

Copyright © 2012 · Magnolia Press





urn:lsid:zoobank.org:pub:DA153881-BAE6-4827-A4D1-9F6F32CC9B63

Taxonomy of spatially disjunct alpine *Teleiopsis albifemorella* s. lat. (Lepidoptera: Gelechiidae) revealed by molecular data and morphology —how many species are there?

PETER HUEMER¹ & MARKO MUTANEN²

¹Tiroler Landesmuseen Betriebsges.m.b.H., Feldstr. 11a, A-6020 Innsbruck, Austria. E-mail: p.huemer@tiroler-landesmuseen.at ²Zoological Museum, Department of Biology, PO Box 3000, FI-90014 University of Oulu, Finland. E-mail: marko.mutanen@oulu.fi

Abstract

The taxonomy of the European alpine species *Teleiopsis albifemorella* (Hofmann, 1867) s. lat. is revised. We sequenced mtDNA markers (COI barcode region) of 44 specimens resulting in a full barcode for 41 specimens. We also sequenced five nuclear markers (CAD, EF-1a, IDH, MDH and wingless) of 12 specimens. Molecular data of nuclear genes combined with weak morphological characters indicate two species: *Teleiopsis albifemorella* from the eastern Alps and the Dinaric mountains and *Teleiopsis paulheberti* **sp. nov.** from the southwestern Alps, the Apennines and the Pyrenees. The COI barcode region groups into seven genetic lineages from geographically coherent areas. Four major haplogroups are assigned to *T. paulheberti* **sp. nov.** whereas three major haplogroups support the eastern alpine *Teleiopsis albifemorella*.

Key words: Lepidoptera, Gelechiidae, *Teleiopsis*, phylogeography, cryptic diversity, DNA barcode, nuclear genes, morphology, Europe, high mountains

Introduction

Disjunct distributions are a common feature in organisms of European mountain systems and reported for a large number of species. Increasing interest in the genetic structure of alpine taxa is reflected in recent literature, and reconstruction of glacial refugia and postglacial colonization is well documented for many plants (Schönswetter *et al.* 2005) but only for relatively few animals (Muster *et al.* 2009, Schmitt *et al.* 2010), among them Lepidoptera such as *Zygaena exulans* (Hohenwarth, 1792), *Parnassius phoebus* (Fabricius, 1793) and *Erebia epiphron* (Knoch, 1783) (Schmitt & Hewitt 2004, Schmitt *et al.* 2006, Todisco *et al.* 2012). The emerging barcoding initiative has resulted in further surprising discoveries, i.e. overlooked cryptic species diversity in several alpine taxa (Huemer & Hausmann 2009, Huemer & Hebert 2011) or taxonomically unresolved genetic clades in different parts of the Alps which are at a first glimpse not reflected by morphology (Huemer 2011, Huemer & Karsholt 2011).

In this paper we try to resolve one of the striking taxonomic problems in an alpine taxon of the genus *Teleiopsis* (Gelechiidae) by combining morphological and genetic data.

The holarctic genus *Teleiopsis* was extensively revised by Pitkin (1988) based on morphology, ecology and biogeography and her species concept was followed in later reviews (Huemer & Karsholt 1999). However, due to the lack of sufficient material and in the absence of molecular data critical taxonomic problems remained unresolved in these foregoing studies. Particularly the *Teleiopsis diffinis*-group as defined by Pitkin (1988) encompassed several cases of possible disjunct cryptic diversity, supported by weak morphological characters and thus indicated as geographical forms only. Recently one of the critical species, *Teleiopsis bagriotella* (Duponchel, 1840), has undergone a thorough, expanded revision (Schmid 2011). The author recognised the specific status of at least three species which he defined by phenotypic characters and morphology of the genitalia. The sympatric occurrence of one new species with *T. bagriotella* in the Swiss mountains furthermore supported specific status. We have tested possible cryptic diversity in another closely related species, namely *Teleiopsis albifemorella*, but in contrast to Schmid (2011) we for the first time used one mitochondrial and five nuclear genes as a supplementary tool of data to resolve the taxonomy.