proceedings

MDPI

Proceedings

Genetic Diversity of the Invasive Sycamore Lace Bug (SLB), *Corythucha ciliata* (Say, 1832) (Tingidae, Hemiptera), in Its Native and Invaded Areas †

Ferenc Lakatos [1,*], Katalin Tuba [1], Jenő Jakab [1], Boglárka Bender [1], Angéla Kalocsai [1], Alexandra Porcsin [1], Réka Szőke-Wittich [1], Hisashi Kajimura [2], and Viktória Tóth [1]

[1] Institute of Forest and Natural Resource Management, Faculty of Forestry, University of Sopron Bajcsy-Zsilinszky u. 4, H–9400 Sopron, Hungary; lakatos.ferenc@uni-sopron.hu (F.L.), tuba.katalin@uni-sopron.hu(K. T.), jakab.jeno@uni-sopron.hu(J. J.), bender.bogi.amelie@gmail.com (B. B.), KalocsaiA15@student.uni-sopron.hu (A. K), porcsin.alexandra@phd.uni-sopron.hu (A.P.), wittichr15@student.uni-sopron.hu (R. S.-W.), toth.viktoria@uni-sopron.hu (V.T.)

[2] Lab. of Forest Protection, Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-8601, Japan; kajimura@agr.nagoya-u.ac.jp

* Correspondence: lakatos.ferenc@uni-sopron.hu

† Presented at the 1st International Electronic Conference on Entomology (IECE 2021), 1–15 July 2021; Available online: https://iece.sciforum.net/.

Abstract: The sycamore lace bug (SLB) (*Corythucha ciliata*) is one of the most abundant and widespread pests on plane (*Platanus* spp.) trees. 38 geographic location of *C. ciliata* from Europe, Asia and North America were analysed by sequencing. Seventeen haplotypes were detected on 1356 bp long fragment of the COI gene from 327 individuals. *C. ciliata* populations from North America showed a higher haplotype diversity (12 HTs), than populations from Europe (6 HTs) or populations from Japan (2HTs). The haplotypes formed two haplogroups, one including only North American HTs and another one including HTs from all continents.

Keywords: *Corythucha ciliata*; population genetics; phylogeny; invasive insect

Citation: Lakatos, F.; Tuba, K.; Jakab, J.; Bender, B.; Kalocsai, A.; Porcsin, A.; Szőke-Wittich, R.; Kajimur, H.; Tóth, V. Genetic Diversity of the Invasive Sycamore Lace Bug (SLB), *Corythucha ciliata* (Say, 1832) (Tingidae, Hemiptera), in Its Native and Invaded Areas, in Proceedings of the 1st International Electronic Conference on Entomology, 1–15 July 2021, MDPI: Basel, Switzerland, doi:10.3390/IECE-10572

Published: 2 July 2021

1. Introduction

To understand the success of an invasive insect species we should to know the source and pathway(s) of invasion and the spatial distribution of intraspecific diversity [1–2]. Without that knowledge we will not be able to set up efficient control measures. In the recent decades several studies have been conducted with various genetic markers to answer these questions [3–7].

The native range of *C. ciliata* is located in North America, where its main hosts are *Platanus* spp. [8]. The invasion history of sycamore lace bug across Europe is well-documented. The first found was recorded in Italy (1964) followed by a high-speed spread across the continent: 1972: Yugoslavia (Zagreb, Rijeka and Ljubljana), 1975: South France, 1976: Hungary, 1978: Spain and Austria, 1983: Switzerland, Czechoslovakia, 1986: Bulgaria, 1988: Greece, 1997: Russia, 2007 Turkey, 2008: Georgia and 2011: Macedonia. No other continent remained free, South-America: Chile (1985); Asia China (2002), Japan (2006), Uzbekistan (2017); Australia (2006); Africa: South Africa (2014) [9–19]. It spread with anemochor and antropochor transportation [10–12, 17, 20–22].

Major host plants of C. ciliata are sycamore trees (Platanus occidentalis, P. orientalis, P. acerifolia) [8, 23], but feeding have been recorded on Fraxinus sp., Morus alba, Brussonetia papyrifera, Carya ovata, Chamaedaphne sp. too [8]. However, other publication [23] reports other possible host plant species as well (Quercus laurifolia, Liquidambar

sytraciflua and Euphorbia pulcherrima), but their list doesn't include Broussonetia, Carya, Chamaedaphne or Fraxinus as host.

In the invaded areas the sycamore lace bug was found mainly on *Platanus* species [11, 21–22, 24]. However, nymphs and adults were detected also on maples (*Acer*) and ash-trees (*Fraxinus*) from Georgia [18]. Sycamore lace bug individuals are sucking on the leaves causing aesthetical damage, but they may have a role as vector of various diseases as well (e.g., *Erysiphe platani*). Sycamore is a widely used ornamental tree species in the northern hemisphere [25–28].

A few numbers of genetic studies have been already conducted on *C. ciliata* in the last decade. One single individual was analysed with microsatellites markers from China [29]. The gene expression profiles were studied [14], as a part of DNA barcode library construction project [30–31]. The whole mitogenomes compared with the avocado lace bug (*Pseudacysta perseae,* Heidemann 1908) using a genome skimming approach was published by Kocher et al. [32]. Ten populations from China, including one outgroup population for Slovenia was analysed by Yang et al. [29]. There are currently 22 COI fragment data entries for *C. ciliata* in the GenBank. Some preliminary results on *C. ciliata* have been published in 2020 [18], but this subset of data incorporates only 22 locations, 117 individuals and a short fragment (546 bp) of the COI gene.

Our aims were (i) reveal the genetic structure of a *Corythucha ciliata*. (ii) exploration of the species' phylogeographic pattern and (iii) to track back the possible introduction events of the species.

2. Materials and methods

2.1. Sampling and molecular methods

We collected nymphs and imagoes from 38 populations of *C. ciliata* from Europe, Central-Asia, Japan and North America and one of *C. arcuata* (Table S1). All samples were stored in 96% ethanol at 4°C. DNA was extracted from entire bodies using GenElute Mammalian Genomic DNA Miniprep Kit (Sigma-Aldrich), following the manufacturer's protocol. Eluted DNA was stored at -20°C.

A 1356bp long region of the COI gene was amplified for 327 individuals by using Pat (5'-TCC AAT GCA CTA ATC TGC CAT ATT A-3'), and LCO1490-J-1514 (5'- GGT CAA CAA ATC ATA AAG ATA TTG G-3') primers [35–36]. PCR conditions included an initial denaturation step at 94 ºC for 2 minutes, followed by 34 cycles at 94 ºC for 30 s, 46 ºC for 1 minute and 72 ºC for 1 minute 30 s with a final extension step that lasted 10 minutes at 72 ºC. Sequences were generated at the Eurofin's Laboratory (Ebersberg, Germany).

2.2. Data analysis

327 individuals were used for mitochondrial DNA (COI) analyses (Table S1). Sequences were visualized using FinchTV 1.4.0 (Geospiza Inc. http://www.geospiza.com/finchtv) and then aligned using ClustalX [37]. After haplotypes were identified, those represented by only a single individual were verified by additional sequencing of an independent amplicon. *C. arcuata* sequences were used as outgroups. Genetic distances were estimated using the Kimura 2-parameter, and computations were done in MEGA 5.02 [38].

2.3. Phylogenetic analyses

Maximum likelihood (ML) analysis was performed under GTR+I model with MEGA 5.02. The level of support for individual nodes was evaluated by bootstrapping with 5000 replicates. We used jModeltest 2.1.2 [39–40] to select the best model of nucleotide substitution with Akaike Information Criterion (AIC) [41].

Population structure

Patterns of molecular diversity based on the mtDNA sequences between and within populations were assessed by estimating: nucleotide diversity (π) [42], transition/transversion ratio, haplotype diversity (h) [43–44] using the software Arlequin version 3.5.1.2 [45].

QGIS 2.18.11 (QGIS Geographic Information System. Open Source Geospatial Foundation Project. http://qgis.osgeo.org) were used to project haplotype distributions and frequencies onto maps.

3. Results

Seventeen haplotypes were detected on 1356 bp long fragment of the COI gene from 327 individuals, from 38 localities (Figure 1, Table S1). Number of the variable sites was 26 (1.92%), approximately half of them were located on the barcoding part of the gene. Haplotypes were differed from each other by 1-10 polymorphic sites.

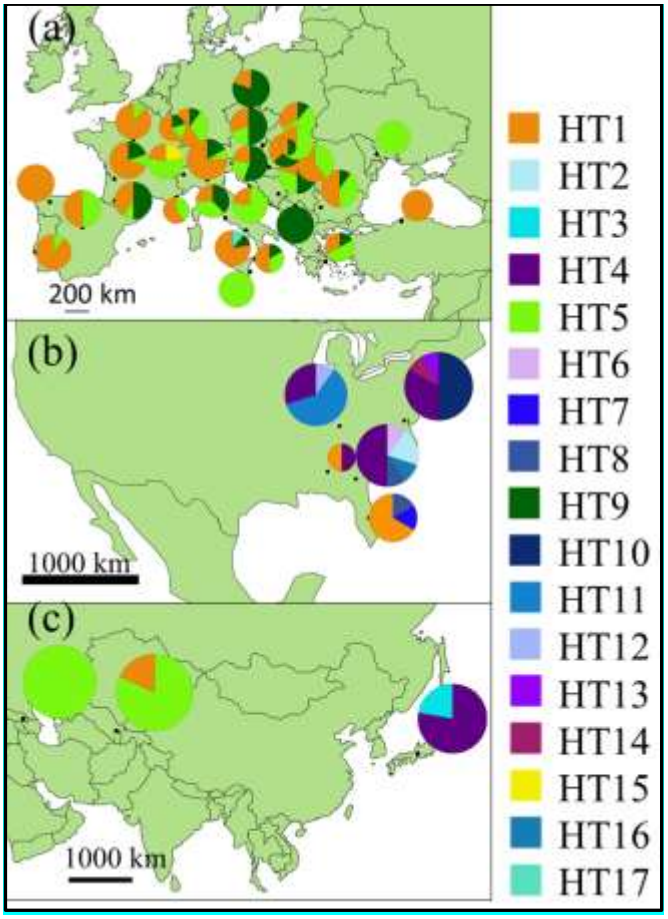

Figure 1. Distribution of *Corythucha ciliata* mitochondrial haplotypes: (**a**) in Europe; (**b**) in North America; (**c**) in Asia.

The haplotypes formed two haplogroups (A & B), which were separated by at least seven mutation steps (Figure 2.). The fourteen intermediate haplotypes were not presented in our data set. The topology of the phylogenetic tree was similar to the haplotype network. Most abundant haplotypes are HT1 (38.23% of the total dataset), HT5 (29.66%), and HT9 (17.74%). HT5 and HT9 were only detected from Europe and Central Asia. HT3 is unique from Japan. Most of haplotypes were detected from North America only (HT2, HT6-8, HT10-14, HT16; six of these are singletons). HT4 (6.12%) was found both in Japan and North America. HT15 and HT17 are unique haplotypes from Europe. The divergence between the haplotypes were 0.07-1.04% much lower than the interspecific divergence between *C. arcuata* and *C. ciliata* 8.49-8.93%.

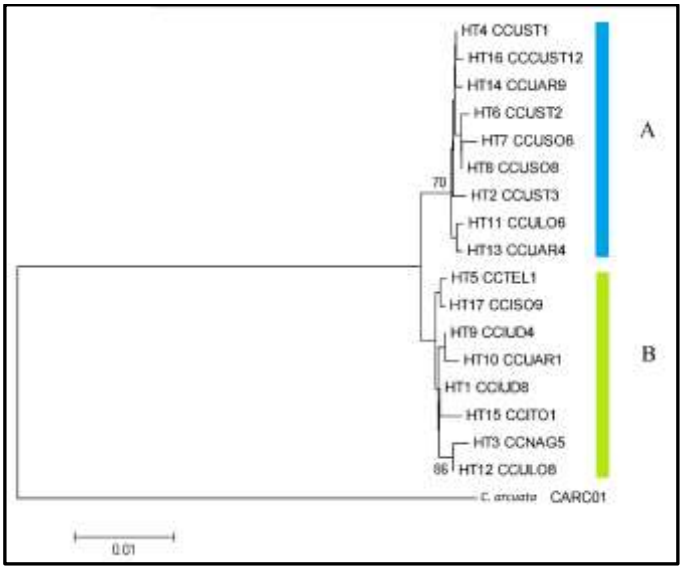

Figure 2. Phylogenetic relationship of *Corythucha ciliata* mitochondrial haplotypes. ML consensus tree of all COI haplotypes. Numbers above branches indicate ML probabilities (>0.60).

The genetic distance between populations 0.00-0.653%; within populations 0.00-0.519%, overall mean distance (TOTAL DATASET) 0.195%. Overall, haplotype diversity (h) was 0.7320 +/- 0.0136, and nucleotide diversity (π) was 0.1945 +/- 0.1152% (Table 1.).

3.1. Genetic diversity and structure in the native range - North America

Altogether twelve haplotypes were detected among the sequences of the 40 specimens collected in North America (five sampling location) and ten of them (HT2, HT6-8, HT10-14 and HT16) were unique. HT4 was the most common one (32.50%), which were found in all populations except Orlando. This haplotype was found also in Japan. HT1 and HT8 revealed two populations, all the other haplotypes were detected at single locations. Both of the two haplogroups A & B were represented in this continent (Figure 1-2). Haplotype diversity (h) was 0.8462 +/- 0.0378, and nucleotide diversity (π) was 0.3630 +/- 0.2005% (Table 1.).

Table 1. Summary of genetic diversity indices for the COI gene: (n) number of individuals sampled; (S) number of polymorphic sites; (No) number of haplotypes; (h) haplotype diversity; (π) nucleotide diversity; (Eur) Europe; (Asi) Asia; (NAm) Nort America.

group	n	No.	S	ts/tv	h ± SD	π (%)± SD
Eur	250	5	6	6/0	0.6542 +/- 0.0123	0.0937 +/- 0.0655
Asi	37	4	12	10/2	0.6562 +/- 0.0555	0.2401 +/- 0.1406
NAm	40	12	21	20/1	0.8462 +/- 0.0378	0.3630 +/- 0.2005
total	327	17	26	25/2	0.7320 +/- 0.0136	0.1945 +/- 0.1152

3.2. Genetic diversity and structure in the invaded range – Europe and Asia

Europe

Five haplotypes were detected among the sequences of the 250 specimens collected Europe (29 sampling location), two of them were common (HT1 44.40% and HT5 31.20%) and HT9 (23.20%), HT15 (0.80%), HT17 (0.40%) were unique for Europe. HT9 were common in the populations from Central Europe and the Balkan Peninsula. Europe is represented in the haplogroup B only. Haplotype diversity was (h) 0.6542 +/- 0.0123, and nucleotide diversity (π) was much lower than in North America 0.0937 +/- 0.0655 (Table 1.).

Asia

Four haplotypes were observed among the 37 specimens collected in Asia (four locations) and one of them is unique (HT3). The population from Japan differ from the other Asian populations unambiguously, because HT3, HT4 were observed only here and no other Asian or European haplotype was detected here. HT1 (24.32%) and HT5 (51.35%), which were common also in Europe, were found from Asia Minor, the Caucasus and Central Asia. Population from Japan represents (together with the north American populations) the haplogroup A, while the other three locations represent the haplogroup B. Diversity indices differ from North American values (0.6562 +/- 0.0555, π=0.2401 +/- 0.1406).

4. Discussion

Interspecific divergence of the COI gene in the plant bugs (Miridae) was reported 6.30% [46]. For the lace bugs (Tingidae), where *C. ciliata* also belongs to, Park et al. [47] detected more than 3% interspecific divergence. In our study the interspecific divergence values between *C. arcuata* and *C. ciliata* varies 8.49-8.93%.

Intraspecific distances for other Heteropteran species were reported 0–7.72% (mean distance 0.74%) [47], and for Apolygus species (Miridae) 0.40% [46]. In our study the overall mean distance was 0.195%, and the distance between populations was 0.00-0.65%. Jung et al. [46] revealed in some cases the average interspecific genetic distance between closely related species 32 times higher than the average intraspecific distance (e.g., genus Scolopocelis). In our cases we also detected 44 times higher interspecific divergence.

COI sequences of SLB showed higher genetic differentiation than avocado lace bug (*P. perseae*), where altogether 9 haplotypes from 469 individuals with 16 polymorphic sites were found [48].

On the total dataset the haplotype diversity is relatively high (h= 0.7320 +/- 0.0136), with low nucleotide diversity (π= 0.1945 +/- 0.1152%) which predict a population bottleneck followed by rapid population growth and accumulation of mutations [49]. We found high haplotype diversity with moderate high nucleotide (h= 0.8462 +/- 0.0378; π= 0.3630 +/- 0.2005) diversity in North America, which suggest a large and stable population with long evolutionary history or secondary contact between differentiated lineages [49]. In the invaded regions we found relative high haplotype diversity with low nucleotide diversity (Europe h=0.6542 +/- 0.0123, π=0.0937 +/- 0.0655; Asia h= 0.6562 +/- 0.0555, 0.2401 +/- 0.1406) which also suggest a population bottleneck followed by rapid population growth and accumulation mutations. Several authors [1, 7, 33, 50] report the loss of genetic diversity for invasive species under the process of biological invasion.

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Table S1: COI haplotypes distributions.

Author Contributions: Conceptualization, F.L., K.T., H.K. and V.T.; methodology, F.L. and V.T.; software, J.J., B.B., A.K., A.P., R.S-W. and V.T.; validation, F.L. and V.T.; formal analysis, V.T.; investigation, F.L., K.T., H.K. and V.T.; resources, F.L.; data curation, V.T.; writing—original draft preparation, F.L. and V.T.; writing—review and editing, F.L. and V.T.; visualization, V.T.; supervision, F.L.; project administration, V.T.; funding acquisition, F.L. and V.T. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by EFOP-3.6.2-16-2017-00018 program at the University of Sopron.

Informed Consent Statement: Not applicable.

Data Availability Statement: Please refer to suggested Data Availability Statements in section "MDPI Research Data Policies" at https://www.mdpi.com/ethics.

Acknowledgments: We would like to György Csóka, Bálint Horváth, Olga Antuhova, Kerry O. Britton, Rossitza Dimitrova, Karel Hradil and Ferenc Rozovits for assistance in collecting some samples.

Conflicts of Interest: The authors declare no conflict of interest.

Table 1. COI haplotype distribution.

Country	Location	n	HT1	HT2	HT3	HT4	HT5	HT6	HT7	HT8	HT9	HT10	HT11	HT12	HT13	HT14	HT15	HT16	HT17
Portugal	Lisabon	9	8				1												
Spain	Valsain	10	5				5												
Spain	Lugo	10	10																
France	Branne	10	7				1				2								
France	Coarse	10	4				1				5								
France	Paris	9	8				1												
France	Le Puy	10	6				3				1								
France	St. Räphael	5	3				2												
Italy	Parma	12	9				1				2								
Italy	Siracusa	9					9												
Italy	Solerno	9	7				0				1								1
Italy	Torino	9	2				5										2		
Italy	Udine	9	2				2				5								
Italy	Ostia	8	2				3				3								
Italy	Scilla	6	3				2				1								
Germany	Freiburg	5	3				1				1								
Czechia	Jičin	10	2								8								
Slovakia	Leva	9	3				5				1								
Hungary	Sopron	10	3				2				5								
Hungary	Sárbogárd	2	1								1								
Hungary	Szekszárd	8	3				5												
Croatia	Virovitica	8	3								5								
Croatia	Zadar	9	2				7												
Bosnia and Herzegovina	Sarajevo	10	2				3				5								
Bulgaria	Sofia	10	5				4				1								

Kosovo	Pejë	10									10								
Serbia	Belgrad	10	6				4												
Greece	Olympus	6	2				3				1								
Moldova	Trisapol	8					8												
Turkey	Karabük	7	7				0												
Georgia	Telavi	10	0				10												
Uzbekistan	Samarkand	11	2				9												
Japan	Nagoya	9			2	7													
USA	Arlington	12				4						6	0		1	1			
USA	Louisville	10				3						0	6	1					
USA	Montgomery	2	1			1													
USA	Orlando	6	4						1	1									
USA	Tifton	10		2		5		1		1								1	
total		**327**	**125**	**2**	**2**	**20**	**97**	**1**	**1**	**2**	**58**	**6**	**6**	**1**	**1**	**1**	**2**	**1**	**1**

References

1. Allendorf, F.W.; Luikart, G.; Aitken, S.N. *Conservation and the Genetics of Populations*; Second Edition.; Wiley-Blackwell, 2013;
2. Bras, A.; Avtzis, D.N.; Kenis, M.; Li, H.; Vétek, G.; Bernard, A.; Colurtin, C.; Rousselet, J.; Roques, A.; Auger-Rozenberg, M.A. A Complex Invasion Story Underlies the Fast Spread of the Invasive Box Tree Moth (*Cydalima Perspectalis*) across Europe. *Journal of Pest Science* **2019**, *92*, 1187–1202.
3. Kirichenko, N.; Triberti, P.; Ohshima, I.; Haran, H.; Byun, B.-K.; Li, H.; Augustin, S.; Roques, A.; Lopez-Vaamonde, C. From East to West across the Palearctic: Phylogeography of the Invasive Lime Leaf Miner *Phyllonorycter Issikii* (Lepidoptera: Gracillariidae) and Discovery of a Putative New Cryptic Species in East Asia. *PLoS ONE* **2017**, *12*, e0171104: 1-22, doi:doi:10.1371/journal.pone.0171104.
4. Carter, M.; Smith, M.; Harrison, R. Genetic Analyses of the Asian Longhorned Beetle (Coleoptera, Cerambycidae, Anoplophora Glabripennis), in North America, Europe and Asia. *Biological Invasions* **2010**, *12*, 1165–1182.
5. Robinet, C.; Imbert, C.-E.; Rousselet, J.; Sauvard, D.; Garcia, J.; Goussard, F.; Roques, A. Human-Mediated Long-Distance Jumps of the Pine Processionary Moth in Europe. *Biological invasions* **2012**, *14*, 1557–1569.
6. Valade, R.; Kenis, M.; Hernandez-Lopez, A.; Augustin, S.; Mari Mena, N.; Magnoux, E.; Rougerie, R.; Lakatos, F.; Roques, A.; Lopez-Vaamonde, C. Mitochondrial and Microsatellite DNA Markers Reveal a Balkan Origin for the Highly Invasive Horse-Chestnut Leaf Miner Cameraria Ohridella (Lepidoptera, Gracillariidae). *Molecular Ecology* **2009**, *18*, 3458–3470.
7. Tóth, V.; Lakatos, F. Phylogeographic Pattern of the Plane Leaf Miner, Phyllonorycter Platani (STAUDINGER, 1870)(Lepidoptera: Gracillariidae) in Europe. *BMC Evolutionary Biology* **2018**, *18*, 135.
8. Drake, C.J.; Ruhoff, F.A. Lacebugs of the World: A Catalog (Hemiptera: Tingidae). *Smithsonian Institution, Washington, DC, United States National Museum Bulletin* **1965**, *213*, 634.
9. d'Aguilar, J.; Pralavorio, R.; Rabasse, J.M.; Mouton, R. Introduction En France Du Tigre Du Platane: Corythucha Ciliata (Say) (Het. Tingidae). *Bulletin de la Société Entomologique de France* **1977**, *82*, 1–6.
10. Jasinka, J.; Bozsits, G. A Platán Csipkéspoloska (Corythuca Ciliata) Fellépése Magyarországon. *Növényvédelem* **1977**, *13*, 42–46.
11. Mutun, S. Corythucha Ciliata, a New Platanus Pest in Turkey. *Phytoparasitica* **2009**, *37*, 65–66.
12. Tzanakakis, M.E. Records of the Sycamore Lace Bug, Corythuca Ciliata, (Say), in Greece. *Entomologica Hellenica* **1988**, *6*, 55–56.
13. Grebennikov, K.A.; Mukhanov, S.Y. *Corythucha Ciliata* (Say, 1932)(Hemiptera: Heteroptera: Tingidae): New Alien Species of True Bugs in Uzbekistan Fauna. *Russian Journal of Biological Invasions* **2019**, *10*, 126–128.
14. Li, F.; Wang, R.; Qu, C.; Fu, N.; Luo, C.; Xu, Y. Sequencing and Characterization of the Invasive Sycamore Lace Bug Corythucha Ciliata (Hemiptera: Tingidae) Transcriptome. *PLoS ONE* **2016**, *11*, e0160609.
15. Picker, M.D.; Griffiths, C.L. Sycamore Tree Lace Bug (Corythucha Ciliata Say)(Hemiptera: Tingidae) Reaches Africa. *African Entomology* **2015**, *23*, 247–249.
16. Prado, C.E. Presencia En Chile de Corythucha Ciliata (Say)(Hemiptera: Heteroptera: Tingidae). *Revista Chilena de Entomologia* **1990**, *18*, 53–55.
17. Rabitsch, W.; Streito, J.C. Corythucha ciliata (Say,1832) – Sycamore lace bug (Heteroptera: Tingidae). In *Alien terrestrial arthropds of Europe*; Roques, A., Kennis, M., Lees, D., Lopez-Vaamonde, C., Rabitsch, W., Rasplus, J.Y., Roy, D.B., Eds.; BIORISK; Pensoft: Sofia - Moscow, 2010; Vol. 4, pp. 964–965.
18. Supatashvili, A.; Goginashvili, N.; Kereselidze, M. Distribution and Some Biological Data of Sycamore Lace Bug–Corythucha Ciliata Say (Heteroptera, Tingidae) in Georgia. *Annals of Agrarian Science* **2016**, *14*, 42–45.
19. Cvetkovska-Gjorgievska, A.; Dedov, I.; Hristovski, S.; Langourov, M.; Lazarevska, S.; Prelik, D.; Simov, N. New Records of Allochtonous, Invasive and Pest Invertebrate Species from the Republic of Macedonia. *Ecologica Montenegrina* **2019**, *20*, 56–70.
20. Dominiak, B.C.; Gillespie, P.S.; Worsley, P.; Locker, H. Survey for Sycamore Lace Bug'Corythucha Ciliata'(Say)(Hemiptera: Tingidae) in New South Wales during 2007. *General and Applied Entomology: The Journal of the Entomological Society of New South Wales* **2008**, *37*, 27.
21. Grosso-Silva, J.M.; Aguiar, A. Corythucha Ciliata (Say, 1832)(Hemiptera, Tingidae), the Nearctic Sycamore Iace Bug, Found in Portugal. *Boletín de la SEA* **2007**, 366–366.
22. Hrubík, P. Alian Insect Pests on Introduced Woody Plants in Slovakia. *Acta Entomologica Serbica* **2007**, *12*, 81–85.
23. Halbert, S.E.; Meeker, J.R. *Sycamore Lace Bug,* Corythucha Ciliata *(Say)(Insecta: Hemiptera: Tingidae)*; Univ. Florida, Coop. Ext. Serv. ENY, 2001; pp. 1–4;.
24. Ripka, G.; Reiderné Saly, K.; Jensen, G.; Rácz, V.; Orosz, A. Díszfák És Díszcserjék Tripsz-, Poloska- És Kabócafaunája a Fővárosban. *Növényvédelem* **1993**, *29*, 569–572.
25. Besnard, G.; Tagmount, A.; Baradat, P.; Vigouroux, A.; Berville, A. Molecular Approach of Genetic Affinities between Wild and Ornamental Platanus. *Euphytica* **2002**, *126*, 401–412.
26. Liu, G.; Bao, M. Adventitious Shoot Regeneration from in Vitro Cultured Leaves of London Plane Tree (Platanus Acerifolia Willd.). *Plant Cell Report* **2003**, *21*, 640–644.
27. Warrick, R.B.; Williams, C.F. Checklist of the Cultivated Trees of St.George, Washington County, Utah. *Great Basin Naturalist* **1991**, *51*, 296–299.
28. Wu, Z.Y.; Raven, P.H.; Hong, D.Y. *Flora of China*; (Pittosporaceae through Connaraceae); Science Press, Beijing, and Missouri Botanical Garden Press, St. Louis., 2003; Vol. 9;.

29. Yang, W.Y.; Tang, X.T.; Cai, L.; Dong, C.S.; Du, Y.Z. Isolation and Characterization of Nine Microsatellite Loci from the Sycamore Lace Bug Corythucha Ciliata (Hemiptera: Tingidae). ,. *Florida Entomologist* **2014**, *97*, 1070–1074.
30. Gwiazdowski, R.A.; Foottit, R.G.; Maw, H.E.L.; Hebert, P.D. The Hemiptera (Insecta) of Canada: Constructing a Reference Library of DNA Barcodes. *PLoS ONE* **2015**, *10*, e0125635.
31. Raupach, M.J.; Hendrich, L.; Küchler, S.M.; Deister, F.; Morinière, J.; Gossner, M.M. Building-up of a DNA Barcode Library for True Bugs (Insecta: Hemiptera: Heteroptera) of Germany Reveals Taxonomic Uncertainties and Surprises. *PLoS ONE* **2014**, *9*, e106940.
32. Kocher, A.; Guilbert, É.; Lhuillier, É.; Murienne, J. Sequencing of the Mitochondrial Genome of the Avocado Lace Bug Pseudacysta Perseae (Heteroptera, Tingidae) Using a Genome Skimming Approach. *Comptes rendus biologies* **2015**, *338*, 149–160.
33. Yang, W.Y.; Tang, X.T.; Ju, R.T.; Zhang, Y.; Du, Y.Z. The Population Genetic Structure of Corythucha Ciliata (Say)(Hemiptera: Tingidae) Provides Insights into Its Distribution and Invasiveness. *Scientific Reports* **2017**, *7*, 635.
34. Tóth, V.; Bender, B.; Tuba, K.; Horváth, B.; Lakatos, F. A Platán Csipkéspoloska (Corythucha Ciliata Say, 1832) Populációgenetikai Mintázata. *Növényvédelem* **2020**, *81*, 168–175.
35. Dinca, V.; Zakharov, E.V.; Hebert, P.D.N.; Vila, R. Complete DNA Barcode Reference Library for a Country's Butterfly Fauna Reveals High Performance for Temperate Europe. *Proceedings of the Royal Society B* **2011**, *278*, 347–355.
36. Lunt, D.H.; Zhang, D.-X.; Szymura, J.M.; Hewitt, G.M. The Insect COI Gene: Evolutionary Patterns and Conserved Primers for Phylogenetic Studies. *Insect Molecular Biology* **1996**, *5*, 153–165.
37. Thompson, J.D.; Higgins, D.G.; Gibbson, T.J. Clustal W: Improving the Sensitivity of Progressive Multiple Sequence Alignment through Sequence Weighting, Position Specific Gap Penalties and Weight Matrix Choice. *Nucleic Acids Research* **1994**, *22*, 4673–4680.
38. Tamura, K.; Peterson, D.; Peterson, N.; Stecher, G.; Nei, M.; Kumar, S. MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution* **2011**, *28*, 2731–9.
39. Darriba, D.; Taboada, G.L.; Doallo, R.; Posada, D. JModelTest 2: More Models, New Heuristics and Parallel Computing. *Nature Methods* **2012**, *9*, 772.
40. Guindon, S.; Gascuel, O. A Simple, Fast and Accurate Method to Estimate Large Phylogenies by Maximum-Likelihood. *Systematic Biology* **2003**, *52*, 696–704.
41. Akaike, H. A New Look Atthe Statistical Model Identification. *IEEE Transactions on Automatic Control* **1974**, *19*, 716–723.
42. Nei, M. *Molecular Evolutionary Genetics.*; Columbia University Press: New York, 1987;
43. Ewens, W.J. The Sampling Theory of Selectively Neutral Alleles. *Theoretical Population Biology* **1972**, *3*, 87–112.
44. Zouros, E. Mutation Rates, Population Sizes and Amounts of Electrophoretic Variation of Enzyme Loci in Natural Populations. *Genetics* **1979**, *92*, 623–646.
45. Excoffier, L.; Lischer, H.E.L. Arlequin Suite Ver 3.5: A New Series of Programs to Performpopulation Genetics Analyses under Linux and Windows. *Molecular Ecology Resources* **2010**, *10*, 564–567.
46. Jung, S.; Duwal, R.K.; Lee, S. COI Barcoding of True Bugs (Insecta, Heteroptera). *Molecular Ecology Resources,* **2011**, *11*, 266–270.
47. Park, D.S.; Foottit, R.; Maw, E.; Hebert, P.D.N. Barcoding Bugs: DNA-Based Identification of the True Bugs (Insecta: Hemiptera: Heteroptera). *PLoS ONE* **2011**, *6*, e18749.
48. Rugman-Jones, P.F.; Hoddle, M.S.; Phillips, P.A.; Jeong, G.; Stouthamer, R. Strong Genetic Structure among Populations of the Invasive Avocado Pest Pseudacysta Perseae (Heidemann)(Hemiptera: Tingidae) Reveals the Source of Introduced Populations. *Biological Invasions* **2012**, *14*, 1079–1100.
49. Grant, W.A.S.; Bowen, B.W. Shallow Population Histories in Deep Evolutionary Lineages of Marine Fishes: Insights from Sardines and Anchovies and Lessons for Conservation. *Journal of heredity* **1998**, *89*, 415–426.
50. Dlugosch, K.M.; Anderson, S.R.; Braasch, J.; Cang, F.A.; Gillette, H.D. The Devil Is in the Details: Genetic Variation in Introduced Populations and Its Contributions to Invasion. *Molecular Ecology* **2015**, *24*, 2095–2111.