



Is accurate taxon identification important for molecular studies? Several cases of *faux pas* in pentatomoid bugs (Hemiptera: Heteroptera: Pentatomoidea)

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Abstract

Recently, DNA has become a major source for phylogenetic inference. Although, in entomology, morphology-based methods of taxon identification and the use of morphological data for phylogenetic analyses remain prevalent, the value of these types of studies (often called “traditional”) are depreciated from time to time. It is obvious, that wrong taxon identification may affect results of any taxonomic study. Here we examine evidence that not only the modern “molecular” taxonomists, but even the so-called “traditional” taxonomists, may be casual and irresponsible in taxa identification, when they do their phylogenomic research. We also argue that a researcher’s responsibility for proper taxon identification and its naming is actually much higher in molecular studies than in any others.

Key words: Hemiptera, Heteroptera, Cydnidae, Dinidoridae, Thyreocoridae, molecular studies, taxonomy, species identification

Introduction

In recent years, methods for generating molecular data are becoming easier, faster, and more cost-effective, thus making DNA a major source for phylogenetic inference (for a review, see, e.g., Vogler and Monaghan 2007, Bybee *et al.* 2010). Although, in entomology, the use of morphological data for phylogenetic analyses remains prevalent (Scotland *et al.* 2003, Bybee *et al.* 2010), the value of these types of studies (often called “traditional”) was recently depreciated (Packer *et al.* 2009; see also reaction to this paper by Hołyński 2010). Nevertheless, this “traditional” taxonomy, despite suffering from a shortage of funds, remains in good health, as also do “traditional” taxonomists (see: e.g., Hołyński 2010, Bybee *et al.* 2010, Assis and Rieppel 2011).

It is obvious, that wrong taxon identification may affect results of taxonomic and phylogenetic studies of any kind. Herein, we draw attention to the fact that a researcher’s responsibility for proper taxon identification and its naming is even much larger in molecular studies than in any other means of identification, because accession to the GenBank database is free for everyone, and the data obtained from GenBank are included in dozens of different phylogenomic and phylogeographic studies each year.

In true-bugs (Insecta: Hemiptera: Heteroptera), molecular data are useful in phylogenetic analyses (for reviews, see: Li 2006, Liu *et al.* 2007). Pending our molecular studies on different pentatomomorph bugs (Lis *et al.* 2011), we have noticed a discrepancy concerning the species names obtained from GenBank, and their current taxonomic status. We have also noticed the disagreements between the GenBank accession numbers for sequences of some pentatomoid taxa, and the accession GenBank numbers published in the original papers where those taxa were analysed.

Methods

Molecular data relating to three pentatomoid families (i.e., Cydnidae, Dinidoridae, and Thyreocoridae) deposited in the NCBI GenBank have been searched through. Taxon information received from GenBank was analyzed with regard to its identification accuracy, a proper taxon name and its genus affiliation, its current taxonomic status, and a GenBank sequence accession number(s).