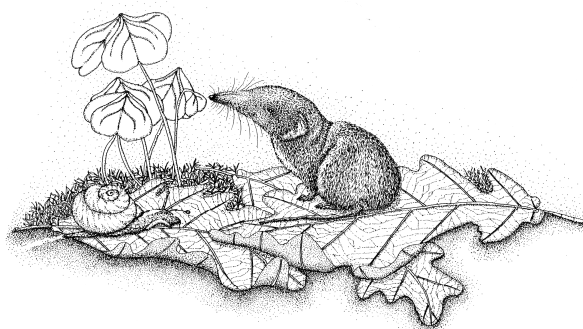


INSECTIVORES AND BATS



A REVIEW OF BAT STUDIES IN IRAN

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Although reports on distribution and abundance of bats from Iran exist since mid nineteen century but these information are very few and have been accumulating very infrequently. The first written report on bats collected from Iran was published in 1876. In 1921 the total number of bat species reported was only eleven. The number of bats identified by European biologist increased gradually and in 1960s and 70s, Iranian scientists reported nine species of Chiroptera new to the Iranian faunal list. In 1980 total bat species reported from Iran was 38 species. Latter a Czech scientist reported one new species from Iran but total species of bat remained 38 because one species has lost its position as a good species. Available data on distribution and abundance of these species are very scarce. For example from the 38 species of bats reported from Iran there are six species that have been reported only once, 21 species are known from only five localities and only two species are known from more than 30 localities. Moreover, there are five bat species which have been reported from neighbouring countries at border areas but not from Iran. Current studies on bats in Iran focus on various aspects of bat biology including bat conservation, regular mistnetting, bat banding, bat echolocating, determination of food habits, postnatal studies, reproductive delay (sperm storage and delayed implantation), and geographic variation in selected species of bats. In this article authors perform a brief review of bat studies in Iran and try to establish that inconsistency of these studies may bear conservation significance.

ALL-IRELAND DAUBENTON'S BAT WATERWAY SURVEY: A
ROBUST MONITORING PROTOCOL FOR THE DAUBENTON'S BAT
MYOTIS DAUBENTONII USING VOLUNTEERS

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A Waterways Survey is being used to monitor the status of the Daubenton's bat in Ireland. The monitoring protocol is based on that developed by the BCT, UK. It focuses on Daubenton's bat activity along waterways as this species is known to have a high dependency on such waterbodies for foraging. The main aim of this scheme is to monitor populations of Daubenton's bat and to collect sufficient data to act as an early warning system for Amber or Red Alert declines. This is also the first systematic survey of this species in the Republic of Ireland. In 2006, a total of 134 waterways were surveyed by 131 volunteer teams, 91% of sites were surveyed twice. Waterways were surveyed in 27 of the 32 counties of the island.

Volunteers were assigned a waterway selected from a dataset of sites currently sampled for biological and chemical water quality parameters. Ten points, 100m apart, were surveyed by volunteers on two evenings in August 2006. At each of the 10 points volunteers recorded Daubenton's bat activity for 4 minutes. 256 completed surveys recorded 12,051 Daubenton's bat passes (Mean = 47.1) and 5,413 'Unsure' Daubenton's bat passes (Mean = 21.1). The proportion of 'Unsure' is considered to be high. Analyses show that identification skills are significant; volunteers that rated their skills as "low" recorded a higher proportion of 'Unsure'. Daubenton's bats were recorded at 122 (91%) of the waterways surveyed. To investigate the relationship between the log-transformed numbers of passes and other variables, an REML model was fitted to the data. Analysis of data suggests that there is an increase in passes with the width of waterways surveyed up to a maximum of 20m. Temperature has a significant influence on the number of passes recorded while rain significantly reduced the number of passes recorded. Power analysis indicates that after 10 years it may be possible to detect Red Alert declines with 90% power if 80 core sites are surveyed annually or 160 sites 40% missing values. Amber Alert declines can be detected with 90% power with 60 sites surveyed annually or approximately 120 sites with missing values.

The scheme is managed by Bat Conservation Ireland with funding from the NPWS, Department of Environment, Heritage and Local Government (ROI), the EHS, Department of the Environment (NI), and Waterways Ireland.

DISTRIBUTION OF DANISH BATS

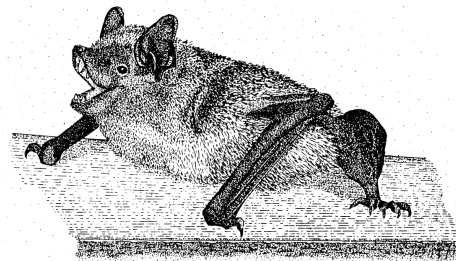
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As a result of the Atlas of Danish Bats and the Atlas of Danish Mammals 17 species of bats have been recorded in Denmark. A strong combination of methods was used: 1) an active search through contact with the public for “specimen localities”, i.e. roosts and other localities where specimens could be identified in the hand, and 2) field identification with high quality ultrasound detectors (bat detectors). A total of 9075 bat species localities (“specimen localities” and “detector localities”) were recorded. During the period 1981-2004 almost all the 647 “terrestrial” 10x10km UTM squares of Denmark were visited for one or more nights with detectors, and this standardized measure of effort makes it possible to analyse the distribution patterns of the species. Examples of some of the most interesting species distributions will be presented. The data were analysed using GIS (Geographical Information System, MapInfo) to describe differences in species richness of bats in different regions of Denmark.



MOLECULAR PHYLOGENY OF ERINACEINAE FISCHER, 1814 OF THE WORLD AS INFERRED FROM MULTIGENE ANALYSIS

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Several contradicting hypotheses on phylogenetic interrelationships among genera of spiny hedgehogs (Erinaceinae) were advanced on morphological grounds. However, they have not been fully tested with molecular data. Our phylogenetic analysis based on sequence data for two nuclear exons (brca, exon 11 and ghr, exon 10), an intron (transferrin, intron 1), and two mitochondrial genes (12S and cytb) produce the first well-resolved and almost complete molecular phylogeny for the subfamily. The results strongly support the monophyly of all contemporarily recognized genera (*Erinaceus*, *Atelerix*, *Hemiechinus*, *Paraechinus*, *Mesechinus*). *Mesechinus* is closely related to *Hemiechinus*, the genetic distance between them falls within the range observed among congeneric species. *Paraechinus* is a relatively divergent sister group to *Hemiechinus*/*Mesechinus* clade, while *Atelerix* is a distant relative of *Erinaceus*. The latter genus comprises four species among which *E. amurensis* is a sister taxon to *E. europaeus* while *E. concolor* is close to *E. roumanicus*. Thus, our results are compatible in most aspects with the morphology-based reconstruction recorded in literature

IS PUGMY WHITE-TOOTHED SHREW (*SUNCUS ETRUSCUS*) A
COMMON AND ABUNDANT SPECIE IN CENTRAL GREECE?

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In Greece, the distribution and population status of pugmy-white toothed shrew is barely known. The existing information comes mainly from islands, and there are some references from continental Greece.

A three year study (2003-2005) was realized in the agricultural ecosystems of Thessaly, central Greece, concerning the trophic ecology of the barn owl (*Tyto alba*). Data were mainly collected in the lowlands with heights varying from 0 to 300m. Pellets were collected from 31 different sampling sites, with 4 successive samplings realized at 6 month intervals.

A total of 10.065 pellets were analyzed which resulted 29.061 prey items. 478 specimens of pugmy white-toothed shrew were recovered from the pellet analyses which form the 1.64% of the Barn owl diet. The total percentage of frequency is low, but attention should be given to the fact that the Pugmy white-toothed shrew was present in 27 of the 31 sites that were sampled. This proves that the specie has a very wide distribution in the agricultural ecosystems of central Greece.

It is also possible that the specie has a high abundance in the study area. The significant difference of a t-test for dependent samples between the two groups of species richness measurements (before and after rarefaction) implies that there are "rare" species in the study area, like the pugmy white-toothed shrew. Nonetheless the specie cannot be considered as "rare" in the field with certainty. The Barn owl rarely chooses to prey on such small species, and although it is a "generalist" predator it is also specialized in small mammals with optimized prey the *Microtus* species, or others of similar biomass. Therefore the term "rare" can be applied to the pugmy white-toothed shrew because the Barn owl rarely preys on it, and not because it doesn't have a high population in the study area. That thought is consistent with the positive correlation between the pugmy white-toothed shrew percentage of frequency and the total prey items in 15 other sites of Greece, where the Barn owl diet was studied. The positive linear relationship proves that as larger samples of pellets are analyzed the percentage of pugmy white-toothed shrew increases. As a result, for mammal species so rarely preyed by the Barn owl, very large samples of pellets have to be analyzed in order to draw conclusions about their abundance in nature. In conclusion, the specie might also present high abundance as well as a wide geographic distribution.

A NON-INVASIVE APPROACH TO ESTIMATE THE DEGREE OF
HYBRIDIZATION BETWEEN TWO SIBLING BAT SPECIES, *MYOTIS*
MYOTIS AND *MYOTIS BLYTHII*, IN NORTH-WESTERN ITALY

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The two sibling species of mouse-eared bat *Myotis myotis* and *Myotis blythii* occur in sympatry over wide areas of Southern and Central Europe, often forming mixed roosting groups. The two species differ in their ecology and physiology, they generally use different feeding habitats, occupy distinct food niches and have different parturition times. Although these species are morphologically almost indistinguishable, a combination of several morphological parameters generally allows an unambiguous discrimination. Recent studies showed that the two species can interbreed and that hybridisation is still ongoing in areas of sympatry. The persistence of well-differentiated nuclear gene pools could be explained by a series of introgression events occurring repeatedly during the recent colonization of Europe by *M. blythii* from Asia.

In this study we report the genetic characterisation of five mixed nursery colonies in North-Western Italy. Because classical sampling techniques, such as mist netting captures, are invasive when applied to bat specimens, we adopted a non-invasive approach based on stool sampling. Moreover a few tissue samples from wing biopsies of unambiguously identified *M. myotis* and *M. blythii* were also analysed, in order to obtain the "parental" classes for subsequent analysis. Five polymorphic microsatellite loci were obtained which allowed to analyze the genetic interactions between the two sibling species and the pattern of nuclear genetic diversity. The genotypes of the individuals sampled in the five mixed nursery colonies were analysed with the program NEWHYBRIDS. This program implements a Bayesian method to detect the presence of hybrids from a sample of individuals of mixed origin, by estimating the allelic frequencies in the two parental populations and for each genotype its posterior probability of being pure or of hybrid origin.

Results obtained confirm that hybrids are present in all five sites sampled, as it was previously demonstrated in just one colony by other investigators. A significant directionality of backcrosses between hybrids and one parental species was observed, thus confirming the asymmetric gene introgression between *M. myotis* and *M. blythii*.

NO EVIDENCE OF GENETIC STRUCTURING AND ISOLATION BY
DISTANCE IN CENTRAL EUROPEAN POPULATIONS OF
MIGRATORY COMMON PIPISTRELLES
(*PIPISTRELLUS PIPISTRELLUS*)

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In two recently discovered European cryptic bat species *Pipistrellus pipistrellus* and *P. pygmaeus* different life strategies were found in some aspects (e.g. echolocation and social calls, foraging habitats, activity patterns, home-ranges). Former data on long-distance migration and hibernation concern *P. pipistrellus* s.l., i.e. either *P. pipistrellus* or *P. pygmaeus*. There is, however, no information whether both species can migrate over long distances and whether they can hibernate in the same hibernacula or not. By examining the degree of population subdivision, a greater understanding of seasonal movements may be attained. Migratory species may be expected to show low levels of structuring while sedentary species may exhibit a greater degree of genetic differentiation among populations. Using a PCR-based species identification method we screened historical (preserved museum samples) and recent (wing membrane tissues) material from underground hibernacula and sites of mass autumn invasions (116 individuals, 10 localities) in central Europe. We found that all individuals in hibernacula and invasion sites were *P. pipistrellus* and there has been no information about the hibernation and mass invasions in *P. pygmaeus* in central Europe.

Ten polymorphic microsatellite markers were used for analysis of population genetic structure. In summer 2006 we collected wing membrane tissues from 202 individuals from 9 maternity colonies of *P. pipistrellus*, 23 to 560 km distant from each other, and situated across the Czech Republic and Slovakia (central Europe). Genetic structuring was very low ($F_{st}=0.0055$) and there were no signs of isolation-by-distance ($P>0.05$) indicating high levels of gene flow among populations even when separated by large geographic distances. These results suggest that mating during migration from summer to winter roosts is important means of gene flow among populations. In the next steps it will be necessary (1) to analyse mtDNA structure to assess relative importance of male and female dispersal and (2) to compare obtained data with those from the cryptic species *P. pygmaeus* to analyse possible differences in mating behaviour between the two species.

This research was supported by the Czech Science Foundation (206/06/0954) and by the Long-term Research Plan (MSM 0021622416) to the Masaryk University.

THE CHROMOSOME RACES OF THE COMMON SHREW
(*Sorex araneus* L.) OF VOLGA REGION

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Three chromosome races of the common shrew occupying huge areas are found in Volga Region: Mologa, Manturovo and Sok. The Mologa race (diagnostic chromosomes are: gm, hn, io, jl, kr, pq) spreads along the right bank of Middle Volga River and occupies the Volga Highland. The Manturovo race (go, hi, jl, kq, mn, pr) is distributed on the left bank of Upper Volga. The Sok race (go, hn, ip, jl, kq, mr) inhabits the left bank of Middle and Lower Volga, its area extends from half-deserts to taiga. We suppose that the Mologa race is separated from two other races by Volga River. Neroosa race (go, hi, jl, kr, mn, pq) occupies huge area and spreads westwards to the Mologa race from the Oka - Don Lowland. The Sok race spreads east toward the Ural Mts. and is substituted by the Yuryuzan race there (go, hi, jl, kr, mn, pq). The Serov race (go, hn, ip, jl, kq, mr) substitutes these races in areas surrounding the Ural Mts.

Chromosome polymorphism caused by dissociation of one or both homologous metacentrics into acrocentrics is observed only in populations of Mologa race; the other races are characterized by metacentric karyotypes. Polymorphism in populations of the Mologa race from the Volga Highland is found in the arm combinations io (frequency 0.25), kr (0.07) and jl (0.03), the polymorphism frequency is growing along with Volga River approaching. The populations from Samarskaya Luka (the highest and the very east site of Volga Highland) are most polymorphic. Chromosome data show that animals from the right bank of Volga and island Serebysh in the bed of the river belong to the same chromosome race Mologa.

Karyotype of the Mologa race differs rather significantly from karyotypes of the other Volga races. Though the Neroosa and Mologa races have two common metacentrics, it looks more probable that Mologa race originated from the Moscow race neighboring from the west. These races have 3 common metacentrics (gm, kr, pq), other metacentrics originating by one WART. Karyotype of the Moscow race is considered as a transformed version of the West European Karyotypic Group (there is also a hypothesis about origin the Neroosa race from the Moscow race). The Mologa race penetrated the Volga Highland between areas of the Manturovo and the Neroosa races, but the expansion of Mologa race was suspended by Volga bed in its middle stream. High level of polymorphism in populations of the Mologa race can mark them as the front line of area.

WHERE ARE OUR WATER SHREWS? THE DISTRIBUTION AND
HABITAT OCCURRENCE OF *NEOMYS FODIENS* IN BRITAIN,
REVEALED BY NATIONWIDE SURVEY

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The Eurasian water shrew (*Neomys fodiens*) is one of Britain's least known mammals. Being small and elusive, with a localised and sporadic occurrence, it has been the subject of few ecological studies either here or elsewhere in Europe. Concerns have been raised about the conservation status of this shrew amongst fears that it may be suffering from habitat loss, pollution and disturbance. In 2004-5 we conducted a nationwide survey of the water shrew on behalf of The Mammal Society and part-funded by the Environment Agency (UK). A large network of volunteers was recruited who were trained to use a sampling protocol based on the 'bait-tube' method to collect scats. Using size, shape, colour and contents it was possible to distinguish scats of water shrews from those of other shrews. Some 506 volunteers surveyed 2159 riparian sites across Britain, supplying scat samples and habitat data. Volunteers were kept informed of the survey's progress by regular reports and newsletters. Evidence of water shrews was found at 387 sites (17.4%). Water shrews were widely distributed across mainland Britain, from the south of England to northern Scotland with a concentration in central and eastern England. They exploited many different freshwater habitats from fast-flowing rivers and streams to ponds, lakes, canals and ditches. They were found by water bodies with a variety of substrates, water depths, bank types and vegetation types, and in sites used for angling, walking and boating. Low BOD and nitrate levels and a pH in the range of 7.0-8.0 were associated with the highest incidence of water shrews. The survey demonstrated that, despite concerns about the status of water shrew, it is an adaptable species which is still widespread in Britain. It also highlights the valuable contribution that volunteers can make to ecological surveys, particularly of elusive species.

ASSESSING FAVOURABLE AREAS FOR THE TWO HEDGEHOG
SPECIES INHABITING MAINLAND SPAIN (WESTERN HEDGEHOG
ERINACEUS EUROPAEUS AND ALGERIAN HEDGEHOG *ATELERIX*
ALGIRUS) USING A SPATIAL DISTRIBUTION MODELLING

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We assessed favourable areas for the Western hedgehog *Erinaceus europaeus* and the Algerian hedgehog *Atelerix algirus*, the only European hedgehog species present in mainland Spain, using spatial modelling based on multivariate geostatistical techniques and geographical information system (GIS). The distribution data of the species (in terms of their presence/absence in the Spanish UTM 10 x 10 km squares) were obtained from the Atlas of Terrestrial Mammals of Spain. To infer the factors affecting the species' distribution, and find out favourable areas for them, we used an initial set of 37 environmentally meaningful variables related to climatic conditions, spatial situation, topography and lithology. Except Altitude, which was directly obtained from the US Geological Survey's EROS Data Center, the majority of the variables were digitized using CARTALINX software ver. 1.2. Mean values for each 10 x 10 km cells were obtained with IDRISI32 by means of an interpolation process from vectorial isoline maps. We applied a favourability function, which is basically a GLM that assesses the local variations in presence probability with respect to the overall species prevalence, and that therefore yields geographical favourability values for the species independently of the proportion of the initial presence/absence rate in the study area. With these values obtained, digital maps of favourable and unfavourable areas for the species in mainland Spain were elaborated. Finally, the variables included in the favourability models were grouped in environmental factors and a variation partitioning procedure was carried out to know the amount of variation of the models that was explained by the pure effect of each factor and by their interactions. The predictive models developed for the two species were remarkably parsimonious, since both included only 7 variables. The results of the variation partitioning procedures showed that climate seems to be the most significant factor determining the Western hedgehog distribution (since purely climatic effect explains 53.36 % of the model variation) whereas the interaction between spatial structuring and climate (which explains 53.75 %) is particularly influential on the distribution of the Algerian hedgehog in the study area.

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MTDNA DIVERSITY OF THE BLIND MOLE
TALPA CAECA SAVI, 1822

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The blind mole *T. caeca* is endemic to southern Europe with a discontinuous distribution. Specimens belonging to this taxon have been reported from the Apennines, the western Alps and the south-western Balkans. In the Italian peninsula the blind mole lives at altitudes between 200 and 2500m asl showing a parapatric distribution with *T. europea* and *T. romana* while in the Balkan Peninsula it can be found from the sea level up to 2000m often in sympatry with *T. europea* and *T. stankovici*. The strong influence posed by the environment on the morphology of these subterranean mammals obscure taxonomic relations between species based on morphological traits alone. Only the use of genetic markers and karyotype analyses allow their unambiguous identification. Several questions regarding the taxonomy of the apparently isolated populations ascribed to *T. caeca* needs to be investigated further.

We carried out a preliminary study of genetic diversity in *T. caeca* from Italy and the Balkan Peninsula using mtDNA. Genomic DNA was extracted from alcohol preserved tissues and from museum specimens (skins and fingers) and cytochrome b sequences were amplified. Levels of genetic differentiation within and between Italian and Balkan populations were evaluated and compared with observed genetic variation within other *Talpa* species.

Preliminary results suggest that the Italian and Balkan populations represent a monophyletic clade. Moreover, mtDNA analysis highlights the existence of a population substructure.

RESOURCE PARTITIONING AMONG INSECTIVOROUS BATS; INSIGHTS FROM STABLE ISOTOPE ANALYSIS

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Sympatric animal species frequently differ in resource use; a mechanism by which these species may be able to co-exist. Understanding whether a pattern of niche differentiation is the result of ongoing competition or whether the outcome of divergent evolutionary histories is still open to debate. Insectivorous bats are one of the most speciose group of mammals, often living and foraging within the same areas and therefore potentially they provide a very interesting model to test theories relating to resource partitioning. Morphologically bats are very similar, however discrete differences of body size and wing morphology coupled with notable differences in their sensory ecology have previously been related to microhabitat use.

The objective of this research was to determine the extent to which resources are partitioned within bats living in different guilds. Stable isotope analysis was used as an ecological tool within this study as it has the potential to determine the trophic level at which the bats are foraging and also provides distinction between aquatic and terrestrial habitats. The insect prey base, which the bats were foraging, was also analysed providing the power to relate foraging choices of the bats to habitat.

I will present results from this study, which provide compelling evidence that bats within these guilds are partitioning their resources at various levels, including between sexes, between species and within species between colonies. The extent and nature of resource partitioning also varies between sites, possibly as an effect of variable levels of resource availability and competition.

HABITAT PREFERENCE OF SORICIDAE IN UNWOODED HABITATS IN WETLAND AREA

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We studied the habitat preference of Soricidae in Kisbalaton wetland area, in Hungary. We compared a dry habitat (with *Solidago gigantea*) with a wet habitat. We trapped 5 times in 2006, catching *Sorex araneus*, *S. minutus*, *Neomys anomalus*, *N. fodiens*, and *Crocidura leucodon*. *C. leucodon* was trapped only in dry habitat; the other species preferred the wet habitat. In wet habitat we distinguished four microhabitats with *Glyceria maxima* (1), *Phragmites australis* (2), *Carex hirta* (3) and *Bidens tripartitus* (4). *Neomys* spp. preferred *Carex* only, while *Sorex araneus* chosen *Carex* and *Phragmites*, too. We suggest, these small species prefer close vegetation, with the possibility of 3D movements.



DISTRIBUTION, HABITAT SELECTION AND ECOLOGY OF
BECHSTEIN'S BAT (*MYOTIS BECHSTEINII*, KUHL 1817)
IN LUXEMBOURG

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Bechstein's bat (*Myotis bechsteinii*, Kuhl 1817) is a tree-dwelling bat which is a typical threatened flag species to old growth broadleaved woodland. However threats to this species are still poorly understood. In order to fulfil its obligations to the Habitat Directive (92/43/EEC), the Luxembourg Water & Forest Administration initiated a three-year study to improve the knowledge on the distribution, the ecology and the habitat selection of this species in Luxembourg forests.

From 2004-2006 22 investigation areas were analysed representative of the major forest growing areas of Luxembourg. During 76 nights all forest dwelling bats were registered by methods of mist netting, detector transects or radio tracking. Bechstein's bat was the second most common bat species from all 399 captured bats in forests. In total 12 nursery colonies were localized with the number of females ranging between 20-70 individuals (mean: 34 ± 18.1). However the distribution of the Bechstein's bat was uneven. The occurrence of the species was significantly positively correlated to mean temperature and the presence of forest vegetation consisting of Melico-Fagetum with old oak trees. However the height, mean precipitation, and the occurrence of Luzulo-Fagetum forest was found to be negatively correlated to the occurrence of *M. bechsteinii*.

By radio tracking 47 individuals, it was found that one nursery colony of *M. bechsteinii* uses a pool of 35-40 roosting trees (> 81 % in old oaks) and mainly woodpecker holes (> 95 %) during a vegetation period. Individuals of female Bechstein's bats foraged on a mean area of 46 ha (MCP) with core feeding areas of 2.1 ha (50 % kernel). Typical forest structures for Bechstein's bats in Luxembourg are characterised by beech forests with old oak trees presenting a closed canopy. The core hunting areas presented a high vertical structure of secondary trees and an unequal distribution of forest stratification.

The results of the present study will allow the Luxembourg Water & Forest Administration to develop a consistent forest management strategy and develop a sustainable forest practice to contribute in the long term to the conservation of the Bechstein's bat.

DISTRIBUTION OF BATS IN THE NATURE RESERVES OF THE SIENA PROVINCE, TUSCANY, ITALY

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Knowledge on the distribution of bats (Mammalia, Chiroptera) in the Province of Siena (Tuscany, Central Italy) is scarce and obsolete. Available checklists reported 18 species in the Province territory, with only 14 of these data being reliable. The aim of our research is to update and critically review the checklist and the distribution of bats in the Nature Reserves of the Province of Siena. Furthermore we investigate basic species-habitat relationships in a poorly studied environment in order to develop habitat suitability models. We utilised various techniques to obtain presence/absence data: such as searching for diurnal roosts, bat-boxes, mist-nets and bat-detector.

Field surveys were carried out during Spring-Summer 2006. We found a total of 14 species, with 3 new records for the area: *Nyctalus leisleri*, *Myotis daubentonii* and *Barbastella barbastellus*. We found many colonies, particularly we have discovered an important maternity roost, with the presence of 5 species (4 of which in reproduction), in the Fosini Castle and the Cornate and Fosini Reserve. This roost is certainly one of the most important reproduction sites in Italy.

Data on species abundance obtained with the eterodinic bat-detector and habitat suitability models allow us to provide basic guidelines for Reserve management, in particular forest management regimes that will improve bat conservation.

DISTRIBUTION AND STATUS OF *NYCTALUS LASIOPTERUS*
(SCHREBER, 1780) IN HUNGARY

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Nyctalus lasiopterus is a rare Palaearctic bat species, which was observed for the first time in Hungary in 1933. Until 1993 only two additional pieces of information about the species were known which are dated to 1960 and 1974. In the early 1990s, the research of forest dwelling bats became more active in North-East Hungary and due to sampling efforts *N. lasiopterus* was mist-netted at a few points of the Northern Hungarian Mountain Range.

To measure the Hungarian distribution of the species all of the published and unpublished data, including the new results of the author were taken into consideration. Data of 98 individuals of *N. lasiopterus* were collected. Based on this information, the species is known from nine locations in Hungary up until now. Lactating females were sampled at five locations (Bükk Mountains, Mátra Mountains, Zemplén Mountains and Aggtelek Karst), which means that the species has nursing colonies in the country. Most of the specimens (81 bats) were mist-netted in the Mátra Mountains, where the only stable nursing population of the species is known. Roosts of the species were located by radio telemetry. The bats occupied the cavities of beeches in an old beech forest (Aconito-Fagetum). In the Bükk Mountains there has been no data about the species since 1997, despite intensive sampling, and there is no data from Zemplén Mountains and Aggtelek Karst since 1996 and 2003, respectively. The Hungarian population of the species is confined to a few points of mountain woodland habitats. However *N. lasiopterus* is a strictly protected species in Hungary, but intensive logging threatens its habitats and that activity could result in the considerable possibility of the local extinctions of the species in this area.

HABITAT SELECTION BY GEOFFROY'S BATS (*MYOTIS EMARGINATUS*) IN THE MEDITERRANEAN: THE IMPORTANCE OF TRADITIONAL FARMLAND

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Most of the little information available on the foraging ecology of the threatened bat, Geoffroy's bat *Myotis emarginatus*, refers to areas outside the Mediterranean Basin. In this study, we analysed habitat selection by this species in a typical Mediterranean landscape. We radio-tracked bats in the Iberian Peninsula in an agricultural landscape dominated by olive groves and analysed different habitat selection patterns in juveniles. Although we confirmed the species' preference for forest habitats, olive groves also turned out to be crucial foraging habitat for both adults and juveniles and ranked first in order of preference. Habitat selection patterns were influenced by age. Juveniles proved to be less mobile than adults, moving on average 1.6 km less than adults in displacements to foraging sites. Deciduous woodland, important for adults, was avoided by juveniles, most probably because it was too far for them to fly. Instead, juveniles preferred more accessible habitats such as coniferous woodland, which was neglected by adults.

We highlight here the importance of traditionally managed olive groves as foraging sites for this threatened bat. The ripping-up of ancient olive groves and their replacement by either intensively managed cropland or coniferous plantations represents a significant threat for this vulnerable species in Mediterranean landscapes.

SEX RATIO AND AGE STRUCTURE IN THE POPULATION OF
LESSER MOUSE-EARED BAT *MYOTIS BLYTHII*
IN NORTHERN CAUCASUS

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Males were not met in 4 largest maternity roosts of Northern Caucasus, with 500-1000 adult individuals. In smaller colonies they consisted from a quarter to half of all adult individuals. Until the end of the gestation period adult males are always situated in roosts separately from congestions of females and juveniles. In general, females consisted more than 90 % of adult animals during roost surveys from May to September. This overestimation is related to their high number in several large reproductive colonies. Males were met in the summer singly or in small groups in a number of roosts, that strongly complicates their counting. During hibernation sex ratio differs in separate colonies depending on temperature conditions, roost size and number of bats in a colony. Sex ratio was equal in the hibernation colony of 150-200 *M. blythii* during 9 years of observation in Canyon cave (Krasnodar Territory). Similar results are received for Shubi-Nykhas cave (North Osetia), winter roost for 2000-2300 *M. blythii*. Rate of tooth wear was investigated in 88 *M. blythii* with known age, ringed and recaptured in Canyon cave. It has allowed determining of an approximate correlation between their ages and wear of the upper canines. On the basis of a tooth wear degree we allocated all individuals, examined in Canyon cave, to 5 age categories. Bats in the age under 1 year consisted there 24 %, in the age of 1-3 years - 18 %, in the age of 4-8 years - 35 %, more than 8 years - 23 %. Sex ratio inside all age groups does not statistically differ from equal. Situation was different in the roosts with a small number of bats, where males and younger bats prevailed. Probably, bats gather in large hibernacula without dependence from their age and sex. Therefore, surveys in mass hibernacula can give the most reliable data on the population structure. Our results indicate relatively long average lifespan of *M. blythii* in Northern Caucasus and importance of mass hibernacula for species conservation.

REPRODUCTIVE CYCLE IN THE GREAT MOUSE-TALLIED BAT
(*RHINOPOMA MICROPHYLLUM*) IN WESTERN IRAN

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The Mouse-tailed bats (*Rhinopomatidae*) are often considered the most primitive of the living *microchiroptera*. This family includes three species: *Rhinopoma microphyllum*, *R. hardwickei* and *R. muscatellum*. All three species of genus *Rhinopoma* occur in southern Iran. Species of genus *Rhinopoma* demonstrate well-developed morphological and physiological adaptation to their desert life. No information is available concerning reproductive biology of this species in its Iranian range. In this study reproductive event of *R. microphyllum* was investigated by macroscopic and microscopic examinations, during a four-month period of winter - spring 2002. Data obtained from this study indicate that unlike most temperate bats, reproductive events of male and female *R. microphyllum* are synchronized. In early March following enlargement of sexual auxiliary glands spermatogenesis and oogenesis began. At this time spermatozoa is stored in epididymis and enlarged follicles can be seen in oviducts. Copulation occurs in mid - March. Based on time lapse between enlarged auxiliary glands and parturition in late June it is estimated that the gestation period is about 100 days. Pups at the time of parturition are 5 grams. Lactation last for four weeks until late July. In early August newborn pups began to forage and gradually the nursing colony disintegrate, into small groups of female and their new born.

CYTOGENETIC ANALYSIS OF THE ITALIAN ENDEMIC MOLE,
TALPA ROMANA (INSECTIVORA, TALPIDAE) BY MEANS OF
DIFFERENT BANDING TECHNIQUES AND FISH

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Talpa romana Thomas, 1902 is an endemic species of the Italian peninsula distributed in the Central and South Italy with a possible exception of the major isles. A number of times, *T. romana* was proposed as a distinct species, but it has been definitely accepted as the one different from *T. europea*, in the late 80th, when investigated through allozyme analysis. Basing on the only morphometric criteria, the species is thought to be structured in four subspecies. On the other hand, *T. romana* is found in extremely diversified environments, from the sea level up to 2000 m above it, and, consequently, the morphological variation may be of adaptive nature. To provide further traits to our comprehension of the species, we conducted classical and molecular cytogenetic analyses in individuals of both sexes. While karyological data are scarce in the species of moles, cytogenetic characterization of *T. romana* has never been computed before. Presently, silver staining of NORs, G- and C-banding and FISH with chromosome markers such as 45S rDNA, 5S rDNA and telomeric repeats were performed. The data are discussed in relation to karyological reports on several congeneric species and other species of Talpidae, and with regard to their peculiar sex chromosome pair including a dot-like Y chromosome.

INSECT PREY AVAILABILITY AND SELECTION BY SEROTINE
BATS (*EPTESICUS SEROTINUS*) IN SEMI-OPEN HABITATS IN
LUXEMBOURG

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From 1996 to 1998 a multidisciplinary project investigated availability and selection of insect prey by serotine bats in Luxembourg. Previous radio-tracking had established the home range of the colony (13.5 km²) and showed that the bats selected woodland, permanent grassland and areas of human settlement as foraging habitats. A grid pattern (1 x 1 km) was laid over the home range and in every grid three different sets of insect traps were operated for five consecutive nights during three periods (gestation, lactation and post-lactation) of the summers of 1996 to 1998. At the same time as insects were trapped, faeces were collected in the roost and analysed by insect taxonomists. Comparison of faecal analyses and insect availability showed which insects were preferred.

The serotine bats of this colony were selective feeders, preying mainly on 10 species of the orders Coleoptera, Diptera, Hemiptera, and Hymenoptera and varying the composition of their diet according to insect availability throughout the summer. The key prey *taxa* were the scarabaeid beetle genera *Aphodius*, *Melolontha* and *Amphimallon*, as well as the dipteran family Tipulidae. The foraging habitats were chosen according to their absolute densities and variety of preferred prey *taxa*, which were associated with semi-open and open habitats such as hay meadows and cattle pastures with tree groups or beside woodland. Dietary diversity varied during the summers and is an indicator of prey availability. It also decreased during adverse weather conditions when bats changed to less weather-sensitive prey *taxa*.

SEASONAL SOURCES OF PROTEIN IN CONTINENTAL AND ANTILLEAN NECTARIVOROUS BATS

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Carbohydrate-rich nectar is considered an inadequate source of protein for nectarivorous vertebrates. New World flower-visiting bats apparently solve this nutritional constraint by ingesting pollen grains and insects, which are rich in protein. Here we examined the importance of plant and animal sources of protein using N stable isotope analysis in three species of nectarivorous bats (*Monophyllus redmani*, *Phyllonycteris poeyi* and *Brachyphylla nana*) in an evergreen forest in Cuba, and one nectarivorous species (*Glossophaga soricina*) in rain and dry forests in Mexico. Animal tissues become enriched in ¹⁵N compared to ¹⁴N with respect to their food sources and their analysis allows one to determine trophic position of the animal. We collected blood from the bats through out the year as well as samples of potential food sources to be used as references. On average, *M. redmani* and *P. poeyi* relied slightly more on plant protein but in both species there were highly insectivorous individuals, and individuals that relied almost entirely on plant protein. *B. nana* showed the same trend but sample size was small (N=4). In both rain and dry forests, *Glossophaga soricina* relied heavily on insects through out the year. Our results indicate that, in spite of their capability to extract pollen contents reported in the literature, nectarivorous bats use animal sources of this nutrient to a large extent although in some species there is considerable inter individual variation. In contrast, neotropical frugivorous bats have been previously shown to rely more heavily on plant sources of protein using a similar isotopic approach. It is perhaps limits on the availability of flowers compared to fruits what explains this contrast in feeding strategies between nectarivorous and frugivorous New World bats.

BATS OF THE EASTERN MEDITERRANEAN: THE GEOGRAPHIC STRUCTURE OF DIVERSITY AND ITS SOURCES

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We databased supposedly all the records of bats available from the E-Mediterranean (essentially contributed from our own field study in the region, partly published in a series of monographs and covering Albania, Bulgaria, Greece, Turkey, Lebanon, Cyprus, Syria, Iran, Israel, Egypt, Libya), analyzed them with aid of several quantitative techniques, identified the chorologic patterns, zones of faunal homogeneity and transitional zones between particular chorologic units. We also summarized the molecular phylogeography data on bats of the region, evaluated the phylogeographic signals of them and compared with the results of chorologic analyses. The essential zone of faunal rearrangements (congruent with the major phylogeographic shed) was found in the Zagros Mts, north of Mesopotamia and S of Talysh Mts., but extensive specificities were found in the Levant region (Lebanon in particular) and Cyprus. The recently identified speciation events are reviewed and correlated to the palaeobiogeography of the region (with particular reference to the Mesinian salinity crisis).

In total, 55 spp. of bats were found to occur in the E-Mediterranean (s.l.), i.e. nearly 46% of the Palearctic bat fauna and markedly more than the European fauna (36 spp.), of which 29 species reach their southern range margins just in the E Mediterranean, while 12 species (including those recently identified by molecular techniques) are endemic to the region. Undoubtedly, the E-Mediterranean represents the most important hot spot of the chiropteran diversity of the W-Palearctic region.

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MOLECULAR DIFFERENTIATION IN A HYBRID ZONE BETWEEN
CHROMOSOMALLY DISTINCT RACES OF THE COMMON SHREW
Sorex araneus IN POLAND

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The common shrew *Sorex araneus* is one of the most variable mammals with respect to karyotype. In the range of this species, 68 chromosome races having characteristic sets of metacentrics and acrocentrics are described. Chromosome races coming into contact give rise to hybrid zones. The present study investigated the genetic structure of the hybrid zone between the Drnholec and Bialowieza races of the common shrew in Poland using four molecular markers: seven autosomal microsatellites (105 individuals studied), Y-linked microsatellite (85 males), 31 allozyme loci (553 individuals) and mitochondrial cytochrome b gene (22 animals). On the basis of specific chromosomes, the Drnholec and Bialowieza races were classified to different karyotypic groups, which were believed to have survived the maximum of last glaciation in independent isolates.

We found that genetic differentiation between the Drnholec and Bialowieza races was weak and not significant in respect to all molecular markers. But these results are in contrast with the chromosomal structure of the hybrid zone under study. We observed very sharp frequency clines of specific chromosomes, what strongly suggests that gene flow between the Drnholec and Bialowieza races was reduced. Gene flow in the studied area can be reduced by selection acting against interracial hybrids, which form decavalents in meiosis I, and by the presence of an environmental barrier in the centre of the hybrid zone. However, we did not find significant correlation between genetic differentiation and the presence of geographical obstacle. Then, analyses of meiosis and spermatogenesis of the hybrid males showed that these individuals suffered from substantial germ cell death and high level of anaphase I nondisjunction. Hence, we supposed that a lack of molecular differentiation between the Drnholec and Bialowieza races is the result of a shared ancestry. Moreover, any genetic differentiation, being a consequence of selection acting against Drnholec/Bialowieza hybrids, is obliterated by genetic drift.

CONSEQUENCE OF MYOTODONTIA AND NYCTALODONTIA
IN TAXONOMY OF VESPERTILIONID BATS
(VESPERTILIONIDAE, CHIROPTERA)

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Two major types of lower molar morphology in Vespertilionid bats some times had been used as a high value taxonomic feature. For example this is one of characteristics dividing genus *Pipistrellus* s.str. from *Hypsugo*, *Falsistrellus*, and some other. It was usually thought that nyctalodontia (connection of postcristid to the hypoconulid) is a primary stage for all Vespertilionidae because of nyctalodont tooth type in relative families (Molossidae, Natalidae and Miniopteridae) and in most archaic fossil forms (e.g. *Stehlinia*). Nevertheless most primitive Vespertilionids of present days - *Kerivoula*, *Cistugo* and *Myotis* - thought to be myotodonts (with postcristid connecting to entoconid). Nyctalodont teeth were known first of all in a set of closely related genera forming tribe Pipistrellinae s.str., which was additional argument for separating of this taxon from Vespertilioninae. There was known only two cases of presence of different dental types in closely related genera: *Plecotus* and *Barbastella*, and *Lasiurus* and *Dasypterus* (myotodont vs. nyctalodont in each pair); and one case of «transitional» dental type (were postcristid may connect to both entoconid and hypoconulid or not to any) in *Lasionycteris noctivagans*.

According to our data situation is not so clear. Nyctalodont molars were found in two branches of *Myotis* s.lato, one including *M. moupinensis* and another including *M. annamiticus*, *M. laniger*, *M. siligorensis* and relatives. In the latter case the «transitional» type also can be seen. Meantime there are typical myotodont molars in *M. longipes* and *M. csorbai* which from our point of view belong to the same species group.

The only member of Vespertilionini s.str. known to be nyctalodont is *Neoromicia nanus*. However closely related *N. helios* is myotodont. Moreover, processing the collections on *N. nanus* we found individuals possessing myotodont teeth, and in some individuals from Kenya we can see «transitional» molar type.

Finally, amongst genus *Murina*, which molars usually can be treated as nyctalodont, we may find wide variety of the feature, including stages not known in any other Vespertilionidae. In series of *M. tubinaris*, however, both «clear» molar types can be found. Two scenarios may be suggested to explain this situation: multiple appearance of myotodontia in evolution of Vespertilionidae (six times at least) or, reasoning from situation in *Noromicia* and *Murina*, multiple reversion in evolutionary dental changes.

CHROMOSOME RACES OF THE COMMON SHREW
Sorex araneus L. (INSECTIVORA) FROM VALDAI HEIGHT AND
ENDEMIC POPULATION OF THE LAST GLACIATION AREA

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Cytogenetic analysis of natural populations of the common shrew *Sorex araneus* over an area of the Valdai Height revealed the presence of four distinct chromosome races ("West Dvina", "Seliger", "St. Petersburg" and "Moscow"). The geographic distribution of the races in relation to the border of the Late Valdai glaciation area is described and discussed. The revealed 5 zones of contact of chromosomal races are located directly on regional formations of a glacier vepsov stages.

Two races, "Seliger" and "St. Petersburg", are located in the former ice sheet area only. Attention is drawn to the fact that many of the races located in the last glacial area from the Valdai Height up to Scandinavia inclusive are characterised by endemic chromosomes (gi, gp, mo, or *et al.*). It was concluded that situation in the area of the last glaciation could favour the preservation of refuges of tundra or forest vegetation and of populations of some small mammal species. It is supposed, that the palaeogeographical situation of the last glaciation differs from what is commonly believed.

THE LONGEST MEIOTIC CHAIN CXI IS THE PROVEN CASE IN INTERRACIAL HYBRID MALES OF *SOREX ARANEUS*

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Two chromosomal races of the common shrew (*Sorex araneus* L.), Moscow and Seliger, form a narrow contact zone in the vicinity of the type locality of the race Seliger (57°10'N, 33°30'E) in European Russia. These two races differ in the full content of variable chromosomes represented by 5 metacentrics in the race Moscow (*gm*, *hi*, *kr*, *no*, *pq*) and 4 metacentrics fused in another arm combination and 2 acrocentrics (*g*, *hn*, *ik*, *mq*, *pr*, *o*) in the race Seliger. Thus, interracial hybrids should be expected to display a complex heterozygote combining 11 Robertsonian metacentrics / acrocentrics (*g/gm/mq/qp/pr/rk/ki/ih/hn/no/o*). Five hybrid karyotypes were detected among 31 overwintered common shrews from the centre of the hybrid zone in April 2006. Meiotic preparations from 2 males showed quite regular chain configuration scored from 86 best spreads at diakinesis-metaphase I. The pairing of homologs at this meiotic phase was obviously normal and did not connect with univalence and/or associations between this exclusive chain-of-11 to either autosomal or sex chromosomal configurations. Besides the three simple heterozygotes reported formerly for the race Seliger (*m/q*, *p/r*, *j/l*), a new heterozygous variant was found in this spring sample. The first case of the heterozygosity for fused "diagnostic" acrocentrics (*g/o*) was recorded in a male which meiotic preparations proved the presence of a Robertsonian trivalent. Still other male was heterozygous for the already known combination *m/q*. In these two variants, autosomal trivalents looked quite as regular as bivalents by the end of meiosis I. No heterozygote was found in the karyotypes of the race Moscow representing the sample studied. These data do not provide an unequivocal evidence for the reduced fertility of hybrids due to meiotic disorders as a result of chromosome rearrangements. As follows from modern meiotic analyses, pairing irregularities existed at pachytene early in meiosis might have been resulted in metaphase II, rather than in metaphase I. So, it can be concluded that hybrid common shrews with the longest chain in meiosis I are not sterile though the lowered fertility of hybrid males cannot be excluded. It was calculated in this study that the observed frequencies of hybrids in the population before breeding season appeared to be lower than what was expected from the Hardy-Weinberg rule ($P < 0.01$). It suggests that selection acts against hybrids in this hybrid zone.

IMPACT ASSESSMENT FROM THE SHUT DOWN OF A MINING FACILITY IN NORTHERN PORTUGAL OVER THE LOCAL BAT COMMUNITY

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Chiroptera present high conservation interest throughout Europe, being protected by legislation resulting from the EU Habitats Directive and the Bern Convention. Twenty seven species are, at the moment, reported for Portuguese territory, representing almost 40% of terrestrial mammal fauna of this country. Some of the species are quite abundant. However a great number of them present small and vulnerable populations, especially cave-dwelling species. Their vulnerability is illustrated by the fact that Chiroptera represent up to 80% of endangered or critically endangered species, according to the Portuguese Vertebrate Red Data Book.

In the last decades, a great number of mining facilities has been shut down in Portugal. The abandonment of extractive activity in these places sometimes results in the emergence of potential danger for human and animal populations, as an outcome from soil and galleries' roof abatement and surface cracks, many times hidden among dense vegetation that grows after abandonment of the mine. However, the system of galleries, hollow spaces resulting from extraction and support structures can provide shelter and breeding locations for bat communities'.

Whenever intervention is needed for providing safe use of the place, by human and animal populations, we are ought to keep in mind that bats are quite sensitive to human disturbance and habitat modification. Consequently, impact assessment studies must be performed any time an intervention might hold the risk of population extirpation.

In this sense, the main objective of this work was to evaluate the possible impact of the mining activity cessation of a tin mining complex in Northern Portugal, over the local bat population. For the purpose, species using mine structures and their surroundings were identified and their conservation status was determined. Six species were found, from which *Rhinolophus euryale/mehelyi* (cf) and *R. hipposideros* are considered to be critically endangered and vulnerable, respectively. Some mitigation measures were suggested for reducing deleterious effects' impact.

Despite its local scope, this study constitutes an important contribute for the knowledge of European bat populations. Keeping in mind the generalized lack of data on the biology and spatial distribution of the populations of this vertebrate group, any contribute presents particular importance, mostly when this information is used for drawing local management and conservation measures.

ON THE ROOSTING ECOLOGY OF GEOFFREY'S BAT (*MYOTIS EMARGINATUS*, GEOFFREY 1806) IN WESTERN EUROPE

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Beyond climatic factors, bat distribution is mainly the result of the availability of summer and winter roosting sites and of adequate feeding habitats. Geoffrey's bat (*Myotis emarginatus*), one of the major endangered house dwelling bat species, is unevenly dispersed at its northern distribution area in Western Europe. In order to analyse the nursing roost selection of *M. emarginatus* in anthropogenic structures, the aim of the study was to determine whether the structure of the roosting site or its microclimatic range are responsible for the roosting choice of this species.

During the year 2003 some 17 abiotic factors from 13 nursing colonies in 5 European countries at the northern distribution edge of this species were analysed. The selected colonies ranged from 30-700 females and were situated in different roosting sites such as church lofts up to semi-undergrounds and World War II bunkers. Measurements of type and volume, roof type and exposure of roosting sites, availability of hanging places, dimension and exposure of flight entrance, light intensity and temperature in relation to the colony size were made.

The results of the study showed the widespread range of ecological factors influencing the nursing habitat selection of *M. emarginatus*. The analysis of the micro-thermic conditions of the hanging places of the nursing colonies in relation to external temperature recordings during different physiological periods as gestation, lactation and fledge time of the young revealed that this species is able to reproduce under a wide range of thermic conditions. The mean thermic range of the nursing colonies hanging places varied from 14.9 ± 2.7 °C up to 24.2 ± 4.9 °C.

As the results of this study show, the capacity of *M. emarginatus* in social thermoregulation offers this species a wide range of potential roosting sites at its northern repartition area. Factors other than microclimatic seem to determine the distribution of this species at its northern border. Further studies on feeding habitats are needed to analyse the reason of the scarce distribution of this species in Western Europe.

HEAVY METAL ACCUMULATION BY URBAN HEDGEHOGS
(*ERINACEUS EUROPAEUS*) IN EASTERN FINLAND

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Samples of urban European hedgehog (*Erinaceus europaeus*) tissues were collected in 2004 and 2005 in eastern Finland (63°N 29°E) and analysed for heavy metals (Cd, Pb, Cu, Zn, Se, Ni) from spine, hair, liver and kidney collected from road-kill hedgehogs (N = 65). The age of each individual was determined by using lower jaw section. The concentrations of lead, copper, nickel and zinc were relatively low in all tissues, while cadmium and selenium levels were elevated in kidneys and liver. The higher concentrations of cadmium and selenium were positively correlated with age, especially so in the kidneys of females. The concentrations of other metals did not correlate significantly with the age of hedgehog. In general, the concentrations of heavy metals in hedgehogs in eastern Finland were lower than those of hedgehogs in central Europe. The results of this study indicate that hedgehog could be used as a bio-indicator of urban environmental contamination.

DYNAMICS OF THE PLEISTOCENE BAT FAUNA (CHIROPTERA)
FROM THE MATUZKA PALEOLITHIC SITE (NORTHERN
CAUCASUS)

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Out of 23 bat species presently inhabiting the northern Caucasus 17 have been found in the Upper Pleistocene (MIS6-MIS2) sedimentary series in Matuzka cave: *Eptesicus serotinus* Schreber, 1774; *Vespertilio murinus* Linnaeus, 1758; *Nyctalus noctula* (Schreber, 1774); *N. leislerii*; *Myotis blythii* Tomes, 1857; *Barbastella barbastellus* Schreber, 1774; *Plecotus auritus* Linnaeus, 1758; *Rhinolophus ferrumequinum* Schreber, 1774; *Miniopterus schreibersii* Kuhl, 1817; *P. pipistrellus* Schreber, 1774; *P. nathusii* Keyserling, Blasius, 1839; *P. cf. kuhlii* Kuhl, 1817; *Hypsugo savii* Bonaparte, 1837; *Myotis brandtii* Eversmann, 1845; *M. nattereri* Kuhl, 1817; *M. bechsteinii* Kuhl, 1817; *M. emarginatus* E. Geoffroy, 1806. Absence of some species in Matuzka oryctocenosis (*Rhinolophus hipposideros*, *R. euryale*, *Myotis daubentonii*, *M. aurascens*, *M. mystacinus* and *Nyctalus lasiopterus*) is most likely caused by taphonomic factors. Thus, by the end of the Middle Pleistocene, the general appearance of the bat fauna had already been formed and remained almost constant to the present time. The preservation and proportions of bat species in Matuzka oryctocenosis suggest that significant part of bat sample comes from birds' pellets. Some part of the fossil material may originated from autochthonous sources supposedly winter colonies of the species roosting in the ceiling fissures in the cave entrance and in the rocky walls surrounding the cave. The general dynamics of the number and structure of Pleistocene bat communities from Matuzka cave are in accordance with those of rodents inhabiting different landscapes and, hence, indirectly reflect environmental changes in the area of Matuzka cave. The bat fauna apparently decreased in time of spread of open-ground habitats. In the Eemian Interglacial, the fauna of bats was the richest and included thermophilic *R. ferrumequinum* and *Miniopterus schreibersii*, besides of the records of *Hypsugo savii* and *Pipistrellus kuhlii*, which demonstrate in the Eemian the ranges corresponding to their Recent distribution. The Valdai glaciation (the time of beds 6-3a accumulation) is characterized by a slightly poorer and less numerous bat fauna, which includes *Myotis nattereri*, *M. emarginatus* and *M. bechsteinii*, and is distinguished by well-pronounced fluctuations of the proportions of taxa. The proportion of psychrophilic faunal elements, such as *Plecotus auritus* and *B. barbastellus*, noticeably increased.

A NEW SPECIES *EPTENONUS GRITSEVI* (VESPERTILIONIDAE,
CHIROPTERA) FROM THE LATE MIOCENE OF THE UKRAINE - A
NEW EVIDENCE OF VESPERTILIONINE BATS EVOLUTION

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The fossil vespertilionid bats have been found in the late Miocene deposits of Ukraine in the Gritsev locality. The dental formula is: I2,3;C1;P2,4;M1-3 and I/1,2,3;C/1;P/2,3,4;M/1-3. The rounded lacrimal foramen is located on the front inner side of orbita. The M/1-3 are the myotodont type. This fossil taxon was named *Eptenonus gritsevi* and was placed into the Vespertilioninae tribe. *Eptenonus* distinguish from *Myotis* in the following: the strong reduction of P/3, I/3 is the smallest one and is shifted outwards, the talonid of M/3 is reduced. *Eptenonus* is most similar to the Early Miocene *Hanakia* Horacek, 2001, and *Paleptesicus* Zapfe, 1970. Unlike *Hanakia* the dentition of *Eptenonus* is shorter and the shape of the mandible is different. In accordance with Ziegler's opinion the lower tooth row of *Paleptesicus* had only one P/2, but the *Eptenonus* had P/2,3. *Eptenonus* differs from *Paleptesicus* as follows: P2 is more reduced, the crown of P4 has additional antero-lingual tip of cingulum, the hypocones of M1-2 are absent, the M1-3 crowns have traces of paralophes, the rostrum part of the skull is wider and shorter. But *E. gritsevi* is similar to *P. priscus* in size. In the Middle Miocene there existed both: the more archaic forms of Vespertilioninae tribe (*H. antiquus*, *P. priscus*), and the forms morphologically corresponding to some modern taxa. The later *E. gritsevi* combines plesiomorphic and more advanced features that can not be referred to any of the known members of the tribe. On the basis of several morphological criteria *E. gritsevi* can be related to *P. priscus*. In this case it is necessary to suppose that *P. priscus* had two small premolars in the lower jaw. So, we may state that species of *Hanakia* must have at least one small premolar in the upper jaw. It is evident that the first stages of *Eptesicus* evolution were characterized by the existence of *Myotis*-like forms like *Hanakia*. We can suggest the two variants of the further evolution: 1) in the process of reduction of small premolars in *Myotis*-like forms first appeared the species similar to the *P. priscus* and then the ones similar to *Eptenonus gritsevi*. It is notable that in *Eptesicus* evolution the reduction of the small premolars in upper jaw took the lead over the lower; 2) there existed several taxa at a time that acquiring the features of modern *Eptesicus* s. str. That can be the reason of mosaic combination of plesiomorphic and apomorphic features in the fossil Miocene taxa.

PLASTICITY IN ROOSTING BEHAVIOUR BY BARBASTELLE BATS
(*BARBASTELLA BARBASTELLUS*): USE OF SUB-OPTIMAL AREAS
SURROUNDING REPRODUCTIVE QUARTERS

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In recent years, we analysed roosting ecology and behaviour of barbastelle bats (*Barbastella barbastellus*) in the Abruzzo, Lazio and Molise National Park (central Italy). We identified a reproductive area where females heavily depended upon the availability of unmanaged beech forest and dead trees for roosting. The species was also recorded in a nearby area, separated from the former by a mountain ridge, where forest was more intensively managed (mainly as coppice) and dead trees were much rarer. In the reproductive area, sex ratio was strongly unbalanced in favour of females, whereas in the neighbouring intensively managed habitat males were much more common. Radiotracking showed that bats moved between the two areas, and that males as well as non-reproductive and pregnant females could also roost at the managed site. Besides dead trees, solitary bats also used rock crevices. However, soon before parturition females crossed the mountain ridge and joined groups roosting in "optimal" habitat to give birth and nurse the young. Our study demonstrates the existence of unexpected plasticity in the species' roosting behaviour. We propose that by decreasing management intensity at sites surrounding reproductive areas (e.g. converting coppice into selective logging), *B. barbastellus* breeding populations might easily expand. This appears to be a main option to increase long-term viability of populations of this threatened bat.

DIVERGENT ECHOLOCATION CALL FREQUENCIES IN INSULAR RHINOLOPHIDS (CHIROPTERA): A CASE OF CHARACTER DISPLACEMENT?

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Rhinolophids have been hypothesised to use echolocation call frequency to recognise conspecifics. Hence, sympatric species calling at similar frequencies should be subject to acoustical character displacement, i.e. a drift in frequency values to minimise the risk of misidentification of conspecifics. If, as proposed, insufficient geographic separation between populations in sympatry and allopatry may counter the establishment of frequency differences by character displacement, then insular populations should exhibit acoustic divergence. We tested the hypothesis that echolocation call frequencies in sympatric rhinolophid bats diverge to avoid overlap when populations are geographically isolated. Time-expanded echolocation calls and body size were recorded from Sardinian populations of *Rhinolophus mehelyi*, *R. hipposideros* and *R. euryale*. *R. mehelyi* calls at frequency values intermediate between the other species. Both call frequencies and forearm length of insular *R. hipposideros* and *R. euryale* were compared with those of populations from Italian areas where *R. mehelyi* is absent to explore the hypothesis that the presence of the latter may determine acoustic divergence in the other species.

Sardinian *R. hipposideros* and *R. euryale* called at frequencies higher and lower respectively than in the peninsula. In this way, overlap with *R. mehelyi* is avoided. Body size showed no difference between insular and peninsular populations, i.e. frequency differences are not a by-product of difference in body size determined by insularity. At least under geographical isolation, character displacement proved a possible causal mechanism for shifts in call frequency of sympatric rhinolophids. The small differences in frequency values among sympatric species are not sufficient to return substantially different target strengths from objects of different sizes and hence allow specialization on different sizes of insect prey, ruling out the existence of ecological character displacement promoted by avoidance of competition for food resources. Species recognition and facilitation of intraspecific communication (with possible implications for mate recognition) therefore constitute the best candidate factors for the phenomenon we observed.

ASSESSING THE INFLUENCE OF ALTITUDE AND LATITUDE ON
BAT DISTRIBUTION AND SEX RATIO: A LARGE-SCALE
GEOGRAPHICAL APPROACH

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In some bat species, sex ratio has been found to depend greatly on altitude. Specifically, elevation represents an important factor affecting food resource availability and may then limit the occurrence of reproductive females which face a high energy demand. To date, no study has addressed the effect of altitude on entire bat species assemblages. Because the ecological effects of altitude are likely to be different at different latitudes, analyses focused on large geographical scales are needed to highlight the interaction between such factors. In this study we analyse the effects of both elevation and latitude on distribution, species composition and sex ratio in Italian bat communities of bats to reveal patterns and species aggregation at two different spatial level: latitudinal and altitudinal. We employed both mist-netting and roost survey data obtained for 25 species from several Italian regions along a north-south transect (Campania, Molise, Abruzzo, Lombardia and Trentino Alto Adige). Sample sites were located at altitudes from the sea level to over 2,000 m a.s.l. The analysis revealed patterns of distributions which may be related to competitive exclusion and different ecological needs both within and between species and highlight different guilds characterising ecosystems at a macro-scale. This analysis offers a sound basis for modelling bat biodiversity and distribution in relation to landscape. Such information is also useful to best address conservation efforts and management plans.

MECHANISMS OF SEGREGATION OF ECOLOGICAL NICHES AMONG SHREWS

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Mechanisms separating ecological niches and reducing interspecific competition among shrews were studied. Based on multi-annual field data and results of laboratory experiments, different dimensions of ecological niches (habitat preferences, circadian activity, diet composition), prey selectivity and food handling, as well as behavioural domination and interspecific interactions were investigated in a four-species community of shrews co-existing in wet habitats. High interspecific overlaps (i.e. little differentiation) in particular dimensions of ecological niches were found, with a simultaneous clear dominance of the larger species over the smaller ones. However, considerable differentiation was observed in prey size preferences, food-hoarding tendency (stronger in small subordinate species), and in the forms of conflict avoidance. This leads to the conclusion that the mechanisms enabling stable co-existence of shrews include: (1) cumulative effects of small interspecific differences in many niche dimensions, without the necessity of great differentiation in one particular dimension; (2) behavioural mechanisms of resource partitioning (territoriality, selection of prey, food hoarding); and (3) behavioural mechanisms of contacts and aggression avoidance (e.g. keeping distance, mutual avoidance, vocal communication) that separate spatially individuals of different species. In other words, since shrews cannot avoid exploitative competition, they have developed a number of behavioural means reducing interference competition.

WINTER ECOLOGY OF SHREWS: HOW DO THEY SURVIVE UNDER THE SNOW?

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The decrease in size of soricine shrews in winter (Dehnel's effect) suggests that this is a difficult time for these tiny, non-hibernating mammals with an extremely high metabolic rate. It is not clear how shrews modify their energy budgets, diets, foraging behaviour, space use and activity to assist their survival through Holarctic winters with snow and sub-zero temperatures when food is assumed to be scarce and elusive. We are investigating winter survival of shrews by a programme of ecological, physiological and behavioural studies at Białowieża (eastern Poland) in a lowland grassland habitat. We present our first data on the space use, circadian activity and feeding ecology of over-wintering *Sorex araneus* in relation to the abundance and location of their invertebrate prey within the soil and litter layers. Shrews were live-trapped under the snow during the coldest months (January-March) and data on population numbers, spatial organisation and daily activity of shrews were collected. Feeding habits were investigated by analysis of scats collected from the traps. The diversity and abundance of invertebrate prey in the litter and soil layers were assessed from soil/vegetation samples. Shrews were active night and day but some increase of activity has been observed between 16:00 and 22:00, whereas decreased activity occurred around 13:00-15:00. Their home ranges were small (100-250 m²) and little overlapping. Shrews foraged in patchily frozen substrata for quiescent prey hidden in leaf litter, roots and soil. There was close correlation between prey eaten and the diversity and numbers of invertebrates present. Shrews subsisted mostly on a few, relatively abundant taxa including oligochaetes, small gastropods, araneids and, surprisingly, diplopods (not favoured as prey in other seasons), and the majority of prey consumed were very small (<3mm). Arthropods and gastropods were most abundant in the litter layer below the snow where temperatures averaged -0.8°C (compared with air temperatures above the snow of -3.7°C) while lumbricids were most abundant deeper in the soil with temperatures averaging +0.8°C. The results suggest that in winter shrews are less selective in choice of prey type and size, and they eat mostly small unprofitable prey because availability of their preferred lumbricids is decreased.

A MORPHOMETRIC CONTRIBUTION TO THE PHYLOGENY OF ELEPHANT-SHREWS (MACROSCELIDEA)

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A geometric morphometric analysis was carried out on 215 skulls belonging to 13 species of elephant shrews (Macroscelidea), an order of African mammals whose phylogeny is still debated. The material included all the four living genera, while specimens came from 14 countries, i.e. nearly all the geographic range of the order.

A total of 22, almost co-planar, landmarks were fixed on digital pictures of the ventral skull side. In order to study shape variation of the skull, morphometric analysis was carried out using computer programs from the 'TPS' (Thin Plate Spline) series, available at the link <http://life.bio.sunysb.edu/morph/>.

As shown by the deformation grids associated to multivariate analysis, the distinction between the genus *Rhynchocyton* (subfamily Rhynchocytoninae) and all the other Macroscelididae (subfamily Macroscelidinae) was mainly based on (1) the lateral contraction of central region of the skull, because of the zygomatic arch and pterigoid bone which moved closer together, (2) the frontal shortening of the premaxillary bones and (3) the nearly parallel position of tooth-rows. Within Macroscelidinae subfamily, the first clear-cut separation could be made between *Macroscelides* and the other genera (*Petrodromus* and *Elephantulus*), due mainly to the central region enlargement of the skull. The most difficult task was to separate *Petrodromus* from *Elephantulus* because the general shape of the skull was very similar. However, the latter showed the premaxillary bones slightly narrower.

On the base of the phenogram obtained by UPGMA on the *Procrustes* distance of the mean shape, the strong difference between *Rhynchocyton* and all the other genera was confirmed, according to the traditional division in the two subfamilies. Within Macroscelidinae subfamily, the analysis supported the monophyly of the genus *Elephantulus* and its closeness to *Petrodromus*, suggesting these two genera could represent a single evolutionary unit. Conversely, *Macroscelides* is a well distinguished taxonomic entity. These conclusions agree with data obtained from previous geometric morphometric and biochemical studies, but differ from those obtained by classic morphological approach and molecular analyses.

LANDSCAPE ANALYSIS OF URBAN AND AGRO-INDUSTRIAL
AREAS OF NORTHERN ITALY HOSTING
RHINOLOPHUS FERRUMEQUINUM COLONIES

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The Greater horseshoe bat is a central Asian-European-Mediterranean chorotype widespread in Europe, though major declines are recorded particularly in the north. In Italy it is present on the whole territory and more than 200 roosts are actually known but only a few are known to be located in highly urbanized and agro-industrialized areas. Greater horseshoe bats' ecology has been deeply studied by several European researchers. In particular in Britain, where Greater horseshoe population dynamics have been deeply studied, researchers stress the importance of a bat friendly land management in the vicinity of the maternity roosts to sustain and possibly enhance the population levels of this species. Authors analyse the way Greater horse shoes manage to exploit areas where human activities are massively present and cause habitat impoverishment and loss.

This paper describes the landscape characteristics found within a 5 Km radius buffer traced around each of the five Greater horseshoe bat nurseries known in the Emilia Romagna plain (northern Italy). The five maternity roosts are located in the central and eastern part of the region at an altitude ranging from 0 to 70 m above sea level. Considering the land use map (2006 update) there are three prevailing land use categories within a 5 km radius from each roost, which alone cover 50% or more of each buffer. According to the main prevalence of such categories it is possible to identify three landscape patterns: crops (C) – crops and permanent cultivation (A, D, E) – crops and urban areas (B).

While permanent cultivations may offer a suitable foraging habitat for Greater horseshoes (i.e. orchards), crops and urban areas usually do not (according to literature) unless hedgerows and/or wooded areas are present. To try and quantify the landscape fragmentation characterizing each buffer, the land use categories were merged in one shapefile using Arcview 3.2 and converted to grid to calculate the mean nearest neighbour distance (MNN) (i.e.: the distance from a patch to the nearest neighbouring patch of the same type, based on edge-to-edge distance) between the patches constituting the presumable commuting and foraging elements selected by the Greater horseshoe bats.

The Nearest Neighbor Standard Deviation (NNSD) was also calculated to have more information about the level of landscape heterogeneity.

Roost buffer C, unlike the others, shows a high standard deviation meaning a more irregular but concentrated pattern of patches, whereas the other buffers have a more regular but dispersed pattern of patches. Overall the distance ranges from ca 70 to 128 metres, that is to say that the patches presumably used by the Greater horseshoe bats within each buffer are not quite connected.

DISTRIBUTION AND ABUNDANCE OF CAVE-DWELLING BATS IN ZAGROS RANGE IN WESTERN IRAN

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On the basis of available information on abundance of cave-dwelling bats in western Iran together with data obtained from recent studied including observations on more than 50 caves an assessment is made on distribution and conservation status of cave-dwelling bats in Zagros Range in western Iran. Approximately over 100,000 bats representing 11 species were recorded. In order to evaluate various elements of karsts topography which my support bats population 32 caves (cavities large enough to create a distinct microclimate) has been investigated in mid-Zagros. One third of caves under study have been visited by various species of bats as nursing colony, summer roosts or temporarily roosting site for migrating bats but only one cave is known to be used as a hibernacula. No association is found between cave volume and cave types (stream cave, vadose, collapse cave, canyon cave) with the presence of bat species. The most abundant species in southern parts of the Zagros range are species of *Rinopoma*. In mid-Zagros range *Myotis blythii* appeared to be more abundant species while in the north *Miniopterus schreibersii* and rhinolophid species are more abundant. Almost all caves have been excavated extensively and vandalism is a major threat to bat in caves. Moreover, in recent years important caves have lost their entire bat populations when the cave converted for tourism activities (three caves including one hibernaculum) or used as water abstraction centre for human settlements. Comparing population estimates made in 4-5 decades ago with recent estimate in some caves indicate shocking loss in population of these animals. Bats which are known to have been evolved superbly many aspect of their morphology, reproductive strategies and activity pattern in association with living in caves appear to be losing all in once because they are trapped defenceless in these caves.

APPLICATION OF INTER-SINE FINGERPRINTS TO RECONSTRUCT
PHYLOGENETIC RELATIONSHIPS IN NEARCTIC SHREWS (*SOREX*)

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The field of molecular systematics has relied heavily on mitochondrial DNA (mtDNA) analysis since its inception. Despite the obvious utility of mtDNA, such data inevitably only presents a limited (i.e., single genome) perspective on species evolution. A combination of mitochondrial and nuclear markers is essential for reconstructing more robust phylogenetic trees. To evaluate the utility of one category of nuclear marker (short interspersed elements or SINEs) for resolving phylogenetic relationships, we constructed an inter-SINE fingerprint for nine putative species of the genus *Sorex*. In addition, we analyzed 1011 nucleotides of the cytochrome b gene. Traditional neighbor-joining and maximum parsimony analyses were applied to the individual cytochrome b and inter-SINE fingerprint data sets, along with Bayesian analysis to the combined data sets. We found inter-SINE fingerprinting to be an effective species level marker; however, we were unable to reconstruct deeper branching patterns within the *Sorex* genus using these data. The combined data analyzed under a Bayesian analysis showed higher levels of structuring within the *Otisorex* subgenus, most notably recognizing a monophyletic group consisting of sister-taxa *S. palustris* and *S. monticolus*, *S. cinereus* and *S. haydeni*, and *S. hoyi*. An additional noteworthy result was the detection of an historic mitochondrial introgression event between *S. monticolus* and *S. palustris*. When combining disparate data sets, we emphasize researcher diligence as certain types of data and processes may overly influence the analysis. However, there is considerable phylogenetic potential stemming from inter-SINE fingerprinting.

POPULATION-GENETIC PARAMETERS OF COMMON SHREW
(*SOREX ARANEUS*) IN CONTEXT OF NATURAL AND
ANTHROPOGENIC BARRIERS

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Natural and also anthropogenic barriers may reduce the gene flow and affect the genetic structure of subdivided populations. The simplest ecological question is then if animals are able to cross various types of barriers. Classical capture-mark-recapture methods are sometimes unable to give satisfactory answer, particularly when number of migrants across barrier is small or the migration occurs rarely, e.g. during some short period of the life cycle. On the other hand, the composition and frequencies of alleles at neutral polymorphic loci provide more exact image of the population structuring and migration pattern. It is known that even small number of effective migrants can preserve the metapopulation genetic variability at the same level as in panmictic population. That is why capture-mark-recapture and genetic studies may sometimes gain different results - no detected recapture at the opposite side of the barrier is not always reliable indication of absent migration. In the present study we genotyped individuals of the common shrew at eight microsatellite loci to reveal the population structure and level of gene flow between subpopulations divided by anthropogenic (road) or natural (river) barrier. Sampling area is the south of Bohemia in the Czech Republic, where the only one chromosomal race (Ulm) is known to occur, so this study deals entirely with intra-racial gene flow in the common shrew. Total number of sampled localities is not known at the time of submitting the abstract, by this time we already have DNA samples of 75 individuals from six localities, and more trapping is planned for spring and summer. Results and interpretations of the genetical analysis will be presented.