



DNA barcodes reveal that the widespread European tortricid moth *Phalonidia manniana* (Lepidoptera: Tortricidae) is a mixture of two species

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Abstract

During efforts to generate DNA barcodes for all North European Lepidoptera, *Phalonidia manniana* (Fischer von Röslerstamm, 1839) was found to comprise two genetically distinct clusters. Morphological investigation further supports the existence of two distinct taxa, *P. manniana* and *P. udana* Guenée, 1845, **sp. rev.** Their biologies also differ, *P. manniana* feeding in stems of *Mentha* and *Lycopus* (Lamiaceae) and *P. udana* feeding in stems of *Lysimachia thyrsoflora* and *L. vulgaris* (Primulaceae). We provide re-descriptions of both taxa and DNA barcodes for North European *Phalonidia* and *Gynnidomorpha*. *Phalonidia tolli* Razowski, 1960, **syn. nov.**, is considered a junior synonym of *Pudana*. *Phalonidia udana* is widely distributed in the North Palaearctic, whereas it seems to be rare or missing in large parts of Central Europe. The study demonstrates the usefulness of DNA barcoding in revealing cryptic species.

Key words: Cochylini, cryptic species, DNA barcoding, *Gynnidomorpha*

Introduction

The idea that a short standard region of organism genome could serve as a universal tag for species identification is less than 10 years old (Hebert et al. 2003a). During that period it has become apparent that the animal barcode, the 5' fragment of the cytochrome c oxidase subunit I gene, works well overall for that purpose. Over 90% of species have unique DNA barcodes (e. g. Hebert et al. 2003b; Hogg & Hebert 2004; Ball & Hebert 2005; Ward et al. 2005; Cywinska et al. 2006; Hajibabaei et al. 2006; Costa et al. 2007; Kerr et al. 2007; Footitt et al. 2008; Rach et al. 2008; Hebert et al. 2009; Kerr et al. 2009; Lukhtanov et al. 2009; Robinson et al. 2009; Sheffield et al. 2009; Zhou et al. 2009; Dinca et al. 2010; Hausmann et al. 2011). There has been much debate whether the allocation of funds for barcoding research will speed up or impede taxonomy (Will & Rubinoff 2004; Ebach & Holdrege 2005a, 2005b; Will et al. 2005; Rubinoff et al. 2006). A growing number of taxonomic works largely based on information on barcodes have shown that barcodes are indeed very useful not only in identification of previously known species, but also in sorting material of poorly investigated taxa (Smith et al. 2005; Smith et al. 2008; Smith et al. 2009), which is the first step towards a better understanding of biodiversity. Barcodes have proven especially useful in revealing species that have remained unnoticed from morphological investigation alone (Hausmann et al. 2009a; 2009b; Segerer et al. 2010; Huemer 2011; Huemer & Hebert 2011). Even though DNA barcoding generates information rather than knowledge at the beginning (Ebach & Holdrege 2005), a large number of taxonomic works have demonstrated that this information makes taxonomists more knowledgeable (see Schindel & Miller 2005) and consequently increases our knowledge of biodiversity. The present work is an example of how careful examination