



Morphology and DNA barcoding reveal three cryptic species within the *Xylophanes neoptolemus* and *loelia* species-groups (Lepidoptera: Sphingidae)

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Abstract

Two species complexes within the genus *Xylophanes* are addressed using a combination of morphological study and analysis of DNA barcode sequences. The existence of two and three cryptic species respectively within the *X. loelia* and *X. neoptolemus* complexes is revealed following consideration of both adult habitus and genital morphology, and the results of a phylogenetic analysis of partial COI sequences—DNA barcodes—for 38 specimens. The taxonomic status of the available names is discussed and to clarify and stabilize the confused nomenclature of this group, a neotype for *Sphinx neoptolemus* Cramer, 1780, and lectotypes for *Choerocampa loelia* Druce, 1878 and *Chaerocampa trilineata* Walker, [1865], are designated. We describe three new species: *X. lolita* n. sp. Vaglia and Haxaire; *X. balcazari* n. sp. Haxaire and Vaglia; and *X. cthulhu* n. sp. Haxaire and Vaglia. The first is endemic to southeastern Brazil and closely allied to *X. loelia*; the second two are relatives of *X. neoptolemus*, of which the first is known only from Guerrero and Michoacán states in Mexico while the second is widely distributed in lowland forests of Central America.

Key words: COI, DNA barcodes, new species, South America, Central America

Introduction

Xylophanes Hübner, [1819] is the most speciose genus of the family Sphingidae (hawkmoths or sphinx moths), with 96 valid species and subspecies names listed in the most recent checklist (Kitching & Cadiou 2000). The present study focuses on a species complex that comprises taxa generally treated as *X. neoptolemus* (Cramer, 1780) and *X. loelia* (Druce, 1878) and represents a first step toward the elucidation of a larger complex that also includes *X. libya* (Druce) and *X. pearsoni* Soares & Motta. In their current sense, both *X. neoptolemus* and *X. loelia* are relatively common species widely distributed across Central and South America. However, it has become apparent, from variation in wingspan and subtle differences in wing pattern and genital structures that these names refer to a complex comprising more than two species. These initial observations are further examined and presented in this paper, and used in association with genetic data to distinguish and describe three new species within this complex. The DNA sequences used are part of a larger project that is assembling DNA barcodes—a part of the COI mitochondrial gene—for all species of sphingids (see <http://www.lepbarcoding.org>). One of the key features of this global campaign is the strong involvement of expert taxonomists and the integration of genetic data within a traditional taxonomic approach. The associ-