MY, while the diversification of the Hengduan clade dates between 5.5 MY and 3.6 MY, i.e. well before the onset of the Quaternary climate fluctuations.

**Key words:** *Niphadomimus*, CO1, DNA barcode, phylogeography, weevils

### Introduction

The weevil subfamily Molytinae contains several thousand species arranged in approximately 430 genera (Alonso-Zarazaga & Lyal 1999) attributed to 57 currently recognized tribes or subtribes (Bouchard *et al.* 2011; Alonso-Zarazaga 2013). All Molytinae species with adequately known biology feed nearly exclusively on live or dead plant tissue both as larvae and adults. The subfamily contains many economically important taxa, including biological control agents against invasive plants, such as the European weevil *Hylobius transversovittatus* Goeze which was introduced in 1992 to the USA and Canada to control Purple loosestrife (*Lythrum salicaria*, see McAvoy & Kok 2002). More important, however, is the role of Molytinae as both forestry and agricultural pests. Best known among them are the two predominantly Holarctic genera *Hylobius* Germar and *Pissodes* Germar, each with a few dozen species, some of which are known as notorious pests of conifers (Lei Guilin *et al.* 2003; Långström & Day 2004). Species of the latter genus are capable of transcontinental travel and establishment, as demonstrated for the North American *Pissodes nemorensis* Germar that had significantly damaged pine plantations in South Africa (Gebeyehu & Wingfield 2003). The wood-associated insects such as Molytinae are the most common among those species that are unintentionally transported with untreated low-grade wood used as dunnage for the international maritime trade. Indeed, specimens of both *Hylobius* and *Pissodes* are the most commonly intercepted wood-associated non-Scolytinae weevils with 181 and 280 interceptions, respectively, recorded at United States ports of entry between 1985 and 2000 (together with species of five other Molytinae genera: *Conotrachelus* Dejean, *Heilipus* Germar, *Marshallius* Kusche, *Niphades* Pascoe and *Rhysomatus* Schoenherr; see Haack 2006). Live larvae and adults of the Molytinae genus *Pimelocerus* Lacordaire, native to Asia Pacific and

Another biological peculiarity of *Niphadomimus* weevils is their remarkable rarity in sifted samples, coupled with occasional abundance. The great majority (70–90%) of samples taken in the seemingly appropriate *Rhododendron*-dominated habitats in the localities where *Niphadomimus* is known to occur failed to record the genus (total number of samples not shown). When detected, the genus would normally be represented by a single specimen of a single species discovered after a few days of intense sampling. Consider that 11 among 14 *Niphadomimus* collecting events pertained indeed to singletons (all four specimens from Nepal, plus seven Chinese records, including the 2010 record of *N. electra* **sp. n.**). Only two samples from the Cang Shan Mountain Range taken within two days of 4–5.vii.2011 resulted in long series of *N. electra* **sp. n.**, and, most uncommonly, one of them additionally included all nine presently known specimens of *N. maia* **sp. n.** (Fig. 15). It is extraordinary that both the exceptionally rich 2011 sites are located within one kilometre from each other, were equally diligently sampled a year earlier (18–19.v.2010) and provided only a singleton of *N. electra* **sp. n.**, the first representative of the genus ever recorded in China. The latter results suggest strong and presently unexplainable temporal fluctuations of adult specimen density.

### Subfamily placement of Molytinae

An important work by Lyal (2014) was published after the manuscript of the present paper has already been completed. In this work the tribes of Molytinae were significantly reorganized and many genera reshuffled, as compared to the earlier standard works of reference (Alonso-Zarazaga & Lyal 1999, Bouchard *et al.* 2011; Alonso-Zarazaga 2013). The most noticeable novelty, however, was the incorporation of the entire former “subfamily Cryptorhynchinae” into Molytinae, the latter presently containing 37 tribes plus ca. 28 genera *incertae sedis* (Lyal 2014: 530, 531). This taxonomic change is not implemented in the present paper for purely technical reasons. Lyal (2014) should be consulted for the most recent in-depth treatment of what is herein considered as the “subfamily Molytinae”; however, changes therein will not affect the results and conclusions of this paper.

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