Systematics and phylogeny of SE Asian bats and their viruses

– final report –

RESULTS

The field trips, collection visits, international cooperation and specimens housed in the Hungarian Natural History Museum provided solid base for the taxonomic and systematic research and viral studies outlined in the project proposal. Target areas of expeditions and taxa of systematic studies partly changed since the submission of the proposal as new opportunities arise what were even more promising than the ones originally planned. These include a new horizon for joint studies with Chinese institutions, an extended cooperation with South Asian (Nepalese, Indian and Sri Lankan) researchers, and cutting-edge studies on bat ectoparasites.

During the five years of the project (including one-year extension) major goals of the original plan were accomplished except for 1) the manuscript of the Tube-nosed bat (Vespertilionidae: Murininae) monograph and 2) the regional revision of *Myotis* species. 1) Due to the wide availability of genetic methodology and the parallel works of different research groups novel discoveries are made continuously in Murininae which would make the planned manuscript premature and far from complete. Nevertheless, the taxonomic-systematic studies of the subfamily were not neglected, as one new species description was published, one more already accepted (not listed herewith) and at least further three species are diagnosed and waiting for description. 2) We are working on the revisions of Indochinese *Myotis* but the morphology-based taxonomy and the tree topology of the phylogenetic reconstructions are in contrast; the situation is further hampered by the fact the mitochondrial and nuclear results are incongruent and we have to suspend these studies until more material will be available. However, other groups of vesper bats were intensively studied, and the results were published in leading periodicals of the field.

SCIENTIFIC PUBLICATIONS

Altogether 32 journal articles were published within the frame of this grant and due to space limitations only short overviews - organised according to the main disciplines - are provided below. Articles with their full details are listed separately.

Articles	Citations	Sum IF	Q1	Q2	Q3
32	159	54.998	12	14	6

Metrics summary of papers published with the support of the K112440 grant

Taxonomy and Systematics

Descriptions of new mammals, including bats are not common and have to be based on very sound results provided by integrative methodologies. Due to the extensive collaborations we described seven new species and one new genus of bats from SE Asia in five years, an unparalleled number in modern era of bat systematics. These results generated great attention on the Hungarian bat systematic studies.

Csorba et al. 2015: Till 2015, three species of the genus *Glischropus* were recognized from the Indomalayan zoogeographic region. During review of material recently collected in southwestern Sumatra, Indonesia, one specimen of a yet undescribed species of Thick-thumbed bat was identified. *G. aquilus* n. sp. markedly differs from its congeners by its dark brown pelage, nearly black ear and tragus, and in skull proportions; the phylogenetic analysis based on cytb sequences also supports its specific distinctness.

Tu et al. 2015: Trident bats of mainland Southeast Asia were subsumed into a single species, *Aselliscus stoliczkanus*. In our study, we examined morphological and genetic traits of different populations from Southeast Asia, and the combined evidence support the existence of a further species, *Aselliscus dongbacana* sp.n. in northeastern Vietnam.

Son et al. 2015: We described a new species *Murina kontumensis* sp.n. based on a specimen collected from the Central Highlands of Vietnam. A taxonomic review of Murininae from Vietnam was also conducted based on combined morphological, DNA, and karyological characteristics. Molecular phylogenetic analyses based on the mitochondrial cytochrome c oxidase subunit (COI) gene supported the monophyly of the subfamily Murininae, whereas the genus *Murina* proved to be paraphyletic in relation to the genera *Harpiocephalus* and *Harpiola*.

Bailey et al. 2016: High-throughput sequencing technologies and associated applications offer new opportunities for obtaining sequence data from museum samples. In this article, samples from horseshoe bats were used to demonstrate the effectiveness of this new technique.

Lim et al. 2016: *Hypsugo macrotis* is restricted to Peninsular Malaysia, Sumatra, Java and adjacent islands, and is known only from a handful of specimens. In this article we reported a new locality record of the species, discussed its phylogenetic affinities with other members of the genus, and a call was made to assess the importance of urban habitats in SE Asia.

Csorba et al. 2016: *Vespertilio oreias* (generally known as *Myotis oreias*) has long been considered an endemic bat species to Singapore but its taxonomic status has been in doubt, and no specimens have been found since its description in 1840. The holotype was re-examined, and we found it to be a composite, consisting of two separate individuals representing two distinct genera, the skin belonging to a *Kerivoula* whereas the skull fragments are of a *Myotis*.

Saikia et al. 2017: *Hypsugo joffrei* is a rare and very little-known bat previously thought to be confined to Myanmar and Vietnam in Southeast Asia. Based on recently collected material and reassessment of museum specimens, this species is being reported for the first time from India and Nepal. We also proposed to recognize the name *H. anthonyi* as the junior subjective synonym of *H. joffrei*. Specimens previously identified as *Philetor brachypterus* from South Asia were found to represent *H. joffrei*, as well.

Tu, Csorba, et al. 2017: In Southeast Asia, bats of the genus *Tylonycteris* have traditionally been classified into two wide-ranging species, *T. pachypus* and *T. robustula*. Our comparative phylogeographic analyses, combined with our multivariate morphological analyses, show that these species represent cryptic species complexes. Accordingly, we proposed several taxonomic changes within the genus *Tylonycteris*: the species *T. fulvida* and *T. malayana* are revalidated, and a new species, *T. tonkinensis* sp. n., endemic to northern Indochina, was described.

Kuo et al. 2017: Since its discovery, the taxonomic status of the only species of *Kerivoula* to be found on Taiwan has been confused. Mitochondrial and nuclear DNA as well as multivariate statistical methods separated *Kerivoula furva* sp. n. from its congeners.

Tu, Hassanin et al. 2017: The taxonomic status of *Rhinolophus macrotis* sensu lato (s.l.) in Vietnam and adjacent territories remains problematic. To address this issue, we performed an integrated study of morphological, acoustic, and genetic characters of *R. macrotis* s.l. specimens and compared these with sympatric species within the *philippinensis* group (*R. marshalli, R. paradoxolophus*, and *R. rex*). Our results reveal that in addition to a cryptic species of *R. macrotis* previously found in Jiangxi and Jingmen, China, *R. macrotis* s.l. in continental Asia includes three further species, namely *R.* cf. *siamensis*, *R.* cf. *macrotis*, and *R.* cf. *macrotis* "Phia Oac."

Ruedi et al. 2018: A new genus, *Cassistrellus* was described based on specimens already known but held in the drawers of museums. A new species in the new genus was also described from Vietnam. This enigmatic Indomalayan lineage - that was previously thought belonging to the genus *Eptesicus* - contains extremely rare species.

Zhang et al. 2018: We performed integrated analyses of the morphology, acoustic and genetic data and constructed the first multilocus phylogeny for the *philippinensis* group of horseshoe bats. The results supported the revised status of *R. paradoxolophus* as a subspecies of *R. rex*, *R.* cf. *macrotis* as a subspecies of *R. macrotis*, and *R. huananus* and *R.* cf. *siamensis* as junior synonyms of *R. siamensis*.

Tu et al. 2018: We undertook a comparative phylogeographic study using molecular, morphological and morphometric approaches to address systematic issues in bats of the *Kerivoula hardwickii* complex in Asia. Our phylogenetic reconstructions using DNA sequences of two mitochondrial and seven nuclear genes reveal a distinct clade containing four small-sized species (*K. hardwickii* sensu stricto, *K. depressa*, *K. furva* and *Kerivoula* sp. n.) previously assigned to *K. hardwickii* sensu lato, as well as *K. kachinensis*, a distinctly larger taxon.

Görföl & Csorba 2018: The vespertilionid genus *Falsistrellus* contained three Asian (*F. affinis*, *F. petersi* and *F. mordax*) and two Australian (*F. tasmaniensis* and *F. mackenziei*) species. We provided sequence data of mitochondrial and nuclear genes for both Australian species for the first time, which, together with combined cranial, dental, and multivariate statistical evidences provide a solid basis to place Asian members of *Falsistrellus* into *Hypsugo* and restrict *Falsistrellus* s. str. to Australia. A new, exclusively Australasian clade of vesper bats was also revealed by the phylogenetic reconstructions.

Yu et al. 2018: After the recently published revision of the *Kerivoula hardwickii*-complex with the description of *K. furva* and re-evaluation of occurrence of *K. titania* in Taiwan, the critical overview of the previous data of Chinese *Kerivoula* was imperative. Forty additional specimens collected from South China were studied through detailed morphological comparisons, multivariate statistical methods and phylogenetic inference. Our results evidently classified these specimens as *K. furva*.

Görföl et al. 2018: The long-toothed pipistrelle (*Hypsugo dolichodon*) was recently described as a new bat species from Laos and Vietnam. During investigations of taxa in the Vespertilionini tribe, we noted that specimens reported as *Hypsugo affinis* from Myanmar and Cambodia have mtDNA sequences and craniodental characteristics like *H. dolichodon* and different from genuine *H. affinis*.

Liu et al. 2019: We applied an integrative taxonomic approach to a case study of *Rhinolophus macrotis* complex, whose taxonomic status remains controversial, to provide insight into the systematics and evolutionary history of these species. By integrating traditional genetic markers with different modes of inheritance, genome-wide SNPs as well as phenotypic characteristics, we clarified the presence of three closely related species, *R. episcopus*, *R. siamensis*, and *R. osgoodi*, within this complex, and proposed a new taxonomic treatment for *R. osgoodi*. Our results suggested that hybridization and introgression are the main causes of low mtDNA divergence in these species.

Faunistics

Faunal studies of protected and would-be protected areas provide irreplaceable data on the presence of rare and threatened species, help to contrate efforts on certain areas with high level of endemism and/or exceptional diversity. These studies can also provide further material to clarify taxonomic status, extend our knowledge on distribution patterns, habitat preference, ecological and behavioural traits.

Tu et al. 2016: With the investigation of the voucher specimens collected by a Vietnamese expedition in 2014, in the frame of the OTKA project, several rare and conservation-dependent species were denoted from the Phia Oac-Phia Den protected area.

Son et al. 2016: The diversity of bats was assessed in the protected forests of Truong Son Mountains, Vietnam. An exceptional high diversity of the forest interior specialist tube-nosed bats (*Murina*) was documented.

Wang et al. 2016: *Myotis indochinensis*, a recently described species from Vietnam, was previously confused with *Myotis montivagus* and *Myotis annectans*. In 2012 and 2015, four medium sized *Myotis* bats were collected in protected areas in South China. Based on their morphological characteristics and phylogenetic inference, they were re-identified as *M. indochinensis*, representing the first records of the species in China.

Guo et al. 2017: *Thainycteris aureocollaris* is a rare vespertilionid bat species reported from remote forest habitats of Lao PDR, Vietnam, and Thailand. In 2015, one specimen was collected in Guizhou Province, China representing the first record of the species from China.

Thong et al. 2018: *Myotis altarium*, was first described in 1911 from southeastern China, and for the next 100 years was thought to be restricted to that country with just one additional individual known from northern Thailand. We captured eight individuals of this species during surveys in northwestern Vietnam and two individuals from East Khasi Hills and East Jaintia Hills districts of Meghalaya state, northeastern India.

Tu et al. 2019: This paper presents the rediscovery of Van Hasselt's Mouse-eared Bat *Myotis hasseltii* after nearly 50 years and its genetic data from Hanoi, northern Vietnam. In addition, a snapshot of the impacts of urbanization on the current distribution and conservation status of this native bat species in Hanoi is also provided.

Mohd-Ridwan et al. 2018: Bat surveys at Gunung Gading National Park in Sarawak, Borneo captured a total of 378 individuals representing 36 species from six families. Rarefaction analysis showed that *GGNP* has the largest number of estimated species compared to other actively surveyed sites in western Sarawak. Correlation analysis showed that there is no statistically significant relationship between lunar phase and the bat capture rate at *GGNP*.

Viral studies

Bats are reservoirs of many potentially zoonotic viruses. To utilize our material collected during field trips, a large extent of viral samples was screened for various viruses. The new viruses found were characterized and placed into deeper evolutionary context. The viral samples are stored in a way to provide material for further research; we now search for new coronaviruses, a study induced by the ongoing coronavirus epidemic originating from Wuhan, China.

Kemenesi et. al. 2017: Members of the viral family Circoviridae are increasingly recognized worldwide. Here, we report a member of the genus *Cyclovirus* detected in the faeces of a great roundleaf bat (*Hipposideros armiger*). Based on structural differences and its phylogenetic position, we propose that our new virus represents a distant and highly divergent member of the genus *Cyclovirus*.

Hron et al. 2018: Endogenous retrovirus (ERV) sequences provide a rich source of information about the long-term interactions between retroviruses and their hosts. However, most ERVs are derived from a subset of retrovirus groups, while ERVs derived from certain other groups remain extremely rare. In this report, we identify the second example of an ERV sequence putatively derived from a past deltaretroviral infection, in the genomes of several species of horseshoe bats.

Zana, Kemenesi et al. 2019: The aim of our study was to investigate the presence of hantaviruses in bat lung tissue homogenates originally collected for taxonomic purposes in Malaysia in 2015. Nanopore sequencing of hantavirus positive samples resulted in partial genomic data from S, M, and L genome segments. The obtained results indicate molecular evidence for hantaviruses in the *M. aenea* bat species. Sequence analysis of the PCR amplicon and partial genome segments suggests that the identified virus may represent a novel species in the genus *Mobatvirus* within the Hantaviridae family.

Zeghbib et al. 2019: The Picornaviridae family comprises important pathogens which may infect both humans and animals. In this study, a bat-related picornavirus was detected from *Minioptreus schreibersii*. Molecular analyses revealed the new virus is related to the *Mischivirus* genus. We examined the co-evolutionary history of all bat-related picornaviruses and explored how the geographical origin, host-genus and host-species relations mirrored in the phylogenetic reconstructions.

Bat ectoparasites

Studies of bat ectoparasites collected during expeditions were added to our previous plan – and proved to be a rich source of new scientific results. Bat ticks are important vectors of zoonotic bacteria; hence the complex host-parasite relationships and the epidemiological relevance of these parasites are hot areas of bat studies.

Hornok et al. 2015: Collections of ticks on one hand resulted in the recognition of a morphologically and genetically distinct species from Vietnam, to be described later. On the other hand, some specimens collected in Vietnam and in Japan formed a monophyletic clade and shared morphological features with *I. ariadnae*, a recently described European species. Phylogenetic relationships showed similar clustering patterns with those of their bat host species.

Hornok et al. 2016: *Ixodes* ticks were collected during our Vietnamese expedition in 2014 and subsequently by our collaborator, Vuong Tan Tu. The combination of morphological and phylogenetic investigations was used in the description of a new tick species, *Ixodes collaris*.

Hornok, Szőke, Tu et a. 2017: The study investigated the morphology, mitochondrial gene heterogeneity and host range of *Argas vespertilionis* in the Old World. Phylogenetic analyses based on two mitochondrial markers suggests that it represents a complex of at least two putative cryptic species.

Hornok, Szőke, Görföl et al. 2017: *Argas vespertilionis* is a geographically widespread haematophagous ectoparasite species of bats in the Old World, with a suspected role in the transmission of *Babesia vesperuginis*. Molecular taxonomic analyses of *A. vespertilionis* and *B. vesperuginis* suggest a genetic link of bat parasites between Central Europe and Central Asia, which is epidemiologically relevant in the context of pathogens associated with bats.

FIELD TRIPS

18–31 July 2015: Financed by the host institution (and not by the present OTKA grant), the PI of the OTKA project participated in a field trip in Jiangxi, China organised by the Guangzhou University. The trip yielded 99 tissue samples and specimens of some rare bat species not represented yet in the HNHM collection.

13–31 August 2015: In connection with an international conference together with the researchers and students of the University of Malaysia, Sarawak (UNIMAS), we organised a collecting trip to two protected areas in Sarawak. The field survey with the participation of PI and Tamás Görföl was successful with many important bat voucher specimens, tissue samples, and over 100 organ virus samples collected.

18 May – 2 June 2016: Fully financed by the host institution the PI of the OTKA project participated in a field trip in Taiwan organised by the Tung Hai University Taichung, Taiwan. The trip yielded 59 samples and a paratype specimen of a new species housed in the HNHM.

25–31 July 2016: Partly financed by the host institution and partly by the present OTKA grant, the PI of the OTKA project participated in a field trip in Yunnan organised by the Northeast Normal University, Changchun, China. The trip yielded 68 specimens, associated tissues samples and echolocation recordings.

25 August–11 September 2016: Partly financed by the host NGO and partly by the present OTKA grant, the PI of the OTKA project participated in field trips in Nepal organised by Small Mammals Conservation and Research Fund, Kathmandu. The trip yielded 16 samples, presently deposited in the Tribhuvan University Zoological Collection.

14 September–6 October 2016: Financed by the present OTKA grant, Tamás Görföl, Gábor Kemenesi and Péter Estók took a field trip in Vietnam, hosted by the IEBR, Vietnam Academy of Sciences. The trip was very successful, with 147 bat tissue samples, 60 voucher specimens and more than 100 viral samples flash-frozen on the spot.

23 May–15 June 2017: Partly financed by the host institution and partly by the present OTKA grant, Gábor Kemenesi participated in a field trip in Vietnam, organised by the Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam. 123 viral samples and 15 bat tissue samples were collected.

14–24 November 2017: Partly financed by the host institution and partly by the present OTKA grant, the PI of the OTKA project participated in a field trip in Yunnan, Xishuangbanna organised by the Nankai University, Tianjin, China. The trip yielded 25 samples including four species not represented yet in the HNHM tissue sample collection.

2–15 August 2019: Partly financed by the host institution and partly by the present OTKA grant, the PI of the OTKA project participated in a field trip in Shaanxi, Qinling Mountains, organised by the Northeast Normal University, Changchun, China. The trip yielded very poor results with only 14 specimens and associated samples collected.

COLLECTION VISITS

6–18 March 2016: Natural History Museum, London. UK
29 May 2016: National Museum of Natural Science, Taichung, Taiwan
20 June 2016: Senckenberg Naturhistorisches Sammlungen, Dresden, Germany
21–23 June 2016: Museum für Naturkunde, Berlin, Germany
1–3 August 2016: School of Environment, Northeast Normal University, Changchun, China
8 June 2017: Natural History Museum, London, UK
14–24 August 2017: Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia
1 December 2017: Institute of Zoology, Chinese Academy of Sciences, Beijing, China

CONFERENCES AND PRESENTATIONS

3rd International Southeast Asian Bat Conference 14-17 August 2015, Kuching, Malaysia
Görföl T., Kemenesi G., Jakab F., Estók P. & Csorba G. (2015): Systematics and phylogeny of SE Asian bats and their viruses – An introduction to our research program (poster presentation)

X. Magyar Denevérvédelmi Konferencia 16-18 October 2015, Körösbánlaka, Romania
Csorba G., Kemenesi G., Jakab F., Estók P. & Görföl T. (2015): Délkelet-ázsiai denevérek és vírusaik szisztematikai és filogenetikai vizsgálata – egy kutatási program ismertetése (oral presentation)

X. Magyar Természetvédelmi Biológiai Konferencia. 1-3 April 2016, Mórahalom, Hungary
Csorba G. & Görföl T. (2016): A magyar denevérkutatás szerepe a trópusi területek természetvédelmében (poster presentation)

8th International Conference on Emerging Zoonoses, 7-10 May 2017, Manhattan, USA
Kemenesi G., Kurucz K., Zana B., Tu V.T., **Görföl T., Estók P**., Földes F., Sztancsik F., Urbán P., Fehér E. & **Jakab F.** (2017): Highly divergent cyclo-like virus in a great roundlead bat (*Hipposideros armiger*), Vietnam (poster presentation)

17th International Congress of Virology, 17-21 July 2017, Singapore
Benkő M., Vidovszky M.Z., Podgorski I., **Görföl T**. & Harrach B. (2017): Recognition of adenoviruses that likely have switched host. (poster presentation)

14th European Bat Research Symposium, 1-5 August 2017, Donostia, The Basque Country
Csorba G., Tu V.T., Furey N.M., Kruskop S.V., Lee L-S. & **Görföl T**. (2017): Towards the clarification of the phylogeny, taxonomy and distribution of South-east Asian Hypsugo (poster presentation)

Global Genome Biodiversity Network Conference 22-25 May 2018, Vienna, Austria
Csorba G., Vörös J., Krizsik V. & **Görföl T.** (2018): Using genomic resources in the systematic and phylogenetic researches of Southeast Asian bats (poster presentation)

4th Southeast Asian Bat Conference 6-9 August 2018, Bacolod, Philippines

Csorba G., Tu V.T., Ruedi M., Kruskop S., Furey N.M. & **Görföl T.** (2018): Revisionary systematics of Asian taxa of the Hypsugine-group (oral presentation)

Tu VT., Furey NM., **Görföl T., Csorba G**. & Hang CT. (2018): Human–bat interactions at sacred sites in Vietnam (oral presentation)

International Meeting on Emerging Diseases and Surveillance 9-12 November 2018, Vienna, Austria

Zana B, Buzás D, **Kemenesi G, Görföl T, Csorba G**, Madai M & **Jakab F**. (2018): Molecular identification of a presumably novel hantavirus in Bronze Tube-nosed Bat (*Murina aenea*) in Malaysia (poster presentation)

A Magyar Mikrobiológiai Társaság 2018. évi Nagygyűlése 17-19 October 2018, Eger, Hungary

Zana B, Buzás D, **Kemenesi G, Görföl T, Csorba G**, Madai M & **Jakab F**. (2018): Új hantavirus molekuláris azonosítása Malajziából származó Murina aenea denevérfajból (oral presentation)

18. International Bat Research Conference 28 July-1 August 2019, Phuket, Thailand

Görföl T., Győrössy D., Szabadi K. L. & **Csorba G**. (2019): Bat tissues in the HNHM Collection of Genetic Resources (poster presentation)

Tuan L. Q., Thong V. D., Son N. T., Tu V. T., Luong N. T., Nguyen V. T., Huang J. C-C., **Csorba G., Görföl T**. & Tuanmu M-N. (2019): Spatiotemporal patterns of bat diversity driven by cimate change in Vietnam (poster presentation)

INTERNATIONAL COOPERATION

The good connections established in the last decades and the joint studies organised within the frame of the present project materialized in different ways. Field trips were organized and enthusiastically supported by local researchers, and the collected materials were shared between HNHM and the partner institutes. Hundreds of specimens were sent or brought to the HNHM for identification which also yielded novel discoveries and, in many cases, further enriched the HNHM collection including precious type material. The extensive scientific connections and common projects resulted in institutional invitations, small-scale additional grants and access to several collections previously practically not available for studies. Fundamentally important outcomes of the international cooperation were the mutual knowledge transfer and capacity building, not to mention the series of joint papers written by these collaborative research groups.

The most important organizations who helped us in the implementation of our grant are as follows:

- Insitute of Ecology and Biological Resources, Hanoi, Vietnam
- Northeast Normal University, Changchun, China
- Guangzhou University, Guandong, China
- The University of Tokyo, Tokyo, Japan
- Durrell Institute of Conservation and Ecology, Canterbury, UK
- Universiti of Malaysia Sarawak, Kuching, Malaysia
- Zoological Museum of Moscow State University, Moscow, Russia
- Indonesian Institute of Sciences, Bogor, Indonesia
- Texas Tech University, Lubbock, USA
- Harrison Institute, Sevenoaks, UK

- Museum National d’histoire naturelle, Paris, France
- Centre for Biodiversity Conservation, Royal University of Phnom Penh, Phnom Penh, Cambodia
- Department of Zoology, University of Mandalay, Mandalay, Myanmar
- University of Ruhuna, Matara, Sri Lanka
- Flora & Fauna International, Phnom Penh, Cambodia
- Natural History Museum of Geneva, Geneva, Switzerland
- Royal Ontario Museum, Toronto, Canada
- National Museum of Natural Science, Taichung, Taiwan
- Taiwan Forestry Research Institute, Taipei, Taiwan
- National Taiwan University, Taipei, Taiwan
- Small Mammal Research and Conservation Fund, Kathmandu, Nepal.

We had several visitors in the Mammal Collection of the HNHM from our international partners: Dr. Vu Dinh Thong from the IEBR, Vietnamese Academy of Science and Technology, Vietnam; Dr. Pipat Soisook from the Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkla University, Thailand; Dr. Juliana Senawi from The National University of Malaysia, Malaysia; Dr. Manuel Ruedi from the Natural History Museum of Geneva, Switzerland; Parvathy Venugopal, University of Bristol, UK; Dr. Sergei V. Kruskop from the Zoological Museum of Moscow State University, Russia.

Memorandum of Understandings with special emphasis on joint bat studies were signed between the HNHM and the following organizations: Indonesian Institute of Sciences, Indonesia; Department of Zoology, University of Mandalay, Myanmar; University of Ruhuna, Sri Lanka; Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Vietnam.

REFERENCE LIBRARY FOR ASIAN BAT ECHOLOCATION

In line with the original task of the project we constructed the Asian Bat Call Database (ABCD) with associated metadata in Darwin Core format (species, voucher reference, locality information, date, call parameters, etc.). Beside the echolocation sounds recorded in flight tent, it also holds calls from free-flying bats identified to species. The ABCD acts as a repository of the original calls (recorded by a Pettersson D1000x detector using the cutting-edge technology in the field) and has the exceptional additional value that each record is linked to a reference, typically a voucher specimen housed in a public collection and is supplemented by a genetic sample and photographic documentation taken on-the-spot allowing further taxonomic-systematic examination. The database presently contains data and parameters of 474 bat individuals representing 107 species. The dataset was cleaned with the help of MSc students and is ready to be published via a dedicated website.

SCIENCE DISSEMINATION

As science dissemination is an important task for every researcher, we wrote several articles in widely read public journals and gave oral presentations to students and to general public, as well. Radio and TV interviews reached even more people and we could transfer the results of our program and the message of the importance of bat protection.

Journal articles

GÖRFÖL T., KEMENESI G. & JAKAB F. 2015: Denevérek és vírusjárványok. – *Természet Világa* 146(6): 242–245.

GÖRFÖL T. & CSORBA G. 2016: Denevérkutatók versenyben – *Élet és Tudomány* 71(50): 1574–1576.

CSORBA G. & GÖRFÖL T. 2016: Denevér- és vírusvadászat Borneón – *GEO Magazin* 2016(10): 55–63.

ANON. (2016): Halálos vírusokra vadásztak Borneón a magyar denevérkutatók – *Blikk Vasárnap* 23 (285): 14, 19 pp.

Oral presentations

Denevér- és víruskutató expedíción Kongóban, 26 January 2015, Garay János Általános Iskola és AMI, Szekszárd

Denevér- és vírusvadászat a trópusokon (Kutatók Éjszakája), 25 September 2015, Budapest

Denevér- és vírusvadászat a trópusokon, 17 October 2015, Körösbánlaka, Románia

Denevér- és vírusvadászat a trópusokon, 31 October 2015, Budapest

Denevérkutatás Gemenctől Kongón át Borneóig, 11 December 2015, Szekszárd

Denevér- és vírusgyűjtés a trópusokon (Utazási Medicina tanfolyam), 12 February 2016, Budapest

Denevér- és vírusvadászat a trópusokon (Kutatók Éjszakája), 29 September 2017, Magyar Természettudományi Múzeum, Kutatók éjszakája, Budapest

Denevér- és vírusvadászat a trópusokon, 1 December 2017, Garay Általános Iskola és AMI, Szekszárd (2 occasion)

Radio and TV interviews

Denevérkutatás az MTM-ben– *Klubrádió, Állatbarát*, 24 January 2016

Mire jók a természetrajzi gyűjtemények? – *Duna TV, Kék bolygó*, 22 June 2016

Denevérek és denevérkutatás – *Civil Rádió, Foggal és örömmel,* 2 November 2016

Denevérek – *MR1-Kossuth Rádió, A tudomány hangjai*, 18 February 2017

A denevérek haszna – *MR1-Kossuth Rádió, A tudomány hangjai*, 8 May 2017