

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

Leland Humble¹, Jeremy de Waard², Robin Floyd³,
João Lima³, and Robert Hanner³

¹Natural Resources Canada, Canadian Forest Service,
Victoria, BC, Canada V8Z 1M5

²University of British Columbia, Forest Sciences Department,
Vancouver, BC, Canada V6T 1Z4

³University of Guelph, Biodiversity Institute of Ontario &
Department of Integrative Biology, Guelph, ON, Canada N1G 2W1

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.