



United States
Department of
Agriculture

Forest Service

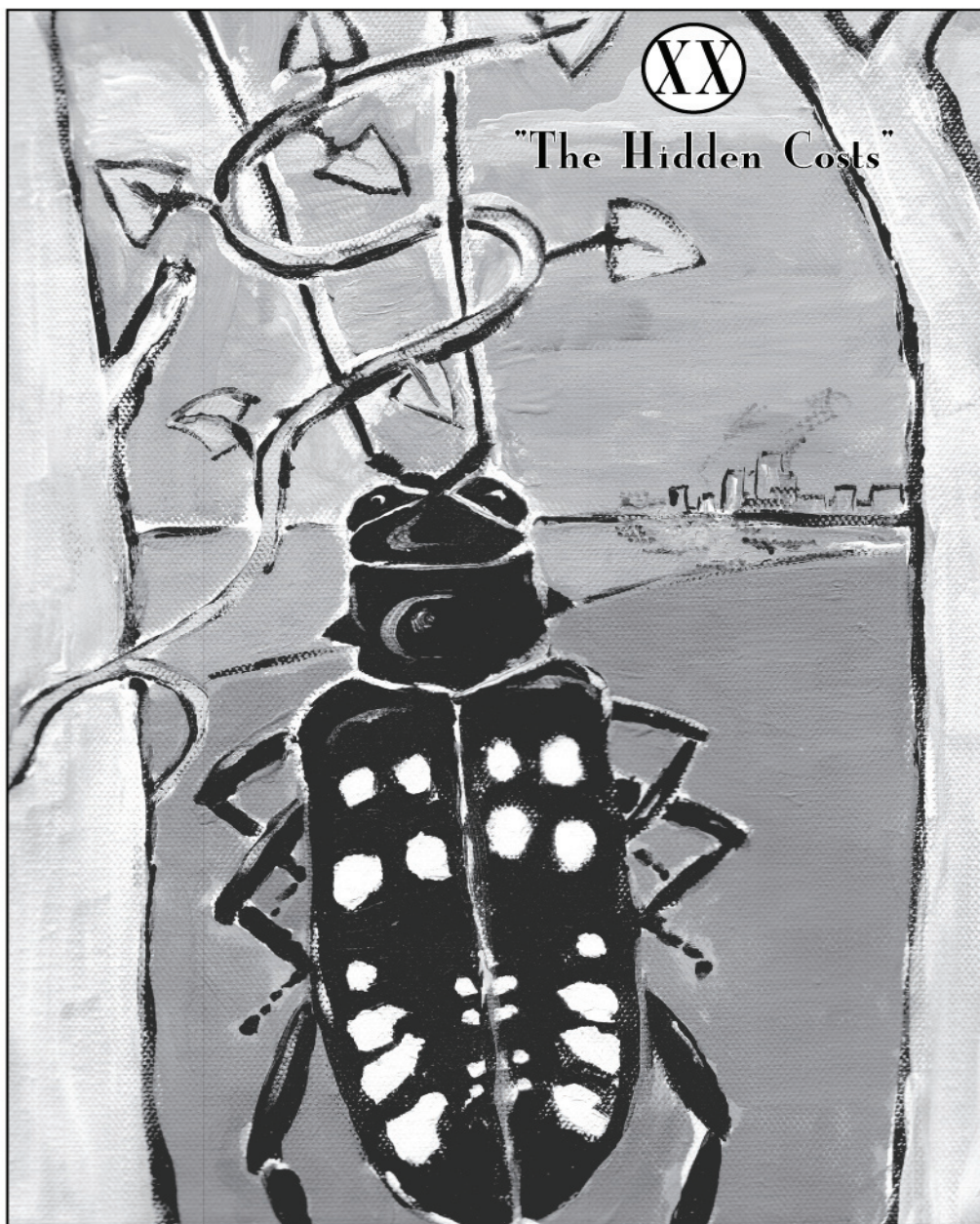
Northern Research
Station

General Technical
Report NRS-P-51



Proceedings

20th U.S. Department of Agriculture Interagency Research Forum on Invasive Species 2009



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"The Hidden Costs"

USDA RESEARCH FORUM
on INVASIVE SPECIES

January 13-16, 2009
Annapolis, Maryland

ADDITIONS AND CORRECTIONS TO BARCODE LIBRARIES FOR *LYMANTRIA* SPP.

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ABSTRACT

The genus *Lymantria* includes a number of destructive forest pests such as the gypsy moth (*L. dispar*) and nun moth (*L. monacha*) in various regions across the northern hemisphere. A number of species have been transported beyond their native range, either intentionally or in conjunction with international trade. Egg masses of both *L. mathura* and *L. dispar asiatica* were recovered from vessels during quarantine inspections on the west coast of both Canada and the United States in the early 1990s. Populations of *L. dispar asiatica* that established in Vancouver, BC, Portland, OR and Seattle, WA, were subsequently eradicated at great expense. Populations of *L. dispar* and *L. mathura* are again increasing in Asia and viable egg masses of both species have been detected on vessels arriving in ports on the west coast of North America.

Multiple molecular studies have used the mitochondrial gene cytochrome c oxidase I (COI) to distinguish species or haplotypes of *Lymantria* species. Nomenclatural changes from a recent morphological revision have given rise to

errors in the species names associated with molecular data deposited in GenBank. We recently sampled additional specimens of *Lymantria dispar asiatica*, *L. mathura* and *L. monacha* from the Russian Far East, *Lymantria dispar* from regulatory interceptions in British Columbia, and additional specimens of *L. mathura* from Japan. The nearest-neighbor joining tree generated from COI data in GenBank in combination with the COI barcodes we generated provides genetic confirmation that *Lymantria mathura* from Japan is conspecific with populations from South Korea and the Russian Far East. The taxon previously reported as *L. mathura* from Japan (Okinawa) was recently described as a new species, *L. flavida*. The GenBank COI records [DQ116087 & DQ116088] attributed to *L. mathura* actually represent sequence data for *L. flavida*. Another five records attributed to *L. dispar* (or the subspecies *L. d. hokkaidensis*) in GenBank [DQ116179, DQ116180, DQ116181, DQ116182 and DQ116126] are now considered to be the species *L. umbrosa*. We also provide additional barcode sequences for *L. dispar* and *L. monacha* from the Russian Far East.