Department of Biology and Ecology
Faculty of Natural Sciences
Matej Bel University in Banská Bystrica
&
The Slovak Limnological Society

This conference is being held under the auspices of
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The major of town Vysoké Tatry

THE 8th CENTRAL EUROPEAN DIPTEROLOGICAL CONFERENCE

Conference Abstracts

Ladislav Hamerlík, Daniela Dobríková & Jaroslav Stoklasa (eds.)

Kežmarské Žľaby, 28th – 30th September, 2015

The 8th Central European Dipterological Conference

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Vysoké Tatry, Slovakia

Date:

28th – 30th September, 2015

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Welcome to the 8th Central European Dipterological Conference held in Kežmarské Žľaby, High Tatra Mountains, Slovakia!

The triennial meetings of dipterists have been organized since 1969, initially as workshops of Czech and Slovak dipterists. However, over the last decades the meeting went through a significant development and owing to the broader interest from researchers of the surrounding countries, it has become a conference.

Similarly to the previous meetings, the current conference provides a place for scientific communication and collaboration in the broad field of Diptera research: taxonomy, phylogeny, physiology, zoogeography, ecology, palaeoecology and applied disciplines such as nature conservation, human/ veterinary medicine and criminology. At the same time they have always been a good opportunity to meet not only colleagues but also old friends and good people.

We wish you a fruitful conference time in Kežmarské Žľaby!

The organizing committee

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Our thanks for support belong to:

CONFERENCE PROGRAM

Sunday, 27.09.2015
16.00 – 22.00: Registration

Monday, 28.09.2015
09.00 – 10.30: Registration
11.00 – 11.30: Opening ceremony
11.30 – 12.30: Lunch

Oral presentations – **Phylogeny of Diptera**
12.30 – 12.45: Zatwarnicki T.: Phylogeny of the tribe Discocerinini (Diptera: Ephydridae)
12.45 – 13.00: Ševčík J., Kaspřák D., Mantič M., Fitzgerald S., Ševčíková T., Tóthová A. & Jaschhof M.: Molecular phylogeny of Bibionomorpha *sensu lato* (Diptera) based on five gene markers
13.00 – 13.15: Mantič M. & Ševčík J.: Molecular phylogeny of the families Keroplatidae and Lygistorrhinidae (Diptera: Bibionomorpha): preliminary results
13.15 – 13.30: Sikora T., Jaschhof M., Kaspřák D., Mantič M. & Ševčík J.: Preliminary molecular phylogeny of gall midges (Diptera: Cecidomyiidae)
13.30 – 13.45: Kaspřák D., Tóthová A. & Ševčík J.: Molecular phylogeny of Mycetophilidae: current state of knowledge
13.45 – 14.00: Burdíková N., Kaspřák D., Mantič M. & Ševčík J.: Molecular phylogeny and host specialization of the family Bolitophilidae (Diptera)

14.00 – 14.30: Coffee break

Oral presentations – **Taxonomy, biogeography, faunistics & conservation biology**
14.30 – 14.45: Cielniak M.: Morphology of the preimaginal stages of *Halmopota salinarius* (Diptera: Ephydridae)
14.45 – 15.00: Pochrząst K. & Ryczko I.: The comparision of proboscis morphology and its influence on food preferences in subfamilies Ilytheinae and Ephydrinae (Diptera: Ephydridae)
15.00 – 15.15: Heřman P. & Koprdová S.: Morphology of male and female terminalia of three Central European *Trypeta* species (Diptera: Tephritidae)
15.15 – 15.30: Sarvašová A. & Kočišová A.: The use of integrative taxonomy in determining of biting midges from genus Culicoides (Diptera: Ceratopogonidae)
15.30 – 15.45: Ballayová N., Goffová K., Čiampor Jr. F. & Čiamporová-Zaťovičová Z.: Taxonomy of *Heterotrissocladius marcidus* (Chironomidae) based on DNA analysis, and genetic variability of its Tatra population

15.45 – 16.15: Coffee break

Oral presentations – **Taxonomy, biogeography, faunistics & conservation biology**
16.15 – 16.30: Dénes A.-L., Kolcsár L.-P., Török E. & Keresztes L.: Pediciidae from the Carpathians Biodiversity Hotspots: from general patterns to case studies
16.30 – 16.45: Kubík Š.: The genus *Thaumatomyia* (Diptera, Chloropidae) in the Palaearctic Region
16.45 – 17.00: Kúdela M.: Species of the genus *Prosimulium* (Diptera: Simuliidae) in Europe
17.00 – 17.15: Kúdelová T.: European species of the *Simulium reptans* group (Diptera: Simuliidae)
17.15 – 17.30: Semelbauer M.: New species of lauxaniids from Slovakia
17.30 – 17.45: Černý M. & Roháček J.: *Cerodontha* (*Poemyza*) *unisetiorbita* (Agromyzidae) – a leaf miner fly on bamboo also found in the Czech Republic

18.00: Dinner

Tuesday, 29.09.2015

Oral presentations – **Taxonomy, biogeography, faunistics & conservation biology**

09.00 **–** *09.15:* Čelechovský A.: Interesting informations about fauna of bee flies from the Czech Republic and Slovakia (Diptera: Bombyliidae)

09.15 – 09.30: Papp L. & Černý M.: Agromyzidae (Diptera) of Hungary – a "European" project

09.30 – 09.45: Tkoč M.: Diptera collection of the Department of Entomology of the National Museum in Prague

09.45 – 10.00: Barták M.: Commented checklists of several families of Czech and Slovak Diptera

10.00 – 10.30: Coffee break

Oral presentations – **Ecology of Diptera**

10.30 – 10.45: Starý J.: How to look for *Rhabdomastix* (*Rhabdomastix*) *incapax* (Diptera, Limoniidae)

10.45 – 11.00: Soltész Z.: Flies of Red-footed Falcon

11.00 **–** *11.15:* Roháček J.: Psammophilous flies (Diptera) on glacial sand deposits in Silesia (Czech Republic)

11.15 **–** *11.30:* Foltánová A., Oboňa J. & Svitok M.: Mosquito (Culicidae) community assembly in tree-holes of oak forest

12.00 – 13.00: Lunch

Oral presentations – **Ecology of Diptera**

13.15 – 13.30: Bulánková E.: Ecological preferences of *Atherix ibis* (Fabricius, 1789) and *Ibisia marginata* (Fabricius, 1781) larvae

13.30 – 13.45: Madsen B. L.: Ecological observations on *Atherix ibis* and *Phalacrocera replicata*

13.45 – 14.00: Andersen T., Baranov V., Hagenlund L.K., Ivković M., Kvifte G.M. & Pavlek M.: Blind flight? A new troglobiotic orthoclad (Diptera, Chironomidae) from the Lukinajama – Trojama cave in Croatia

14.00 – 14.15: Čerba D., Milošević D., Turković Čakalić I., Ergović V., Koh M. & Vuković A.: Functional role of chironomid larvae (Chironomidae, Diptera) within a Danube floodplain

14.15 – 16.45: Individual program

17.00: Transfer to conference dinner in village Ždiar

Wednesday, 30.09.2015

Oral presentations – **Ecology of Diptera**

09.00 – 09.15: Milošević D., Stojković Piperac M., Petrović A., Čerba D., Paunović M. & Simić V.: Concordance of Diptera taxa with different groups of freshwater biota in lotic system

09.15 – 09.30: Stojković Piperac M., Milošević D., Petrović A., Čerba D., Paunović M. & Simić V.: Can dipterans be used as a surrogate for rapid assessments of freshwater biodiversity?

09.30 – 09.45: Brabec K.: Changes in chironomid communities related to intensity of degradation in small streams

09.45 – 10.00: Hamerlík L., Novikmec M., Svitok M., Veselská M. & Bitušík P.: Chironomidae (Diptera) in the ponds of the Tatra Mts.: diversity and interesting records

10.00- 10.30: Coffee break

Oral presentations) – **Ecology of Diptera and Applied Dipterology**

10.30 – 10.45: Rettich F., Šebesta O. & Vyskočil R.: Beavers caused massive occurrence of mosquitoes

10.45 – 11.00: Čičková H., Kozánek M. & Takáč P.: Pros and cons of the use of *Lucilia sericata* eggs in maggot debridement therapy

11.00 – 11.15: Dobríková D., Hamerlík L., Szarłowicz K., Reczynski W., Kubica B., Šporka F. & Bitušík P.: The impact of human activities on the chironomid communities (Diptera: Chironomidae) of lake Popradské pleso over the last 200 years

11.15 – 12:00 Conference closing remarks and discussion

12.15: Lunch

Poster presentations

1. Bocková E. & Kočišová A.: Species composition of mosquitoes (Diptera: Culicidae) in selected areas in Eastern Slovakia
2. Katona P.: Potential geographic distribution and a new locality of *Eclimus gracilis* Loew, 1844
3. Szentiványi T., Szőke K. & Estók P.: Host associations of bat flies (Diptera: Nycteribiidae) in Hungary
4. Špaček J.: Distribution of Athericidae (Diptera) in the Czech Republic
5. Špaček J.: Some interesting chironomid taxa in the Krkonoše (Giant) Mts.
6. Török E., Jöst H., Horváth C., Cadar D., Tomazatos A., Lühken R., Becker N., Keresztes L., Popescu O. & Schmidt-Chanasit J.: Longitudinal mosquito surveillance study in Danube Delta and the first report of *Ochlerotatus hungaricus* (Mihalyi, 1955) for Romania

ABSTRACTS OF ORAL PRESENTATIONS

Blind flight? A new troglobiotic orthoclad (Diptera, Chironomidae) from the Lukina jama – Trojama cave in Croatia

Trond Andersen[1], Viktor Baranov[2], Linn Katrine Hagenlund[1], Marija Ivković[3], Gunnar M. Kvifte[1,4] & Martina Pavlek[5]

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[1,4]*Department of Zoology, Institute of Biology, University of Kassel, Kassel, Germany*
[5]*Department of Molecular Biology, Ruđer Bošković Institute, Zagreb, Croatia and Croatian Biospeleological Society, Zagreb, Croatia*

Keywords: Chironomidae, Orthocladiinae, new genus, caves, Croatia

During expeditions to the Lukina jama – Trojama cave system in the Velebit Mountain in Croatia in 2013, several females of a pale Chironomidae belonging to the subfamily Orthocladiinae were collected in a chamber at 980 m below the surface. The specimens were found to belong to an undescribed chironomid genus, which will hopefully be published during the autumn. Molecular phylogenetic analysis groups it with the genera *Tvetenia*, *Cardiocladius* and *Eukiefferiella* in the "tribe Metriocnemini".

Morphological features like pale color, strongly reduced eyes and very long legs make it a typical cave animal. Surprisingly, it has also retained large wings and appears to be capable of flight which would make it the first flying troglobiont worldwide, disproving previous beliefs that bats are the only animals capable of flying in complete darkness.

The species appears to be parthenogenetic, as only females were collected. The discovery confirms the position of the Dinaric arch as a highly important hotspot of subterranean biodiversity.

Commented checklist of Czech and Slovak species of Fannidae (Diptera: Muscomorpha)

Miroslav Barták[1] & Jiří Preisler[2]

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Keywords: Diptera, Muscomorpha, Fanniidae, Czech Repblic, Slovakia, new records

Commented checklist of Czech and Slovak Fanniidae is presented. The following five species are first recorded from the Czech Republic: *F. collini* d'Assis-Fonseca, 1966 (simultaneously first record from Central Europe), *F. lugubrina* (Zetterstedt, 1838), *F. melania* (Dufour, 1839), *F. slovaca* Gregor & Rozkošný, 2005, and *F. brinae* Albuquerque, 1951 (simultaneously first record from low altitudes) rising the total number of Czech species to 69. Another species, *F. alpina* Pont, 1970, is first recorded from Slovak Republic, rising the total number of Slovak species to 51. Another two species are first recorded from Bohemia [*F. verrallii* (Stein, 1895) and *F. vespertilionis* Ringdahl, 1934] and two from Moravia [*F. limbata* (Tiensuu, 1938) – this species, considered in Central Europe very rare, was found in large numbers but always near water both running and standing in early spring under unusually warm temperature conditions and *F. norvegica* Ringdahl, 1934]. The occurrence of two very rare species is confirmed in the Czech Republic [*F. conspecta* Rudzinski, 2003 and *F. cothurnata* (Loew, 1873) – simultaneously first recorded from Kazakhstan]. The existing keys are improved for *F. carbonaria* (Meigen, 1826), *F. nidica* Collin, 1939, and *F. conspecta*. Some variability in key characters was found in *F. carbonaria* (specifically, t2 has 1-5 pd setae) which may cause confusion in existing keys.

Změny struktury taxocenózy pakomárovitých (Diptera: Chironomidae) v závislosti na intenzitě degradace malých vodních toků

Changes in chironomid communities related to intensity of degradation in small streams

Karel Brabec

Centrum pro výzkum toxických látek v prostředí, Přírodovědecká fakulta Masarykovy univerzity, Kamenice 753/5, 625 00 Brno, e-mail: brabec@sci.muni.cz

Klíčová slova: Chironomidae, larvy, organické znečištění, hydromorfologie
Keywords: Chironomidae, larvae, organic pollution, hydromorphology

Gradient intenzity eutrofizace (organického znečištění) a hydromorfologické degradce malých vodních toků byl hodnocen z hlediska odezvy taxocenózy larev pakomárovitých (Diptera: Chironomidae). Přestože bylo snahou vybrat lokality zasažené jen jedním ze studovaných stresorů, zvláště na intenzivně degradovaných lokalitách nebylo možné vyloučit spolupůsobení více stresorů. Intenzita stresorů byla vyjádřena pomocí chemických ukazatelů (koncentrace dusičnanů, fosforečnanů, chloridů, BSK_5) a souhrných indexů systému River Habitat Survey.

Taxocenózy pakomárovitých byly hodnoceny z hlediska druhového složení, autekologických charakteristik (species traits), podílu jednotlivých podčeledí/tribů na abundanci i počtu taxonů a citlivosti vůči stresorům (saprobní valence). Pakomárovití reagují na gradient eutrofizace změnou struktury společenstva z hlediska taxonomického složení I zastoupení potravních strategií. Naproti tomu i nejvíce hydromorfologicky poškozené lokality poskytovaly podmínky pro značné množství druhů pakomárů. To se dá přisuzovat existenci mikrohabitatových podmínek vytvářejících značnou heterogenitu prostředí v prostorovém měřítku odpovídajícím malým larvám pakomárů (řasové nárosty na umělém substrátu, homogenní štěrko-písčitý substrát s dostatkem organické hmoty vyskytující se mezi strukturami regulovaného koryta.

Ve studii byly vyhodnoceny vazby taxocenóz pakomárovitých na chemické parametry vody, hydromorfologické charakteristiky říčního koryta a příbřežní zóny i charakteru povodí studovaných lokalit. Výsledky ukazují na indikační potenciál často opomíjené součásti společenstev makrozoobentosu – larev pakomárů. Vzhledem k tomu, že vetšina říční sítě střední Evropy je vystavena spolupůsobení kombinace stresorů, má vyhodnocení vazby indikátorů na jednotlivé prvky degradace význam pro ochranu ekologické hodnoty říčních ekosystémů.

Ecological preferences of *Atherix ibis* (Fabricius, 1789) and *Ibisia marginata* (Fabricius, 1781) larvae

Eva Bulánková

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e-mail: bulankova@fns.uniba.sk

Keywords: *Atherix ibis, Ibisia marginata*, preferences, climate change impact

Although *Atherix ibis* and *Ibisia marginata* larvae play important role in function of running waters, their ecological preferences have not been completely evaluated till yet (www.freshwaterecology.info). According to the freshwater organisms categories (Schmidt-Kloiber, Hering, 2009) we find out altitudinal preferences, temperature range, pH preference and climate change impact for both species.

The study was supported by the fund VEGA 1-0176/12.

Molecular phylogeny and host specialization of the family Bolitophilidae (Diptera)

Nikola Burdíková, David Kaspřák, Michal Mantič & Jan Ševčík

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Keywords: Diptera, Bolitophilidae, molecular phylogeny, mycophagous insects, host specialization

Results of the first molecular phylogenetic analysis of the family Bolitophilidae are presented. For 10 Central European species of the family Bolitophilidae, DNA extraction and subsequent polymerase chain reaction (PCR) was performed using four gene markers, one nuclear (28S) and three mitochondrial (12S, 16S and COI). Dataset was analysed using the maximum likelihood method. The phylogenetic relationships are studied in relation to host fungi. The results will be presented in the presentation. Current knowledge about host fungi associations for individual species of the family Bolitophilidae will also be summarized.

Morphology of the preimaginal stages of *Halmopota salinarius* (Diptera: Ephydridae)

Magdalena Cielniak

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Keywords: shore flies, larva, puparium

Shore flies (Ephydridae) are known to inhabit environments not tolerated by other Diptera. Quite a few species are specialized to live in waters of exceptionaly high salt concentration. The ability to withstand high osmotic pressure occurred in various lines of shore flies independently. *Halmopota salinarius* (as *Ephydra salinaria*) was described by Bouché (1834) basing on the specimens collected in "Schlesien" (Silesia, SW Poland). The short description of the species also included inprecise illustration of the larva. The more detailed descriptions and illustrations of the mature larvae and puparium are provided. Materials were collected from the graduation tower in Bad Rothenfelde (Germany).

Zajímavosti ve fauně dlouhososek České republiky a Slovenska (Diptera: Bombyliidae)

Interesting informations about fauna of bee flies from the Czech Republic and Slovakia (Diptera: Bombyliidae)

Alois Čelechovský

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Klíčová slova: Bombyliidae, Česká republika, Slovensko, rozšíření, faunistika
Keywords: Bombyliidae, Czech Republic, Slovakia, distribution, faunistics

V čeleď dlouhososkovití (Bombyliidae) je na světě popsáno více jako 4500 druhů, z toho v Evropě bylo zjištěno cca 335 druhů. Larvy jsou predátoři, ektopariziti, endoparazitoidi či hyperparizitoidi různých bezobratlých, hlavně hmyzu: blanokřídlých (Hymenoptera), dvoukřídlých (Diptera), motýlů (Lepidoptera), kobylek (Ensifera) či sarančí (Coelifera). Z území ČR a SR je uváděn výskyt 55 druhů. Některé druhy jsou zoogeograficky významné, mají na území střední Evropy severní hranici svého rozšíření s velmi lokálním výskytem. K těmto druhům patří *Phthiria gaedei, Phthiria canescens, Bombylisoma nigriceps, Systoechus gradatus, Exoprosopa minos* a *Lomatia lachesis.* V příspěvku jsou prezentovány informace o celkovém rozšíření uvedených druhů, zajímavé poznatky z jejich biologie a výskytu na území ČR a Slovenska.

Functional role of chironomid larvae (Chironomidae, Diptera) within a Danube floodplain

Dubravka Čerba[1], Djuradj Milošević[2], Ivana Turković Čakalić[1], Viktorija Ergović[1], Miran Koh[1] & Ana Vuković[1]

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Keywords: Chironomidae, ichthyofauna diet, periphyton, *Glyptotendipes* sp.

In the Pannonian part of the Danube there is a large floodplain area, between 1383 and 1410 rkm, Kopački Rit, supporting very diverse biocoenoses. Freshwater invertebrates form different communities such as periphyton on various substrates, or benthos, and Chironomidae larvae present one of the most constant and abundant taxa groups within them. These communities can be very suitable feeding sites for fish. To test whether chironomids represent the main food in lake's ichthyofauna, we examined the fish stomach contents. Sampling was conducted using gill net in May 2014 in Kopačko Lake. Fish were weighted, measured and their intestines were emptied, and its contents separated and inspected under a stereoscopic microscope. Out of 258 fish, we found Chironomidae larvae in 98 specimens, most of which belonged to the species *Gymnocephalus baloni*. Chironomids presented 70% of sorted invertebrates (larvae 64% and pupae almost 7%) and only dipterans which could be indentified among eaten Insecta. The main food source for fish was most likely periphyton, since the recorded chironomid species composition differed from that found in the sediment, and the dominant species, *Glyptotendipes* sp., *Polypedilum nubeculosum*, *Cricotopus* gr. *sylvestris* and *Endochironomus albipennis*, are typically found on macrophytes and have been previously recorded as dominant phytophylous species in Kopački Rit. The results confirmed the significant functional role of chironomids in hydrobiocoenoses of lentic systems.

Pros and cons of the use of *Lucilia sericata* eggs in maggot debridement therapy

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Keywords: larval therapy, green bottle fly, eggs, chronic wounds

Maggot debridement therapy (MDT) has become an established method of treatment of chronic non-healing wounds. In classic larval therapy, live medicinal-grade larvae of Lucilia sericata (Meigen) are applied in the wounds to remove necrotic tissue and initiate the healing process. However, preparation of maggots and ensuring their sterility are time consuming and labor-intensive. Our laboratory experiments show that L. sericata eggs can be used instead of live larvae with the added benefits of easier handling and longer shelf life of the eggs compared to live larvae. Major challenges associated with application of the eggs during MDT include development of rapid sterility tests to confirm microbiological safety of the eggs, maintenance of suitable transport conditions and optimum moisture of the wound environment to allow hatching of the eggs.

This research was funded by the Operational Program of Research and Development and cofinanced with the European Fund for Regional Development (EFRD), Grant ITMS 26240220030: Research and development of new biotherapeutic methods and their application in the treatment of some illnesses.

The impact of human activities on the chironomid communities (Diptera: Chironomidae) of lake Popradské pleso over the last 200 years

Daniela Dobríková[1], Ladislav Hamerlík[1], Katarzyna Szarłowicz[2], Witold Reczynski[2], Barbara Kubica[2], Ferdinand Šporka[3] & Peter Bitušík[1]

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Keywords: Chironomidae, paleocommunity, loss-on-ignition, ^{210}Pb dating, cultural eutrophication, High Tatra Mts., Slovakia

The goal of the present study is to identify the effect of increasing anthropic impact since the second half of the 19th century on the lake Popradské pleso. The boost of tourist activities and construction of chalets close by the lake are well documented and served as supporting data for the paleoecological reconstruction. The lead dating indicates that the 0–8 cm section of the short core taken from the deepest part of the lake represents the past ~ 200 years, dating back to ~ 1814 AD. In the 10 cm portion of the sediment core, a total of ~ 1700 chironomid head capsules representing 37 taxa of 5 subfamilies were found. The dominating taxa all over the sediment core were *Heterotrissocladius marcidus*-type, *Psectrocladius sordidellus*-type and *Tanytarsus lugens*-type representing the 80 % of all head capsules found. Beside the lacustrine taxa, taxa preferring flowing waters (rheophils and rheobionts) made up a significant portion of the taphocaenosis. We assumed that meteorological conditions such as precipitation, temperature and relative moisture could be the controlling factors for those taxa indicating the intensity of the inlet stream. Neither touristic activity, nor early cottage development around the lake had considerable influence on the chironomid community structure or organic content of the lake. Changes of most of metal elements concentrations reflected rather bigger scale changes of industrial activities than local scale human disturbances.

Mosquito (Culicidae) community assembly in tree-holes of oak forest

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Keywords: lenght – mass relationships, mosquitoes, biomass, competition

The work provides first comprehensive information about mosquitoes communities organization in treeholes in Slovak oak forest. The aims were 1) to establish lenght-mass relationships for three mosquito species (*C. pipiens, A. plumbeus, O. geniculatus*) and to estimate biomass 2) to evaluate relationship between mosquito biomass and characteristics of the environment and 3) to assess the level of competition in mosquite assemblages of treeholes. Samples of mosquitoes were collected from treeholes on oaks (*Quercus* sp.) from September 2010 to January 2012. The lenght-mass relationships were established using power model. We found significant relationship between mosquito biomass and variation coefficient of conductivity and marginally non-significant relationships between biomass, conductivity and size of treehole opening, respectively. The level of competition was assessed using Czekanowsky index of temporal niche overlap. Because the index reached substantially lower values than for simulated communities without competition we conclude that the species were significantly separated in time in several treeholes. This can be interpreted as an indirect evidence of competition. The significant relationship between level of competition and conductivity variability suggests that fluctuating environment promote temporal separation of mosquito species.

This work was supported by the Slovak Research and Development Agency under the contract number APVV-0059-11.

Chironomidae (Diptera) in the ponds of the Tatra Mts.: diversity and interesting records

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Keywords: Chironomidae, biodiversity, alpine ponds, first records, Tatra Mts.

Even though the lakes of the Tatra Mountains (Slovakia/Poland) have been studied intensively over the last decades, there is very little known about the limnology of the ponds in the region. Thus, between 2000 and 2013, 66 Tatra ponds located between 1,089 and 2,201 m a.s.l. were sampled for benthic invertebrates. Out of the total 122 taxa collected, Chironomidae constituted the richest group with 58 taxa. The most diverse pond supported 13 chironomid taxa and, mean diversity was 6 taxa/pond. *Lasiodiamesa* sp., *Derotanypus* cf. *sibiricus* and *Rheocricotopus reduncus* were firstly recorded in Slovakia and represent species/taxa with very rare distribution patterns. While total diversity was decreasing with elevation considerably (b=-0.01, r2=0.24), chironomid diversity showed weak response to altitude (b=-0.003, r2= 0.08). Significant changes were, however, obvious in the chironomid assemblage structure: while the proportion of Tanypodinae and Chironominae on the total chironomid diversity was decreasing with increasing altitude, ratio of Diamesinae and Orthocladiinae increased. This interesting pattern is most likely a result of phylogeny features and in turn different competitiveness of particular chironomid taxa.

The project was funded by the Slovak Research and Development Agency, contract no. APVV-0059-11 and by the Slovak Scientific Grant Agency, VEGA, contract no. 2/0081/13.

Morphology of male and female terminalia of three Central European *Trypeta* species (Diptera: Tephritidae)

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Keywords: *Trypeta*, morphology, terminalia, identification

Male terminalia and female aculeus of three Central European *Trypeta* species – *Trypeta artemisiae*, *T. immaculata* and *T. zoe* – have been studied. New diagnostic characters are presented and their distribution is discussed. The three species are clearly separated on the basis of easily visible genitalic characters.

Molecular phylogeny of Mycetophilidae: current state of knowledge

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Keywords: fungus gnat, Mycetophilidae, Bibionomorpha, molecular phylogeny, systematics

The fungus gnats (Mycetophilidae) represent one of the most abundant and diverse families of the infraorder Bibionomorpha. The relationships within this family are still little-known. The molecular phylogeny of Mycetophilidae was reconstructed based on five mitochondrial (12S, 16S, COI, COII, cytB) and three nuclear (18S, 28S, ITS2) gene markers using maximum likelihood and Bayesian inference. We sampled more than 70 genera or subgenera of Mycetophilidae. DNA was extracted and sequenced in the years 2011–2015. Sequences of several additional taxa were obtained from the GenBank database. The preliminary results revealed subfamilies Leiinae (including *Allactoneura* DeMeijere), Manotinae, Mycetophilinae, Mycomyiinae and Sciophilinae as monophyletic groups. The subfamily Gnoristinae appears as paraphyletic. The tribe Metanepsiini has not been found to be monophyletic but rather a heterogeneous group of genera within Gnoristinae. Also the monophyly of *Dziedzickia* Johannsen is not supported. Individual trees will be demonstrated and discussed in the presentation but the datasets and results are still being updated.

The genus *Thaumatomyia* (Diptera, Chloropidae) in the Palaearctic Region

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Keywords: Chloropidae, Thaumatomyia, species, distribution, faunistic

The genus *Thaumatomyia* Zenker, 1833 is a relatively small genus of the subfamily Chloropinae (Diptera, Chloropidae) belonging to the *Thaumatomyia* genus group together with genera *Formosina* Becker, 1911 and *Thressa* Walker, 1860. The species are characterized by interfrontal setae in one or more rows on the frontal triangle, flattened scutellum with approximated apical scutellar setae, more or less convex scutum and large oval tibial organ on third tibia. Larvae are often predators of aphids. Seven species are known from the Palaearctic Region, three species are disputable and three additional species of this genus are new to science.

Druhy rodu *Prosimulium* (Diptera: Simuliidae) v Európe

Species of the genus *Prosimulium* (Diptera: Simuliidae) in Europe

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Kľúčové slová: *Prosimulium*, cytotaxonómia, cytochróm c oxidáza I
Keywords: *Prosimulium*, cytotaxonomy, cytochrome c oxidase I

Mušky rodu *Prosimulium* majú holarktické rozšírenie a vačšina druhov je viazaných na horské vodné toky. Celosvetovo je známych približne 44 druhov, v Európe 11. Študovali sme materiál z rôznych častí Európy s použitím kombinácie morfologických, cytotaxonomických a molekulárnych metód. Predbežné výsledky ukazujú, že je potrebná revízia väčšiny druhov. V prípade druhu *Prosimulium hirtipes* (Fries, 1824), ktorého areál siaha od Škótska cez väčšinu Európy až po východnú Čínu, bolo na tomto širokom území opísaných päť poddruhov, resp. príbuzných taxónov, tri z nich s výskytom v Európe. Poddruh *P. hirtipes italicum* opísaný z Apeninského polostrova bol neskôr synonymizovaný s *P. hirtipes*. Molekulárna a cytotaxonomická analýza populácií *P. hirtipes* naznačuje, že v Európe ide o komplex cytoforiem, pričom jedna z nich zodpovedá *P. italicum*. *Prosimulium latimucro* (Enderlein, 1925) je vysokohorský druh s ostrovčekovitým rozšírením v pohoriach strednej a južnej Európy a Britských ostrovov. Cytotaxonomická analýza ukázala, že od Britských ostrovov cez Pyreneje, Alpy až po Karpaty ide o jeden taxón, avšak v Prímorských Alpách bol zistený iný reprodukčne izolovaný a sympatricky sa vyskytujúci taxón. V prípade druhu *Prosiumulium rufipes* (Meigen, 1830) sa ukázalo, že morfologicky identifikované jedince z Álp, Karpát a Balkánu zodpovedajú inému taxónu, predbežne označovanému ako *P.* sp. aff. 3. Ďalšia nová cytoforma rodu *Prosimulium* bola zaznamenaná na Peloponéze.

Európske druhy skupiny *Simulium reptans* (Diptera: Simuliidae)

European species of the *Simulium reptans* group (Diptera: Simuliidae)

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Kľúčové slová: *Simulium reptans*, *Simulium colombaschense*, cytochróm c oxidáza, cytotaxonómia
Keywords: *Simulium reptans*, *Simulium colombaschense*, cytochrome c oxidase, cytotaxonomy

Skupinu druhov *Simulium reptans* tvorí 16 druhov mušiek, z ktorých väčšina je svojím vývinom viazaná na veľké rieky. Mnohé z nich spôsobujú v čase premnoženia značné škody na hospodárskych zvieratách a tak isto môžu ohroziť zdravie ľudí. Príkladom takéhoto druhu je *Simulium colombaschense*, ktorý bol v minulosti zodpovedný za masové hynutie dobytka v okolí Dunaja na Balkánskom polostrove. Napriek významu skupiny reptans je stav taxonómie jednotlivých druhov problematický a nedoriešený. U jedincov patriacich do skupiny *reptans* zo strednej Európy, Balkánu a Škandinávie sme porovnali morfologické znaky, štruktúru polyténnych chromozómov a genetickú variabilitu v úseku mitochondriálneho génu COI. *Simulium reptans* (Linnaeus, 1758) a *Simulium reptantoides* Carlsson, 1962 sú dva dobre definované druhy. V rámci oboch druhov boli zaznamenané dve genetické línie (A a B). V prípade *S. reptantoides* sa líne A a B vyskytovali sympatricky na všetkých lokalitách, okrem Talianska, kde sme zaznamenali len líniu B. V prípade *S. reptans* sa línia *reptans* A vyskytovala len v Škandinávii a Veľkej Británii a v strednej Európe sme zaznamenali výhradne reptans B. Medzi severoeurópskymi a stredoeurópskymi populáciami boli male rozdiely v morfológii kukiel a lariev. U druhu *Simulium colombaschense* (Scopoli, 1780) všetky jednince z povodia Dunaja patrili k jednej cytoforme (colombaschense A). Ďalšia cytoforma bola zaznamenaná v Taliansku (B) v rieke Belá (C) a dve nové cytoformy v Grécku (D a E).

Ecological observations on *Atherix ibis* and *Phalacrocera replicata*

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Keywords: water snipefly, cranefly, larval ecology, Jutland, Denmark

Atherix ibis (water snipefly) is well known for egg-bearing female aggregation in crust-like clusters on bridge ceilings and trees facing stream surfaces. Danish distribution data showing the species to be widely distributed in streams in the Jutland peninsula, but absent from the numerous islands. Females aggregate in a short period in early summer in warm and calm weather only. Adverse weather may result in very few clusters. The females are attracted to an initiated cluster by pheromones. The flies fasten to the surface and to each other by minute Velcro-like structures on their feet. Wing coloration, swarming pattern and cluster shape may protect against predators by mimicking some aggressive wasps. The tiny larvae stay in the cluster for a few days before they drop into the water. Contrary to common belief no signs of larval feeding on dead mothers has been observed. The majority of larvae left the cluster during nighttime. The biological relevance of night drops may be to avoid predation from trout-fry.

The cranefly larvae, *Plalacrocera replicata,* is densely covered by long, thin outgrowths. Their silvery appearance indicates a respiratory function. SEM studies shows plastron-like gill structures. Scirtid-larvae (Coleoptera) may be symbionts feeding on microorganisms covering the “gills”, thus preventing reduction in oxygen-uptake.

Molecular phylogeny of the families Keroplatidae and Lygistorrhinidae (Diptera: Bibionomorpha): preliminary results

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Keywords: Keroplatidae, Lygistorrhinidae, Sciaroidea, phylogenetic analysis, molecular markers

With nearly 1000 species and about 100 genera, the family Keroplatidae (Diptera: Sciaroidea) belongs to the most diverse families in the infraorder Bibionomorpha. In the current concept, it contains 4 subfamilies – Arachnocampinae and Sciarokeroplatinae, distributed only in the Australasian and Oriental region, respectively, Macrocerinae, consisting of the tribes Macrocerini and Robsonomyiini, and the largest subfamily Keroplatinae, formed also by two tribes, Keroplatini and Orfeliini. The family Lygistorrhinidae is usually considered as a separate family but there are also opinions, based on both morphological and molecular characters, that it should be placed inside the family Keroplatidae, as its subfamily Lygistorrhininae.

Here we present a new phylogenetic study, based on three mitochondrial (12S, 16S, COI) and two nuclear (18S, 28S) gene markers, that confirms the inclusion of Lygistorrhinidae in the family Keroplatidae, but also shows that some relationships inside the family still need to be resolved. Current dataset includes more than 60 taxa from the families Keroplatidae and Lygistorrhinidae. The phylogenetic tree, based on the maximum likelihood analysis, revealed some interesting results which will be presented and discussed at the conference.

Concordance of Diptera taxa with different groups of freshwater biota in lotic systems

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Keywords: Diptera taxa, community concordance, lotic system, Self-organizing map

Community concordance is a degree to which different taxa groups of freshwater biota similarly respond to different environmental gradients. Due to identification problem, Diptera taxa have been excluded from community concordance studies, or applied with poor taxonomic resolution. The main objective of this study was to test the distributional concordance of Diptera taxa with other freshwater taxa along the longitudinal gradient of lotic systems. Furthermore, we wanted to define the concordant taxa groups for lotic habitats with different levels of water quality. The Artificial neural network (Self-organizing map (SOM)) was used to ordinate and classify macroinvertebrate and fish taxa with similar distributional patterns, sampled along the Southern Morava river basin. The SOM obtained four groups of neurons with concordant taxa. Group A was consisted of 31 taxa mainly from Chironomidae group. Representatives of cluster A were distributed in most polluted sites. Group B were presented with 28 taxa distributed at moderately polluted sites. Group C was presented with 65 taxa from habitats with high water quality. Finally, group D was consisted of 113 taxa without specific distributional pattern. Diptera group presents one of the most dominant and frequent groups within hydrobiocoenoses and has to be included in all biodiversity and bioassessment studies.

Agromyzidae (Diptera) of Hungary – a "European" project

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Keywords: mining flies, Agromyzidae, identification, Carpathian Basin

The mining flies are important pests of a number of cultivated plants. The damage caused in field crops is seldom extensive but the number of agromyzid species recorded as pestiferous is very high. On the contrary, no comprehensive book on the Central European Agromyzidae has been published after Hendel's (1931–36) in the Lindner's series. Now the authors plan a book series (4 vols) for the safe identification for the c. 750 species of Agromyzidae, which may occur in the Carpathian Basin. The identification of all agromyzid species of the middle areas of Europe is mostly possible.

Vol. 1 with 1300 (mostly original) figures on more than 300 pages (published in September 2015) includes the general part (morphology of adults and larvae, phylogenetic relationships of Agromyzidae, classification, life-habits, economic importance, the history of studies on the Hungarian Agromyzidae). The systematic part contains a key to genera (adults) and the subfamily Agromyzinae with 157 spp. in the genera *Agromyza, Hexomyza, Melanagromyza* and *Ophiomyia*. A catalogue with occurrence data in Slovakia and in the Czech Republic, the references and a taxonomic index are attached.

The species entries on each species include *Diagnostic features* (particularly of the male genitalia) - *Faunistic status* - *Life-habits* - *Economic importance* - *Comments*.

In Vol. 1 twelve species new to science and fifty-eight other species as new for the fauna of Hungary are reported. Vols 2 to 4 will be published one volume/year to 2018.

The comparision of proboscis morphology and its influence on food preferences in subfamilies Ilytheinae and Ephydrinae (Diptera: Ephydridae)

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Keywords: shore flies, larval feeding, Poland

The present phylogenetic classification of the shore flies (Zatwarnicki, 1992) is based on morphological structures and the male terminalia. The first phylogenetic reconstruction with an emphasis on structures of proboscis in Hyadinini (Ilytheinae) was presented recently (2014). Three elements of adult mouthparts have phylogenetic importance for taxonomy: the number of pseudotracheae, structure of cibarium and lacinia.

We demonstrate the comparison of the proboscis and its structures within two sister-groups: Ilytheinae and Ephydrinae. Both subfamilies contain species with different food preferences. We can distinguish algae, diatoms and cyanobacteria feeders, which show a great variety of modifications of pseudotracheae and cibarium parts. The dagger-like or teeth-like modifications occurring in pseudotracheal rings are most likely used to graze and filter food substrate from surfaces. The ground plan of cibarium in presented subfamilies also differers significantly. Variations are visible in the shape of hypopharynx and arrangement of cibarial sensilles. The foregoing characters can be used to better understanding of food preferences occurring in the family Ephydridae.

Bobři způsobili lokální komáří kalamitu

Beavers caused massive occurrence of mosquitoes

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Klíčová slova: záplava lužního lesa, bobr evropský, *Aedes*, komáří kalamita
Keywords: floods, flood-plain forest, beaver (*Castor fiber*), massive occurrence of *Aedes* spp. mosquitoes

V období dlouhotrvajícího extrémního sucha a minimálního výskytu komárů rodu Aedes (Diptera, Culicidae) byla v polovině července 2015 v polesí Tvrdonice, na hranici katastrálního území města Lanžhot a obce Kostice, na lokalitě s místním názvem Liščí hora zjištěna lokální záplava téměř 500 ha lužního lesa. Záplavu způsobili bobři evropští (*Castor fiber*) svými hrázemi, kterými přehradili kanály napájené řekou Moravou a které slouží k zavodňování lesa. Výskyt larev komárů byl v době záplavy enormní, místy až 500 larev/dm^2. 24. července byla již pozorována výrazná aktivita enormního množství čerstvě vylíhlých komárů. Dne 28. července zde byl proveden odchyt komárů pomocí světelné EVS pasti s atraktantem CO_2 . Past byla exponována od 16:00 do 8:00 následujícího dne. Bylo odchyceno 1709 samic komárů. Dominovaly druhy byly *Ae. vexans* (77,5%) a *Ae. sticticus* (21,3%). Další odchyt byl zde proveden 6. srpna. To již bylo odchyceno 3489 komárů což odpovídalo tzv. „kalamitnímu“ výskytu. Dominovaly opět druhy *Ae. vexans* (85,7%) a *Ae. sticticus* (13,3%). Na kontrolní nezaplavené lokalitě Lanžhot – Soutok vzdálené cca 15 km bylo v tu dobu do pasti chyceno pouze 77 komárů. Na druhé kontrolní lokalitě Tvrdonice, vzdálené pouze 3 km od zaplavené lokality, bylo odchyceno 545 komárů (*Ae. vexans* byl zastoupen v 95,6 %). Na této lokalitě došlo proti odchytu z 15. července k výraznému nárůstu počtu bodajících komárů v důsledku záletu *Ae.vexans* z bobry zaplavené lokality. V druhé polovině srpna bobři opravili pobořené hráze a lužní les byl opět zaplaven.Výskyt larev a později dospělců komárů bude i nadále sledován.

Psammophilous flies (Diptera) on glacial sand deposits in Silesia (Czech Republic)

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Keywords: Diptera, psammophilous species, distribution, glacial sands, Hlučínsko, Czech Republic

Preliminary results of a study of dipterous communities on sandy habitats of glacial origin in the Hlučínsko area (Czech Silesia, NE Czech Republic) are presented. The glaciolacustrine sand deposits in the area under study were formed after the Saalian Glaciation (cca 160 000 ya) on shores of postglacial lakes which had arisen from a melted glacier. The psammophilous insect fauna only occurs in sites where the sand is exposed, i.e. mostly in sand-pits. Because no research of sand-loving Diptera has previously been conducted in the area, the author began to study this group by sampling flies in the largest active sand-pit (Závada nr. Hlučín, about 49°56'25''N, 18°09'56''E, cca 265 m) and in a small abandoned sand-pit and a nearby sandy hill (Bělá ve Slezsku, 49°58'25''N, 18°09'05''E, cca 245 m) in 2013 and 2015. Flies were collected by sweeping and netting on these sandy habitats once a month with the aim to obtain as wide a species spectrum as possible. The sampling hitherto performed yielded a number of psammophilous or even psammobiont species, the most interesting of which are: *Aspistes berolinensis* Meigen, 1818 (Scatopsidae), *Tetanops myopina* Fallén, 1820 (Ulidiidae), *Trixoscelis obscurella* (Fallén, 1823) (Trixoscelididae), *Eutropha variegata* Loew, 1866, *Thaumatomyia hallandica* Andersson, 1966 (Chloropidae) and *Curtonotum anus* (Meigen, 1830) (Curtonotidae). In addition, several xerophilous and/or thermophilous species were also recorded, including *Desmometopa discipalpis* L. Papp, 1993 (Milichiidae). Judging from their distribution the sand-loving species found on glacial sands in the Hlučínsko area seem to be of different origins. Besides the species of distinctly southern origin (e.g. *Curtonotum anus*) and taxa widespread in the W. Palaearctic (most other species), it seems that at least some of them could have spread from the Baltic Sea coasts by a growing continental glacier during the Saalian Glaciation and survived on sand dunes formed on the shores of postglacial lakes. This is the case of *Tetanops myopina*, a species widespread on sand dunes of Irish, North and Baltic Seas having its only inland records on glacial sands in northern Ukraine and the NE part of the Czech Republic. These inland populations are therefore considered to be glacial relicts.

New species of lauxaniids from Slovakia

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Keywords: Lauxaniidae, *Sapromyza slovaca*, new species, Slovakia

During faunistical research of Slovakia, a new lauxaniid belonging to the genus *Sapromyza* named *S. slovaca* was discovered. The new species is closely related to *S. sexpunctata* and *S. opaca*, as revealed by phylogenetic analysis of three molecular markers (16S rRNA, elongation factor 1-alfa and 28S rRNA). In the key of Papp (1979) and Shatalkin (2000) it can be easily confused with *S. zetterdterti*. Both species are small in body size and share the presence of 2 pairs of black spots on 5th and 6th abdominal tergites. Both species are easy to recognize, especially by the structure of male genitalia and some other morphological characters, like the presence of brown rectangular spot on the occiput, antennae widely separated and flat frons (present in *S. zetterstedti*, absent in *S. slovaca*). Both species differ also by habitat preference. The new species prefers warm and open places (up to date it is known from western Slovakia), while *S. zetterstedti* occurs typically in high altitude (High Tatra Mountains) or high latitude (the type locality is Norway).

Preliminary molecular phylogeny of gall midges (Diptera: Cecidomyiidae)

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Keywords: Diptera, Sciaroidea, Cecidomyiidae, molecular phylogeny, systematics

Family Cecidomyiidae (Diptera: Sciaroidea), with about 6,000 described species, is one of the most species-rich families of flies in the world. The family is currently subdivided, based on morphological characters, into six subfamilies – Catotrichinae, Lestremiinae, Micromyinae, Winnertziinae, Porricondylinae and Cecidomyiinae. Representatives of all these subfamilies were included in this study. The phylogeny was reconstructed based on combined analysis of five gene markers – three mitochondrial (12S, 16S, COI) and two nuclear (18S, 28S). Our results support the monophyly of the family as well as the monophyly of all the subfamilies. The phylogenetic tree obtained from the maximum likelihood analysis will be presented and commented on in the presentation.

Flies of Red-footed Falcon

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Keywords: blood-sucking flies, vector, bird, Culicidae, Ceratopogonidae, Carnidae

The strictly protected Red-footed falcon (*Falco vespertinus* Linnaeus, 1766) was studied: Kardoskút, South Hungary 2010-2012, Mezőcsát East Hungary 2009, 2010. Two sampling methods were used: gel trap and breeding. For the gel trap plastic plates (10×15cm) were used covered with baby oil gel on one side. The gel traps were fixed on the nest boxes (24h) during the three different phases of the incubation period (eggs, young and old nestlings). The flies were removed by clean petrol, thus the files did not damage, whichallowed the identification of these fragile flies. Near Mezőcsát in 2009 that was a period when the nest boxes weren't cleaned for 3 years. Nest material has been collected from 44(2009) and 17 (2010) nest boxes. The material has been stored in linen bag, and in the winter season stored in a cellar. The imagoes of flies have been breeded.

A total of 16668 (gel trap) and 50550 (breeding) diptera specimens were catched during the studies. The most abundant species were Culicidae and Carnidae. Four Ceratopoginidae species and one Fannidae species proved to be new to the Hungarian fauna.

Significant correlation was found between the numbers of the mosquitoes and the nestlings and detected the West-Nile Virus (lineage 2) in *Culex pipiens* Linnaeus, 1758 in Kardoskút. The number of blood-feeding *Carnus hemapterus* Nitzsch, 1818 was drastically reduced 2010 compared to 2009, most likely due to our cleaning efforts thus necessarity the cleaning of the nest boxes.

Jak se hledá *Rhabdomastix (Rhabdomastix) incapax* Starý, 2005 (Diptera, Limoniidae)

How to look for *Rhabdomastix* (*Rhabdomastix*) *incapax* (Diptera, Limoniidae)

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Klíčová slova: Diptera, Limoniidae, *Rhabdomastix (Rhabdomastix) incapax*, nová samice, redukce křídel, ekologie, chování
Keywords: Diptera, Limoniidae, *Rhabdomastix (Rhabdomastix) incapax*, new female, wing reduction, ecology, behaviour

Znovuobjevení druhu *Rhabdomastix (Rhabdomastix) incapax* Starý, 2005 na Sardinii umožnilo aktualizovat popis samce a podat první popis samice tohoto druhu. Jsou připojeny poznámky k redukci křídel, ekologii a chování.

Rediscovery of *Rhabdomastix (Rhabdomastix) incapax* Starý, 2005 in Sardinia made it possible to update the description of the male and to provide the first description of the female of this species. Notes on the wing reduction, ecology, and behaviour of this species are appended.

Can dipterans be used as a surrogate for rapid assessments of freshwater biodiversity?

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Keywords: surrogate, biodiversity, diversity indices, river basin

The assessment of biodiversity using all taxa in the given area is usually a time-consuming and expensive process since it requires taxonomic expertise for each group of aquatic biota. Therefore, the selection of surrogates to reliably represent freshwater biodiversity is an important topic in many recent studies. However, according to the available literature, a very few cross-taxon correlations can be considered as high enough to be used as a potential surrogate. In this study, we tested the utility of Diptera taxa to assess the freshwater biodiversity in lotic systems of central Balkan Peninsula. The total number of species, abundance, and diversity indices (Shannon-Wiener diversity index – H', Simpson index – 1-D) have been calculated for four taxa groups: Diptera, Ephemeroptera-Plecoptera-Trichoptera (EPT) group, macroinvertebrates without Diptera and fish. Spearman rank-correlation coefficients revealed that diversity of Diptera and other macroinvertebrates are correlated along the longitudinal gradient of the river basin, when the diversity was presented by 1-D ($r=0.391$, $P<0.05$). In addition, Diptera diversity was also correlated with EPT group (H', $r=0.391$, $P<0.05$). Such low level of correlation indicates a different diversity patterns among the investigated taxa groups. The obtained diversity information from different taxa groups is rather complementary, what diminishes the reliability of a surrogate approach in the biodiversity management.

Molecular phylogeny of Bibionomorpha *sensu lato* (Diptera) based on five gene markers

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Keywords: lower Diptera, Sciaroidea, phylogenetic analysis, molecular markers, systematics

The phylogeny of the megadiverse insect infraorder Bibionomorpha (Diptera) was reconstructed based on the combined analysis of three mitochondrial (12S, 16S, COI) and two nuclear (18S, 28S) gene markers. All the analyses (maximum parsimony, maximum likelihood and Bayesian inference) strongly support the monophyly of Bibionomorpha in both the narrow (*sensu stricto*) and the broader (*sensu lato*) concepts. The major lineages of Bibionomorpha *sensu lato* (Sciaroidea, Bibionoidea, Anisopodoidea, and Scatopsoidea) and most of the included families are supported as monophyletic groups. The position of Axymyiidae outside Bibionomorpha as well as the paraphyly of Bibionidae and Keroplatidae are demonstrated and discussed. Most of the included Sciaroidea *incertae sedis* genera were found to be related to Cecidomyiidae, but the relationships within this group require further study.

Dipterologická sbírka Entomologického oddělení Národního muzea

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Klíčová slova: Diptera, kurátorské a výzkumné aktivity, Psychodidae, webová prezentaca
Keywords: Diptera, Psychodidae, curator and research activities, online presentation

V příspěvku bude představen vznik a krátce popsána historie sbírky dvoukřídlých Entomologického oddělení Národního Muzea v Praze. Dále bude nastíněn stav a vývoj sbírky v letech 1961–2014 (v těchto letech sbírka sídlila v Kunratickém zámku) a dále bude informováno o nejvýznamnějších přírůstcích a o sběrných expedicích z tohoto období. Od začátku roku 2015 je sbírka deponována v nových depozitářích v Horních Počernicích a nyní probíhá její reorganizace. Bude představen plán této reorganizace a možnost zapojení externích specialistů do těchto prací. Autor představí hlavní kurátorské a výzkumné aktivity, včetně již ukončených, rozpracovaných a také těch plánovaných. Především bude představen katalog typů sbírky koutulovitých (Psychodidae) a nová webová prezentace sbírky (www.diptera.cz), kde lze nalézt podrobnější informace o sbírce a činnostech kurátora. Budou představeny nejvýznamnější části sbírky a je nabídnuta možnost jejich studia příslušnými specialisty (distanční v podobě výpůjček a prezenční – návštěvy).

Phylogeny of the tribe Discocerinini (Diptera: Ephydridae)

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Keywords: Diptera, Ephydridae, Discocerinini, phylogeny, proboscis

The tribe Discocerinini belongs to the subfamily Gymnomyzinae and is composed by 13 genera and 2 subgenera (1 genus and 2 subgenera are described as new). Generic relationship of the tribe was suggested by Zatwarnicki and Mathis (2001). The characters of proboscis support generic status for recently established taxa (*Orasiopa*, *Lamproclasiopa*, *Galaterina*, and *Facitrichophora*) and allow separating three new taxa. Genera *Polytrichophora* and *Orasiopa* are divided into subgenera and *Hydrochasma* is divided into separate genera, while one group of species is more related to *Discocerina*, than to the rest of *Hydrochasma*. Two types of cibarium were found and different number of pseudotracheae (from 2 to 11). The revised relationship among Discocerinini resulted in four groups 1) *Gymnoclasiopa* group with nominate genus, 2) *Diclasiopa* group with *Diclasiopa*, *Ditrichophora*, *Hecamedoides* and *Pectinifer*, 3) *Lamproclasiopa* group with *Galaterina*, *Lamproclasiopa, Orasiopa* and 4) *Discocerina* group with, *Discocerina,* New genus, *Facitrichophora*, *Hydrochasma*, and *Polytrichophora.*

EXTENDED ABSTRACTS

Taxonómia druhu *Heterotrissocladius marcidus* (Chironomidae) na základe analýzy DNA a genetická variabilita jeho populácie na území Tatier

Taxonomy of species *Heterotrissocladius marcidus* (Chironomidae) based on DNA analysis and genetic variability of its Tatra population

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Úvod

Tatranské jazerá vytvárajú unikátny habitat pre mnohé vodné bezstavovce. Výskum dvojkrídlovcov doposiaľ prebiehal na druhovej, resp. rodovej úrovni najmä v rámci faunistických, ekologických a paleolimnologických štúdií. Druhová diverzita spoločenstiev vodného hmyzu plies je celkovo dobre spracovaná, avšak štúdium druhov a populácií na molekulárnej úrovni je len v začiatkoch.

Z publikovaných dát o zložení spoločenstiev makrozoobentosu tatranských plies je zrejmé, že najpočetnejšou skupinou je čeľaď Chironomidae (Hamerlík et al. 2014). Na území Tatier bol potvrdený výskyt 58 druhov pakomárov (Novikmec 2015). Modelový organizmus *Heterotrissocladius marcidus* (Walker 1856) bol zvolený predovšetkým z dôvodu jeho vysokej frekvencie výskytu vo veľkých, ale i malých jazerách. Jeho vodné larvy majú eurytopné rozšírenie na celom území Tatier a tvoria významnú súčasť makrozoobentosu tatranských plies. Imágo aktívne lieta, no pre jeho nízku hmotnosť môže byť zanášané vzdušnými prúdmi. Naopak, v larválnom štádiu nie je schopný migrácie, čo umožňuje presnú lokalizáciu zozbieraných jedincov. Larvy je možné determinovať na základe kombinácie morfologických znakov: tenké, štíhle telo, mliečnobiele zafarbenie, výrazne tmavé submentum (časť hlavovej kapsuly) (Bitušík 2010).

V rámci komplexnejšieho štúdia populačnej genetiky *H. marcidus* v Tatrách bol okrem iných markerov analyzovaný aj fragment mitochondriálnej DNA: *cytochróm c oxidáza podjednotka I* (ďalej mtCOI). Práve analýza sekvencií mtCOI, ktoré sa často využívajú aj na molekulárnu determináciu druhov (Hebert et al. 2003), naznačila nesúlad s klasifikáciou založenou na klasických morfologických znakoch a možné taxonomické zmeny.

Kľúčové slová: mtDNA, *cytochróm c oxidáza I*, pakomáre, plesá, Vysoké Tatry
Keywords: mtDNA, *cytochrom c oxidase I*, chironomids, glacial lakes, High Tatras

Materiál a metódy

Odber a determinácia materiálu. Analyzované jedince H. marcidus boli zozbierané v rokoch 2009 až 2013 v tatranských plesách a menších jazierkach v nadmorskej výške 1311 až 2157 m n. m. na slovenskej (8 dolín) a poľskej (3 doliny) strane Vysokých Tatier, ale i v Západných Tatrách (2 doliny). Odber vzoriek bol vykonávaný v dostupnej litorálnej zóne jazier. Substrát pozostával z balvanov, štrku a štrkopiesku. V sedimente menších pliesok bol zaznamenaný vysoký podiel partikulovanej organickej hmoty. Vzorky boli odobrané kvantitatívnou metódou kick-sampling (Frost et al. 1971) do hydrobiologickej sieťky s kruhovým rámom s veľkosťou ôk 300 µm. Materiál bol na mieste dekantovaný, premytý, uložený do plastových nádob a fixovaný čistým liehom. V laboratóriu boli vzorky s použitím stereomikroskopu rozdelené do vyšších taxonomických skupín a druh H. marcidus bol determinovaný podľa dostupných kľúčov na určovanie pakomárov (Bitušík 2000, Brooks et al. 2007). Na identifikáciu do druhu nebolo potrebné vytvárať trvalé preparáty. Materiál zostal po určení neporušený a jedince mohli byť použité na izoláciu DNA.

Molekulárne metódy. DNA bola izolovaná z 563 jedincov pomocou Chelexovej metódy. PCR reakciami bol pomocou primerov Pat a Jerry (Simon et al. 1994) amplifikovaný fragment mitochondriálneho génu mtCOI. PCR reakcie prebehli v termocykléri (Eppendorf Mastercycler Pro) za nasledujúcich podmienok: počiatočná denaturácia (94°C, 5 min), 30 cyklov: denaturácia (94°C, 30 s), anelácia (48°C, 90 s), polymerizácia (72°C, 60 s), záverečná terminácia (72°C, 10 min). Úspešnosť amplifikácie bola skontrolovaná pomocou gélovej elektroforézy (PowerPac Basic, BIO-RAD) v 1% agarózovom géli s následnou vizualizáciou v UV transluminátore (Gel Logic 2/2 PRO). PCR produkty boli zaslané na sekvenovanie do extermého laboratória Macrogen Europe Inc. (Amsterdam, Holandsko). Z 563 jedincov sa podarilo úspešne osekvenovať 382 fragmentov mtCOI s dĺžkou 723 bázových párov.

Analýza a vyhodnotenie dát. Sekvencie mtCOI boli skontrolované a manuálne upravené v programe Sequencher 5.1. Konečná matica znakov bola vytvorená v programe MEGA 6.0. (Tamura et al. 2013). Ako sesterské skupiny („Outgroups“) boli použité príbuzné taxóny *Pseudodiamesa branickii* (Nowicki, 1873) (čeľaď Diamesinae) a *Macropelopia sp.* (čeľaď Tanypodinae). V rovnakom programe bola analyzovaná príbuznosť, resp. maximálna podobnosť vzoriek metódou maximum-likelihood (Tamura a Nei 1993) a vypočítaná hodnota genetickej vzdialenosti (uncorrected p-distance) medzi hlavnými vetvami vzniknutého kladogramu. Spoľahlivosť topológie vetiev stromu bola otestovaná metódou bootstrap pri počte opakovaní 300, pričom spoľahlivosť uzlov je preukazná nad hodnotou 50%. Vytvorený kladogram bol zobrazený a upravený v programe FigTree v1.4.2 (www.tree.bio.ed.ac.uk). V programe Network 4.6.1.3 (Bandelt et al. 1995) bola vytvorená haplotypová mapa.

Výsledky a diskusia

Plesá a plieska Tatier sú ľadovcového pôvodu a ich vek sa odhaduje na približne 10 000 rokov. Populácie tatranských jazier sú preto z evolučného hľadiska pomerne mladé. Pri tak recentnom veku tatranskej populácie *H. marcidus* sme predpokladali, že DNA jedincov patriacich do subpopulácií 21 plies a menších pliesok (zozbieraných v priebehu piatich rokov) nebude výrazne diverzifikovaná. Avšak, molekulárna vzdialenosť medzi analyzovanými jedincami bola značne variabilná. Metódou maximum-likelihood bol vytvorený kladogram, na ktorom sa v rámci študovaného druhu jasne oddelili 3 skupiny jedincov – evolučné línie (Group 1, Group 2, Group 3) (Fig. 1).

Celková spoľahlivosť uzlov (bootstrap hodnota) všetkých troch identifikovaných skupín jedincov bola 99%, čo potvrdzuje ich samostatnú evolučnú históriu.

Odlišnosť jednotlivých skupín je demonštrovaná určením genetickej vzdialenosti (Tab. 1). Identifikované vývojové línie sa líšili pomerne vysokým percentom v rozmedzí od 3,3% po 8,3%. Vzdialenosť „Outgroups“ sa od Group 1–3 pohybovala v rozmedzí 15,7% až 18,4%. Vo všeobecnosti platí, že horná hranica vnútrodruhovej variability je 5,2% (Weis et al. 2013), ale napr. Hebert et al. (2003) uvádza, že hranica medzidruhovej úrovne sa pohybuje okolo 3%.

Genetická vzdialenosť medzi jedincami v rámci skupín sa pohybovala v rozmedzí (0,001 – 0,019), hodnoty genetickej vzdialenosti medzi zistenými skupinami však výrazne prevyšujú obidve publikované hranice.

Tab. 1. Hodnoty genetickej vzdialenosti (uncorrected p-distance) medzi „outgroups“ a skupinami vzoriek *Heterotrissocladius* cf. *marcidus* vyčlenených na základe analýzy mtDNA fragmentu pre *cytochróm c oxidázu podjednotku I.*

	Group 1	Group 2	Group 3	Outgroup 1	Outgroup 2
Group 1					
Group 2	7,00%				
Group 3	8,30%	3,30%			
Outgroup 1	18,10%	17,50%	18,40%		
Outgroup 2	15,90%	15,60%	15,70%	16,80%	

V programe Network 4.6 bola analyzovaná genetická štruktúra populácie *H. marcidus* tatranských plies. Vzhľadom k tomu, že maximum likelihood analýza mtCOI fragmentu potvrdila prítomnosť geneticky výrazne odlišných skupín, ktoré naznačujú prítomnosť viacerých taxónov (?druhov), haplotypové siete boli vytvorené samostatne pre každú skupinu (Fig. 2). Celkovo bolo identifikovaných 85 haplotypov s rôznou početnosťou medzi jednotlivými skupinami. Počtom vzoriek bola najbohatšia skupina Group 1, v ktorej bolo identifikovaných 22 haplotypov. Ostatné skupiny boli zastúpené menším počtom vzoriek, geneticky však boli pestrejšie - Group 2 – 39 haplotypov, Group 3 – 24 haplotypov.

Výsledky analýzy DNA tatranských vzoriek *H. marcidus* potvrdili, že tmavo sfarbené submentum ako rozlišovací znak pre larvy druhu *H. marcidus* nemusí byť dostatočný, podobne ako to uvádza Saether (1975). V budúcnosti sa na izoláciu DNA nebude využívať celá larva, ale iba hruď a bruško. Hlavová kapsula bude uložená ako dočasný preparát aby bola možná následná podrobnejšia analýza morfologických znakov jedincov reprezentujúcich jednotlivé evolučné línie. Okrem toho bude potrebné získať materiál dospelých jedincov, aby bolo možné prípadne podporiť prítomnosť viacerých samostatných taxónov (druhov) vo vzorkách z Tatier, doposiaľ určovaných ako *H. marcidus.*

Táto štúdia jasne preukázala opodstatnenosť a význam analýzy molekulárnych znakov v kombinácii s morfologickými znakmi. Bez analýzy taxonomicky dôležitých DNA markerov by sme jednak nepoznali skutočnú diverzitu študovaných organizmov a následná analýza populačnej štruktúry (napríklad s využitím hypervariabilných jadrových fragmentov) by obsahovala zmes viacerých taxónov a jej výsledky by tak strácali svoj význam.

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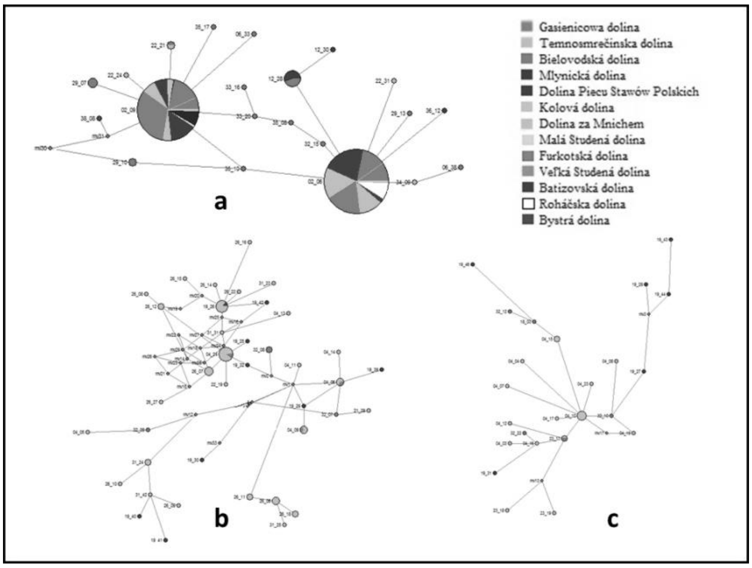
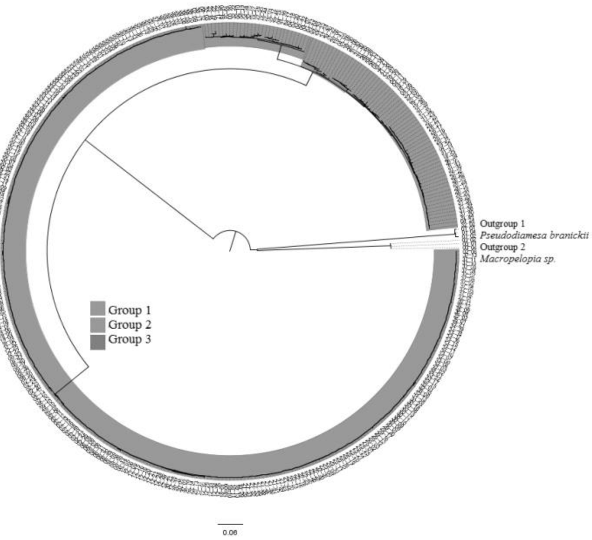


Obr. 1. Maximum-likelihood kladogram 382 jedincov *Heterotrissocladius* cf. *marcidus* vytvorený na základe analýzy mitochondriálneho fragmentu pre *cytochróm c oxidázu podjednotku I*.

Fig.1. Molecular phylogeny of 382 *Heterotrissocladius* cf. *marcidus* specimens based on *cytochrom c oxidase subunit I* gene sequences. Cladogram is based on maximum-likelihood.



Obr. 2. Haplotypové mapy tatranskej populácie druhu *Heterotrissocladius* cf. *marcidus* (a – Group 1, b – Group 2, c – Group 3) v 13-tich tatranských dolinách. Veľkosť kruhu zodpovedá množstvu jedincov prislúchajúcich danému haplotypu, farebná výplň predstavuje jednotlivé doliny. Červené čísla označujú pozíciu, na ktorej nastala mutácia v sekvencii. Červené body reprezentujú nezachytený alebo vyhynutý haplotyp.

Fig.2. Haplotype maps of *Heterotrissocladius* cf. *marcidus* population (a – Group 1, b – Group 2, c – Group 3) from 13 Tatra Mts. valleys based on *cytochrom c oxidase subunit I* fragment. The sizes of the circle are proportional to the number of individuals sharing that haplotype. The colors are belonging to the valleys. Red numbers represent position of mutation in sequence. Red points represent not catched or extinct haplotype.

Prehľad druhovej skladby komárov (Diptera: Culicidae) na vybraných lokalitách východného Slovenska

Species composition of mosquitoes (Diptera: Culicidae) in selected areas in Eastern Slovakia

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Úvod

Komáre (Culicidae) patria k najviac študovanej skupine dvojkrídlovcov. Nutnosť intenzívnej surveillance s ohľadom na druhovú diverzitu, populačnú dynamiku, rozšírenie a paraziticko-hostiteľské vzťahy vyplýva predovšetkým z ich schopnosti prenášať celý rad patogénov. Východné Slovensko má v súvislosti s výskytom komárov výnimočné postavenie. Charakteristické klimatické podmienky tohto územia spojené s teplou, mierne suchou klímou, priaznivým ročným úhrnom zrážok a častými záplavami, vytvárajú ideálne podmienky nielen pre prežívanie vektora, ale aj patogénov, na prenose ktorých sa podieľajú. Osobitosť územia sa už niekoľkokrát potvrdila aj v minulosti. V povojnových rokoch sa vo východnej a juhovýchodnej časti krajiny šírila malária, dnes sa tu nachádza jedna z endemických oblastí dirofilariózy.

Aktuálne je na Slovensku zaznamenaných 50 druhov komárov. Najkomplexnejšie informácie o faune *Culicidae* z územia Slovenska pochádzajú z 50. až 60.-tych rokov (Kramář et al. 1952, Kramář 1958, Trpiš 1965 a,b). Štúdie z ostatných 20 rokov (Halgoš & Dovoedo, 1993, Jalili & Degma 1998, Jalili et al. 2009, Minář et al. 2007, Stralková & Halgoš, 2012) pochádzajú prevažne zo západnej časti krajiny, kde sú komáre sledované nepretržite už takmer 60 rokov. Vo východnej časti krajiny po eradikácii malárie prieskumy postupne stratili na intenzite a doteraz chýba ucelenejší obraz o aktuálnej druhovej diverzite. Našou prácou sa snažíme nadviazať na takmer 50 rokov staré faunistické práce z toho územia, resp. na mladšie práce publikujúce výsledky z príležitostných odchytov komárov robených na východe Slovenska.

Kľúčové slová: komáre, larvy komárov, východné Slovensko, druhová diverzita
Keywords: mosquitoes, mosquito larvae, Eastern Slovakia, species composition

Materiál a metódy

Výskum bol sústredený na lokality situované v Košickom, Prešovskom a Trebišovskom okrese. Na odchyt lariev sme používali sitko s priemerom 12 cm, pričom v každom liahnisku boli robené 3 výlovy. Larvy sme konzervovali v 75% alebo v 96% alkohole a diagnostikovali v laboratóriu. Morfologicky úzko príbuzné druhy sme pre presnejšiu diagnostiku zalievali do kanadského balzamu do formy trvalých mikroskopických preparátov. Imága sme odchytávali lapačmi typu CDC Miniature Light Trap s CO_2 návnadou vo forme suchého ľadu (2 kg mikropeletiek). Lapače sme exponovali do výšky približne 150 cm nad zemou, v podvečerných hodinách, zapínali vždy v približne rovnakom čase (17-18.30) a vypínali o 8-9 hodine ráno nasledujúceho dňa. Ako doplnkovú metódu sme používali odchyty entomologickou sieťkou a exhaustorom. Samice sme diagnostikovali pod stereolupou na základe morfologických znakov a determinačných kľúčov (Kramář, 1958, Becker et al. 2010). Druhovej identifikácii samcov predchádzalo zhotovenie mikroskopických preparátov hypopýgií.

Pri každom terénnom odchyte sme zaznamenávali vybrané ekologické parametre (teplotu vody, pH vody, teplotu, vlhkosť a prúdenie vzduchu). Informácie o priemerných, minimálnych a maximálnych hodnotách teploty vzduchu, vlhkosti vzduchu, rýchlosti vetra a denného úhrn zrážok nám poskytoval slovenský hydrometeorologický ústav v Košiciach (SHMU).

Výsledky a diskusia

V priebehu sledovaného obdobia (2010-2013) bolo celkovo odchytených 24 druhov komárov, patriacich do 6 rodov (*Aedes, Anopheles, Culex, Culiseta, Coquillettidia, Ochlerotatus*).

Diferenciálnou diagnostikou sme zistili 16 druhov lariev s eudominantným zastúpením (relatívna abundancia >10 %) *Culex pipiens* (33,80 %), *Aedes vexans* (19,27 %) a *Ochlerotatus cantans* s. l. (15,99 %). Dominantnú zložku (relatívna abundancia 5 – 10 %) tvorili *Ae. cinereus* (5,94 %), *Oc. sticticus* (5,54 %) a *Oc. punctor* (5,05 %). V sezónnom výskyte lariev v jednotlivých rokoch sme zaznamenali rozdiely v druhovom zložení a abundancii (Tab.1), ktoré vyplývali z meteorologickej situácie, predovšetkým z prítomnosti resp. absencie vody v liahnisku, ktorá ovplyvnila ich vývin.

Odchytmi adultných komárov sme zaznamenali 22 druhov (Tab. 2). Celkovo sme odchytili 64 434 komárov, ako druhy s eudominantným výskytom boli zistené *Ae. vexans* (36,6 %), *Oc. sticticus* (12,1 %) a *Cx. pipiens* s. l. (42,3 %). Tri druhy (*Oc. cataphylla, Oc. communis* a *Oc. punctor*) boli odchytené iba entomologickou sieťkou. Zaujímavým nálezom v rámci odchytov boli 4 samičky pôvodom ázijského komára *Aedes (Stegomyia) albopictus*, ktorého sme odchytili v roku 2012 na lokalite v Šebastovciach (okres Košice). Podobne ako v Českej republike (Šebesta et al. 2012) a v Rakúsku, aj na Slovensku (Bocková et al. 2013) sa jednalo o jeho prvý nález v rámci územia a nový záznam v strednej Európe.

Významnú úlohu v sezónnom výskyte lariev ako aj dospelcov zohrávali vonkajšie faktory, predovšetkým teplota ovzdušia a množstvo atmosférických zrážok. Z meteorologického pohľadu, boli všetky 4 sledované roky extrémne, najmä v súvislosti so zrážkami (rok 2010) a teplotou ovzdušia (roky 2012, 2013). Abundancia lariev priamo úmerne závisela od úhrnu zrážok, t.j. početnosť lariev sa zvyšovala vždy po nástupe, resp. doznení zrážok (Bocková, 2013). V obdobiach extrémnych horúčav, početnosť výrazne klesala. Druhová diverzita sa čiastočne menila v závislosti od kalendárneho mesiaca, avšak prežívateľnosť lariev bola vyššia u druhov teplomilných. Populačná dynamika u adultov nebola poveternostnými vplyvmi tak výrazne ovplyvnená ako v prípade lariev, nakoľko nie sú striktne viazané na vodné prostredie. Navzdory vysokým teplotám vzduchu (priemerná ročná teplota 10,2 °C) a malému množstvu, nepravidelne rozmiestnených zrážok v rokoch 2012 a 2013 (548,9 a 616,3 mm zrážok) sa odchytávalo počas celej sezóny relatívne veľké množstvo imág (Tab.3).

Cieľom našej práce je intenzívna a podrobná entomologická surveillence z čo najväčšej časti východného Slovenska, poskytnúť aktuálne poznatky z oblasti druhovej diverzity a bionómie komárov. Vzhľadom ku zmenám klímy je potrebné nepretržite sledovať zmeny v druhovom zložení komárov, zmeny v sezónnej dynamike, interakcie vektorov s prostredím, hostiteľmi a patogénmi.

Tab. 1. Porovnanie druhovej skladby a abundancie lariev odchytených v rokoch 2010 – 2013.

Druh	**Rok 2010**		**Rok 2011**		**Rok 2012**		**Rok 2013**		**Spolu**	
	A	%	A	%	A	%	A	%	A	%
Ae. cinereus	146	1,47	924	10,37	578	10,73	86	1,73	1734	**5,94**
Ae. refiki	0	0,00	2	0,02	0	0,00	0	0,00	2	**0,006**
Ae. rusticus	0	0,00	1	0,01	0	0,00	0	0,00	1	**0,003**
Ae. vexans	3655	36,83	0	0,00	234	4,34	1732	35,01	5621	**19,27**
An. maculipennis	273	2,75	0	0,00	74	1,40	38	0,80	385	**1,32**
Cs. annulata	9	0,09	1159	13,01	94	1,74	17	0,34	1279	**4,38**
Cx. territans	0	0,00	6	0,06	0	0,00	0	0,00	6	**0,02**
Cx. pipiens	4757	47,93	524	5,90	2897	53,80	1679	33,94	9857	**33,80**
Oc. cantans/annulipes	454	4,57	3110	34,93	625	11,60	474	9,60	4663	**15,99**
Oc. cataphylla	8	0,08	1076	12,10	302	5,60	50	1,01	1436	**4,92**
Oc. flavescens	0	0,00	364	4,10	46	0,90	2	0,04	412	**1,41**
Oc. geniculatus	6	0,06	0	0,00	0	0,00	9	0,20	15	**0,05**
Oc. leucomelas	0	0,00	244	2,74	0	0,00	0	0,00	244	**0,83**
Oc. punctor	13	0,13	1148	12,90	232	4,30	81	1,63	1474	**5,05**
Oc. sticticus	602	6,10	193	2,16	135	2,50	688	13,90	1618	**5,54**
Oc. communis	0	0,00	151	1,70	167	3,10	90	1,81	408	**1,30**
Počet druhov	**10**		**13**		**11**		**12**		**16**	
Počet jedincov	**9923**		**8902**		**5384**		**4946**		**29155**	

A=abundancia, A>10%=eudominantý druh, A=5-10 % dominantný druh, A<5 %=satelitný druh

Tab. 2. Porovnanie druhovej skladby a abundancie adultov odchytených v rokoch 2010-2013.

Druh	**Rok 2010**		**Rok 2011**		**Rok 2012**		**Rok 2013**		**Spolu**	
	A	%	A	%	A	%	A	%	A	%
Ae. albopictus	0	0,00	0	0,00	4	0,01	0	0,00	4	**0,01**
Ae. cinereus s. l.	34	5,90	9	2,61	1128	3,94	311	0,91	1482	**2,33**
Ae. rossicus	0	0,00	0	0,00	127	0,44	336	0,99	463	**0,72**
Ae. vexans	152	26,40	20	5,81	3034	10,61	20036	59,05	23252	**36,65**
An. claviger	0	0,00	0	0,00	6	0,02	51	0,15	57	**0,08**
An. hyrcanus	0	0,00	0	0,00	2	0,006	0	0,00	2	**0,003**
An. maculipennis s.l.	33	5,70	0	0,00	317	1,10	283	0,83	633	**0,99**
An. plumbeus	0	0,00	0	0,00	2	0,006	3	0,008	5	**0,008**
Cq. richiardii	0	0,00	0	0,00	9	0,03	254	0,74	263	**0,41**
Cs. annulata	0	0,00	20	5,81	125	0,43	30	0,09	175	**0,26**
Cx. modestus	0	0,00	0	0,00	16	0,05	5	0,01	21	**0,03**
Cx. pipiens/torrentium	212	36,90	158	45,93	19454	68,08	7046	20,76	26870	**42,36**
Cx. territans	70	12,20	0	0,00	0	0,00	106	0,31	106	**0,17**
Oc. annulipes	0	0,00	0	0,00	0	0,00	6	0,01	6	**0,009**
Oc. cantans s.l.	0	0,00	70	20,34	541	1,89	707	2,08	1388	**2,19**

Oc. caspius	0	0,00	0	0,00	213	0,74	658	1,93	871	**1,37**
Oc. cataphylla	0	0,00	8	2,32	0	0,00	7	0,02	15	**0,02**
Oc. communis	0	0,00	6	1,74	0	0,00	0	0,00	6	**0,009**
Oc. flavescens	0	0,00	0	0,00	0	0,00	3	0,008	3	**0,004**
Oc. geniculatus	0	0,00	0	0,00	24	0,08	42	0,123	66	**0,10**
Oc. punctor	8	1,40	29	8,43	0	0,00	0	0,00	37	**0,06**
Oc. sticticus	66	11,50	24	6,97	3574	12,50	4045	11,92	7709	**12,15**
Počet druhov	**7**		**9**		**16**		**18**		**22**	
Počet jedincov	**575**		**344**		**28576**		**33929**		**64434**	

A=abundancia, A>10%=eudominantý druh, A=5-10 % dominantný druh, A<5 %=satelitný druh

Tab. 3. Porovnanie vybraných environmentálnych faktorov a abundancie imág komárov v rokoch 2012 a 2013.

Rok	**2012**			**2013**		
Mesiac	**Počet adultov**	**Teplota vzduchu [°C]**	**Úhrn zrážok [mm]**	**Počet adultov**	**Teplota vzduchu [°C]**	**Úhrn zrážok [mm]**
apríl	211	11,1	44,4	1 146	11,4	26,1
máj	1 557	16,3	39,9	3 090	15,8	147,7
jún	8 102	19,9	83,1	8 965	20,0	82,8
júl	9 999	22,2	127,6	15 635	19,6	62,0
august	8 707	19,6	62,0	5 093	19,7	21,7
SPOLU	**28 576**	*17,8	357,0	**33 929**	*17,3	340,3

**priemerná teplota ovzdušia za obdobie apríl-august*

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Cerodontha (*Poemyza*) *unisetiorbita* (Agromyzidae) – a leaf miner fly on bamboo also found in the Czech Republic

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Introduction

The Agromyzidae is a family of Acalyptrate Diptera with 3,017 phytophagous species unequally distributed in 30 genera. The host-plant are currently known for only 42% of the agromyzids species which are distributed in 146 families and 899 genera of plants (Benavent-Corai et al. 2005). The genus *Cerodontha* Rondani, 1861, with seven subgenera (*Butomomyza* Nowakowski, 1967, *Cerodontha* Rondani, 1861, *Dizygomyza* Hendel, 1920, *Icteromyza* Hendel, 1931, *Phytagromyza* Hendel, 1920, *Poemyza* Hendel, 1931 *and Xenophytomyza* Frey, 1946) and comprising altogether 291 species, is the most diverse group of the the family Agromyzidae. The species-richest subgenus *Poemyza* Hendel, 1931 includes 81 species distributed in all the biogeographical regions of the world. A total of 30 species belonging to *Poemyza* are currently know from Europe (Nowakowski 1973, Zlobin 1993). Species of *Poemyza* are miners of leaves of grasses (Poaceae) but the information about their biology has hitherto been available for only 29 species of the subgenus worldwide. Only 3 leaf miner species of the subgenus *Poemyza* are known to use bamboo species (subfamily *Bambusoideae*) as host-plants (Spencer 1990) of which only *Cerodontha* (*Poemyza*) *unisetiorbita* Zlobin, 1993 is known also from Europe. This species was described from Japan (Zlobin 1993) and its occurrence was latter also confirmed from Italy (Süss 2001). The new records from the Czech Republic, Germany and Switzerland („Rai Hannover“ 2013) demonstrate spreading of this species in Europe. The high number of the mined leaves found on host-plants as well as the number of reared specimens indicate that the occurrence of the species is already firmly established in these localities (see below).

Keywords: Diptera, Agromyzidae, *Cerodontha* (*Poemyza*) *unisetiorbita*, new records, Czech Republic, distribution, biology

Material and methods

Material examined: CZECH REPUBLIC: Moravia, Štípa near Zlín, ZOO Zlín - Lešná, 49°16'24"N, 17°42'39"E, 265 m a.s.l., 11.viii.2014 and 15.vii.2015 on *Phyllostachys nuda*, ex. puparium in leaf mine, 11 adults (4♂♂ 7♀♀) emerged 13.-21.viii.2014 and 1 ♀ emerged 17.vii.2015. All specimens were reared from larvae and puparia found in mined bamboo leaves.

Rearing methods: Larvae were left in leaves placed in microtene bags up to the pupariation. For rearing adults the puparia were removed from mines and placed separately in small glass vials corked by rolled blotting paper enabling air exchange and suitable humidity. Vials with puparia were put in small plastic box with foam plastic which was regularly wetted by drops of water. The emerged adults were captured and kept separately but killed only after 24 hours when maturated, subsquently they were dry-mounted on triangular pinned cards together with associated (empty) puparia.

Results and discussion

C. (*P.*) *unisetiorbita* was described by Zlobin (1993) from Japan. This species very closely resembles *C.* (*P.*) *bisetiorbita* Sasakawa, 1955 being known from Japan and Taiwan but is characterized in having orbital setulae in a single row, the ultimate section of vein M_{3+4} long about 1.8 times as long as penultimate and legs entirely black. The specimens studied from C. Europe have legs lighter, with fore knees and tarsi pale brown. The structures of the male genitalia are in both species distinctly different (cf. Sasakawa 1961: Fig. 49c, d, e, f and Zlobin 1993: Figs 77-81). The larva forms a pale green, short and relatively broad ophionom mine (Fig 3) on upper side of the leaf, the older mines are somewhat browned. On larger leaf more larvae can mine together and their mines can sometimes be connected. The pupariation occurs in the leaf mine. Puparium (Fig 2) is reddish brown to brown, 1.65–1.85 mm long, somewhat dorsoventrally flattened, intersegmental grooves are slightly wrinkled and shallow, posterior spiracles long, each with 8–9 bulbs.

The occurrence of *C.* (*P.*) *unisetiorbita* in Evrope was first recorded in 2000 from Italy (Süss 2001) on bamboo *Phyllostachys mitos* near Arizzano in the vicinity of Lago Maggiore in the province Verbania and subsequently also in Milano and Liguria: Pozzuolo in the province La Spezia. In August 2013 mines of *C.* (*P.*) *unisetiorbita* have been found in growths of bamboo species *Phyllostachys* sp. a *Fargesia* sp. in a bamboo garden near Zürich in Switzerland („Rai Hannover“ 2013). Subsequently, in summer 2014 and 2015 the mines of the same species have been found by on *Phyllostachys nuda* in ZOO Zlín – Lešná, in Štípa near Zlín (Czech Republic). The identical mines were also found on the species *Phyllostachys atrovaginata*, *P. parvifolia* a *P. aureosulcata „spectabilis*“ in bamboo garden in Hannover (Germany). All adult flies reared from puparia from the latter two populations clearly belonged to *C. (P.) unisetiorbita*.

Seedling bamboos grown in Europe are mostly importeds from China but many *Phyllostachys* species from China have a long history of cultivation in Japan. Thus it is not always possible to reveal the origin of the bamboo species imported to Europe. Because the occurrence of leaf miners (Agromyzidae) in bamboo growths has hitherto not been specially investigated it can be expected that *C.* (*P.*) *unisetiorbita* will plausibly be found also in other countries of Europe and/or America where various bamboo species are planted from seedlings imported from China or Japan.

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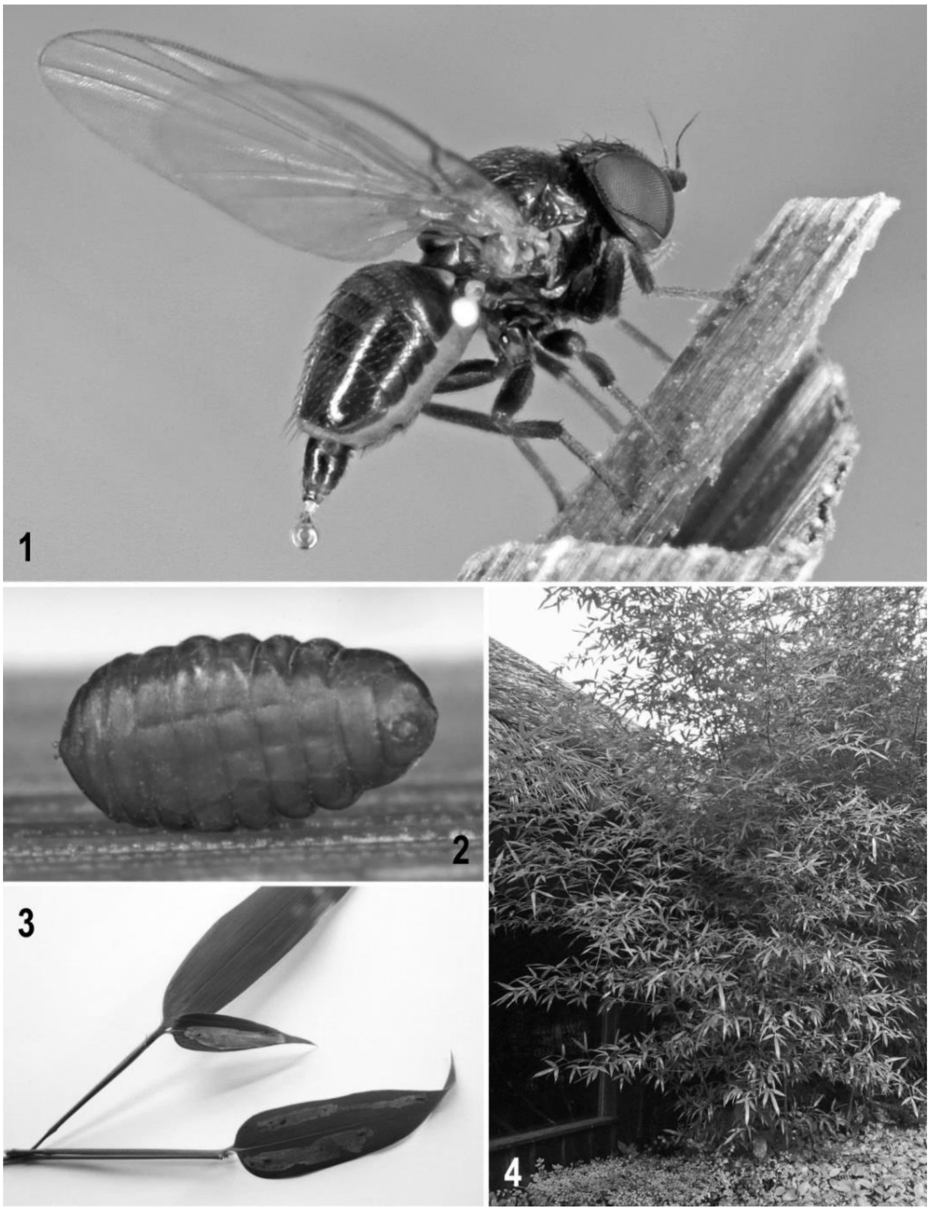

Figs 1–4. Adult, puparium, mines and host plant of *Cerodontha* (*Poemyza*) *unisetiorbita* Zlobin from the Zoological garden Zlín-Lešná: **1** – female, laterally, **2** – puparium, ventrally, **3** – a mined bamboo leaf of *Phyllostachys nuda,* **4** – habitat with host plant *P. nuda* in the Zoological garden Zlín Lešná. Photo by J. Roháček (Figs 1, 2) and M. Černý (Figs 3, 4).

Pediciidae from the Carpathians Biodiversity Hotspots: from general patterns to case studies

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Abstract

Carpathians are recognized as one of the most important hotspots for aquatic biodiversity in Europe. In the present study sequences of the mtCOI gene and morphometric measurements of 11 characters of the male genitalia were used to study phylogeographic pattern of a range-restricted endemic dipteran group belongs to Pediciidae from here. Molecular data supports the taxon status of the allopathic sibling pairs *Pedicia apusenica*, *Pedicia staryi* and *Pedicia lobifera* with limited distribution in small enclaves of the Carpathian Area. Additionally, in the case of the most widespread *Pedicia staryi* the results revealed further divergent structures between populations from geographically isolated mountain groups, already identified as important centers of endemism. An unexpected high genetic diversity was identified in the populations from the Rodnei Mountains, where the northern and southern slope harbor highly divergent genetic structures and support the importance of this mountain range to preserve autochthonous diversity. This pattern brings important new evidence on the complex autochthonous evolutionary history of spring habitats in the Carpathians, as these patterns are most likely the result of long-term isolation in so called cumulative microrefugia in the Carpathians, caused by aridization and forest fragmentation in the Miocene-Pliocene period and continued during the Quaternary Glaciations, due to their specific habitat requirements to wet and humid environment of headwater springs.

Keywords: crane fly, cryptic diversity, microrefugia, mtCOI, speciation

Introduction

The biogeographic studies of the last decades are mostly focused on the Pleistocene climate changes as the mechanism that shaped distribution and influenced differentiation of lineages at specific level due to isolation in different refugia (Ferchaud et al. 2012). However in many cases recent morphological and molecular studies revealed that speciation events often predate Pleistocene climatic changes and can frequently be related with repeated insularity of the Carpathians during the Miocene transgression and regression periods of the Parathetys and associated with insular speciation in different isolated land-masses (Pop et al. 2010) or volcanism (Habel & Assmann 2010).

The *Pedicia* (*Crunobia*) *staryi* species complex was established by Savchenko in 1986, and according to the present classification schemes is represented by five species: *Pedicia (C.) apusenica* Ujvárosi & Starý, 2003, *P. (C.) lobifera* Savchenko, 1986, *P. (C.) stary* Savchenko, 1978, *Pedicia (C.) spinifera* Starý, 1974 and *P. (C.) straminea* Meigen, 1838. *P. lobifera, P. stary* and *Pedicia apusenica* are narrow endemics and are closely related to wet and moist environment of headwaters in the Carpathians, and the Apuseni Mountains at altitudes between 1000-1500m. *P. staryi* shows a disjunct distribution with populations in the northern part of the Eastern Carpathians (Czarnohora-Maramures and Rodnei Mountains) and in the eastern part of the Southern Carpathians (Bucegi Mountains). In the Bulgarian Mountains they are replaced by *P. spinifera*. The last member of this species group, *P. straminea* is widely distributed in various headwater habitats at different altitudes in Europe (Oosterbroek 2014). The aim of this study was to infer the phylogenetic relationship among the five species of the group and to identify the molecular divergence of the three Carpathian species.

Materials and methods

The individuals used in the study were collected with entomological net and stored separately in collection tubes containing 96% ethanol, in the Zoological Museum of the Babes Bolyai University, Cluj Napoca.

Tissue samples from a total 126 specimens of the five *P.* species were used in the molecular analysis. DNA extraction, PCR amplification and sequencing followed standard protocols employed at the Canadian Centre for DNA Barcoding (Ivanova et al. 2006, Ivanova et al. 2012, Ivanova & Grainger 2012a,b). The phylogenetic relationships between all five species of the *P. staryi* complex were inferred based on the haplotype data set using a Bayesian inference (BI) algorithm BEAST 1.7.4 (Drummond & Rambaut 2007), using the previously selected substitution model (HKY+G).The consensus tree was visualized in FigTree 1.4 (http://tree.bio.ed.ac.uk/software/figtree/). Differentiation between groups was analyzed with the hierarchical analysis of the molecular variance (AMOVA) using Arlequin 3.5 (Excoffier & Lischer 2010).

Morphological variation among lineages of *P. staryi* were quantified by comparing 11 morphological characters of the male genitalia. The measured morphological variables were compared with Kruskal–Wallis tests and principal component analysis (PCA) in R 3.2.1.

Results and discussion

This study is the first assessment of the phylogenetic relationship of the five species belonging to the *P. staryi* species complex based on mitochondrial DNA sequence data. Our results suggest the monophily of the group and thus confirm Savchenko's (1986) findings based on the morphological characters.

The BI tree inferred based on the 658 base pair mtCOI alignment shows that the Balcanian endemic *P. spinifera* is the oldest species strongly differentiated from the the other species of the group. *Pedicia starminea* is the sister species of the three Carpathian taxa. *P. lobifera* is monophyletic (PP=1.00). The topology of the trees show four well supported *P. staryi* lineages (*Fig. 1*). The *staryiR+staryiG* lineage consists of haplotypes from Rodnei and Gutin Mountains and form two distinct groups corresponding to the two mountain ranges. One haplotype from the Rodnei Mountains forms a separate clade (*staryiR2*) that is basal to the unsupported group formed by the third *P. staryi* lineage (*staryiB*) and *P. apusenica. StaryiB* is a genetically cohesive and geographically well separated group consisting of haplotypes from the Bucegi Mountains. *P. apusenica* is also well supported (PP=1.00) and monophyletic (Fig. 1). However the low support of nodes on the phylogenetic trees show that the relationship between the species is not clearly resolved by the *mt*COI data at hand. AMOVA showed the highest amount of variation 79.55%) when the five clades (*P. apusenica*, *staryiB, staryiG, staryiR1* and *staryiR2*) were treated separately.

The PCA analysis based on the morphometrical measurements also shows tree separated lineages corresponding to *staryiR1*, *staryiR2* and *staryiG* (Fig. 2). *StaryiB* overlapped with the other three groups but several statistically supported differences were found by the Krustal–Wallis test (example Fig. 3) confirming the existence of this fourth group.

The results of this study show similarly deep divergent morphological and genetic structures from the Carpathians as in the case of some fish species (Kotlík & Berrebi 2002), aquatic insects like caddis flies (Bálint et al. 2011) and other Pediciidae crane flies (*Dicranota martinovskyi* Stary, 1974 group) (Kolcsár et al., pers. com.) or terrestrial species with limited dispersal ability (Varga, 2010) from this region. Thus presenting an important arguments that these areas should not simply be viewed as "glacial refugia", but rather as "long term" or cumulative refugia (Tzedakis et al. 2013).

Aknowledgements

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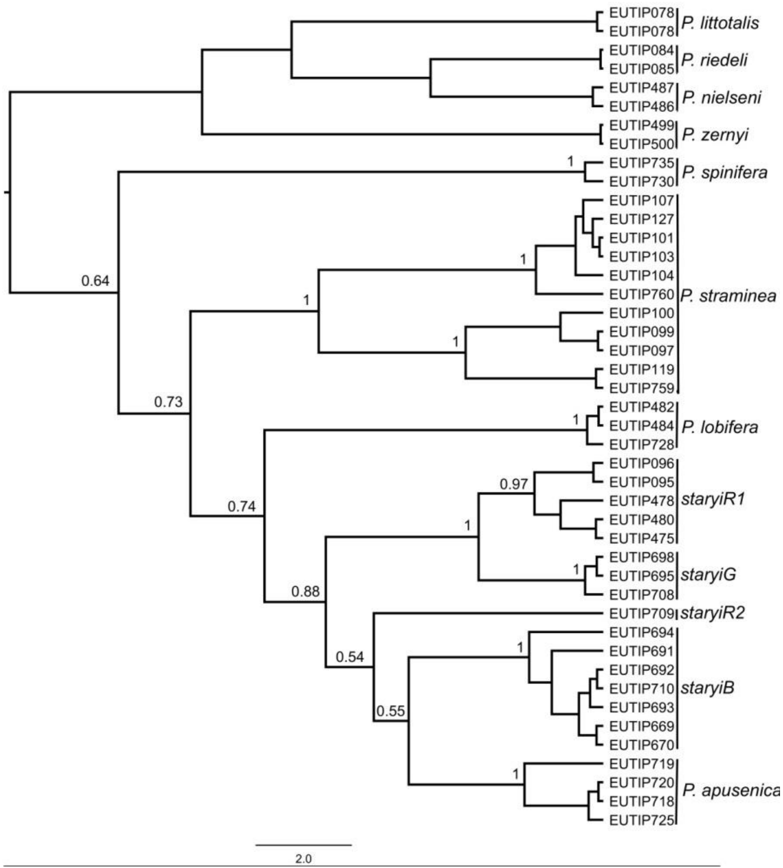

Fig. 1. Bayesian inference (BI) tree showing the phylogenetic relationship among the five species of the *P. staryi* group.

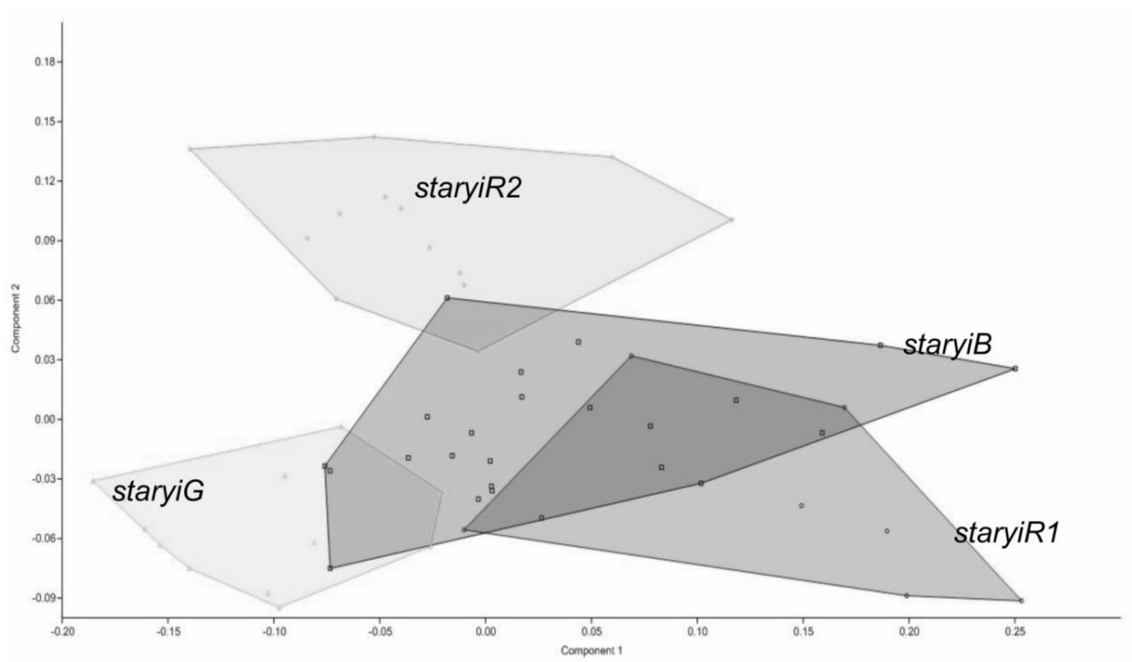

Fig. 2. Result of PCA analysis of the four *P. staryi* lineages.

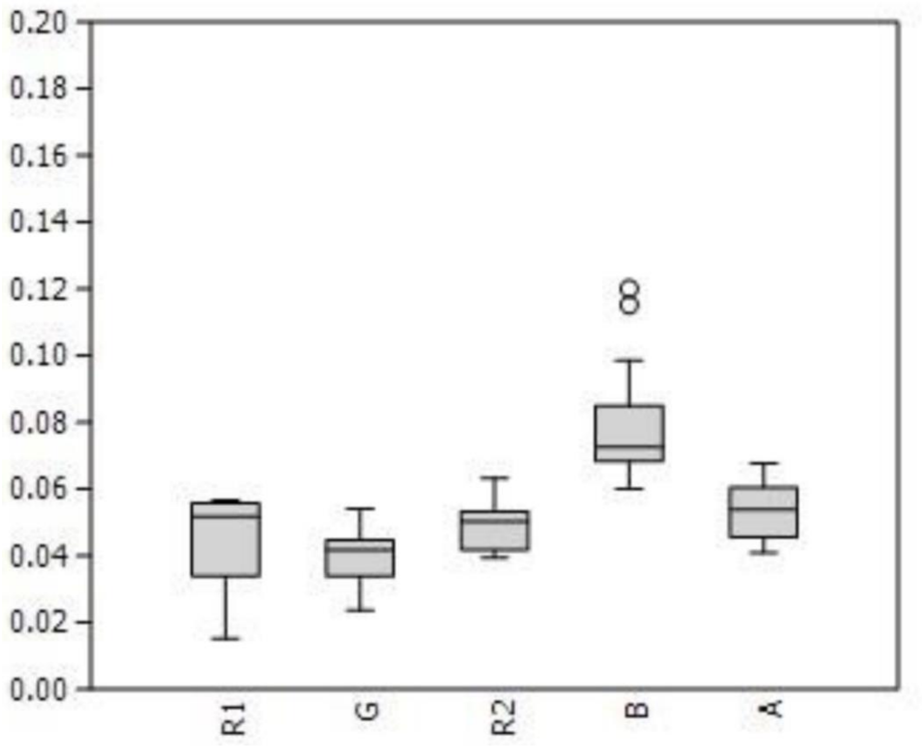

Fig. 3. Boxplot showing differences between the four *P. staryi* lineages and *P. apusenica* in case of the angle of the 9th tergit lobe from lateral view.

Druhová skladba dvojkrídlovcov (Diptera) potenciálnych vektorov patogénov v chovoch koní

The species composition of the Dipterans (Diptera) as potential vectors of pathogens in horsebreeding

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Úvod

Prostredie chovu koní je integrovaný dynamický systém, v ktorom sú vo vzájomnej interakcii mnohé fyzikálne, chemické, biologické a sociálne faktory. V ostatnom období je zvýšená pozornosť venovaná biologickej zložke chovného prostredia, ktorá sa významnou mierou podieľa na prenose patogénov. Jedná sa predovšetkým o krv cicajúce dvojkrídlovce, ktoré sú schopné prenášať pôvodcov rôznych chorôb aj so zoonotickým potenciálom, ako sú napríklad chrípka, rhinopneumónia, bronchopneumónia, antrax, anémia, encefalitída West Nile, žalúdočné červy napr. *Habronema* spp. (Knapp, 1985) a pod. Dosiaľ bolo opísaných asi 150000 druhov dvojkrídlovcov, ktoré sú zaradené do 10000 rodov, 180 čeľadí, 22-32 nadčeľadí, 8-10 infraradov a 2 podradov (Yeates a Wiegmann, 1999). Podľa Franca (2005) sa na Slovensku vyskytuje viac než 6000 druhov dvojkrídlovcov, ktoré sú zaradené do asi 100 čeľadí. Z hľadiska prenosu patogénov majú význam najmä Psychodidae, Ceratopogonidae, Culicidae, Simuliidae, Tabanidae, Muscidae, Sarcophagidae, Calliphoridae, Oestridae, Glossinidae a Hippoboscidae.

Naša štúdia predkladá výsledky viac než desaťročného pozorovania druhovej skladby potenciálnych vektorov patogénov z radu dvojkrídlovcov (Diptera) v 6-tich chovoch koní na východnom Slovensku.

Kľúčové slová: muchy, ovady, pakomáriky, komáre, výskyt, kôň
Keywords: flies, horse flies, biting midges, mosquitoes, occurrence, horse

Materiál a metódy

Entomologickú surveillance sme vykonávali v rokoch 2000-2014 pravidelným týždenným monitorovaním vybraných chovov (Košice, Poľov, Mudrovce, Ruskov, N. Myšľa a Poprad) počas hlavnej sezóny, t.j. v mesiacoch máj-september. Dospelé jedince sme odchytávali ručne ľahkou polopriehľadnou sieťkou, exhaustormi z koní alebo prostredia, a tiež pomocou svetelných lapačov. Druhovú diagnostiku sme robili mikroskopicky podľa dostupných kľúčov na základe morfologických znakov (Gregor a Rozkošný 1977, Kramář 1958, Chvála a kol., 1981, Délecole 1985).

Výsledky a diskusia

Celkove sme odchytili 5786 múch (Muscidae), z toho 68,4 % (3955 ks) *Musca domestica*, 27,9 % (1615 ks) *Stomoxys calcitrans*, 1,6 % (93 ks) *Haematobia irritans*, 1,3 % (77 ks) *Musca autumnalis*, 0,7 % (39 ks) *Hydrotaea floccosa* a 0,1 % (7 ks) *Fannia arnata*. V ustajňovacích priestoroch boli dominantné *M. domestica* a *S. calcitrans*, ostatné druhy sa vyskytovali vo výbehoch a blízkych pastvinách. Podobné spektrum múch uvádzajú aj Říha a kol. (1983) u ťažných koní.

Z pakomárikov (Ceratopogonidae) sme odchytili 5 443 jedincov, z toho 93 % (5062 ks) bolo zo skupiny *Obsoletus* komplex, 4,7 % (256) *Pulicaris* komplexu a 2,3 % (125 ks) sme zaradili do skupiny iných druhov pakomárikov.

Z ovadov (Tabanidae) sme pri koňoch odchytili 116 ks dospelých ovadov. V severovýchodných chovoch boli dominantnými druhmi *Tabanus autumnalis* (20 %), *Haematopota pluvialis* (18 %), *H. subcilindrica* (18 %) a *Chrysops relictus* (18 %). Z ďalších druhov sme zaznamenali výskyt *Hybomitra bimaculata*, *Tabanus maculicornis* a *T. mikii*. V nížinných oblastiach v pásme od 162 do 205 m n.m. sme zaznamenali ojedinelý výskyt *Haematopota pluvialis* a *Chrysops relictus*.

Priamo vo výbehoch sledovaných chovov koní a ich blízkom okolí sme zachytili pomerne málo komárov (435 ks). Najčastejšie sme diagnostikovali druhy *Ochlerotatus sticticus* (32,6 %), *Aedes vexans* (16,1 %), *Culex pipiens/Culex torrentium* (15,1 %) a v severnejších okresoch (Poprad) aj *Culiseta annulata* (36,2 %).

Zástupcov čeľade Hippoboscidae sme diagnostikovali iba v jednom chove v okrese Poprad, kde na koňoch paradoxne parazitoval ovčí druh *Melophagus ovinus*.

Záver

Z vektorov, ktoré môžu priamo ohrozovať naše chovy koní prenosom patogénov si v budúcnosti zaslúžia viac vedeckej pozornosti komáre rodov *Culex* a *Aedes* vo vzťahu k prenosu togavírusu vyvolávajúceho encefalitídu West Nile, ovady (*Tabanus*) ale i bodavky (*Stomoxys*) ktoré sú schopné prenášať reovírus infekčnej anémie koní. V neposlednom rade sa náš ďalší výskum bude zaoberať aj sledovaním pakomárikov (*Culicoides*) a ich schopnosti prenášať pôvodcov onchocerkózy.

Poďakovanie

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Využitie integratívnej taxonómie v determinácii pakomárikov z rodu *Culicoides* (Ditera: Ceratopogonidae)

The use of integrative taxonomy in determining of biting midges from genus Culicoides (Ditera: Ceratopogonidae)

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Úvod

Taxonómia druhov je základom pre všetky teoretické aj praktické biologické výskumy. Celé storočia bola tradičná taxonómia založená na princípe komparatívnej morfológie. Tento tradičný prístup nesie však subjektivitu pri interpretácii znakov, z čoho vyplývajú nepresnosti pri identifikácii čo vedie k nestabilnej systematike. Novodobá taxomómia je postavená na syntéze morfologických, molekulových a biologických dát.

Druhová determinácia pakomárikov z rodu *Culicoides* (Diptera: Ceratopogonidae) na základe morfologických znakov je komplikovaná a časovo náročná. V súčasnosti mnoho vedcov využíva moderné molekulové metódy na zvýšenie kvality a aj kvantity vedeckých výstupov. V ostatných rokoch bolo uskutočnených množstvo štúdií zameraných na identifikáciu druhov a na rekonštrukciu fylogenetických vzťahov medzi pakomárikmi s využitím rôznych úsekov DNA – COI génu, ITS-1 či ITS-2 úseku (Ander *et al.* 2013, Augot *et al.* 2013, Gomulski *et al.* 2006, Meiswinkel *et al.* 2004, Stur & Borkent 2014). Na tieto výskumy sa najviac osvedčil gén COI mitochondriálnej DNA, ktorý preukazuje nízke vnútrodruhové a vysoké medzidruhové variácie. COI gén predstavuje najviac využívaný gén pri výskume pakomárikov a taktiež najviac dostupných sekvencií pakomárikov v GenBank (GB) sú sekvencie COI génu.

Cieľom tejto práce bolo zrevidovať biodiverzitu fauny pakomárikov na východnom Slovensku využitím morfologickej determinácie a barcodingu COI génu mtDNA na princípe integratívnej taxonómie.

Kľúčové slová: *Culicoides*, DNA barcoding, integratívna taxonómia
Keywords: *Culicoides*, DNA barcoding, integrative taxonomy

Materiál a metódy

Pakomáriky použité v tejto štúdii boli odchytené svetelnými lapačmi v rámci entomologického prieskumu vo vybraných lokalitách východného Slovenska – na farmách s hospodárskymi zvieratami (Michaľany, Veľaty, Tulčík) a v oborách (Rozhanovce, Byšta) v rokoch 2011-2014.

Za účelom morfologickej identifikácie sme z jednotlivých druhov zhotovili trvalé preparáty a určovali ich pod stereomikroskopom na základe znakov – počet a tvar spermaték, tvar článkov tykadiel a prítomnosť sezíl na jednotlivých článkoch, veľkosť a tvar tretieho palpálneho článku a tvar senzíl, počet tŕňov na druhom páre končatín atď. Morfologickú identifikáciu sme robili na základe dostupných štandardných diagnostických kľúčov (Delécolle 1985, Glukhova 1989, 2005) a interaktívneho kľúča (Mathieu *et al.* 2012).

Na analýzy fylogenetických vzťahov a identifikáciu barcodingom, sme pripravili 62 sekvencií COI génu z 38 druhov pakomárikov. Do analýz sme zahrnuli aj sekvencie z rôznych oblastí Európy, ktoré boli dostupné v databáze GenBank. Sekvencie COI génu druhov *C. manchuriensis*, *C. subfasciipennis*, *C. fascipennis*, *C. achrayi*, *C. griseidorsum*, *C. kibunensis*, *C. tauricus*, *C. segnis*, *C. riouxi* a *C. gejgelensis* neboli dostupné v databáze, a preto sme spolu s našimi vzorkami amplifikovali a sekvenovali aj COI gén z menovaných jedincov poskytnutých z Francúzska (Dr. Mathieu, Inštitút parazitológie a tropickej patológie v Štrasburgu). Na určenie fylogenetických pozícií našich druhov sme 196 sekvencií podrobili analýze algoritmu najvyššej pravdepodobnosti ML (*maximum likelihood*) s HKY+I+Γ modelom nukleotidovej substitúcie a algoritmu najvyššej úspornosti MP (*maximum parsimony*).

Výsledky a diskusia

V tejto práci sme sa snažili skĺbiť morfologickú determináciu s molekulovými metódami na dosiahnutie čo najdôveryhodnejších výsledkov. Z 38 morfologicky určených druhov, 31 jednoznačne vytvorilo klaster s identickými druhmi z GB. Pri zvyšných vzorkách sme zistili nesúlad medzi klasickou determináciu a barcodingom DNA. Nízku medzidruhovú divergenciu s maximálnou genetickou vzdialenosťou 0,034 sme zaznamenali medzi druhmi *C. pallidicornis* a *C. subfasciipennis*. Jedince týchto dvoch druhov sú však morfologicky takmer úplne totožné, až na prítomnosť veľmi jemnej svetlej škvrnky na krídlach. Je preto otázne, či tieto dva druhy nie sú len synonymá a nevýrazná škvrna nie je len druhová variácia. Ďalšie dvojice druhov s nízkou maximálnou genetická vzdialenosťou boli *C. salinarius* a *C. manchuriensis* (2.4 %) a *C. festivipennis* a *C. clastrieri* (1.3%). Tieto druhy sú však jednoznačne odlíšiteľné na základe morfológie.

Naopak vysoká vnútrodruhová divergencia bola medzi jedincami morfologicky determinovanými ako *C. kibunensis. C. kibunensis* vytvoril klaster jedincov s priemernými vnútrodruhovými variáciami 3,7 % a maximálnymi až 6,2 %. Navyše aj medzi jedincami z rôznych oblastí Slovenska sa vyskytli variácie 5,5 %. Podľa Avise et al. (2000) vnútrodruhová divergencia je zriedka vyššia ako 2 % a väčšinou je nižšia ako 1 % (Hebert *et al.* 2003). Aj Lassen et al. (2012) uvádza vnútrodruhové variácie menej ako 1 %. Vyššia miera vnútrodruhovej variability môže súvisieť s geograficky alebo enviromentálne podmienenými vnútrodruhovými variáciami, ale môže pramениť aj z nesprávnej morfologickej determinácie či omylov v GB. Predpokladáme však, že *C. kibunensis* je pravdepodobne skupina blízko príbuzných kryptických druhov, existenciu ktorej naznačovali aj štúdie z rôznych oblastí Bieloruska, Ukrajiny, Turkmenistanu a Kazachstanu, ktoré odhalili isté morfologické variácie (Glukhova 1989, 2005).

V GenBank neboli dostupné sekvencie druhov *C. tauricus* a *C. slovacus*. Po zaradení sekvencií *C. tauricus* z Francúzska do analýz, sme zistili, že *C. tauricus* z Francúzska aj napriek morfologickej podobnosti tvaru spermaték s našimi jedincami, tvoril parafyletickú vetvu a genetická vzdialenosť slovenských jedincov *C. tauricus* a *C. slovacus* je 0,087, ale dvoch *C. tauricus* (SK a FR) 0,157.

V priebehu druhovej determinácie sme zaznamenali aj 2 druhy (Spe A a Spe B), ktoré sme na základe morfologických znakov zaradili do podrodu *Culicoides*, ale pozorovali sme pri nich isté morfologické odchýlky a na základe dostupných morfologických kľúčov sa nám ich zatiaľ nepodarilo druhovo určiť.

Jedince Spe A a Spe B tvorili v kladograme samostatné vetvy a ich sekvencie sa nezhodovali so žiadnymi sekvenciami získanými z GenBank. SpeA je z fylogenetického hľadiska najbližšie príbuzný novopopísanému druhu *C. boyi* z Dánska (Nielsen & Kristensen 2015), od ktorého sa líši minimálnou medzidruhovou vzdialenosťou 8 %.

Aj napriek názorom mnohých vedcov, že DNA barcoding predstavuje spoľahlivú a nenáročnú molekulovú metódu druhovej identifikácie známych i nových druhov aplikovateľnú na široký okruh metazoí (Jinbo *et al.* 2011, Virgilio *et al.* 2010), zistili sme mnohé obmedzenia využitia danej metódy. Tieto nedostatky môžu byť vylepšené integratívnou taxonomickou revíziou kombinujúcou genetické a morfologické údaje (Dayrat 2005, Schlick-Steiner *et al.* 2010).

Na základe komplexného prístupu prelínajúceho morfológiu s molekulovými metódami sme úspešne určili 41 druhov *Culicoides* a rozšírili ich zoznam na Slovensku o minimálne 5 druhov (Sarvašová *et al.* 2014). Barcodingom sme prispeli 67 sekvenciami COI génu do databázy GenBank (KJ624068-KJ624135), z toho sekvenciami 6 nových druhov (*C. griseidorsum*, *C. gejgelensis*, *C. tauricus*, *C. slovacus*, *C. riouxi* a *C. odiatus*), ktoré ešte neboli v čase realizácie tejto štúdie v databáze.

Poďakovanie

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ABSTRACTS OF POSTER PRESENTATIONS

Potential geographic distribution and a new locality of *Eclimus gracilis* Loew, 1844

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Keywords: Bombyliidae, *Eclimus gracilis*, distribution modelling, Albania

In 2013 a specimen of *Eclimus gracilis* (Diptera: Bombyliidae) was found in Albania and it is proved to be a new species to the Albanian fauna. Based on Maximum Entropy Species Distribution Modelling (MAXENT) I made the potential distribution of the species. I had only 13 locality data but MAXENT worked well despite of the low number of localities and the overall performance of the model was high (AUC = 0.942). The model worked well considering the small sample size and it is predicted suitable habitat to the Albanian locality as well. The used environmental variables were the follows: mean temperature of driest quarter, precipitation of wettest quarter, precipitation of warmest quarter and precipitation of coldest quarter. Until this study the species were known from France, Greece, Israel, Italy, Libya, Macedonia, Morocco, Turkey and I successfully found it in Albania as well. The distribution model predicted additionally suitable habitat to the following countries: Algeria, Bosnia and Herzegovina, Croatia, Iran, Iraq, Lebanon, Portugal, Spain, Syria and Tunisia.

Host associations of bat flies (Diptera: Nycteribiidae) in Hungary

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Keywords: bat fly, Pupipara, ectoparasite, Chiroptera, sex ratio

On our poster we summarize the results of our study on bat flies collected in the Bükk Mountains, in 2012 and 2013. During the survey 779 bat specimens (of 24 species) were examined for bat flies, 93 bats (nine species) were infected by these ectoparasites. 116 specimens of nine bat fly species (*Basilia italica, B. nana, B. nattereri, Nycteribia kolenatii, N. latreillii, N. schmidlii, N. vexata, Penicillidia conspicua* and *P. dufourii*) were collected. *Basilia nana*, *Nycteribia kolenatii* and *Nycteribia schmidlii* were the most frequent bat fly species (n > 20). The prevalence rate of bat species and the host specificity of bat flies showed differences. The most infected bat species by bat flies were *Miniopterus schreibersii* (42.85%), *Myotis daubentonii* (29.76%), *M. bechsteinii* (14.89%), *M. alcathoe* (13.79%) and *M. myotis* (13.63%). The mean intensities of these species are 1.3, 1.3, 1.1, 1.3 and 1.3, respectively. The least specialized bat fly (oligoxenous species) was *Basilia italica,* which had four host species from three bat genera (*Barbastella barbastellus, Myotis alcathoe, M. brandtii,* and *Plecotus auritus*), moreover this is the first report of *B. italica* from *P. auritus*. The sex ratio of bat flies showed significant differences in two species: *Nycteribia schmidlii* ($p = 0.0105$) and *Penicillidia conspicua* ($p = 0.0325$)*,* in both species female dominancy was observed. The occurrence of bat flies did not show significant differences in regard to the sex of hosts (males n = 546, prevalence = 11.5%, females n = 233, prevalence = 12.8%).

Distribution of Athericidae (Diptera) in the Czech Republic

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Keywords: Athericidae, distribution, Czech Republic

In the Czech Republic the Athericidae family contains three species: *Atherix ibis, Atrichops crassipes* and *Ibisia marginata*. Grubs of all the three species live in running waters. *Atherix ibis* and *Atrichops crassipes* are included in The Red List of the Czech Republic. Between the years 2007 – 2014 *Atherix ibis* species was discovered in 565 localities, *Atrichops crassipes* in 73localities and *Ibisia marginata* in 195 localities. Generally we can talk about constant and numerous occurence in all the localities. In several cases they were all found together. It is interesting that *Atrichops crassipes* species which is considered to be rare in the Czech Republic occurs mainly in the anthropogenic heavily modified streams, modified both by technical alterations as well as by the quality of water.

***Atrichops crassipes* (Meigen, 1820)**
Prefers alfa - mesosaprobic and beta - mesosaprobic waters. The size of the stream does not determine its appearance. This species prefers bog and clay substrate near banks zone. Distribution mainly on heavily modyfied water bodies. Altitude in which these species appear is 150 – 500 m.

***Atherix ibis* (Fabricius, 1798)**
Prefers running reaches of medium-sized and large-sized streams with gravel and stone substrate. Wide of reaches more than 5 m. Beta-mesosaprobic waters are characteristic for *Atherix ibis*. Altitude in which these species appear is 120 – 985 m. Very sensitive species to acidification.

***Ibisia marginata* (Fabricius, 1781)**
Prefers small-sized and medium-sized submontane streams with small amount of anthropic adaptations. Wide of reaches up to 5 m with broadleaveson banks. Preferring oligosaprobic to beta-mesosaprobity waters. Altitude in which these species appear is 190 – 850 m. Very sensitive species to acidification.

Some interesting Chironomid taxa in the Krkonoše (Giant) Mts.

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Keywords: Chironomidae, Diptera, Giant Mts., Czech Republic, distribution

Krkonose is the highest mountain range in the Czech Republic. The very first enquiry of the natural resources is dated back to the year 1563, when an Italian doctor P. O. Mattioli (1500 – 1577) carried out his botanical research. The initial research of insects was done in 1846 by E.A.H. von Kiesenwetter and J.C.F. Markel. J. Gerhard (1868, 1896) did research on aquatic beetles of the spring areas and pools. Important entomologists active in the area of Krkonoše were for example F. Klapálek, J. Obenberger, K. Hůrka and others. However the systematic research started only at the end of the 20th century, in 1980s. A lot of specialists on different species of insects have been cooperating on the research of Krkonoše insects. A big variety of entomological methods are being used to gain the material and these methods have also been enriched by the hydrobiological principles. Until now more than 100 taxons of family Chironomidae have been discovered in Krkonoše (Giant) Mts. But chironomid fauna is still little known in this area.

Boreoheptagyia dasyops Serra-Tosio, 1989
Lysečinský brook, near Lysečinská bouda, altitude 950 m, 7.5.2010, 8 larvae. Larvae in blue-green and green filamentous algae on splash zone near waterfall.

Diamesa* cf. *bohemani Goetghebuer, 1932
Albeřický brook under confluence with Lysečinský brook, 645 m n.m. 25.5.2012, 1 male (maturation from larva in laboratory), 15.3.2013, 1pupa.

Diamesa latitarsis (Goetghebuer, 1921)
Lysečinský brook, near Lysečinská bouda, altitude 950 m, 1.8.2012, 11 larvae, 4 pupas.

Dratnalia potamophylaxi (Fittkau & Lellák, 1971)
Zlatý brook, Sklenářovice, altitude 687m, 7.5.2011, 2 larvae (in cases of caddisfly Potamophylax luctuosus).

Syndiamesa edwardsi (Pagast, 1947)
Lysečinský brook, near Lysečinská bouda, altitude 950m, 25.5.2012, 19 larvae, 1pupa, 1 male (maturation from larva in laboratory), 22.6.2012, 15 larvae, 1.8.2012 2 larvae. Larvae in blue-green and green filamentous algae on splash zone near waterfall. Albeřický brook tributary, altitude 730m 4.5.2014, 1 male.

***Syndiamesa* sp.** Kieffer, 1918
Bolkovský brook, altitude 580m 4.5.2010, 1 larva, concrete pipe culvert with mosses.

***Sublettea* sp.** Roback, 1975
Mosses and algae periphyton on trickle rock face, Labský důl, 1210 m n.m., 21.9.2012, 10 larvae. In Europe mentioned only *Sublettea coffmani.*

Longitudinal mosquito surveillance study in Danube Delta and the first report of *Ochlerotatus hungaricus* (Mihalyi, 1955) for Romania

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Keywords: Mosquito surveillance, new records, mtCOI, *Ochlerotatus hungaricus*, Danube Delta

Human and animal diseases caused by mosquito-borne viruses are of growing importance in many countries of Europe including Romania. Pathogen surveillance in mosquitoes and animals was not performed regularly and therefore, longitudinal data sets are missing, especially from Romania. Thus, we initiated intensive mosquito surveillance in the Danube Delta to analyze its mosquito's communities and collect vector data from different types of ecosystems. During 2014 a number of 240,679 female mosquitoes were collected with CO2-baited EVS traps at four sampling sites. All mosquitoes were identified using morphological characteristics and species were confirmed by sequence analysis of the mtCOI gene. The most common species were *Coquillettidia richiardii* (41%) and *Anopheles hyrcanus* (34%). Identified by both morphological and molecular tools, *Oc. hungaricus* was identified for the first time for Romania. We collected two specimens in June in Letea floodplain forest. However *Oc. hungaricus* is not a frequent species and its biology is not well known. Phylogenetic analysis show its close reltationship to an *Oc. hungaricus* specimen collected in 1998 from the Tisza River in Hungary and also to *Oc. dorsalis* specimens from Danube Delta. The data of this longitudinal study provide a solid base to determine the seasonal fluctuations in mobovirus activity and the relative abundance of the mosquito vector species.

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