

Population genetic structure of the invasive plane leaf miner (*Phyllonorycter platani* STRG. 1870)

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The plane leaf-miner (*Phyllonorycter platani* Stgr. 1870) is one of the most important invasive leaf miner species in Europe. This moth is oligophagous, its host plants are restricted to the genus *Platanus* and the primary hosts are *Platanus orientalis* and *P. × hispanica*. We hypothesize, that the major host is *Platanus orientalis*, and *Phyllonorycter patani* is native to the autochthonous distribution area of *P. orientalis*.

Our aims were to test: Whether the native area of the moth correlates with the native area of *Platanus orientalis*? Where is the gene pool of this moth species? What is the level of genetic variation in its native area? Whether the genetic variability dispersal models are similar to the available faunistic models? Is there any bottleneck effect?

In order to answer these questions we have collected *P. platani* populations from Europe, Central-Asia and North-America (altogether 21 populations, including 4 from autochthonous *P. orientalis* stands). We have analyzed a 1400bp long fragment of the mitochondrial DNA (COI gene).

We identified altogether 16 haplotypes. Three of them are unique for Central-Asia, one of them for North-America. HT-1 and HT-2 (the most common haplotypes) are represented in all European population and in North-America. Populations in the autochthonous area (South-Italy and Greece) show higher diversity, in Italy with one, in Greece with five unique haplotypes.

Our first results support the hypothesis, that *P. platani* is native to the autochthonous distribution of its main host *P. orientalis*. However, there are still several open questions. To find an adequate answer to them we have to increase the number of the investigated populations and apply other molecular genetic methods.

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