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A revision of the *Schinia volupia* (Fitch) species complex (Lepidoptera: Noctuidae: Heliothinae)

MICHAEL G. POGUE[1,4], GARY D. OUELLETTE[1] & CHARLES E. HARP[2,3]

[1]*Systematic Entomology Laboratory, PSI, Agricultural Research Service, U. S. Department of Agriculture, c/o Smithsonian Institution, P.O. Box 37012, NMNH, MRC-168, Washington, DC 20013-7012, USA.*
E-mail: michael.pogue@ars.usda.gov; gary.ouellette@ars.usda.gov
[2]*Research Associate: C. P. Gillette Museum of Arthropod Diversity, Colorado State University, Ft. Collins, CO 80523.*
[3]*8834 Quarto Ave., Littleton, CO, 80128, USA. E-mail: cehmoth@aol.com*
[4]*Corresponding author*

Abstract

DNA barcode analysis of cytochrome oxidase I (COI) could not differentiate between the species of the *Schinia volupia* (Fitch, 1868) complex including *S. volupia, S. masoni* Smith, *S. fulleri* (McElvare, 1961); *S. sanrafaeli* Opler, 2004; *S. miniana* (Grote, 1881); and *S. biforma* Smith, 1906. Genitalic characters could only differentiate *S. biforma* from the *S. volupia* complex. Based on forewing color and pattern, larval host plant utilization, and geographic distribution, *S. volupia*, *S. sanrafaeli*, *S. fulleri*, and *S. miniana* are recognized as valid species and *S. masoni* is considered a **new synonym** of *S. volupia*. *Schinia volupia, S. fulleri, S. sanrafaeli, S. miniana,* and *S. biforma* are diagnosed and described. A variety of adult images are presented to show the range of variation among these species. Male and female genitalia of all included taxa are illustrated. Host plant utilization is discussed and illustrated. Distribution maps for examined specimens are provided.

Key words: DNA barcoding, COI, taxonomy, synonymy, host plants

Introduction

Four species were recognized as being closely related to the widespread *Schinia volupia* (Fitch, 1868): *S. masoni* (Smith, 1896); *S. sanrafaeli* Opler, 2004; *S. fulleri* (McElvare, 1961); and *S. miniana* (Grote, 1881). Using routine DNA barcode analysis of cytochrome oxidase I (COI) these species could not be differentiated. *Schinia biforma* Smith would sometimes be distinguished in neighbor joining tree runs and in other runs *S. biforma* would be included in the *S. volupia* complex. When male and female genitalia were studied, no distinguishable differences were found, except for differentiating *S. biforma* from the *volupia* complex. Based on forewing color and pattern and larval host plants five species were recognized: *S. volupia, S. sanrafaeli, S. fulleri, S. miniana,* and *S. biforma*.

DNA barcoding uses a 648-bp region of COI as a tool for differentiating species and for finding cryptic species imbedded within presumed morphologically distinct species (Burns and Janzen 2001, 2005; Hebert *et al.* 2004; Ball and Armstrong 2006; Hajibabaei *et al.* 2006; Smith *et al.* 2006; Burns *et al.* 2007, 2008). There has been discussion involving closely related species that have identical or overlapping barcodes that can lead to a varying degree of misidentification using COI barcodes (Hajibabaei *et al.* 2006 (Lepidoptera: Hesperiidae); Elias *et al.* 2007 (Lepidoptera: Ithomiinae); Wiemars and Fiedler 2007 (Lepidoptera: Lycaenidae)). In a study of 315 species of Lepidoptera from the Area de Conservación Guanacaste (ACG) in Costa Rica, only 2.1% could not be differentiated based on the COI barcode (Hajibabaei *et al.* 2006). The examples given were all in the family Hesperiidae and included three species in the genus *Phocides* and two species in the genus *Polyctor* that formed mixed-species clusters, or COI was unable to differentiate the species within each mixed cluster. However, these taxa were deemed to be morphologically and ecologically distinct (Hajibabaei *et al.* 2006). In a study of 58 species of Ithomiinae from two sites across the Rio Napo in eastern Ecuador only 68–77% were successfully identified

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