

GENETIC ASPECTS OF INVASIVE LEAF MINERS—EXAMPLES OF THREE SPECIES INTRODUCED RECENTLY TO EUROPE

Ferenc Lakatos¹, Zoltán Kovács¹, Christian Stauffer², Charles Covell³ and Donald R. Davis⁴

¹Institute of Forest and Wood Protection, West-Hungarian University, Sopron, 9400, Hungary

²Institute of Forest Entomology, Forest Pathology & Forest Protection, BOKU, University of Natural Resources & Applied Life Sciences, Vienna, 1190, Austria

³Department of Biology, University of Louisville, Louisville, KY 40292, USA

⁴Smithsonian Institution, National Museum of Natural History, Washington D.C., 20560-0127, USA

Abstract

Three invasive leaf miner moth species *Parectopa robiniella* Clemens 1863, *Phyllonorycter robiniella* Clemens 1859 and *Cameraria ohridella* Deschka et Dimic 1986 using mtDNA sequences and PCR-RAPD were investigated during this study. Populations were from North America and Europe.

All three, invasive species belong to the Gracillariidae (superfamily Gracillarioidea), a large, cosmopolitan family of over 2000 recognized species, with probably even greater number of species awaiting discovery. The genus *Parectopa* is a member of the largest, but far most diverse subfamily, Gracillariinae. *Phyllonorycter* and *Cameraria* are the largest genera within the Lithocolletinae, a subfamily currently including approximately 10 genera. *P. robiniella* and *Ph. robiniella* originated from North America. *C. ohridella* was first described in 1986 from the Ohrid lake region in Macedonia and in only a few years the moth dispersed over the entire European continent.

We used mitochondrial DNA markers for screening genetic diversity. 500-600 bp long fragments of the COI

gene were sequenced. A significant variation of 0.7% in the mtDNA was detected in *P. robiniella* and in that species the European and North American populations could be separated. The statistical analysis indicates that the Hungarian haplotypes are derived from the American ones. In the other two species, *Ph. robiniella* and *C. ohridella* no substitutions could be detected among the populations. The complement PCR-RAPD analysis in *C. ohridella* revealed differences in the genetic similarities according to their spreading. However, more populations and markers have to be analysed to obtain a more stable dataset.

The origin of *C. ohridella* is still not known. Thus it might be reasonable to investigate either the host tree or the origin of closely related species living on the same tree. Both in North America and in Asia (Japan) *Cameraria* species can be found on different *Aesculus* species. Regarding host switches from *C. ohridella*, species living on *Acer* (e.g. *A. rubrum* L.) like *Cameraria aceriella* Clem. should be taken into consideration for analysis.