Erratum: Complex MtDNA Variation and Species Delimitations in the Phyciodes tharos Species Group (Nymphalidae: Melitaeini): A Second Look in Michigan and Ohio

Author: Proshek, Benjamin

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ERRATUM: COMPLEX MTDNA VARIATION AND SPECIES DELIMITATIONS IN THE *PHYCIODES THAROS* SPECIES GROUP (NYMPHALIDAE: MELITAEINI): A SECOND LOOK IN MICHIGAN AND OHIO

Editor's note: The above article (Proshek and Houghton 2012) was published in issue 66(1) with an unfortunate error. Throughout the manuscript, one species name (*batesii*) was replaced by another (*cocyta*) (excluding the figures, table and appendix). This error rendered the meaning of much the article unintelligible. This short note is meant to give a brief synopsis of the text so that, when combined with the figures, table and appendix in the original article, readers of the article may understand the significance of the research. Readers are also reminded that the corrected original article is available in .pdf format online from the Lepidopterists' Society website or by contacting the author at the email address given at the end of this note.

The Nearctic genus *Phyciodes* is a taxonomically interesting group of butterflies. In particular the North American *P. tharos* species group (*P. tharos*, *P. cocyta*, *P. batesii* and *P. pulchella*) has posed several historical taxonomical challenges due to their phenotypic similarity and variability and apparently incomplete reproductive isolation (Oliver 1980; Porter and Mueller 1998; Scott 1998). The specific status of *Phyciodes tharos* and *cocyta* in particular are controversial, the latter having been relatively recently raised to species status from a subspecies of *tharos* (Scott 1994), but not to a consensus of lepidopterists (e.g., Glassberg 1999).

Wahlberg et al. (2003) conducted the first molecular analysis of the genus *Phyciodes*, sampling 140 specimens from all ten North American *Phyciodes* species and sequencing 1450 base pairs of the mitochondrial gene cytochrome oxidase I (COI). Their findings largely supported previous research based on morphology and ecology, except for the suggestion that *P. cocyta* was not as closely related to *P. tharos* as it was to *P. batesii*. The purpose of Proshek and Houghton (2012) was to re-examine the relationship between *P. tharos*, *P. cocyta* and *P. batesii* in a limited geographic area (the lower peninsula of Michigan and northwest Ohio), where the ranges of those three species coincide (*P. pulchella* is not found in the East) (Fig. 1).

We sequenced 40 novel COI sequences (5 *P. tharos*, 10 *P. batesii*, and 25 *P. cocyta*) and constructed a split network. We also combined those sequences with 78 sequences from Wahlberg et al. (2003) and generated a maximum-likelihood phylogenetic tree.

In the split network, two distinct clusters were formed: one containing all five *P. tharos*, and the other all 10 *P. batesii* (Proshek and Houghton 2012, Fig. 2). Of the 25 *P. cocyta* sequences, 20 were found with the *P. tharos* sequences, and five with the *P. batesii* sequences. Of those five, two were two of the three *P. cocyta* collected from Otsego Co., MI, the only sampling location where *P. batesii* was the most numerous *Phyciodes* present. On the other side of the network, one of two *P. cocyta* sequences that clustered most closely to the *P. tharos* sequences was the lone *P. cocyta* collected from Ionia Co., MI, which was by far the geographically closest site to where all the *P. tharos* were sampled (Lucas Co., OH) (Appendix).

In the combined maximum-likelihood tree, our results closely mirrored the parsimony tree of Wahlberg et al. (2003) in topology and branch support (Fig. 3). The tree of Wahlberg et al. (2003) had a "*tharos*" clade, a "*cocyta/batesii*" clade, and a "*pulchella*" clade. Of our novel sequences, all of the *P. tharos* and 20 of the 25 *P. cocyta* clustered in the "*tharos*" clade, and the remaining five *P. cocyta* along with all of the *P. batesii* clustered in the "*cocyta/batesii*" clade (Table 1).

Our results suggest that: (i) mitochondrial introgression may be occurring between *P. cocyta* and both *P. tharos* and *P. batesii* in our area of study, and (ii) that *P. cocyta* is in fact more closely related to *P. tharos* than *P. batesii*, at least in our area of study, in contrast to the conclusion suggested by Wahlberg et al. (2003). The evidence for assertion is that: (i) in Fig. 1 (Proshek and Houghton 2012), none of the three species form an exclusive split; (ii) two of the three *P. cocyta* from Otsego Co., MI cluster with the *P. batesii* samples from Otsego Co., MI, despite three-quarters of the *P. cocyta* sequences clustering with the *P. tharos* sequences; (iii) in Fig. 3 (Proshek and Houghton 2012) four-fifths of our novel *P. cocyta* sequences, as well as all five of our *P. tharos*, cluster in the "*tharos*" clade of the phylogenetic tree, not the "*cocyta/batesii*" clade.

It is hoped that this study will help to clarify some questions on the relationships among the members of the *Phyciodes tharos* species group, and especially that it may inspire future research. An analysis incorporating nuclear genes in particular may help to clarify matters.

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BENJAMIN PROSHEK, *Department of Biology, Hillsdale College, 33 East College Street, Hillsdale, MI 49242; email: bproshek@gmail.com*

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