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## RESEARCH ARTICLE

# Genetics of currant clearwing moth (Lepidoptera: *Sesiidae*)

Gábor Gyulai<sup>1</sup>, Renée P Malone<sup>2</sup>, Gábor Zs Gyulai<sup>3</sup>, Péter Lehoczky<sup>3</sup>, Zoltán Tóth<sup>3</sup>

<sup>1</sup>Institute of PhD Schools, MATE University, Gödöllő, Hungary

<sup>2</sup>TUDublin University, Dublin, Ireland

<sup>3</sup>MATE University, Gödöllő, Hungary

Corresponding author: [gyulai.gabor@uni-mate.hu](mailto:gyulai.gabor@uni-mate.hu) and [gyulaigabodr@gmail.com](mailto:gyulaigabodr@gmail.com)

**Abstract** – A group of clearwing moths *Sesiidae* (*Syn.: Aegeriidae*) is analyzed here with special emphasis on genetics of *currant clearwing moth* (*Synanthedon tipuliformis*, CLERCK 1759). DNA sequences of the longest (1544 nt) available sequence of *Sesiidae* genes *Co1* (cytochrome oxidase subunit-1 of mitochondrial DNA, mtDNA) (mtDNA; *NCBI# AJ864359.1*) were analyzed after *In silico* data mining, and dendrogram was edited to reveal molecular diversity and genetic distances among *Sesiidae* species. Batesian mimicry, sexual dimorphism, and genetics and genomics of *Sesiidae* are indicated.

**Keywords** – *Sesiidae*, DNA sequences, dendrogram analysis

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## INTRODUCTION

Clearwing diurnal moths of *Sesiidae* (*Hung.*: “*üvegszárnyú lepkék / darázslepkék / szitkárók*”) comprise about 1500 species of 160 genera with about 51 subspecies in the world. By global regions, *Sesiidae* show different species numbers including Australia and Pacific Island (58 species) (Kallies, 2020), Ethiopian region (237 species), Nearctic region (121 species), Neotropical region (268 species), Oriental region (415 species), Palearctic region (347 species) (Pühringer and Kallies, 2004).

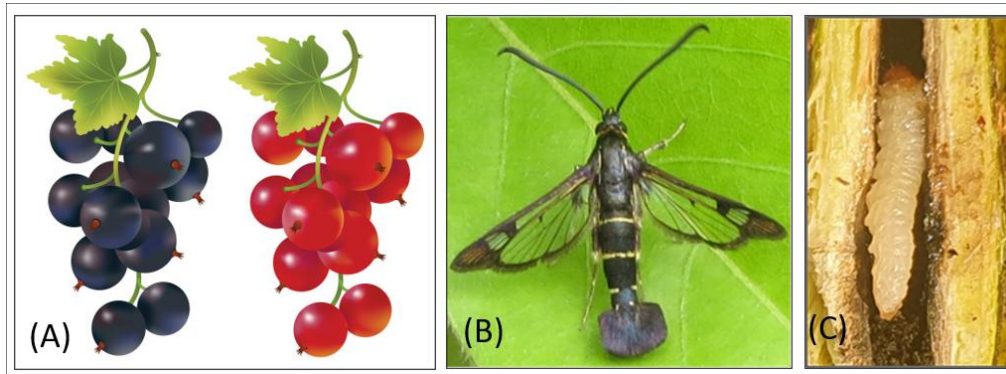
In Europe 107-120 species have been recorded including the 46-47 species described in Hungary (Mészáros and Szabóky, 2005; Lastuvka and Lastuvka, 2001; Gozmány, 1979; Szelényi, 1964; web1-3) (Fig. 1). In Japan, 39 *Sesiidae* species have been identified (Arita, 1994).

The global spread of *Sesiidae* species presents new challenges to plant protection. *E. g.*, *Synanthedon tipuliformis* (Fig. 2) (*Eng.*: currant clearwing moth; *Hung.*: “*ribizliszitkár*”) seriously damages black- and red currant (*Ribes nigrum* and *-rubrum*) (Simoncsics, 2017) plantations in Hungary (personal communication, 1986, Sándor Gyulai, 1923–2000).

The first occurrence of currant clearwings moth in Japan was reported in 2010 (Murai *et al.*, 2010). New *Sesiidae* species (Edwards, 1981) and forms (Edwards, 1982) are discovered continuously (Liang and Hsu, 2015). New species of *Scalarnathia [Bombecia] kaszabi* (Kallies and Pühringer, 2004). a long-legged clearwing moth (*Teinotarsina aurantiaca*) (Yagi *et al.*, 2016), and *Bombecia pallasi* (Gorbunov, 2020) was registered also recently.



**Figure 1.** The hornet clearwing (*Sesia apiformis*) of male (left; ♂) and female (right; ♀) and living in poplar trunk. (*NCBI# txid748215*). Photo by *D Balogh* (source: *web1a*)



**Figure 2.** Berries of black and red currant (*Ribes nigrum* and *-rubrum*) (A) (source: [web1a](#)); a photo of currant clearwing moth (*Synanthedon tipuliformis*) (female, ♀; wingspan: 1.5 – 2.0 cm) (B) (Hung.: “ribizliszitkár”) (photo by [S Nagy](#); source: [web1b](#); license CC BY 4.0); and its larva (C) bored into *Ribes* trunk (length: ~1 cm) (photo by [G.Zs. Gyulai](#)).

Larvae of *Sesiidae* bore into trunks, stems, roots or bark of trees, shrubs, and annual plants. In case of fruit trees like apple and shrubs like *Ribes* the damage is considerable. Nevertheless, borers of *Sesiidae* larvae may have roles in the turnover of lignin in the ecocycles, similar to the other wood boring insects such as Coleoptera (Eng.: beetles; Hung.: “bogarak”) like *Lucanidae* (Eng.: stag beetles; Hung.: “szarvasbogarak”), and *Cerambycidae* (Eng.: longhorn beetles; Hung.: “cincérek”).

#### MOLECULAR EVOLUTION

Evolutionarily, *Sesiidae* seem to follow Batesian mimicry (named after HW Bates, 1825–1892) by exhibiting a wasp like appearance similar to hower flies (Hung.: “viráglegyek”) (*Syrphidae*) with 6000 species including the 390 species described in Hungary (Tóth, 2011), and *flower longhorn beetles* (*Lepturinae*) (Hung.: “virágcincérek”) with about 35.000 species found globally

Henry Walter Bates assumed that harmless species could survive (*i.e.*, evolve / change) more successfully by imitating (*i.e.*, mimicry) the bodies of harmful species (*e.g.*, wasps and bees). For this appearance the wings of *Sesiidae* species lost the wing scales (the colored powder of butterfly wings), and it was coupled with wasp-like yellow/white/red belts appearance in the abdomen of moths (Fig. 1, and 2).

However, unlike Bates or Darwin (1859), geneticists, recently, seem to assume that mimicry in the evolution happens accidentally without any evolutionary directions, except natural selection and drift (Behe, 2007).

Natural selection in butterflies coupled with sex preference were analyzed recently in *Colias crocea* populations (Eng.: sulfur; Hung.: “sáfránylepke”) where two female (♀) types were identified (personal communication, 1969, László Bizsilla, 1903 – 1983; Gyulai *et al.*, 1969, 1978). Sex advantage of orange winged females (♀) “remained” stronger compared to the “new” white winged females (♀), which developed by transposon insertion (Alzohairy *et al.*, 2014) from orange winged female (♀); and the transposon broke the development of orange/yellow wing color by

suppression of *BarH-1*, a homeobox transcription factor gene (Woronik *et al.*, 2019). The name ‘Bar’ comes from a *Drosophila* sex-linked narrow eye mutation ‘barred’ (which looks ‘like a bar’) (Tice, 1914).

#### GENETICS AND GENOMICS OF *SESIIDAE*

DNA sequences (Jenser, *et al.*, 2001; Gyulai *et al.*, 2011) of total genomes of three *Sesiidae* species are available at Genbank NCBI (by 2022).

The median total genome length of *Synanthedon vespiformis* (Eng.: yellow-legged clearwing; Hung.: “szederszitkár”) has a 0.267886 x 10<sup>9</sup> DNA nt size genome (NCBI# *ilSynVesp1.1*); *Bembecia ichneumoniformis* (Eng.: six-belted clearwing; Hung.: “fűrész szitkár”) has a genome of 0.47526 x 10<sup>9</sup> DNA nt genome (NCBI# *ilBemIch1.1*); and the *Sesia apiformis* (Eng.: hornet clearwing; Hung.: “darázslepke”) has 0.513794 x 10<sup>9</sup> DNA nt (NCBI# *txid748215*) (Fig. 3.a) (NCBI - National Center for Biotechnology Information). Genbanks provide further sequences data of 56 *Sesiidae* species (by 2022).

*Sesiidae* genome sizes compared to other butterflies show the same range; *e.g.*, *Papilio machaon* (Eng.: swallowtail butterfly / Hung.: “fecskefarkú lepke”) has a 0.255982 x 10<sup>9</sup> DNA nt size genome (NCBI# *ilPapMach1.1*); and *Bombyx mori* (Eng.: silkworm; Hung.: “selyemhernyó”) has a some larger of 0.429019 x 10<sup>9</sup> DNA nt size genome (NCBI# *txid7091*).

For comparative genetic analysis, the longest (1544 nt) available sequence of *Sesiidae* genes *Co1* (cytochrome oxidase subunit-1 of mitochondrial DNA, mtDNA) was analyzed here to find the closest related genera and species to *Synanthedon tipuliformis* (NCBI# *AJ864359.1*) (branch-I, Fig. 3.b) which was found to be *S. soffneri*.

*S. soffneri* feeds on *Lonicera* bushes. *S. spheciformis* feeds on *Alnus* trees; *S. formicaeformis* feeds on *Salix* trees. These wide ranges of host plant patterns seem not to show correlations with appearances of *Sesiidae* species and the source of feeding plants.



**Figure 3.a.** Samples of two DNA stretches (60 nt each) with low (a) and high (b) levels of DNA nucleotide differences (block letters in color) of sequences of *Co1* gene subunit-1 (mtDNA; NCBI# AJ864359.1; 1544 nucleotides) of currant clearwing (*Synanthedon tipuliformis*) and related species. Sequences were downloaded from NCBI (source: web7) and

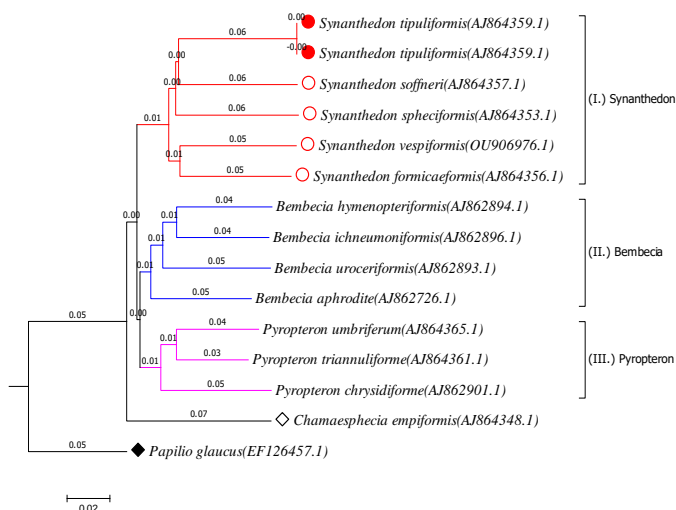
**SEXUAL DIMORPHISM**

*Sesiidae* species show high rates of sexual dimorphism by wing and body coloration and sizes. Females (♀) have larger body size than males (♂) (Fig. 1). *E.g.*, the uniquely large hornet clearwing moth (*Sesia apiformis*) (Hung.: “darázslepke”) (Fig. 1) which lives in poplar (*Populus* ssp.) trunk has a wingspan of about 2.8–3.3 cm (males, ♂), and 3.4–5.0 cm (females, ♀) (source: web4-6).

The clearwing character is not rare in Lepidoptera; the clearwing hummingbird moths (*Hemaris thysbe*), and the gardenia bee hawk (*Cephonodes kingii*), both of *Sphingidae* (Hung.: “szenderek”), are also clear winged by losing the wing-scales early after developing from pupa.

**CONCLUSIONS**

*In silico* genetic analysis of a small, impressive but very harmful pest of currant clearwing moth (*Synanthedon tipuliformis*) showed the closest relation to *Synanthedon soffneri* based on sequences analyses of *Co1* gene subunit-1 (mtDNA) (source: web7). Species of the three main *Sesiidae* genera of *Synanthedon*, *Bembecia* and *Pyropteron* were sharply discriminated based on dendrogram analysis. The wide ranges of host plants of *Sesiidae* species were not found to correlate with the diverse source of feeding plants. Mimicry and pest damage of larvae of clearwing moth species and their role in the turnover of wood lignins (Gyulai *et al.*, 2018) in the ecological cycles were indicated.



**Figure 3.b.** Genetic distances among *Sesiidae* species. Sequences of *Co1* gene subunit-1 (mtDNA) of currant clearwing (*Synanthedon tipuliformis*) (●) (Hung.: “ribizliszitkár”) were aligned (1544 nucleotides, NCBI# AJ864359.1). Dendrogram analysis was run by Neighbor Joining algorithm of NCBI server (source: web7) and edited by MEGA7 computer program (Kumar *et al.*, 2016). Main branches (I.-III.), branch lengths, NCBI gene bank numbers, and unit of genetic distance (0.02) are indicated, which gives the numbers of nucleotide substitutions along a 100 nt DNA stretch. For outgroup, diurnal butterfly *Papilio glaucus* (◆) are indicated.

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## WEB SOURCES

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web1b. <https://www.google.com/search>

web2. [microlepidoptera.hu](http://microlepidoptera.hu)

web3. <http://www.pyrgus.de>

web4. *Catalogue of Lepidoptera of Belgium*

web5. <https://projects.biodiversity.be/lepidoptera/species/4911/#>

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web7. <https://www.ncbi.nlm.nih.gov>

