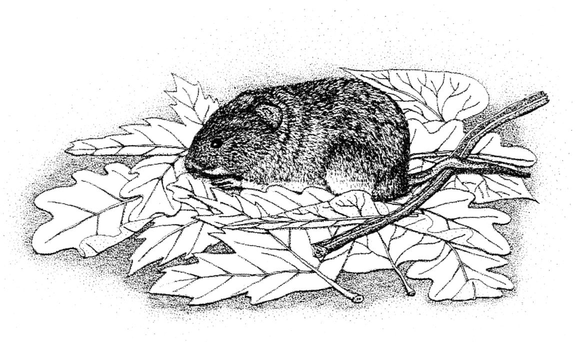
RODENTS AND LAGOMORPHS



A COMPARATIVE GEOMETRIC MORPHOMETRIC ANALYSIS OF NON-GEOGRAPHIC VARIATION IN TWO SPECIES OF MURID RODENTS, *AETHOMYS INEPTUS* FROM SOUTH AFRICA AND *ARVICANTHIS NILOTICUS* FROM SUDAN

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Non-geographic morphometric variation particularly at the level of sexual dimorphism and age variation has been extensively documented in many organisms including rodents, and is useful for establishing whether to analyse sexes separately or together and for selecting adult specimens to consider for subsequent data recording and analysis. However, such studies have largely been based on linear measurement-based traditional morphometric analyses that mainly focus on the partitioning of overall size- rather than shape-related morphological variation. Nevertheless, recent advances in unit-free, landmark/outline-based geometric morphometric analyses offer a new tool to assess shape-related morphological variation. In the present study, we used geometric morphometric analysis to comparatively evaluate non-geographic variation in two geographically disparate murid rodent species, *Aethmoys ineptus* from South Africa and *Arvicanthis niloticus* from Sudan**,** the results of which are also compared with previously published results based on traditional morphometric data. Our results show that while the results of the traditional morphometric analyses of both species were congruent, they were not sensitive enough to detect some signals of non-geographic morphological variation. For example, while one series of analysis could detect the presence of sexual dimorphism, the other could not. These results highlight the importance of the need for a careful evaluation of size- and shape-related non-geographic mophological variation prior to subsequent analyses of geographic variation and the delineation of species. Erroneous analysis of non-geographic variation may also have implications in the interpretation of evolutionary and geographic processes that may be responsible for morphological differences at both the inter- and intra-specific levels.

PHYLOGENY AND HISTORICAL DEMOGRAPHY OF ECONOMICALLY-IMPORTANT RODENTS OF THE GENUS *ARVICANTHIS* (MURIDAE) FROM THE NILE VALLEY: OF MICE AND MEN

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Our investigation clarified the taxonomy, phylogeny and historical demography of semi-commensal Nile rats (*Arvicanthis*) from the Nile Valley in Sudan. Nile rats are important crop pests and zoonotic disease reservoirs; whilst not occupying human dwellings they are closely associated with agricultural settlements in the Nile Valley. Phylogenetic analysis of the complete cytochrome-*b* gene (1140 bp) of 23 individuals from six localities in Sudan (from two previously recognized species, *A. niloticus* and *A. testicularis*), together with available Genbank sequences, supported the monophyly of the genus *Arvicanthis* and its sister-group relationship with *Lemniscomys*. The data supported the existence of only a single species, *A. niloticus*, from the Nile Valley. Historical demography and population genetics of the Sudanese Nile Valley population indicated a very recent exponential population expansion event (*ca* 300 years ago), which corresponds with the most recent period of exponential human population expansion in the Nile Valley inferred from archaeological evidence. Two African *Arvicanthis* clades were supported (with 100% bootstrap support) by the broader phylogenetic analysis: 1) *A. niloticus*, *A. abyssinicus* and *A. neumanni*, and 2) *A. rufinus* and *A. ansorgei* from Western Africa. Within the first clade, divergence between lineages of *A. niloticus s. s.* from West and North-East Africa (8.9%) suggests specific recognition, but sampling of geographically intermediate localities is required. Based on hypothesized palaeodrainage and palaeoclimatic patterns, we propose a simple model for speciation of *Arvicanthis* in Africa.

APPLICABILITY OF DIFFERENT DNA-MARKERS TO THE RECOVERY OF PHYLOGENIES AT A DIFFERENT TAXONOMIC LEVEL: CASE STUDY OF SUBFAMILY ARVICOLINAE (CRICETIDAE, RODENTIA)

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Application of molecular markers became the most popular method in the studies of phylogeny and systematics of various organisms. However, the adequate choice of a molecular marker in correspondence with taxonomic level of the group under study rarely deserves a special attention. We compare the resolving power and limitations of mtDNA (cyt b) and nuclear (LCAT, GHR, p53, Fbgb) markers for the recovery of phylogeny at different taxonomic levels within subfamily Arvicolinae. A wide range of data sets (morphological, palaeontological, cytogenetic and others) was already applied to the study of phylogenetic relationships of the main phyla within the group. It makes this subfamily and ideal model for testing hypothesis on applicability of various DNA - markers to the recovery of phylogeny due to the possibility of cross-validation. Despite the good support of some clades, the basal splits both as within the most speciose genus *Microtus* and within subfamily in a whole remain uncertain. Molecular studies with the application of cyt b as a marker both to the recovery of phylogenetic structure in *Microtus* and the subfamily did not clarify the situation and "hard" polytomies" in both cases were explained by several pulses of rapid radiation. We argue that these polytomies are evident result of mutational saturation, accelerated and uneven rate of cyt b evolution resulting in high degree of homoplsy. It is especially evident in the case of *M. gregalis*. We studied variation of this marker in this species within the different isolated parts of its range and our results demonstrate extremely high variation and high rate of it evolution. Comparison of the cyt b trees and trees obtained from the analysis of nuclear markers showed that the latter gave much better resolution than the cyt b. Moreover phylogenies obtained from nuclear markers are in better agreement with a number of other data sets and confirmed the earlier findings of cytogenetic, biochemical and paleontological research. The LCAT appeared to be most appropriate marker for the study of phylogenies at the supraspecies level and p53 - for the the close species and species groups. GHR gives good resolution for the order of divergence at generic level. According to our findings the cyt b is an appropriate marker for the study of intraspecies (phylogeography) and species level phylogenies in Arvicolinae.

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COMPARATIVE PHYLOGEOGRAPHY OF RED-BACKED VOLES IN RUSSIA WITH SPECIAL REFERENCE TO THE FORMATION OF SYMPATRIC ZONE IN BANK AND RUDDY VOLES (*MYODES*, CRICETIDAE, RODENTIA)

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Bank (*Myodes glareolus*) and ruddy (*M. rutilus*) voles have wide overlapped ranges.. Despite the fact that these species split from a common ancestor not later than 2.5Ma, they are very similar in morphology, behaviour and karyotypes. Sympatric zone of these species formed gradually with the bank vole dispersing to the north and east and ruddy vole westward. Up to now there are a lot of data concerning the history of distribution and genetic structure of bank vole in Europe but analogous data are lacking for the most part of the species range in Russia. We analyzed the variation of the cyt b (1000bp) in the bank vole from 32 sites (225 specimens) in central and northern parts of European Russia, Ural and Transural regions and in ruddy voles (51) from the same sites in sympatric zone. We found that part of the haplotypes of the bank vole cluster within the haplotypes of a ruddy vole, phenomenon of introgression that was known earlier. Further on we outlined in details the geographic zone of introgression and show its scale. We found populations of bank voles with both types of haplotypes and show that the zone of introgression do not completely coincide with sympatric zone of two species. All bank voles in Murmansk area and north Karelia have "ruddy" mtDNA haplotypes, then the percent of these haplotypes decreases dramatically through Arkhangel area and Komi to Middle Urals and locally increases in southern Transural region. Single specimens with "ruddy" haplotypes occur in St.Petersburg and Novgorod regions. It is worth noting that "ruddy" haplotypes of bank voles are not identical too that of *M. rutilus* from the same sites what evidence for ancient hybridization event. Putatively it may happen during maximum of Holocene warming (5-3 thousand BP). Phylogeographic structure within the cluster of the proper bank voles is poorly pronounced. It is characterized by high haplotype and low nucleotide diversity what speaks for rapid recolonization of territory from Kaliningrad to Ural by population with a small effective size.

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MOLECULAR AND CYTOGENETIC CHARACTERIZATION OF SEVERAL REPEAT DNA SEQUENCES IN *MICROTUS THOMASI* FROM GREECE

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Extensive karyological analysis has demonstrated that the underground vole *Microtus thomasi* presents with several karyotypic forms in Greece (*thomasi*, *atticus*, s*ubalpine* and Rb-subalpine). The cytotypes '*thomasi*' and '*atticus*' feature a diploid chromosome number of 2n=44 but FN=44 and FN=46, respectively. The main difference between these two karyotypic variants concerns the X chromosome morphology, being characterized as acrocentric in '*thomasi*' and subtelocentric in '*atticus*'. In addition with regard to the sex chromosomes, there has been detected remarkable heterochromatin content variability, both within, as well as, between the above two cytotypes.

Digesting genomic DNA from '*atticus*' with the endonuclease AluI we have observed in gel electrophoresis several intense bands, corresponding to repeated DNA sequences. Three of these sequences have been cloned, sequenced and localized by fluorescence in situ hybridization (FISH). Two of them, with approximately 900 bp and 300 bp are fragments corresponding to the L1 retrotransposon. Southern blot demonstrated that both L1 fragment are present in all the Microtidae species analyzed. Both L1 fragments are distributed homogeneously in the euchromatic regions of all chromosomes but not in the pericentromeric heterochromatin, and are especially abundant in X chromosome euchromatin and absent from its heterochromatic bands.

The third repeat DNA sequence with approximately 900 bp that was analysed, did not show any homology with either repeat or single sequences available in GenBank. Southern blot analysis demonstrated that this repeated sequence is restricted exclusively to the genome of M. thomasi. FISH demonstrated that this sequence corresponded to the pericentromeric satellite DNA, since it is located in the pericentromeric heterochromatin of most chromosomes, and also in the heterochromatic block of the X chromosome.

Finally, methylation analysis demonstrated that none of the three repeat DNA sequences cloned from '*atticus*' are methylated.

PALEOENVIRONMENT AND CONDITIONS OF THE HABITABILITY OF PALEOLITHIC MAN IN NORTH-WESTERN ALTAI AS AN EXAMPLE

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The purpose of the study was to reconstruct the structure and dynamics of Pleistocene mammal communities, as manifestation of dynamics of natural environment. Research problems are:

1. The general pattern of the recent population of small mammals of the northwestern Altai is of forest pattern but includes isolated steppe and nival elements.
2. Pleistocene small mammal associatiation of Anuy basin (northwestern Altai testify to significant changes of structure of the population small mammals of a Anuy valley during late Pleitocene. In Pleistocene fauna of northwestern Altai prevailed voles (*Stenocranius gregalis*, *Alticola strelzovi*), inhabitants of dry steppes and tundras or high-mountainous steppes. However in fossil and in recent faunas are steadily kept endemic of this territory: Altay mole, *Asioscalops altaica* and zokor, *Myospalax myospalax*, some characteristic westsibirien species: longteil ground squirrel, chipmunk, Siberian red vole, Alticola, daurien hamster. There is evidence that the changes of ecological structure of communities proceeded on a background stable as a zoogeography situation.
3. The entire data pool suggests that humans primarily used Denisova cave during the autumn and winter seasons. Hyenas need a refuge for brining up the litter only in springs and early summers. Thus, humans and hyenas could have used the cave in different seasons.
4. The life of humans in the cave was accompanied by certain inconvenience. The field of view was limited and it was difficult to perform anticipatory actions in relation to ungulate herds. Therefore, with the onset of the warm season, humans moved to temporary open sites, such as Ust'-Karakol, wherefrom the whole of the Anui and Karakol valleys and adjacent mountain slopes are visible. It provided the control of extensive area and, hence, a rapid and adequate response of the human hunting team to the appearance of an ungulate herd.
5. Apparently, certain other factors influenced seasonal migrations of humans from the cave. In particular, in the spring and summer seasons, the air temperature inside the cave is much lower than outside. Under such conditions, it was essential to move to open summer sites.

PARASITE LOADS AND GENETIC DIVERSITY OF THE BROWN HARE, *LEPUS EUROPAEUS*, IN SPAIN

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The relationship between genetic diversity and parasites has been often studied, but there are few that report natural populations and multiple pathogen systems. Parasite resistance is expected to be higher in genetically diverse or heterozygote individuals. However this heterozygote advantage has been recently discussed.

North-East Iberian Peninsula is the south-western range edge of *Lepus europaeus*. In this region, the brown hare is in contact with two other hare species (*L. granatensis* and *L. castroviejoi*), and occurs in low densities. Although hybrids are not detected fenotipically, recent genetic studies have reported the past and ongoing hybridization among these species. In addition, a massive mitochondrial introgression by the extant mountain hare (*L. timidus)* has been described. Altogether, these facts make this region as an interesting evolutionary place, likely to develop local adaptation and then to test coevolution host-parasites. In this work, we analyse the parasites of 24 *L. granatensis*, 70 *L. europaeus* and 18 *L. castroviejoi* from the North-Central Iberian Peninsula. Nuclear and mitochondrial neutral markers of these animals were also examined by a set of six microsatellites and a RFLP-PCR of cyt b.

By means of exploring the contact zone and the peripheral core populations of these three *Lepus* sp. species, we tested: a) in what way heterozygosity advantage to parasite infection is present; b) if this relation is similar among the three species and c) if the introgression of *L. timidus* DNA mitochondrial has any influence in this relation.

HABITAT USE OF THE RED SQUIRREL (*SCIURUS VULGARIS* LINNAEUS, 1758) IN MEDITERRANEAN WOODLANDS WITH DIFFERENT MANAGEMENT REGIMES

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In the Italian peninsula the Red squirrel (*Sciurus vulgaris* Linnaeus, 1758) is usually associated with conifer and mixed broadleaved woodlands. The management of woodlands could affect the distribution of the species, since it is often considered an obligate of mature forests. The aim of our work is to analyse seasonal patterns of habitat use in different woodland typologies in an area of central Italy (one site in the Grosseto Province, Tuscany and four sites in the Viterbo Province, Tuscany).

A hair tube survey was carried out for tree sessions: June-July (2006), September-October (2006), February-March (2007) in the following cover typologies: artificial conifer woodlands (*Pinus halepensis, Pinus pinea, Pinus nigra, Pinus pinaster,Cupressus sempervivens, Cupressus lusitanica, Cupressus macrocarpa*), mixed broadleaved woodlands both termophilous (*Quercus cerris* with *Ostrya carpinifolia, Acer* spp., *Fraxinus ornus* and *Quercus pubescens*) and mesophilous (*Quercus cerris* with *Carpinus betulus, Fagus sylvatica*).

In order to account for false absences we examined habitat-use patterns by fitting occupancy models through program PRESENCE to detection history data. We defined a set of a priori models to test the effects of season and cover type on the probability of presence and on the detection probability. A multi-model inference approach was followed to account for model selection uncertainty, thus model averaging was used to estimate parameters. Red squirrel signs of presence were found in 10% of the hair tubes in both broadleaved and conifer forests. Number of sites where the species was found and statistical estimate of proportion of sites occupied are very close, suggesting that few false absences occur in our data. We interpret the results evaluating effects of woodland management on seasonal habitat use patterns of the red squirrel accounting for variation in detection probability.

ACTIVATION OF INNATE IMMUNITY INCREASES ENERGETIC COST OF AGGRESSIVE BEHAVIOUR

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Aggression, as an important component of social interactions, takes part in hierarchical and territorial organizing in rodent populations. Investigation of a new territory increases an infection risk or risk of encountering with uncommon immunogenic bacterial compounds. Most of them, bacterial lipopolysaccharide (LPS), bacterial DNA, flagellins etc., activate innate immune system. Since both, territorial competition and immune defense, are costly, we predict higher energy demands for aggressive behavioral in LPS-treated male mice.

Special apparatus which let us measure oxygen consumption (OC) just after social conflict was used in pair-wise tests on ICR male mice. Behavioural and metabolic response to social conflict were studied in males 3 h after injection with LPS (type 055:B5 Sigma; 50 mkg/kg) or with saline (control).

Number of aggressive acts were higher in control pairs than in LPS- treated pairs (18.8±4.3 N=7 and 2.9±1.4 N=10, consequently, Z=3.84, P<0.01, Mann-Whitney test). Appreciable increase of OC was found just after tests in both LPS-treated and control males. Social dominance was more expensive for LPS-treated males than for control males. LPS-treated dominants showed growth of OC on 1.4±0.2 ml/g*h from basal level. And it was significantly higher in comparison with control dominants (0.47±0.14 ml/g*h, t=2.7, P<0.05, Student t-test). Thus the activation of innate immune system cause an increase of energy cost of the establishing social hierarchy.

THE COMMON HAMSTER *CRICETUS CRICETUS* IN POLAND: STATUS, CURRENT RANGE AND GENETIC DIVERSITY

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The current range of the common hamster, *Cricetus cricetus* in Poland was established. The range of the species has dwindled substantially in the course of just 30 years and the process is still going on. The Polish populations are isolated from Belarusian, Czech and German ones; there is low probability of some exchange with Ukrainian hamsters. Moreover, the areas of hamster distribution in Poland are isolated from one another. In view of the marked shrinkage and fragmentation of the range, we propose changing the status of this species in Poland from unknown (DD) to endangered (EN).

The genetic diversity of 12 populations in the present range was established. The control region of mtDNA was sequenced for 150 individuals and partial sequence of cytochrome b for 40 individuals. Only seven haplotypes of mtDNA control region were found and hamsters with the same haplotype inhabited large areas. Such pattern of variation cannot be the result of present genetic drift, but is rather a consequence of historical, postglacial bottleneck.

The differentiation of cytb sequences showed the presence of two phylogenetic lineages in Poland. One of them, so far specific for Poland, most probably recolonized Polish uplands from the east. The other one migrated from the south, as it is identical with Pannonia described from Czech and Hungary. The hamsters of Pannonia group are more endangered in Poland as they are represented by small, isolated populations. On the other hand, Polish lineage seems viable, however immediate conservation efforts are necessary.

MATE-CHOICE IN TWO SPECIES OF BATHYERGIDS (GENUS *FUKOMYS*): IS INFIDELITY AN OPTION?

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Subterranean Zambian mole-rats of the genus *Fukomys* live in colonies where reproduction is restricted to a single breeding pair living in monogamy. The eusocial colony structure with lifelong philopatry of the offspring is retained by restriction of mating due to incest avoidance. Colony members are generally xenophobic towards unfamiliar "intruders" of the same sex, but encounter of individuals of opposite sex often results in mating.

The mechanisms of new colony formation in the field are not known, and dispersal as well as extra-pair copulations with non-related animals are technically impossible in the laboratory. However, behavioural fidelity tests of the reproductive pair might shed light on the intensity of pair-bonding. In this study we tested reproductive *Fukomys mechowii* and *Fukomys anselli* for their preferences in mate choice.

The tested subjects could move freely in the middle part of a 2-choice-labyrinth that connected the grid-separated terminal boxes containing the animals of choice. During each 30 min. test session the sniffing times and positives responses (approaching, vocalizing, agitated quivering) towards each animal of choice were recorded.

The breeding males (kings) in both species, *F. mechowii* and *F. anselli*, spent significantly more time sniffing a strange reproductive female (queen) than their own mate. If given the choice between a strange queen and her non-reproductive daughter, the tested kings significantly preferred the queen. Reproductive females on the other hand did not show a preference for either their own mates or a strange king.

We conclude that although the eusocial colony structure of the Zambian mole-rats implies social monogamy, infidelity seems to be an option. Field studies are necessary to prove whether extra-pair copulations actually do take place in these species. In this case we expect, however, that after mating with a "strange" female, the king returns to his own colony to help his queen raising the offspring. This phenomenon ("social monogamy" but "genetic polygamy" if chance occurs) thus parallels the system that has been recognized in many bird species.

WHAT DOES SENSORY ECOLOGY OF AFRICAN MOLE-RATS TELL US ABOUT THAT OF EUROPEAN MOLES AND “RATS”?

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Subterranean mammals live in self-constructed burrows which they rarely, if ever, leave. Prevalent features of the underground ecotope are darkness and limited signal transmission, so that the subterranean world appears monotone in comparison to the situation found above. Sensory ecology has been studied profoundly in the blind mole-rat *Spalax*, some African bathyergids (*Cryptomys*, *Fukomys*, and *Heterocephalus*), and African golden moles (*Chrysochloridae*), recently also in South American octodontids, but (with exception of a highly specialized Condylura cristata) it remains neglected in Eurasian and North-American species of subterranean mammals.

Here, we summarize recent findings on hearing, vision, magnetoreception, and distant heat sensing revealing that most sense organs are specialized rather than degraded (as suggested by some earlier studies). Since European subterranean mammals (e.g. moles and voles) live under similar environmental conditions as their African counterparts, we expect to find many shared characteristics molded by convergent evolution. However, studies on subterranean European species are underrepresented, and we will here follow up the question why. Especially the European mole - a popular study subject until the 80's of the previous century, but then seemingly forgotten - could be a real sensory ecology gold mine.

The studies on subterranean species have taught us to take a closer look at the animals' ecotope to avoid misinterpretations but also to venture new approaches. Some of the new techniques developed in the studies of subterranean species, may be also applied to standard laboratory rodents as has recently been shown for magnetoreception in mice.

MORPHOLOGICAL VARIABILITY AND TAXONOMY OF THE GENUS G*ALEA* MEYEN, 1832 (RODENTIA, CAVIINAE): A PRELIMINARY GEOMETRIC MORPHOMETRIC APPROACH

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Size and shape changes in the skull of yellow-toothed cavies *Galea* spp. were investigated using both geometric and linear morphometrics. 150 specimens from the all four currently recognised species (*G. musteloides, G. spixii, G. flavidens* and *G. monasteriensis*) from 20 populations were analyzed. Skull size and shape were analysed after Procrustes analysis of two dimensional landmarks collected over its dorsal and ventral sides. No significant sex effect was observed, but was significant for age effect. The ontogenetic effect was suppressed by size-free discriminant analysis use on the weight matrix. This analysis was carried out initially for the six larger samples, which comprised six individuals or more. Size allows the recognition of two groups, the small-sized composing by populations from Argentina and Bolívia (*G. musteloides* and *G. monasteriensis*) and the large-sized including only the Brazilian populations (*G. spixii* and *G. flavidens*). Shape differences are significant for the majority of the comparisons. Five morphometric groups were identified among the *G. musteloides* populations, while *G. spixii* and *G. flavidens* grouped together in the same cluster. "Small" samples were probabilistically allocated to the "large" samples based on the least squared Mahalanobis multivariate distances estimated in 1,000 random bootstrap interactions. The only one representative from *G. monasteriensis* grouped with *G. musteloides* populations. These results suggest the presence of grouping that do not match with the current taxonomy proposed for the genus *Galea*. A better framework will include more specimens from less representative populations as well as molecular analysis.

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HIGH BROWN AND BLACK RAT (*RATTUS NORVEGICUS* AND *R. RATTUS*) BIOMASS CONTRIBUTION IN THE BARN OWL DIET DURING NON-BREEDING SEASONS IN CENTRAL GREECE, THESSALY

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The Brown and Black rats are considered to be among the largest prey items that the Barn owl captures in Mediterranean Europe. The Black rat is very common in Mediterranean countries, whereas the Brown rat is less widespread in the Mediterranean region. Very few studies exist about the distribution of the species in Greece, and the latest distribution maps show that the species are almost absent from the region of Thessaly, central Greece, a fact which is inconsistent with our results.

In the present paper we firstly present new data about the distribution of the species in Thessaly, central Greece. We make two comparisons: one with the rest published studies in Greece concerning the Barn owl diet, and another with selected studies realized in similar environments in Mediterranean Europe, specifically in Italy and Spain.

We mainly focus on the rats’ energetic contribution. Since rats are among the "largest" Barn owl preys in Europe, it is quite important to outline the biomass spectrum with which a large prey participate in a raptor's feeding habits.

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. Pellets were analyzed according to the "dry" method and prey was identified with the use of reference books. The Brown and Black rat appeared in the Barn owl diet in 25 of the 31 sampled sites in Thessaly. There was a very significant difference between the breeding and non-breeding seasons, with the rats showing a high biomass contribution during the non-breeding seasons, and minor appearance during the breeding seasons. In comparison with other studies from Greece, in no other case have the *Rattus* spp. presented such high biomass contribution, neither had they been preyed greatly in numbers. A similar result was produced from the comparison of our data with those of selected studies realized on the Barn owl diet from similar environments of Mediterranean Europe, a fact that makes the Thessaly case a remarkable example.

THE EFFECTS OF HABITAT TYPE ON THE POPULATION GENETIC STRUCTURE OF THE GENERALIST WOOD MOUSE (*APODEMUS SYLVATICUS*)

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We examined the effects of distinct habitat types at a microgeographic scale on the genetic structure of natural populations of the European wood mouse, *Apodemus sylvaticus*, a highly vagile, habitat generalist species. Ecological and behavioural studies indicate that this species exhibits considerable dispersal relative to its home range size. Thus, there is potential for high gene flow among populations. As levels of population genetic structure are related to gene flow, we hypothesised that, despite of habitat type, population genetic structuring at the microgeographic level should be negligible, increasing only with geographic distance. We sampled natural wood mouse populations in inner forest, edge of forest and hedgerow locations on nearby pastoral farmland, at three replicate, matched sites. Within each replicate site samples were from 1.0-2.5 km apart. Contrary to our initial hypothesis, variation at seven microsatellite loci indicated unambiguously that the wood mouse population was highly structured across the three habitat types with no significant correlation between genetic and geographical distances. Temporal sampling at one site had confirmed genetic temporal stability within sample while genetic heterogeneity tests suggest that the association between genetic variation and habitat block arose independently at the three sites. In the absence of physical barriers to dispersal, habitat appears to have a strong influence on gene flow. Thus, populations of *A. sylvaticus* in landscapes comprised of patches of different habitat types, represent a genetically based metapopulation. Under favourable conditions, such population pattern can lead to genetic isolation. This process is likely to be accelerated by genetic drift where effective population size is reduced. This finding has major implications for understanding the population dynamics and dispersal of habitat generalists, and is critical in understanding the dynamics of populations occupying discrete, variable habitat patches.

CHANGES IN THE NUMBER AND MORPHOTYPES OF B-CHROMOSOMES IN MOUSE *APODEMUS PENINSULAE* FOR 26 YEARS

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Among 429 mouse *Apodemus peninsulae* Thomas, 1906 from Altai, Siberia, Pribaikalye and Mongolia only three mice had no B-chromosomes. Almost all mice have various systems of combinations of several classes B-chromosomes (from 1 up to 24 B-chromosomes) various dimension and morphology. 213 (65 %) from 429 mice studied had an individual variant of system B-chromosomes.

For the certain populations the variants are peculiar B-chromosomes, and they are kept during tens years (the known period of researches). Dynamics in various years, as a rule, have cyclic character, with preservation of originality in this population. Analysis of six populations of mice *A. peninsulae* from Siberia, Pribaikalye and Primorski Krai for a period of 26 years (1971-1997) revealed a trend of cyclicity of rise and recession of the number of B-chromosomes in two populations of Siberia. Apparently, the pattern of variants of system B-chromosomes in investigated populations of *A. peninsulae* during long intervals of time remains stable enough and its variability is regulated by processes. At infringement of these processes, in particular, as a result of anthropogenous loading, cyclicity of rise and recession of the number B-chromosomes can be broken.

In a population of the Altai Mountain (coast of the lake Teletskoe) almost three multiple (2.8 times) increases in an average B-chromosomes in 2002 and 2006 in comparison with 1980 is found. For 22 years the average B-chromosomes has grown from 2.3 up to 6.5. In 2006 the average B-chromosomes also was equal 6.5.

At such, almost triple growth of number B-chromosomes the parity of morphotypes has essentially changed B-chromosomes. In 2002 and especially in 2006 the number fine biarmed, acrocentric and dot elements have considerably grown B-chromosomes. Last two morphotypes have been not noted among 34 mice in 1980. Primary fine B-chromosome are fragments A-chromosomes (FISH results).

DIRECT AND INDIRECT IMPACT OF PREDATORS ON VOLE POPUALTION DYNAMICS

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Predators generate both direct (via killing) and indirect (via presence) pressure on prey populations. Some theoretical consideration and empirical data suggests that specialist predators (small mustelids and raptors) can shape vole population in cyclic dynamics (top down process). Whereas another studies (both theoretical and empirical) indicate that predators can not be a main factor explaining the cycles. Additionally, empirical evidence of the non-lethal effect of predators in natural ecosystem is still unexploited. This is why, we try to evaluate direct and indirect impact of predators (small mustelids and vole eating raptors) on cyclic free-living root vole (*Microtus oeconomus*) population. The study was conducted in Biebrza National Park, Poland from 2003 to 2006. Vole population dynamics was monitored on three trapping grids (0.6 ha each) situated in homogenous grassland habitats. Small mustelids population was monitored on two permanent transects - each 3 km long. Population dynamics of vole and mustelids was monitored every 8 weeks by CMR procedure. Vole eating raptors were counted monthly and from September 2005 till November 2006 raptors exclusion experiment was conducted. Indirect impact of small mustelids on vole behaviour was studied in experiments with weasel odour. The risk from raptors was counted with usage of GUD method (habitat structure, presence/absence of raptor). In studied population small mustelids generated small negative impact on vole population only during the late summer and early autumn (August - September), raptors create strong negative impact only during the early spring (March - April). Indirect effect of small mustelids was opposite to their density - when weasel population density was low, voles avoided their scent and vice versa. The level of predation risk generated by raptors was closely related with habitat structure and light intensity. The highest risk occurred in habitats with high light intensity (low vegetation) The presence of predator model did not effect vole behaviour. It was concluded that: 1) small mustelids play a minor role in regulation of studied vole population; 2) vole eating raptors generate strong negative pressure on vole population in early spring; 3) paratrophic impact of predators play a minor role in prey behaviour and in their population dynamics; 4) population cycles in voles are not primarily driven by prey -predator interactions.

IBERIAN HARE (*LEPUS GRANATENSIS*) DIURNAL BEDDING SITES IN DOÑANA NATIONAL PARK (SW IBERIAN PENINSULA)

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The Mediterranean hare (*Lepus granatesis*, Rosenhauert, 1856) is an endemic species to the Iberian Peninsula and it is largely distributed in a great part of the Iberian Peninsula. However, there are no much works done on its spatial ecology, as the grazing and the use of its habitat and microhabitat. No research has specifically addressed microhabitat features that may be important in selecting diurnal bedding sites.

Research was conducted on Doñana National park (SW Iberian Peninsula) since November 1996 to August of 1997. The study areas were "La Vera", a transition area (ecotone) between the scrubland and the salt marsh characterized with a hight diversity of species and the marshland with typical macrophytes plants communities. Average precipitation was 560 mm (1980-2002). The mean monthly temperature was 23, 6 º C for summer and 10, 7 ºC for winter.

To evaluate characteristic habitat feature 11 habitat variables were measured at 38 diurnal hares bedding sites and were compared to the same variables at 38 random sites according a previous established protocol. Univariate analyses of the habitat variables were used to test for differences between bedding sites and random sites. There were observed several significant differences in number of species of plants, bearings and cover.

The Iberian hare choose the diurnal bedding sites based on the level of cover protection. Patches with high aerial, right and left cover and less cover in front. That provided the best visual observation capacity of diurnal bedding sites. Dense cover probably protection from extreme temperatures too, as well as concealment and escape cover from predators.

INSULARITY EFFECT ON THE HELMINTFAUNA OF *MUS DOMESTICUS* IN ALEGRANZA ISLET (CANARY ISLANDS)

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Alegranza is an uninhabited islet located at 17 km from the northern coast of Lanzarote Island. With a surface of 11.72 km^2 belonging to the protected area of Archipielago Chinijo. Between 1998 and 2000, a total of 108 house mouse were dissected. Five helminth species were found: *Rodentolepis microstoma* (Hymenolepididae), *Catenotaenia pusilla* (Catenotaeniidae) (Cestoda); *Gongylonema musculi* (Gongylonematidae), *Mastophorus muris* (Spirocercidae) and *Syphacia obvelata* (Oxyuridae) (Nematoda). The helmintfauna presents in *Mus domesticus* in Alegranza islet is impoverished in relation of continental populations. Introduced species, use to introduce at same time their parasites in new colonized habitats. These parasite species that can survive are present in higher prevalence and intensities than in continental habitats. In general, they are direct life cycle species or heteroxenous species not having strong specificity for their intermediate hosts. In Alegranza, the single species with direct life cycle is *S. obvelata*, a nematode specific of hosts of genus *Mus*, showing a direct transmission between hosts. The rest of species recovered from Alegranza Island present an indirect life cycle with scarce specificity for the different species of arthropods that act as intermediate hosts. Different microhabitats are occupied for this species [oesophagus and stomach mucosa (*G. musculi*); free in stomach (*M. muris*); intestine (*C. pusilla*); coledoc and biliary ducts (*R. microstoma*); caecum (*S. obvelata*)], being interspecific competition reduced.

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PAST AND CURRENT HYBRIDIZATION IN HARES (*LEPUS* SPP.)

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Hares (genus *Lepus*) have a remarkable worldwide distribution and are present in a great variety of habitats. Some species are clearly adapted to cold environments while others inhabit preferentially warmer regions. Considering this obvious adaptation to diverse habitats, it is expected that the climatic fluctuations that characterized the Pleistocene influenced differently the species, forcing them to change their range of distribution, and eventually promoting novel contacts between them. The description of ancient mitochondrial introgression from an arctic species, *L. timidus*, into three other species of hares in the Iberian Peninsula supports these types of past interactions. Although *L. timidus* is presently absent from Iberia, it left molecular traces that sustain its historical presence in the region, in accordance with palaeontological records. The extent of this mitochondrial introgression is remarkable, manly in the north, where it is fixed in some brown hare populations. The introgression phenomenon involving *L. timidus* is not exclusive from the Iberian Peninsula since it has been described in Sweden and Russia and is probably occurring in other regions of Asia and North America. In addition, evidences of ongoing hybridization were also detected in the north of the Iberian Peninsula between *L. europaeus* and *L. granatensis*. Thus, in the Iberian Peninsula there is a combination of past and current hybridization events involving four hare species, which makes it an extraordinary place to study different evolutionary aspects of this mammal group. Taking all these evidences together, the hybridization in hares seems to be a relatively frequent phenomenon.

PHYLOGENETIC RELATIONSHIPS AMONG MEMBERS OF THE *MICROTUS ARVALIS* COMPLEX USING MORPHOMETRIC, MOLECULAR AND KARYOLOGICAL DATA: FOCUS ON THE ALTAI VOLE

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Within the *Microtus arvalis* complex, two forms have been described on the basis of chromosomal morphology and hybridization results: the eastern "*obscurus*" and the western "*arvalis*". The form *obscurus* ranges to the east and south of the distribution of *M. arvalis*.. It seems that *obscurus* and *arvalis* can interbreed in captivity, but their hybrids demonstrate low fertility. On the other hand, some authors treat "*obscurus*" as a separate species.

Some recent molecular data on the cytochrome b gene suggest a recent split between "*arvalis*" and "*obscurus*". The cytochrome b divergence is 2-4% between *arvalis* and *obscurus*, whereas the divergence between *M. arvalis* and two closely related species, *M. rossiaemeridionalis* (*M. levis*) and *M. kirgisorum* (*M. ilaeus*), is about 7.0% and 9.2%.

We investigated the karyological, genetic (mitochondrial sequences from the cytochrome b gene) and morphological (global morphological analyses from teeth) structure of Altai vole populations from China in order to clarify the systematic status of the Altai vole and its hypothetic implication in the evolutionary history of *M. arvalis*. Our first results, notably from a molecular point of view, display close phylogenetic relationships between *obscurus* from China and Russia. On the other hand, the divergence between the *obscurus* and the different *arvalis* lineages is much more important than previously observed: around 4% between *obscurus*-*arvalis* and around 2.5% among *arvalis* lineages. These molecular results are also supported by cytogenetic analyses: 2N=46, FN=72 for *obscurus*; 2N=46, FN=84 for *arvalis*. For these reasons, *Microtus obscurus* could be considered as the sister species rather than a sub-species of *Microtus arvalis*.

CHROMOSOMAL FORMS OF THE SPECIES *NANNOSPALAX NEHRINGI* (SATUNIN, 1898) (RODENTIA, SPALACIDAE) FROM VAN LAKE BASIN, EASTERN ANATOLIA, TURKEY

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Twenty-one (12 males and 9 females) specimens of *Nannospalax nehringi*, collected from Van Lake basin, Eastern Anatolia -Turkey, were used for karyological studies. Two different chromosomal forms of *Nannospalax nehringi* have been found in Van Lake basin, Eastern Anatolia. The diploid number of chromosomes in the Muş (Malazgirt) and Van (Erciş;) populations are 2n = 48. The fundamental number of chromosomal arm (NF) is 72 and the number of autosomal arm (NFa) is 68. Their karyotypes consist of 11 pairs of meta/submetacentric and 12 pairs of acrocentric autosomes. The X chromosomes are large submetacentric, whereas the Y chromosomes are large acrocentric. This result is a new record for Turkish mole rats. So, the new record from Muş (Malazgirt) and Van (Erciş) have enlarged the distribution range of this form (2n=48) south westward. The Bitlis population has 2n = 54 chromosomes. The number of chromosomal arm (NF) is 74 and the number of autosomal arm (NFa) is 70. The autosomal set has 9 pairs of meta/submetacentric and 17 pairs of acrocentric chromosomes. The X chromosomes are large and submetacentric, whereas the Y chromosomes are minute acrocentric. When these results are compared with previous studies, *Nannospalax nehringi* specimens from Eastern Anatolia have some differences in their chromosome morphology.

CONSERVATION OF SICISTA *SUBTILIS TRIZONA*. LET THE WEED SPREAD?

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The Southern Birch Mouse *Sicista subtilis* (Pallas, 1773) is one of the rarest and least known small mammal species of Europe. Admittedly the only occurrence of its subspecies, the *S. subtilis trizona* (Frivaldszky, 1865) is confined to Hungary. The elimination and contamination of the undisturbed lowland habitats are the main reasons of its endangerment besides a natural eastward area-regression that began in the Holocene. The Hungarian *Sicista*-population collapsed at the 1960s like many other species due to the dynamic intensification of agriculture. Today the range of this subspecies has shrunken into only one locality.

The last living specimen was caught in Hungary in 1926 and till 2006 it was detected only from owl-pellets, but at less and less localities. In 2006 the *S. subtilis* were trapped exclusively in thistly weed vegetation *Carduetum acanthoidis*. These patches mostly border on abandoned plough-land vegetation (*Convolvulo-Agropyretum repentis*) dominated by annual grasses. The habitat of *S. subtilis* adjoins solonetz steppe (*Artemisio santonicae-Festucetum pseudovinae*), too. Most part of the habitat were ploughed a short time ago (10-15 years) and on a smaller part of it barns and other farm-buildings stood.

The survival of the population here is due to the underdevelopment and closeness and not to special vegetation or other special environmental factors. The sustainment of this "ideal" state would be desirable but it is not compatible easily with the socio-economic development of the region. The solution can be a *Sicista* Biosphere Reservation where building new roads, bituminizing the actually heavy roads and using chemicals are not permissible. Within its mosaic area the agriculture and the farming which contribute to form weed-patches consist with the natural habitats. These undisturbed, wide, connected patches are the most important factors for the conservation of *Sicista subtilis*. So we need to protect the weed for this species.

LONG-TERM MONITORING OF HUNGARIAN BIRCH MOUSE (*SICISTA SUBTILIS TRIZONA*)

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Since 1995 a long-term monitoring of endangered Hungarian subspecies *Sicista subtilis trizona* (Frivaldszky, 1865) has been carried out in the Borsodi Mezőség Landscape Protection Area by owl-pellet examinations (sites: Nagyecsér, Nagyház-tanya, Salamonta) and life-trappings (site: Nagyecsér).

On site Nagyház-tanya *Microtus arvalis* was the most frequent species while *Crocidura leucodon*, *Sorex araneus*, Sorex minutus were subdominant and *Apodemus* sp., *Apodemus agrarius*, *Crocidura suaveolens*, *Sicista subtilis* were also detected with a decreased prevalence. In 1998 a considerable gradation of *Sicista* with high frequency (27%) must be emphasized and a significant difference has been found in community structure, too. However in average years the relative frequency of *Sicista subtilis* in owl-pellets is around 1 %.

On site Salamonta *Microtus arvalis* was the most prevalent species, followed in the dominance order by *Sorex araneus, Sorex minutus, Crocidura leucodon*. On the other hand *Apodemus sp., Apodemus agrarius, Crocidura suaveolens, Microtus minutus, Mus* sp. and *Sicista subtilis* showed very low rates. In 2006 the *Sicista*-population also showed to became stronger (5%) than former years.

On the most important site, Nagyecsér, based on owl-pellets, *Microtus arvalis* was proved to be the dominant species of the small mammal community, while *Sorex araneus*, *Crocidura leucodon* were subdominant and *Apodemus agrarius*, *Microtus minutus*, *Mus* sp., *Sorex minutus* and *Sicista subtilis* added diversity to the community, but with very low rates. In 1998 a gentle gradation was found in this site, since 8% of the prey specimens were *Sicista subtilis*. According to the life-trapping on Nagyecsér in 2006, *Apodemus agrarius, Microtus arvalis* and *Sorex araneus* were the dominant species, while prevalence rates of *Microtus minutus, Neomys anomalus, Sicista subtilis* and *Sorex minutus* were lower. Note that *Sicista subtilis* showed 5% relative frequency using life trapping method.

The increase in *Sicista* in 1998 and 2006 coincided with decrease in *Mus* and *Sylvaemus* but it is unverifiable that the *Sicista*-gradation was directly caused by the low-point of these potential competitors. The connection with the high amount of rainfall in spring is more probably. The two most water-dependent species, *Neomys anomalus* and *Arvicola terrestris* show dynamics like *Sicista*.

REPRODUCTIVE BIOLOGY OF SARDINIAN HARE *LEPUS* (*CAPENSIS) MEDITERRANEUS* REVEALED BY STAINED PLACENTAL SCARS

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Sardinian hare L*epus (capensis) mediterraneus* is present all over the Sardinia island, mainly on hilly areas covered by Mediterranean maquis, small woods, natural prairies and seminative.

Data recorded in recent years show low densities (1-5 ind./km^2) in most of the suitable habitat. The population dinamics of Sardinian hare is still poorly known. The hunting season goes on 3 weeks from September to October.

Indispensable requirements for a correct hunting management are the knowledge of the reproductive pattern of the species and the estimation of the reproductive success of the populations.

We used placental scar analysis to determine the reproductive history of female sample of Sardinian hare collected during the 2004 hunting season in all the Sardinian provinces.

We observed most of females in reproduction (50% pregnant and 29% with resorptions in progress) while the remnant are non fertile females (18%). The mean number of pregnancies per female was 2.64 (± 1.34 SD). The mean number of placental scars and/or foetuses per female was 3.57 (± 1.83 SD), while the mean number of placental scars and/or foetuses per pregnancy was 1.35 (± 0.63 SD). The reproductive activity last throughout the year, confirming data collected in captivity during 9 years of monitoring. However the pattern observed in captivity looks different from that observed in the wild. The summer regressive phase of the reproductive activity recorded in the wild could be affected by the Mediterranean climate that limits availability of food resources, while the gradual increasing of the activity at the beginning of autumn could be coincide with the end of the dry season.

However an intense sampling is recommended to define the best period for hunting activity, taking in account the biological cycle of the species.

FIRST DATA ON REPRODUCTIVE BIOLOGY OF ITALIAN HARE *LEPUS CORSICANUS*

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The Italian hare *Lepus corsicanus* is an endemic species occurring in central and southern Italy and in Sicily. In Corsica this species has been introduced in historical times. Its distribution and some ecological aspects suggest that Italian hare is a species adapted to Mediterranen habitat. However the biology of this endemic species is poorly known, including reproductive phenology that should be influenced by climate as in other Lagomorphs.

Italian hare is a game species in Sicily (15 October-30 November). The knowledge of the reproductive pattern of the species is an indispensable requirement for a correct hunting management. The present study was aimed at defining the breeding season, estimating the litter size and measuring fertility.

We recorded the reproductive status of the females collected in Sicily and on the Peninsula for the project on the Italian hare and shot in Sicily during 2004 hunting season. Some uteri were coloured for counting and aging placental scars.

We observed most of females in reproduction (61.54% pregnant and 15.38% with resorptions in progress). The mean number of pregnancies per female was 2 (maximum value recorded: 4). The mean number of placental scars and/or foetuses per female was 3 (maximum value recorded: 6), while the mean number of placental scars and/or foetuses per pregnancy was 1.5 (± 0.71 SD).

The reproductive activity last throughout the year, with a maximum in spring and a minimum during winter and summer; in autumn the activity is moderate. This preliminary data seem to show an influence of the dry and cold seasons.

An intense monitoring is recommended especially in Sicily to better define the reproductive phenology and to develop conservation and management strategies.

DISPERSION AND COLONIZATION OF PLANT SPECIES BY ENDOZOOCHORY IN SAN DUNE SYSTEMS

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The Rompido Spit is a complex dune system located in Gulf Cadiz, southern west of Spain. This natural place has the characteristic that grows an average of thirty meters per year in length and it is formed by mobile and stabilized san dunes. Mobile sand dunes are harsh ecosystem where the colonization is limited by the stressful environment condition. In this natural place wild rabbit is the most abundant herbivorous. The goals of this study were: a) to know the species that geminate from rabbit pellets, b) to estimate the number of seeds that geminate by seasons and pellets, c) to know if wild rabbit contribute to arrive and colonization of vegetation species to new areas. Fresh pellets were collected over one hundred and ten parallel belt transects of 10 m wide and separated from each other by one hundred meters. In laboratory pellets were placed for germination and growth seedling were observed daily during 8 month. The seed shadow was estimated with a 1m wide belt transect across each of the fourteen youngest dune ridges located at the end of the spit. The dune ridges are in an age-gradient of formation (from oldest to youngest) and *R. monosperma* colonization. All pellets within 1x1 square meters segments of transects were collected and they were place for germination. At least 14 species geminated from pellets. The most abundant were: *Retama monosperma*, *Silene nicaensis*, *Sedum andegavense*, *Malcolmia littorea* and *Solanum alatum*. In relation to seed size, *R. monosperma* and *S. alatum* had assist dispersion; the others species would be consume jointly with the plant or part of them. *R. monosperma* was dispersed along all trough year even thought fruit down the tree at the beginning of august. The numbers of seed germinated were significantly greater in summer whereas the number of pellets were significantly greater in winter. Seed shadow was observed all trough of year. Wild rabbit disperse 8% of the plant species present in the study area and they contribute to arrive and colonization of germinable seed to young dune ridge.

INTEGRATIVE SYSTEMATICS OF THE ALIEN SCIURID (RODENTIA) FROM ANTIBES (SOUTH EAST FRANCE): AN ATTEMPT OF TAXONOMIC IDENTIFICATION

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In Antibes city in French Riviera, parks and gardens are invaded by an alien squirrel species. Described for the first time in 1972, this species has been tentatively attributed to *Callosciurus erythraeus-flavimanus* complex. Introduced since 70's this species has not yet extended its range outside the city. Other invasive squirrels of the same genus are known in Italian cities and have been attributed to *C. finlaysoni*.

In order to better determine the Antibes alien species and understand its origin, we have performed a cytogenetical, morphological, morphometrical analyses on fresh collected specimens. Morphological and morphometrical (distances analyses, PCA and DFA) comparisons have been made with Museum material of South East Asia and when possible with type specimens. Molecular sequences (cytb) will be obtained for two specimens.

As results four specimens have been karyotped and exhibit 2N=40, NF=78, NFa=74, thus sharing the same diploid number with the three other congeneric species (*C. flavimanus*, *C. finlaysoni* and *C. notatus*) studied earlier However chromosome banding and molecular cytogenetic studies are needed to elucidate the nature of minor karyotypic differences related to NF equal to 78 (our study), 76 (CFL) and 74 (CFI and CNO). From morphology and morphometrcis we have not yet found any Asiatic relative appropriate for a precise knowledge of its origins and we wait for cyt.b DNA sequences results.

Such integrative systematics approach should be generalized to the study of invasive species.

OCHOTONIDS OF EURASIA: SYSTEMATICS, TAXONOMIC DIVERSITY, DISPERSAL AND EVOLUTIONARY DEVELOPMENT

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Eurasian ochotonids (Ochotonidae, Lagomorpha) include 15 extinct genera and one extant genus *Ochotona* with 64 extinct and extant species. It is known that ochotonids show general evolutionary trends in cheek teeth from rooted towards rootless, enamel structure on the occlusal surface of cheek teeth from simple to complicated in P^3 and P_3, hypostria of P^4-M^2 from shallow to deep, and talonids of P_4-M_2 from narrow to wide.

The earliest records of the family Ochotonidae, with two subfamilies Sinolagomyinae and Ochotoninae, are known from the Middle Oligocene and they are represented by the genus *Sinolagomys*. During the Miocene a high diversity of ochotonids have been observed; these forms flourishied throughout the world and were represented by not less than 15 genera. At the end of Miocene all taxa of subfamily Sinolagomyinae disappeared in all continents, and Ochotoninae species continued to exist Eurasia, and two new genera *Bellatonoides* and *Ochotona* appeared in Asia. At the beginning of the Pliocene, another new genus *Ochotonoma* appeared in Asia and *Pliolagomys* in the Europe. Ochotonids of Eurasia continue to be rather diverse, especially the genus *Ochotona* which was represented by rather numerous species.

During Pliocene the climate changed towards cool and arid and open landscapes became widely distributed. Such kind of environment was favourable for dispersal of ochotonids. At that time the genera *Ochotona*, *Pliolagomys* and *Ochotonoides* were widely distributed in Eurasia. Towards the end of Pliocene the abundance of ochotonids decreased in this region. Probably the reason was a diversification and rapid expansion of arvicloids from the end of Early Pliocene. They could become the main nourishmental competitors of grass-feeding ochotonids. The genera *Pliolagomys* and *Ochotonoides* having teeth with peculiar complicated structure disappeared and from the end of Pliocene sole genus *Ochotona* with simple structure of teeth survived and they could adapted to different biotopes: different type of steppes, subdesrets, deserts, mountain slopes and high mountains even mountain tundra.

By the end of the Middle Pleistocene the distributional range and diversity of *Ochotona* greatly decreased in Europe. During the Late Pleistocene the vast periglacial plain of Europe and western Asia was occupied by pikas of the “pusilla” group. In contrast to it, the Asian region was inhabited by many different endemic species some of which were ancestral forms of modern *taxa*.

The current distribution of ochotonids has decreased considerably from their Pleistocene distribution in Europe and at the present time mainly concentrated in Asia which is inhabited by 28 living species, two modern species are Northamerican forms and in Europe *Ochotona pusilla* occupies restricted steppe area in upper Volga River.

ARVICOLA LACÉPÈDE, 1799 (RODENTIA): SYSTEMATIC REVISION AND MORPHOLOGIC VARIABILITY

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The water vole, genus *Arvicola*, is characterised by a broad geographic distribution throughout Europe and a wide climatic tolerance, since the Quaternary. As a result, this genus is present in both glacial and interglacial periods and is widespread during the late Middle and Upper Pleistocene. Its rapid evolution and successive migration waves permit the use of the genus as a major biostratigraphical tool within the Quaternary. *Arvicola* is one of the most important components of the "short chronology" theory, based on Mammalian assemblage and expansion.

Today, two main species are distinguished. *Arvicola sapidus*, the largest in size, is restricted to Spain and France and is completely aquatic. The second extant species, *Arvicola terrestris*, is characterised by a terrestrial lifestyle, and a geographic distribution covering the whole of Europe except Spain. *Arvicola* made its first appearance in Central Europe around 500,000 years ago, and in Eastern Europe around 400,000 years ago. Both the extant species and the fossil, *Arvicola cantiana* (Hinton, 1910), were probably derived from *Mimomys* (*M. occitanus - M. polonicus - M. pliocaenicus - M. ostramosensis - M. savini*) as suggested by the great similarity in molar occlusal surfaces. In *Arvicola*, the enamel band of salient angles underwent differentiation, and m1 length increased during the Quaternary. *Arvicola cantiana* follows the *Mimomys* enamel pattern, the enamel is thicker on the posterior wall and thinner on the anterior wall, while in modern *Arvicola* the enamel is thinner on the posterior wall and thicker on the anterior wall. The thinning of the enamel band on the posterior wall continually reduces and thus, corresponds to an irreversible trend. In previous works performed by W.D. Heinrich, W. van Koenigswald, T. van Kolfschoten and E. Desclaux, the enamel differentiation and the length of M1 are used to specific determinations, relative dating and correlations of Archaeological records and have led to increase species number.

In our study, we suggest (1) to reappraisal the *Arvicola* genus in term of morphodiversity and morphospace and to (2) estimate the morphologic variability, in using outline analysis (CDFT) which take account the tooth shape in its whole.

Therefore, we show that the extant species seem to derive from one single species *Arvicola cantiana* (Hinton, 1910) and that this one has a large phenotypic plasticity without obvious temporal, geographic and climatic clines.

EARLY ARVICOLIDS, THEIR POTENTIAL ANCESTORS AND RELATED FORMS

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Arvicolids originated as a branch of cricetid rodents within the Late Miocene and became extremely divers in the Northern Hemisphere during the Pliocene and Quaternary. Despite their abundant fossil record, their early phylogenetic history is still not sufficiently known. This contribution is a critical compilation of data on early arvicolids and related cricetid taxa, so-called microtoid cricetids. On the base on dentalmorphological characters possible evolutionary tendencies and relationships are suggested.

Up from MN 4 (early Miocene), *Democricetodon* and *Megacricetodon* are the most common cricetid genera. Still undiscovered members of this group branch to the microtoid cricetids and arvicolids. The Late Miocene brachyodont cricetid *Rotundomys bressanus* displays a tendency towards a creation of lophs on its molars, which seems to be close to that of the potential ancestor of true arvicolids.

In response to environmental changes, cricetids evolve several independent lineages with mesodont/hypsodont and prismatic molar pattern during Late Miocene. Some of these early "experiments" become extinct soon: *Microtocricetus* and *Microtoscoptinae*, aberrant lineages with prismatic molars but without alternating triangles. The only exception is *Paramicrotoscoptes*, the molars of which possess slightly alternating triangles. Other lineages establish firm long-lasting evolutionary pathways since the Late Turolian/Ruscinian (Eurasia) and Early Hemphillian (North America) respectively, e.g., the *Trilophomyini*, a group of European aberrant cricetids inc. sed. The Baranomyinae are a conservative group close to *Microtodon*, since the anterior part of m1 does not develop additional triangles. *Anatolomys* is a basal genus of this group.

To the most primitive representatives of the arvicolids belong the Ischymomyinae that appear in MN 10-11 with *Pannonicola* (= *Ischymomys*), which possesses mesodont molars with a prismatic structure. This taxon is presumably ancestral to *Dolomys* and perhaps even to *Dicrostonyx*. Most likely *Microtodon* evolves into *Promimomys*, the ancestor of *Mimomys*. The latter gives rise to *Microtus* and *Arvicola*. Thus, the hypothesis of a diphyletic origin of arvicolids is supported by two separate groups in the Turolian and the co-occurrence of *Mimomys* and *Dolomys* in the Ruscinian.

The origin centre of arvicolids is most likely situated in Asia. However, the American *Copemys* might also be included in the ancestry of modern arvicolids.

REPRODUCTIVE ISOLATION BETWEEN CHROMOSOMAL RACES OF *MUS MUSCULUS DOMESTICUS* REVEALED BY MULTIPLE UNLINKED LOCI

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* This contribution is dedicated to our dear and irreplaceable friend Marco

The repeated occurrence and rapid fixation of Robertsonian (Rb) fusions have led to the formation of several chromosomal races in the western house mouse, *Mus musculus domesticus*. Since the discovery of the first race in the Swiss-Italian Alps, there have been several studies, with particular attention being paid to the contact zones between different Rb races and between Rb races and surrounding standard populations (2n = 40). In this work we analysed a parapatric contact area between two metacentric races in Central Italy, the Cittaducale race (CD; 2n = 22) and the Ancarano race (ACR; 2n = 24) in order to estimate gene flow at this boundary. Hybrids between these two races show high level of structural heterozigosity and are expected to be highly infertile. A sample of 88 mice subdivided in 14 localities was used. Mice were genotyped by mean of 8 microsatellite loci mapped in 4 different chromosome arms. Results showed a clear genetic differentiation between the CD and the ACR race as revealed by the differences in allele frequencies along the contact zone. The genetic differentiation between the races was mainly highlighted by assignation analyses, in which all the individuals were correctly assigned by their genotypes to the source chromosomal race. This result is stressed by the absence of any geographical or ecological barrier in the parapatric contact zone that occurs within a village. In these conditions, the observed genetic separation leads to suppose a drastic reduction of gene flow between the races. The CD-ACR contact area constitutes a rare example of a final stage of a speciation process between chromosomal races in rodents due to their chromosome incompatibility.

MORPOHOLOGICAL VARIATION BETWEEN CHROMOSOMAL RACES OF *MUS MUSCULUS DOMESTICUS* IN CENTRAL ITALY

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* This contribution is dedicated to our dear and irreplaceable friend Marco

The house mouse, *Mus musculus domesticus*, exhibits a high level of chromosomal polymorphism due to the occurrence and fast fixation of Robertsonian fusions between telocentric chromosomes. For this reason, since the discovery of the first metacentric population in 1969, it has been an emblematic example of chromosomal speciation. In this work we analysed two contact areas between chromosomal races in Central Italy using geometric morphometry. The first area is characterized by the parapatric contact of standard populations (2n = 40) and the Cittaducale race (CD; 2n = 22), the second one by the two metacentric races CD and Ancarano (ACR; 2n = 24). While the CD-Standard area presents a hybridization zone about 20 kilometres wide, there is no evidence of hybridization between the CD and ACR races. The total sample is composed by 207 mice and 15 landmarks on the left mandible were collected. A population sampled in the coastline of Rome is also analysed in order to examine the morphological variation of individuals living in different ecological conditions and in absence of gene flow with the contact zones. In the hybrid zone, the statistical analyses revealed significant conformational differences between the populations, while a weak differentiation between the chromosomal groups is shown. The pair-wise comparisons between the populations lead to hypothesize the presence of stochastic influences in the shape variations. In the contact area, the high genetic differentiation between the metacentric races has produced a distinguishable morphological pattern in the CD and ACR individuals, despite the occurrence of stochastic influences in the observed variations. Through morphological variations observed in the two areas, these results showed in the hybridization zone an example of a form of reproductive isolation which still has to be completed and in the contact area a final stage of a speciation process.

MORPHOLOGIC AND BEHAVIOURAL TRAITS OF COMMENSAL *ACOMYS CAHIRINUS* POPULATION FROM EGYPT (RODENTIA: MURIDAE)

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Acomys cahirinus is one of the few rodent species that locally switched to commensalism. It is possible to compare traits and characteristics of commensal populations with those living freely in the nature. Since commensal way of living presents an enormous change in environment, as well as change in selective pressures, we might assume significant change in variety of traits.

We examined differences in particular traits of postcranial skeleton between commensal and non-commensal populations of genus *Acomys.* Skeletons of the following species were available: commensal and non-commensal *A. cahirinus* population from Egypt, *A. cilicicus* from Turkey, *A. dimidiatus* from Israel and *Acomys sp.* from Iran. 29 postcranial parameters and 5 parameters on the body were measured on the total number of 230 individuals. In addition, we examined behaviour of individual populations in a simple test of free exploration. Tested individual were allowed voluntarily to leave starting home cage. 170 experiments with equal number of males and females were evaluated. 12 behavioural factors were monitored, focusing on their frequency and duration.

Multivariate statistics (PCA, DFA, ANCOVA) of morphometric data indicate that Iran population is most differentiated from the rest of cahirinus-dimidiatus group. On the other hand, postcranial morphology of commensal and non commensal populations is fairly similar.

It contrasts with the results of behavioural data. In the free exploration test, commensal *A. cahirinus* population significantly differed from the most related taxa, including non-commensal *A. cahirinus* population. The main difference between commensals and non-commensals lied in latency, i.e. time duration until the individual decides to leave familiar environment and gets out of its home box. No gender differences were detected.

The assumption, that different ecology (commensal environment vs. nature), has an influence on behavioural characteristics, was confirmed. Differences between commensal and non-commensal populations in behavioural traits are much more pronounced than corresponding differences in morphology. It supports the hypothesis that behavioural characteristics are changing faster and that their change precedes the change in morphology.

POPULATION VIABILITY ANALYSIS AND GENETIC FEATURES IN *LEPUS CORSICANUS* AND *L. EUROPAEUS* LIVING SIMPATRICALLY

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The Cilento-Vallo di Diano National Park hosts an endangered population of Italian hare, endemic in South Italy. The Italian hare suffers predation pressure by pest species, illegal hunting and habitat reduction. Moreover, it may be threatened by competition with sympatric European hare (*L. europaeus*), introduced in last decades by man. European hare yearly spread in the Park, where the hunting is forbidden, from annual restocking populations made out of the Natural Park. An indication of troublesome of these factors on the Italian hare can derive from an evaluation of genetic variability and singleness at population level. We studied genetic status of two hare species according to populations and metapopulation approaches. From organic tissue were extracted nucleic acids, amplifying and screening Cytb and Control Region of mtDNA. Eight microsatellite DNA polymorphic loci were analysed to investigate population structure and gene flow. Recent bottleneck signature and low gene flow among isolated Italian hare populations were found. These results and information on low density of population encouraged us to perform a Population Viability Analysis (PVA) using VORTEX. We investigate the Italian hare's risk, the key factors influencing the dynamics of the population and the effect of future management actions. Simulation trends and sensitivity tests indicated that factors greatly acting on the population survival are illegal hunting and juvenile predation. The first causes extinction in short time if hunting depresses the population size more then 13 percent/year. Whereas, if the population has a juvenile mortality up to 80%, it achieves extinction slowly, but population will undergo a worrying reduction of gene diversity. Hypothetical management action plans, to improve the status of Italian hare, must to consider eradication of European hare, a fight against illegal hunting, an increase of habitat areas and the introduction of genetically safe breeding specimens.

ITERSPECIFIC HABITAT SELECTION BETWEEN ITALIC AND EUROPEAN HARES SYMPATRIC POPULATIONS

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Recent studies have shown the presence of an endemic species of hare, Italian hare (*Lepus corsicanus*), in central and southern Italy. One of the most important aspects of population management is the presence of alloctonous European hare (*Lepus europaeus*). In fact, in the past brown hares was repeatedly introduced in the same areas, in order to hunting management policy and since the presence of autoctonous species was unknown. So, these species are locally sympatric, such as on Cilento and Vallo di Diano National Park. In this situation the ecological pressure of European hares may be a risk for the endemic and rare Italian hare and studies on ecological selection allow us important information to a conservation plan.

In this contribution we show results of researches on habitat selection between these species on a mountain territory in the Park.

The occurrence of hares was checked during the night, using a spotlight. Species identification was made by means of morphological patterns, only whether it was possible by distance and environmental conditions. All the unidentified detections were not considered. Indirect survey was also made by using faeces size, when differences allow the species detection. Each detection of hares was georeferenced and recorded in a spatial database.

We considered a buffer area of 300 m radius around each detection, and eco-geographical variables were described in: land cover, elevation, slope, aspect, man made structures.

Species seem to select habitat differently within foraging areas. European hares maintain a lot of grass covered areas, while beech forests and shrubs occur widely in the Italic hare habitats.

THE NOCTURNAL ACTIVITY OF COMMON DORMOUSE (*MUSCARDINUS AVELLANARIUS*) IN RELATION TO SEASON AND SEX

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Common dormouse, *Muscardinus avellanarius* (Linnaeus, 1758), is a widespread glirid species observed in a variety of woodland types. The aim of this study was to determine if common dormouse selects different habitat types for feeding, moving and nesting. The study was carried out in the Natural Reserve "Castel di Guido", placed at 10 km north of Rome (41°54'N, 12°31'E). This area is characterized by a high environmental heterogeneity, encompassing both natural and artificial patches of vegetation. Natural patches are represented by thermophilous mixed oak woodland, while artificial patches consist of an assemblage of planted trees belonging to several deciduous or evergreen species. A total of 23 animals were radiotagged (14 males, 9 females). Radiotracking was performed in five sessions: two in autumn (November-December 2004 and 2005) and three in spring (March-April 2004 and 2006, April-May 2005). Each session lasted three weeks. Locations were obtained by using both triangulation and "homing-in" methods by approaching the animals on foot. Activity was recorded at sight or by listening to amplitude and direction changes of the radio signal, and classified into three categories: 1) feeding, if the signal amplitude was fluctuating and the direction came from the same point; 2) moving, if the signal amplitude was fluctuating and its direction changed quickly; 3) resting, if the signal amplitude was constant and came from the same direction. Dormice selected habitat only for feeding and resting, and consequently moved along connecting patches between resting sites and foraging areas. Distribution activity of dormice varied seasonally. During autumn, they fed mainly in natural patches (rich in acorns), and rested in artificial pine stands that offered shelter. In spring, resting and foraging activities were carried out within the same patches, either artificial (as downy oak and pine stands) or natural. Furthermore, in this season, dormice fed in artificial maple stands. Dormice resulted to be more selective in autumn than in spring, probably because in the latter season resources were more uniformly distributed. Females resulted to be more selective than males as for concerned habitat use, probably in relation to reproductive behaviour. Patterns of habitat selection varied among seasons, and the same habitat type can have a different role (as resting or foraging area) over the time.

GENETIC FACTORS INFLUENCE MATERNAL CARE IN PINE VOLES

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The initiation and maintenance of maternal behaviour after parturition are controlled by endocrinal and neural mechanisms. Maternal (parental) behavioural processes are likely to affect offspring development. Strain comparisons in mice have confirmed that genetic factors influence maternal behaviour as well. In the European pine voles (*Pitymys subterraneus*) there are two coat-colour morphs. The wild type is black agouti (A); the other shows coat colour dilution and pink eyes (D). Diluting mutants connected with P and/or D series of alleles show deep morphological and physiological effects.

Maternal behaviour in the A and the D females during 3 weeks after parturition was observed under laboratory conditions. Weight of nest material did not differ significantly between A and D females. However pregnant and lactating A females build more completely enclosed nest than do D females. Daily checking and/or repairing nests was impressively different: A females tended to the nest for 5 times longer periods than D females. As for nursing posture and pup licking, D mothers tended to engage in less arched-back nursing and pup licking. They also spent 9.6 per cent less time inside the nest with the offspring in comparison to A mothers. Blanket nursing was observed more frequently in A females.

Additional testing ("test of shyness") of the both coat-colour females have been conducted. The D females stay in secluded places for 56 per cent of the observation periods, while the A females 11 per cent only.

Genotypic traits in European pine voles affect their maternal behaviour and patterns of development in their offspring. Body weight of D voles is 8.5 g at 22nd day after birth, while in A voles it is 10.1 g at the same age. Maximum metabolic rate differs significantly between D voles and A ones. Behavioural processes may play a larger role than previously suspected in the development and maintenance of interindividual variation.

GENETIC VARIABILITY AND POPULATION GENETIC STRUCTURE OF YELLOW-NECKED MOUSE (*APODEMUS FLAVICOLLIS*) IN THE HETEROGENEOUS LANDSCAPE

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In this study we applied analysis of microsatellite markers to investigate: (i) genetic variability within local populations of yellow-necked mouse, inhabiting forest patches of different size, and (ii) genetic differentiation among local populations from forest patches, separated by different distances and habitat barriers.

Animals from north-eastern Poland in the Mazury Landscape Park were investigated. The field study were carried out during 2003-2005 at the landscape scale (approximately 600 km2) in eight spatially separated forest patches of different sizes and in extensive forest complexes. The shortest distance between particular trapping locations was 275 m and the longest was approximately 40 km.

The basic study methods involved rodent live-trapping, ear lobe collection as a source of DNA and molecular genotyping of individuals using automatic capillary electrophoresis.

A total of 338 yellow-necked mice was trapped and put forward subsequent molecular analysis in 7 microsatellite loci. On base of obtained genotypes we estimated allelic richness and level of heterozygosity for each forest patch, as well as genetic differentiation between pairs of local populations applying FST and RST statistics. We also provided assignment test and identified the first generation migrants to infer about the level of isolation and short-time gene flow among habitat patches.

Our results indicated that the level of genetic variability of local populations depends on patch size and degree of its isolation. We also showed that different types of habitat barriers have diverse effects in induction of pronounced genetic structure of yellow-necked mouse population.

MOLECULAR SYSTEMATICS OF PIKAS OF THE SUBGENUS *PIKA* (*OCHOTONA*, LAGOMORPHA)

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The structure of the subgenus *Pika* and the interspecies variability of its component species were discussed on the basis of sequences of the mtDNA Control region (C-region). 37 specimens from 14 species were studied. The subgenus *Pika* includes the previously described species *O. alpina, O. hyperborea, O. hoffmanni, O. pallasi, O. argentata, O. collaris, and O. princeps*. According to preliminary results, the subgenus *Pika* does not include the dwarf pika (*O. pusilla*). Within the confines of the subgenus, *O. pallasi* and *O. argentata* are united in one cluster with a new, yet-to-be-described species from Central Yakutia. The molecular-genetic variability is lower in this branch of the phylogenetic tree as compared with clusters of Altai and Northern pikas, although all three forms (*O. pallasi, O. argentata* and *Ochotona* sp.n.) are long-divergent, good Linnaean species. The Khentei pika (*O. hoffmanni*) forms one cluster with the scorodumovi form from the interstream area between the Shilka and Argun rivers. The scorodumovi form undoubtedly deserves species status. However, the name of this species depends on the taxonomic position of the mantchurica form from the Great Hingan Ridge. At the same time Chinese specialists suppose - based on a sequencing of cytochrome-b from mtDNA - that pikas from northern Manchuria belong to two different species. Moreover, pikas from Da Hinggan Ling (near *O. scorodumovi*'s range) are called *O. hyperborea mantchurica*, following Thomas (1909), while pikas from Xiao Hinggan Ling are called *O. alpina cinereofusca*, following Zimmermann (1964). We have shown that the structure of cytochrome-b in mantchurica and scorodumovi forms is very similar (6 replacements for 541 bp) and differs sharply from *O. alpina sensu* Yu et al., 2000 on Xiao Hinggan Ling (53 replacements for 541 bp), as well from *O. hyperborea yesoensis* from Hokkaido Island (GenBank NCBI: www.ncbi.nlm.nih.gov) (50 replacements for 541 bp). Thus the proper species name of pikas from Shilka - Argun must be *O. mantchurica scorodumovi*, but the taxonomic status of pikas from the Lesser Khingan Ridge (China) needs to be specified.

The subspecies status of *O. alpina turuchanensis* was confirmed. Pikas from the alpina group with caryotype 2n=40 were found near the middle Lena River. The definition of their status will require more research.

PHYLOGEOGRAPHY AND POST-GLACIAL HISTORY OF THE EUROPEAN SQUIRREL, *SCIURUS VULGARIS*

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The red squirrel, *Sciurus vulgaris*, has declined dramatically in Europe during the last century. Nevertheless, phylogeographic data covering its entire distribution area, which provide the basis to identify the evolutionary significant units of this species and to establish an effective conservation strategy, are still missing. In order to assess genetic variation and differentiation of this species, we sequenced parts of the mitochondrial DNA gene (D-loop and cytochrome b), as well as nuclear genes of *S. vulgaris* across Europe. The data show no strong genetic structuring according to geography for most individuals analyzed. This pattern is probably the result of a rapid population expansion about 40,000 years ago, following an expansion of forests during an interglacial warming. However, squirrels collected in the southern-most part of the Italian peninsula (Calabria) are more differentiated, with genetic distances to Northern and Central Italian populations much greater than to the Russian ones. This would indicate that the separation of the Calabrian lineage happened at least 150,000 years before present. An explanation for this surprising differentiation of the Calabrian squirrel might be a close association to its food plant, the endemic Calabrian pine tree. Conclusively, the Calabrian populations of *S. vulgaris* have to be considered as a separate conservation unit in the future. Protection of this endemic mammal lineage should be prioritized.

PARENTAL CARE AND ITS RELATIONSHIP TO SOCIAL ORGANISATION OF THREE VOLE SPECIES (ARVICOLINAE) WITH DIFFERENT MATING STRATEGIES

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This research aims to examine sex difference, or lack thereof, in parental care of three vole species with different mating strategies: red-backed vole (RBV) *Clethrionomys rutilus*, common vole (CV) *Microtus arvalis*, and Brandt vole (BV) *Lasiopodomys brandti*. The subjects were ten adult pairs of every species housed in terraria with two nest chambers. Pairs rearing their first litter were observed on day 2 postpartum and hereafter every next day till day 21 (time of weaning). The following adult activities were recorded: duration of nest-residence (DNR), frequency of mate grooming, duration of pup grooming.

There was no significant difference in DNR between females of three vole species. 5 of 10 RBV males did not share the nest with the female and did not display paternal behaviour excluding last 4-5 days. No sex difference was found in DNR in CV and BV. RBV parents spent together in the nest and groomed each other less time that did parents of CV and BV. RBV litters spent more time alone in the nest than did litters of CV and BV. DPG was greater in females compared with males of every species. In BV females, DPG was much greater than that one in females of two other vole species. DPG in CV and BV males was greater than that one of RBV males. Totally, young RBV received less parental care that did young CV and BV.

Thus, an essential relationship between mating systems of the vole species and their pair bonding and parental care: promiscuous mating in RBV is associated with weak bonding and mainly sole maternal care; polygynous/monogamous mating in CV and BV is associated with more tight bonding and biparental care. Interspecific variation in the level of parental care is related mainly to the direct parental care. I hypothesise that tactile stimulation (side-by-side contacts in the nest, huddling over the pups, and pup grooming) could be considered a proximate mechanism promoting pair bonding and family-group mode of life in arvicoline rodents.

MULTIPLE PATERNITY IN WILD POPULATION OF YELLOW-NECKED MOUSE (*APODEMUS FLAVICOLLIS*)

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Occurrence of multiple paternity is a result of the female's insemination by more than one male within a single estrus period. This phenomenon have been already described for a wide range of taxonomic groups (e.g. mammals, birds, reptiles, fishes, invertebrates) with a special regard on small rodents.

Statement of this kind of behaviour and evaluation of its frequency in wild population of yellow-necked mouse was the primary aim of our study. This common rodent species has still unexplained mating system. Animals were trapped in north-eastern Poland, in 2004-2006. In order to find multiple paternity of the offspring of 10 pregnant females, seven microsatellite loci, described for members of genus Apodemus were applied. The analyses were performed using multiplex PCR method and estimating the length of amplified fragments by automated sequencer.

The presence of additional alleles, indicating multiple paternity, were found in 33% (3 of 10) of investigated litters. The offspring fathered by single male prevailed in each litter, proportion of individuals originated from other males varied from 16.7% to 20%.

Our findings revealed that previously suggested monogamous or polygynous mating system in wild living yellow-necked mouse populations are not obligatory. The promiscuous mating system may be considered as a realized strategy in this species.

LONG-TERM MONITORING OF HUNGARIAN BIRCH MOUSE (*SICISTA SUBTILIS TRIZONA*)

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The Southern Birch mouse *Sicista subtilis* (Pallas, 1773) is one of the rarest and least known small mammal species of Europe. Since 1995 a long-term monitoring of Hungarian subspecies *S. subtilis trizona* (Frivaldszky, 1865) has been carried out in the Borsodi-Mezőség Landscape Protection Area using owl-pellet examinations (sites: Nagyecsér, Nagyház-tanya, Salamonta) and life trappings (site: Nagyecsér).

On the site of Nagyecsér based on owl-pellets, *Microtus arvalis* proved to be the dominant species of the small mammal community, while *Sorex araneus*, *Corcidura leucodon* were subdominant and *Apodeums agrarius*, *Microtus minutus*, *Mus sp.*, *Sorex minutus* and *Sicista subtilis* added diversity to the community, but with very low capture rates. At the same time, in 1998 a gentle gradation was found in these *Sicista* populations, since 8% of the captured specimens were *Sicista subtilis*. According to the life-trapping on the site of Nagyecsér in 2006 *Apodemus agrarius, Microtus arvalis* and *Sorex araneus* were the dominant species, while prevalence rates of *Clethrionomys glareolus*, *Microtus minutus, Neomys fodiens*, *Sicista subtilis*, *Sorex minutus* were lower. It is worth noting that Sicista subtilis showed 5% prevalence using life trapping method.

In the case of site, named Nagyház-tanya *Microtus arvalis* was the most prevalent species while *Corcidura leucodon* (mostly before 1998), *Sorex araneus* (mostly after 2000), *Sorex minutus* (mostly 1996) were subdominant and *Apodemus* sp., *Apodemus agrarius, Crocidura suaveolens*, *Sicista subtilis* were also detected with a decreased prevalence. As regards Southern Birch Mouse, in 1998 a considerable gradation with high prevalence (27 %) should be emphasized and a significant difference has been found in community structure, too.

On the third important site (Salamonta) *Microtus arvalis* was the most prevalent species, followed in the dominance order by *Sorex araneus*, *Sorex minutus*, *Corcidura leucodon*. On the other *hand Apodemus sp.*, *Apodemus agrarius, Crocidura suaveolens, Microtus minutus, Mus* sp. *and Sicista subtilis* showed very low capture rates.

MICROHABITAT PATCH USE OF MEHELY'S ROOT VOLE (*MICROTUS OECONOMUS MEHELYI*)

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In the framework of this study the dominance relationships, the spatial distribution and microhabitat patch use of individuals of the strictly protected subspecies of root vole *Microtus oeconomus mehelyi* were studied in three different regions, such as Kis-Balaton, Szigetköz and Tóköz.

During the investigated period, the root vole showed high prevalence in all of the three sample sites. According to data obtained in the territory Kis-Balaton, *M. oeconomus* seems to be a bit more dominant species compared to the other glacial relict vole species *M. agrestis*. Fluctuation of habitat-structure either could induce a drastic change in population size of *M. oeconomus* or in extreme case could faster extinction of root vole populations. At the same time, it seems that vegetation structure is only one of the factors, but on this microhabitat scale it is not necessarily the most important niche dimension determining the spatial distribution of individuals of root voles. Beside composition of vegetation, some other properties of the area, first of all its water coverage and the seasonal changes thereof, act as background variables that influence the spatial distribution and patch use of *M. oeconomus* individuals. On the other hand, a positive discrimination has been found in intermediate vegetation usage confirming our former hypothesis, that the Hungarian root vole prefers semi-aquatic margins of reed-beds.

INTRASPECIFIC VARIATION IN REPRODUCTIVE STRATEGIES OF MOUNTAIN HARES (*LEPUS TIMIDUS VARRONIS*) AT DIFFERENT ALTITUDES

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Many studies have shown a positive correlation between litter size and latitude in hares (*Lepus* sp.). This phenomenon is mainly due to differences in climatic conditions at various latitudes. Consequently, hares produce fewer litters but larger litter sizes at higher latitudes. In this study I tested whether climate is also a strong evolutionary factor along various altitudes. For this, I analysed female fecundity of mountain hares by staining placental scars. Samples derived from hunted individuals shot between 1000 and 3000 m a.s.l. in Grisons (Switzerland). Females produced between three to 14 young in one to three litters per year. Corrected for age (by dried eye-lens weight), body constitution and other factors I found the following: Mountain hares produce fewer litters and larger litter sizes at higher altitudes. Therefore, altitude seems to be a similar environmental factor like latitude affecting reproductive strategies in hares. Altitudinal effects might be one explanation why exceptions of the linear relationship between litter size and latitude can be found.

I thank Hannes Jenny and his colleagues from the Office of Game Management and Fisheries of Grisons for his support and the hunters for collecting hare samples.

DISPERSAL: DEMOGRAPHIC AND SPATIO-TEMPORAL IMPLICATIONS IN THE COMMON VOLE (*MICROTUS ARVALIS*)

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The importance of dispersal in fragmented landscapes has long been recognised. Work on dispersal, however, is often theoretically based or indirectly inferred by population genetics. In six 50x50 m semi-natural enclosures separated by vole-tight fences we investigated the population dynamics and spatio-temporal behaviour of individually marked common voles (M*icrotus arvalis*) during 2005 and 2006. Naturally occurring meadow vegetation, representing the voles' habitats, was surrounded by a frequently mown 2.5 m wide matrix stripe, avoided by the animals due to increased perceived predation risk. A point system based on trappings in at least two matrix traps revealed individuals sacrificing safety for the intention to leave the population. Dispersers were manually transferred within two separate experimental systems from source into transition and into sink enclosures. Frequent trapping sessions within the habitats gave information on the population dynamics. Automatically recording of above-ground activity and radiotracking of 45 dispersers and residents, respectively, revealed the voles' spatio-temporal behaviour. Altogether, we transferred 128 pre-saturation and saturation dispersers. Due to significantly higher male dispersal rates and higher survival rates among resident females the populations became female biased. Survival rates were neither density nor treatment dependent. Densities in the treatment phase significantly increased from source over transition to sink enclosures. Compared with residents, male dispersers grew faster, female dipersers more slowly. Activity data showed that transferred females significantly avoided residents, whereas male dispersers showed temporal avoidance with residents only when not been transferred, suggesting male dispersers to be more competitive than females. About 800 tissue samples of resident and disperser individuals are about to be analysed to reveal the establishing success and the impact of dispersal on the populations' genetic heterogeneity.

DEMOGRAPHIC VARIABILITY IN THE COMMON VOLE (*MICROTUS ARVALIS*)

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The demography of the common vole was intensely studied in the 50th and 60 th by German researchers in an attempt to identify the factors responsible for vole density cycles and often amazing outbreaks. Since this research was driven by the applied aspect of pest control, the concern of this species diminished when the vole cycles faded out in Central Europe, and cycle research concentrated on other species in Fenno-Scandia, the UK, and North-America. Only recently *M. arvalis* is reconsidered as rewarding for cycle research, because one and the same population can switch between the three dynamic patterns, i.e. annual density fluctuations, occasional outbreaks, and regular density cycles. However, since the older studies are rather descriptive than quantitative and analytical, and for the most part were published in German, few data are internationally available to model the demographic machinery of the different dynamic patterns. We measured demographic key parameters in six enclosed common vole populations over one annual cycle in parallel, starting with very small founder populations of two males and three females. Although considerable variation in the demographic key parameters occurred, the resulting general course of density was highly comparable among populations. This suggests that extremes in one demographic parameter were compensated by others, which hints to possible self-regulatory feed-back loops. The data will allow a modern quantitative analysis of the common vole demography. In addition, modelling of the population dynamics with setting all key parameters to the average, the minimum, and the maximum, respectively, will reveal the demographic power within the normal range of parameter variability.

PREDATION PATTERNS ON NORWEGIAN LEMMINGS AND GREY-SIDED VOLES

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A predator's functional response to variation in prey density is a key element in predator-prey systems, and recent research on small mammal dynamics both in Europe and North America has demonstrated the pivotal role of predators' functional responses in shaping fluctuations of several prey species. However, only a few studies have been devoted to studies of predation patterns on Norwegian lemmings (*Lemmus lemmus*), the classic enigma of population ecology, and co-existing vole species (*Clethrionomys spp*. and *Microtus spp*.) on the low alpine tundra in Fennoscandia. Consequently, the relative importance of predation in this system is not fully understood, and few previous studies have estimated functional responses or prey preference. During a peak year of rodents in subarctic Sweden, we used prey remains to quantify the functional responses of the rough-legged buzzard (*Buteo lagopus*; the most common raptor in the Fennoscandian mountains) to the two most important prey species in this community: Norwegian lemmings and grey-sided voles.

The rough-legged buzzards strongly preferred Norwegian lemmings over grey-sided voles and showed a steep type II functional response to lemmings. They also showed a different functional response to grey-sided voles, best described by a type III function. The different shapes of the two functional responses were probably an effect of the strong preference for lemmings, due to the combined effect of differences between lemmings and grey-sided voles in habitat utilisation, anti-predator behaviour and size-dependent vulnerability to predation. Lemmings are more frequently found in more open micro-habitats where buzzards prefer to hunt; lemmings are further more sluggish than the more agile vole species and should therefore be easier to catch for hunting raptors.

The distinguished differences in vulnerability to predation between lemmings and voles suggest that these species should be treated separately in future time-series analyses and theoretical models in order to better understand the role of predation in this study system.

IS THE IRISH HARE A SUBSPECIES OR A SPECIES?

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Ireland has a reduced number of mammal species relative to Britain and Europe and controversy has surrounded the time and means by which terrestrial fauna colonised the island. The Irish mountain hare (L*epus. t. hibernicus*) is one of six currently recognised subspecies of mountain hare (*L. timidus*) and is among the oldest members of the Irish fauna with fossil records dating back to 28,000 radiocarbon years BP. Its taxonomic status has been uncertain since its first description by Bell (1837) as a full species *(Lepus hibernicus*). Despite accumulating evidence showing significant morphological, ecological and behavioural differences between Irish and other mountain hares an overlapping degree of phenotypic plasticity complicates taxonomic resolution. Considering that most of Ireland was covered by ice some 20,000 years ago, the origin of present day populations is uncertain. Two main hypotheses have emerged. The first argues that hares did not survive during the last ice age and current populations are descendants of founder individuals that colonised Ireland post-glacially through a putative temporary landbridge connection with Britain and/or Europe. According to this prediction, Irish hares would have a low level of diversity and be genetically similar to other mountain hares from outside Ireland. A second hypothesis suggests that Irish hares are descendents from populations that have survived in glacial refugia in or near to southern Ireland. According to this hypothesis, current populations would have a high level of diversity following isolation and expansion from a cryptic refuge. We investigated these contrasting hypotheses from a molecular perspective. Thirty seven Irish hares were sequenced for 3215bp of mtDNA comprising ND4/5, D-loop and Cytochrome b genes. These were compared with available data for 751 hares from 14 Lepus species at the D-Loop, 451 hares from 13 *Lepus* species at Cytochrome b, and 41 hares from three *Lepus* species at the ND4/5. In addition, 21 Irish hares were sequenced for 405bp of the nuclear Transferrin gene and compared with 30 hares from 7 other *Lepus* species. Results revealed Irish hares comprise a unique genetic lineage which has been continually evolving in isolation from other mountain hare lineages since before the last glacial maximum. This finding provides the first evidence of a terrestrial mammal's survival and expansion from a cryptic Irish refuge and challenges the current subspecies status of the Irish hare.

BIOLOGICAL PECULIARITIES OF THE EDIBLE DORMOUSE IN THE ZHIGULI MOUNTAINS

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The edible dormouse (*Glis glis* L., 1766) is a typical representative of the broad-leaved forest community whose distribution in Eastern Europe is limited by different kinds of oak forests. At present the most Eastern population of the edible dormouse inhabits the Zhiguli Mountains.

This study of dormice biology was carried out in 2003-2006 in the north of the Zhiguli Mountains (53′25° N, 49′42° E). Dormice were captured by metal live-traps fixed in lines on trees. Regular censuses were carried out monthly in 3 permanent lines; episodical captures were made in 14 trial lines. After weighing, sexing and aging the dormice were released at their point of capture. The animals were marked by ear tattoos. Altogether 189 dormice were captured, 163 of them were marked, 67 animals were captured more than once.

The active period of the edible dormouse lasts 4-5 months. Time constraints of the hibernation period differ between years and for animals of different ages. Breeding of dormice occurs once a year. Most juveniles leave their maternal nests when the adults begin to hibernate. In some years there is a failure of reproduction (in 2004 and 2006 for example). Oscillations of the species abundance in different years were observed. The highest number in the monitoring lines was in 2006 (9 dormice per 100 trap nights), the lowest was in 2004 (1.1 dormice per 100 trap nights).

Males were slightly more numerous than females in population, the average ratio being 1.3:1. Juveniles predominated in the captures of 2005. In 2006, when reproduction failure was observed, yearlings predominated.

The breeding season of the edible dormouse in the Zhiguli lasts from the first ten-day period of June to the middle of July. Reproductive activity of young males was linked to body mass. Postnatal development of the species was observed.

Analysis of biotope preferences of dormice revealed that the most suitable type of forest for them is oak with admixtures of linden and maple, with dense hazel undergrowth and thin ground cover. The number of dormice in the forest depends on the extent of development of the undergrowth and tree holes. Analysis of 200 faecal samples showed that food composition of dormice in different biotopes is very similar, but strong differences occur with seasonal changes of food.

THE TAXONOMIC RECONSIDERATION OF THE MOLES FROM VIETNAM WITH A REFERENCE OF DISTRIBUTIONS

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The mole inhabiting in Vietnam was known since 1932 in the official report published by Field Museum of Natural History, Chicago. These specimens collected from Sapa, Lao Cai Province, northern Vietnam were identified as Kloss's mole, *Euroscaptor klossi* (Thomas, 1929), and no taxonomic reconsideration have been done. In 1940, Miller described a new species of mole, *E. parvidens*, from Bao Loc, Lam Dong Province, and southern Vietnam. After that, almost no record about the mole in Vietnam was published so far. Recently, the authors had some expeditions of the mole in the northern to southern Vietnam. In the results of field works, about 40 specimens of the mole were collected and identified based on the comparisons with previously recorded museum specimens including the type materials. The moles are distributing in the wet montane forests and farms located in relatively high elevation area, primary from Chinese border to south along the Annamese Mountains. In conclusion, two species belonging two genera of the mole, *E. longirostris* (Milne-Edwards, 1870) and *Mogera latouchei* Thomas, 1907, peripatrically occur in northern Vietnam, and another species, *E. parvidens* (Miller, 1940), has patchy distribution areas in southern part of Vietnam.

THE ROLE OF VOMERONASAL ORGAN IN RECEPTION OF ANDROSTENONE IN MICE

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Pheromones play a key role in social and sexual behavior of house mouse (*Mus Musculus*). Androstenone (AND) is well known as sex boar pheromone, but also provokes some pheromone-like effects in mice (Ingersoll, Launay, 1986). A genetic model of specific anosmia to AND was developed based on two inbred strains of mice: highly sensitive to AND CBA/J (CBA) mice and almost insensitive NZB/B1NJ (NZB) mice. CBA mice detect AND 2000-fold more diluted than NZB mice (Voznessenskaya, Wysocki, 1994). In our recent study we investigated the role of vomeronasal organ (VNO) in reception of AND using this model. AND thresholds were established in both strains of mice using Y-maze paradigm. Re-testing AND thresholds after surgical removal of VNO (VNX) showed 4-16-fold decrease in sensitivity in highly sensitive CBA mice, but did not affect thresholds in NZB mice. Patterns of c-fos expression were registered in sensory tissue of VNO after 1,5-hour exposure of mice to 0,1 % (w/v) AND. VNO receptor sensory tissue contains two anatomically and functionally separate groups of neurons: V1R and V2R. In CBA mice activated cells were located in the basal and apical zone of VNO receptor tissue. Consistent pattern of activation in basal zone may indicate the existence of specific AND receptor belonging to V2R family. In NZB mice activated cells were found only in apical zone. We observed individual variation in number and location of activated cells in apical zone of VNO of NZB mice. Behavioral and histochemical data indicate the involvement of both systems: main olfactory and VNO in reception of AND in CBA mice. In low sensitive to AND NZB mice involvement of VNO in reception of AND requires further investigation. Given the involvement of VNO receptor tissue, especially V2R zone, in reception of AND and its behavioral effects, AND functioning as a mouse pheromone may be proposed.

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VOCALIZATION OF THE JUVENILE SILVERY MOLE-RATS (*HELIOPHOBIUS ARGENTEOCINEREUS*)

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The environment of underground burrows is dark, monotonous, simple and stable. Lack of visual cues and nearly no air currents that can transport scents make acoustical signals of special importance. Adult silvery mole-rats live solitarily and meet only for mating; juvenile period is the only one when they live in social group. Therefore, it is very interesting to monitor their communication during this period, observe context of vocalization and its slight change to adult vocalization. Juveniles are nursed till three months; one female has one litter per year with one to four youngs. According to relatively small vocal repertoire of adults (eight types of calls), we assumed that also juveniles will have only few vocal signals.

We recorded four types of true and one type of mechanical vocalization produced by juveniles. Most of calls were produced when they were in group, isolated pup vocalized only seldom. The pups were the noisiest during nursing. They produced long (0.37-0.5 s) calls with many harmonical frequencies and energy concentrated between 0.9 to 2 kHz if in stress (during fight with siblings, impossibility to get to mother). Two individuals concentrated energy to higher harmonical frequencies in 5.5 kHz. As a reaction to painful stimuli (biting by sibling, manipulation), they produced short (0.09 s) screams with most of the energy in around 1.7 kHz, and during very strong stimuli in 4.2 kHz. Vocalization was most frequent during nursing; signal was short (0.2 kHz), simple with maximally two harmonics and the energy concentrated between 0.6 to 1.5 kHz. They produced short (0.11 s) clicks with frequencies around 1.2 kHz during contacts among pups (play, getting over each other). Mechanical signal was produced by teeth chattering and occurred during cleaning and as a warning in stress situations.

SIBLING VOLES ARE COMPETITIVELY SUPERIOR TO FIELD VOLES IN THE ABSENCE OF PREDATORS, BUT SUFFER MORE FROM PREDATION

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Interspecific competition is assumed to generate negative effects on coexisting species, possibly including slower population growth and lower survival. The field vole (*Microtus agrestis*) and the sibling vole (*M. rossiaemeridionalis*) are sympatric close relatives which compete for similar resources. We studied the effects of coexistence on population densities, reproductive parameters, and survival in these two species by means of experimentation in large, predator-free outdoor enclosures (0.5 ha). While populations of both species reached higher densities in the absence of the other, field voles appeared to suffer more from interspecific competition than sibling voles. On a population level, the sibling vole seems to be a superior competitor in the absence of predators due to better survival and possibly a higher reproductive capacity. However, predators can alter such interspecific competitive interactions substantially. We tested the effects of predation on the two species in large outdoor enclosures by predisposing vole populations to radio-collared freely-hunting least weasels (*Mustela nivalis nivalis*) for three weeks. Lethal and non-lethal impacts of predation limited the population growth of both species during and after the experimental period, but the magnitude of effect was different for the two species. The population growth of field voles became stabilized under weasel predation, while populations of sibling voles decreased markedly in size. At the population level sibling voles seem to be superior competitors to field voles, yet more vulnerable to predation. We suggest that predation risk probably has a profound effect on the relationship between the two species in nature and may even facilitate their coexistence.

MODULATIONS OF BEHAVIOUR AND CHEMOCOMMUNICATION OF MALE MICE

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For create model of the beginning stage of parasite penetration we used injection with bacterial lipopolysaccharide (LPS - component of the wall cell of gram-negative bacteria), which activates innate immune system.

In experiment on mice ICR one male group were treated with LPS (type 055:B5 Sigma, μg/kg, i.p.) and other one with saline (control). Through 3 h after injection LPS-treated males were lose competitiveness in pair-wise with control contestants ($Z=2.5$; $p<0.01$; $df=18$, Mann-Whitney U-test). On 5 days after injections they were recovered up to control level.

To estimate sexual attractiveness of the scent samples of these males we collected soiled bedding and urine in the 1st and 5th nights after injections. Scent attractiveness of urine and bedding samples collected in the 1st night after treatment did not differ between saline and LPS treated males ($Z=1.4$, $p=0.17$; $df=18$ for urine; $Z=1.7$, $p=0.09$; $df=58$ for bedding). Urine and soiled bedding of LPS-treated males sampled in the 5th night after injection were more attractive in comparison with control males ($Z=3.4$, $p<0.001$ equally for both samples). So, in contrast to immunogenic stimuli (SRBC) addressed to adaptive immunity, activation of innate immunity can increases male scent attractiveness, at least, in the time of behavioral recovering after LPS injection.

REPRODUCTIVE ISOLATION OF CLOSELY RELATED *MUS* SPECIES: THE ROLE OF CHEMICAL CUES

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The *Mus musculus* s.lato species group includes closely related *taxa* in different stages of divergence. We recorded patterns of c-fos expression in main olfactory bulb (MOB) and in the accessory olfactory bulb (AOB) in males in response to stimulation with urine from oestrus either con- or heterospecifics. *M. musculus*, *M. spicilegus and M. domesticus* males showed clear elevated c-fos expression in both MOB and AOB in response to stimulation with urine from conspecific oestous female. *M. spicilegus* males responded with elevated c-fos expression only in MOB to stimulation with urine from estrous female. In *M.musculus* and *M. domesticus* males also we did not observed c-fos expression in AOB in response to stimulation with estrous female urine from *M. spicilegus*. Under laboratory experiment patterns of behavior in mice were investigated in long-term (1.5 hour) dyadic encounters on neutral territory by means. Data analysis was made by means of Observer Video-Pro, Version 4.1. Elements of sexual, agonistic and amicable behavior were recorded. We did not found any qualitative differences in behavioral patterns of *M. spicilegus* and *M. musculus* including copulatory behavior but frequency and duration of some elements of agonistic and amicable behavior differ significantly. Male *M. spicilegus* made from 6 to 71 mounts with intromissions which terminated by ejaculation. After 8-10 min of rest cycle of sexual behavior was repeated. Male *M. spicilegus* can ejaculate during test from 2 to 9 times, mean – 6.4. Males of commensal taxa made from 4 to 115 mounts with intromission which terminated by one ejaculation. Mean ratio the number of mounts with intromission per one ejaculation in male *M. spicilegus* was 6.1, in males of commensal forms - 45.3 ($P>0.05$). Ejaculations in male M. spicilegus occurred significantly more often than in males of commensal mice. Different stereotypes of mating behavior during encounter of potential sexual partners can disturb communicative process and prevent successive copulation. *M. musculus* -*M. spicilegus* and *M. macedonicus* - *M. spicilegus* species distinguish between the urine odours of con- and heterospecifics and investigated conspecific urine odours more than heterospecific odours. The data obtained support the hypothesis that behavioral interactions and chemical cues can play role in reproductive isolation of closely related *Mus* species.

POLYMORPHISM OF THE MHC CLASS II DQA AND DRB GENES IN BROWN HARES (*LEPUS EUROPAEUS*) AND MOUNTAIN HARES (*LEPUS TIMIDUS*) FROM SWITZERLAND

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Elucidating how natural selection promotes local adaptation in interaction with migration, genetic drift and mutation is a central aim of evolutionary biology. In all vertebrates studied to date, the major histocompatibility complex (MHC) is a multigene family acting at the interface between the immune system and infectious diseases. Despite the fact that numerous candidate genes potentially under the influence of positive selection have been identified in model organisms the MHC remains a potential model for testing competing hypotheses on the causes and consequences of selection. This study aimed to provide preliminary data on the genetic variability of the MHC class II of the brown hare (*Lepus europaeus*) and mountain hare (*Lepus timidus*) two well-separated species that co-exist in Switzerland and, as previous genetic studies showed, hybridised in both direction. We analysed DQA and DRB genes in 116 individuals of *L. europaeus* and in 90 individuals of *L. timidus*, using Single Strand Conformation Polymorphism (SSCP) combined with direct sequencing. Eight alleles in *L. europaeus* and 5 alleles in *L timidus* were found for DQA. The percentage heterozygosity in *L. europaeus* and *L timidus* was 47.4% and 18.2% respectively. Nine alleles in *L. europaeus* and 7 alleles *L timidus* were found for DRB. The percentage heterozygosity in *L. europaeus* and *L timidus* was 28.6% and 57.6%, respectively. The construction of phylogenetic trees in both species and genes showed that several DQA (or DRB) sequences of *L. europaeus* are more relative to those of *L. timidus* and vice-versa, with high percentages of recombination. These findings are discussed in relation to genetic background, possible hybridization phenomena, life history of populations and immune reaction.

INTRINSIC AND EXTRINSIC MACHINERY OF POPULATION CYCLES IN SMALL MAMMALS

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The cyclic dynamics of many small mammals has been interesting for ecologists through decades, but the ecological machinery behind population cycle remains one of the intriguing puzzles in population ecology. We investigated the long-term population dynamics of two main vole species: the bank vole (*Clethrionomys glareolus*) and the red-backed vole (*C. rufocanus*) inhabiting the primary dark coniferous forests. The study was carried out at the Visimsky State Nature Biosphere Reserve (Middle Urals, N57°22′402″ E59°46′409″, 566 m a.s.l.) three times per year (spring, summer and autumn) in 1995-2006. We used arcsin(p) as density index (DI) of small mammals. The harmonic analyses of vole time series revealed two peaks of spectral density: first (weak) on the 1-yr and the second (strong) on 3-yr periods. According to the phase diagrams every year was classified into one of the three phases: trough (1996, 1999, 2002, 2005), increase (1997, 2000, 2003, 2006) and peak (1995, 1998, 2001, 2004). The vole spring densities in the peak considerably exceeded those in the increase, whereas corresponding autumn density was lower. The log-linear analysis of three way contingency tables phase(3)´age(3)´sex(2) indicated that age structure is not independent on phase. The lack of matured young both sexes in bank vole (males only in red-backed vole) in the peak is a certain evidence for density dependent asymmetrical scramble competition between immature and mature (territorial) conspecifics. When the population exceeds some density threshold in the beginning of a reproductive season the maturation of juveniles would be inhibited. On the other hand, for successful specialized predator reproduction (delayed numeric response) the sufficient prey density is necessary, as well. Not surprisingly, that mustelids (mainly *Mustela nivalis*) were captured every autumn (sometimes in summer too) in the prey peak only. The vole troughs were observed in the next springs after years when mustelids were captured in all cases (2´2 table: 0/4/8/0, exact 2-side Fisher's test, P=0.002). We suppose, that seasonality and the impact of specialist predators are the main causes (at least at the study area) of observed 3-yr cycles. The intra-specific interactions (self-regulation) supposed to be stabilizing loop that prevents population overshoot and resource exhausting. The interspecific synchrony of multi-annual dynamics both rodents and shrews may be explained as shared predation.

SURVIVAL ANALYSIS TO PREDICT THE PREDATION RISK IN REINTRODUCED POPULATIONS OF THE COMMON HAMSTER (*CRICETUS CRICETUS*) IN THE NETHERLANDS

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The common hamster (*Cricetus cricetus*), a rodent species inhabiting farmland in parts of west- and central-Europe, has suffered a dramatic decline over the last 20 years in the western part of its geographical range. Populations in France, Belgium, Germany and the Netherlands, collapsed mainly due to land-use intensification. In 2002, a breeding program was started to reintroduce the common hamster in the Netherlands. From 2002-2006, a total of 460 captive-bred hamsters were released at 6 locations with adjusted agricultural management, aimed to reduce predation risk. Part of the released hamsters and of (re)captured wild-born hamsters received a radio-transmitter. In this way, a total of 379 hamsters were monitored. Predation was the main mortality factor, with 95% killed by foxes, polecats, birds of prey, and other predators. Survival rate analysis revealed that mean yearly survival rate varied from 2-22% and was mainly dependent of: a) agricultural measures, b) origin of hamsters, i.e. wild-born or captive-bred, c) gender, d) site of release, e) month of release, and f) year. Perspectives for long-term conservation of common hamster populations on farmland are discussed.

POPULATION DYNAMICS OF THE *APODEMUS SYLVATICUS* IN THE NORTH WEST OF THE IBERIAN PENINSULA

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Although the wood mouse (*Apodemus sylvaticus*) is a large distribution species, it is scant the knowledge about its population dynamics in the Iberian Peninsula. In the present study it is contributed preliminary data about the species dynamics in the Burgos region, north peninsular.

It has been made seasonal samplings in three areas with different environmental characteristics: Orbaneja del Castillo, Covanera and Mozuelos de Sedano.

The samplings were made during three consecutive nights by life traps, being revised at daybreak. The captured specimens were identified at species level, weighted and sexed. The reproductive state and the age have been written down too. All specimens were marked and subsequently released. It was applied a capture rate which is expressed as (number or captured specimen / number of trap-nights) x 100. The capture efforts have been similar in all the three places.

During the first campaign there were captured 2 specimens of *Apodemus sylvaticus* in Orbaneja del Castillo. In Covanera 30 mice were captured and in Mozuelos de Sedano it was captured 15 wood mice and 2 *Microtus* sp. During the spring campaign it was captured 17 specimens in Orbaneja, in Covanera it was captured 32 specimens and in Mozuelos de Sedano it was captured 4 wood mice and 2 *Microtus* sp.

The biggest rates of capture obtained for the wood mouse were found in Covanera, being those 27.03% and 26.67%, in December and April respectively. On the other side, in December, Mozuelos showed a high level, 12.50%, coming down this to 3.33% in April. In the case of Orbaneja, it has been observed similar behaviour but opposite, being this 1.67% the obtained value in December and 14.17% in April. None the sampling areas have shown significant differences at sex rate.

BEHAVIOURAL DIFFERENCES AMONG INDIVIDUALS - PERSONALITY OF THE COMMON VOLE (*MICROTUS ARVALIS*)

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Selection impact on phenotype is one of the most important issues in evolutionary biology and ecology. By studying inter-individual variation, we would attempt to found whether there is a single best strategy for an individual to adopt or whether there are several viable alternatives.

The tendency for individuals to differ consistently in behavior is quantified as a behavioral correlation across situations. Therefore, we tested nearly 100 common voles in three experiments (1. New environment test, 2. orientation in an eight-arm radial maze and 3. feeding behavior in a cafeteria test) and then correlated behavior among them. Additionally, we were interested in measuring behavioral dependence on the intraspecific competition (number of animals in the breeding group and sex ratio in the group) and sex.

In the New environment test we monitored frequency, latency and total duration of various components of behavior. According to shy-bold continuum we assigned some individuals as completely shy or completely bold, whereas remnant animals, showing no apparent trend in behavioral components, occupied the middle part of this continuum.

The experiment in radial maze focused on the orientation and learning abilities of voles (they had to found and eat all pieces of food). Results from this experiment are not so clear but it seems that bold animals made more faults at the beginning but then they learn more quickly how to optimize their foraging activity.

In the cafeteria test we found out that animals differed in consummation of various types of food and this preference was also dependent on the position of the food in the experimental box. However, this behavior had no relationship to the personality of the animal, which contrasted with our expectations. It is probable that the forces of natural selection that promote individual differences for one activity can be different from those for other activities.

Moreover, the personality of studied animal was neither dependent on the number of animals in a breeding group nor on the sex ratio in the group. We didn't find any difference in behavior in our experiments between males and females.

To conclude, our experiments suggested that it is not necessary to live in fluctuating environments to maintain a mixture of different behavioral strategies but in fact, even in homogeneous environment interactions between individuals can favor the adoption of alternative tactics.

MOLECULAR PHYLOGENY OF THE GENUS *ALTICOLA* (CRICETIDAE, RODENTIA): EVIDENCE FOR PARALLEL PROGRESSIVE EVOLUTION

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Central Asian mountain voles *Alticola* is a yet poorly known group of voles which belongs to the tribe Clethrionomyini comprising also red-backed voles *Clethrionomys* and oriental voles *Eothenomys*. Phylogenetic relationships among the three constituent subgenera (*Aschizomys*, *Platycranius*, *Alticola* s.s.) as well as their affinities within the tribe are still unclear. Phylogenetic analysis of the sequence of mitochondrial cytochrome b gene reveals that *Alticola* s.l. is not a monophyletic group since the representatives of subgenus Aschizomys are closely related to *Clethrionomys*, whereas *Alticola* s.str. and subgenus *Platycranius* form a separate clade. Moreover, *Aschizomys* appeared to be polyphyletic as well, since *A.* (*Ashizomis*) *macrotis* is part of a well-supported group together with *C. centralis* and *C. glareolus* while *A.* (*Aschizomys*) *lemminus* tends to represent the basal branch within the poorly resolved complex of lineages including *C. rutilus*, *C. californicus*, *C. glareolus*+*C. centralis*+*A.* (*Aschizomys*) *macrotis*, and two forms of *C. gapperi*. The position of the flat-headed vole *A.* (*Platycranius*) *strelzowi* as the closest relative of *A. (Alticola) semicanus* is inconsistent with the monophyly of the nominative subgenus. The results of the relaxed-clock analysis suggest that *Alticola* s.s /*Clethrionomys* split dates to early Middle Pliocene. Basal cladogenetic events within *Alticola* s.str. can be attributed to the late Middle - early Late Pliocene. *A.* (*Aschizomys*) *macrotis* branched from *Clethrionomys* in late Early - early Middle Pleistocene. The proposed scenario of evolution in Clethrionomyini implies rapid parallel morphological changes in different lineages of *Clethrionomys*-like ancestral forms resulting in independent origin of several *Alticola*-like descendant taxa adapted to mountain and arid petrophilous habitats.

MORPHOMETRICS OF THE MOLARS AS A MARKER OF RECENT PHYLOGEOGRAPHIC EVENTS IN THE BANK VOLE (*CLETHRIONOMYS GLAREOLUS*)

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Phylogeographic analyses based on mitochondrial DNA evidenced a complex history for the bank vole *Clethrionomys glareolus* during the Quaternary, resulting today in several lineages: "Western" and "Eastern" (with respect to Eurasia), "Spanish", "Italian", "Balkan", "Ural". The last is characterized by a mtDNA signature typical of ruddy vole *Clethrionomys rutilus*. These phylogroups are interpreted as the result of repeated isolation in glacial refugia. Their differentiation is therefore recent, being less than 300 000 years.

Morphological criteria cannot compete with molecular markers for unraveling such recent and complex history. Yet, they can shed light on the selective context of the differentiation, and open the potential for a confrontation with the fossil record. As a first step, we investigated the patterns of differentiation of *C. glareolus* based on its third upper molar. The shape of this feature was quantified using a Fourier analysis of its 2D outlines.

The two species *C. glareolus* and *C. rutilus*, differentiated some 2.5 - 1.8 Myrs ago, can be differentiated based on their molar shape. Furthermore, the main phylogroups of *C. glareolus* display substantial morphological differentiation despite their recent divergence. Gene flow appeared to maintain a relative homogeneity within each phylogroup despite large geographic distances. This suggests that the molar differentiation among the phylogroups was driven more by drift during glacial isolation and subsequent expansion that local selection in the modern environments.

Finally, the M3 shape of the Ural lineage is clearly glareolus-like, hence showing a major discrepancy with mtDNA markers. The further analysis of nuclear genes is require to understand the processes that led to a bank vole morphology combined with ruddy vole mitochondrial DNA.

SHAPE ANALYSIS OF MANDIBLES AND FIRST UPPER MOLARS OF *APODEMUS* FIELD MICE: INFLUENCE OF PHYLOGENY AND GEOGRAPHY

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The field mice (genus *Apodemus*) are generalist murine rodents, with a broad Eurasian distribution area. The numerous species of the *Apodemus* genus have been grouped into four genera based on molecular phylogeny. In the present study we focused on the *Sylvaemus* and *Apodemus* groups. We investigated the patterns of shape differentiation of the first upper molar and mandible, in order to quantify the morphological variations among and within species and assess the relative importance of phylogeny and geography.

Several species of the *Sylvaemus* and *Apodemus* subgenera were sampled from a set of localities ranging from East-Asia to Europe. We quantified the shape of the mandibles and first upper molars using Fourier analyses, applied to their two-dimensional outline.

A high-level phylogenetic signal was first investigated by comparing both subgenera *Sylvaemus* and *Apodemus.* The molar clearly shows a shape differentiation between the two groups, whereas the mandible shape does not seem to be a good marker of phylogeny.

A smaller scale of variation was investigated by focusing on a set of Chinese localities sampling valleys isolated by deserts and high mountain ranges, where several *Apodemus* species occur in sympatry. Within each species, an important morphological differentiation separates the populations, suggesting that the mountain ranges and the overall complexity of the landscape constitute an efficient barrier to gene flow.

EFFECTS OF MAMMALIAN AND AVIAN PREDATORS ON OPTIMAL FORAGING TRADE-OFFS

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Studying adaptive foraging behaviour of small mammals under laboratory conditions reveals how they perceive their environment and permanently trade off, their feeding needs and predatory risks. Using a homogenous environment (for predators and prey mostly do use the same scale) with evenly spread predation risk, we conducted a series of foraging experiments using wild captured bank voles (*Clethrionomys glareolus*). In an arena with 25 food patches, different levels of risk where created by using a 2x2 factorial design. Avian predation risk was simulated by providing cover for the arena or no cover at all, and additional weasel odour was distributed in the arena at any start of an experiment. The results show that the manipulation of the type and combination of risks influence feeding strategies. In addition, the number of visited feeding stations and the feeding effort per tray change. In save situations (full cover, no odour) all trays are visited, with a lower local foraging effort but a high overall intake. Is feeding risky (no cover or occurrence of weasel odour), the overall intake is reduced, but a higher effort in a lower number of trays is made, resulting in a skewed distribution of space use. Video-analysis showed a temporal allocation of risk, depending on the presence or absence of the weasel. For example voles delayed their start of activity up to two hours and shortened their activity phases in the weasel treatments. Therefore animals differ between ground predation, where temporal allocation is more important, and avian predation, where spatial allocation seems to be the better strategy. Video-analysis of foraging activities were an useful tool of examining optimal foraging, for changes of strategies on a temporal axis play an important role in antipredatory behaviour.

HOT TOPICS IN PIKAS' (*OCHOTONA*) TAXONOMY

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Taxonomy of pikas was always one of the knotty problems in mammal systematics. Only a negligibly small number of Palaearctic *taxa* from this genus has ever been revised. More or less established taxonomy, which was reflected in MSOW II (Hoffmann, 1993), actually serves as a compromise between fragmentariness of our knowledge about pikas and the necessity of formalization. Application of genetic methods shifted the focus of interest to the problem of the subgeneric structure, which was reflected in MSOW III (Hoffmann and Smith, 2005). However, small percent of covered *taxa* and low bootstrap support in recent genetic studies, do not allow us to make strong conclusions about the subgeneric structure per se. Instead, some «hot topics», study of which can give some appreciable results, have been clearly outlined. For example, we can mark some groups such as *macrotis-roylei* and *erythrotis-gloveri*, phylogeographic study of which will be a noticeable contribution in perception of the history of fauna of Tibet and adjacent country. However, the main guideline in pikas taxonomy should be conducting of comprehensive taxonomic research. Prospects for development of pikas' taxonomy seem rather vague without combination of at least data on morphology and genetics. A glaring example of this thesis is a result of investigation of the group of "burrowing species" (*cansus*, *thibetana*, *curzoniae*, *dauurica* etc).

An example of comprehensive approach to pikas' taxonomy is the recently completed revision of *alpina-hyperborea* group. Combination of morphological, bioacoustic and genetic data allowed to essentially revise the concept of taxonomy and phylogeny of the group and made it possible to find the keys for diagnostics of earlier problematic populations. As a result, the group has been shown to comprise five species-level *taxa*: *O. alpina* (Altay-Sayan Mts, Hangayn Nuruu), *O. hyperborea* (Polar Ural, Putorana plateau, Yakutia, Russian Far East, Transbaikalia, Sayan Mts, Tuva, Hangayn Nuruu), *O. turuchanensis* (territory between the Yenisey and Lena Rivers), *O. hoffmanni* (Dutalan Ula - the Mountaine Range lied to the south-east from the upper Onon River), *O. mantchurica* (territory to the south from the Onon-Shilka-Amur Rivers, except Russian Primorye), the poorly known taxon *O. m. coreana* from Changbai Shan on the border of China and Korea is preliminary attributed to this species.

DISTRIBUTION AND DENSITY OF MEDITERRANEAN HARE (*LEPUS CAPENSIS MEDITERRANEUS*) AND WILD RABBIT (*ORYCTOLAGUS CUNICULUS*) IN SARDINIA (ITALY)

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Mediterranean hare in Italy occurs only in Sardinia. Wild rabbit in Italy occurs in just a few areas in the North of the country, in Sicily and Sardinia. In spite of the lack of information about the distribution and the population dynamic of these two species, both of them are game species in Sardinia. We investigated the distribution of both species by means of game bag records from 183 game preserves. We also estimated the population density by means of nocturnal spotlight censuses from 2003 to 2005.We performed one-way ANOVA to test significance in density differences between years or seasons, and the Multifactorial Analysis of Variance to test for significant interactions between factors (year-season) possibly influencing population density. Mediterranean hare occurred in the 76.6% of the total surface area of Sardinia. Mean hunting bag densities were low: 2 hares/Km^2 (min=0; max=30.6; SD=2.75). Taking into account data from all sampled areas, on the whole, spring-summer increase was of 99.4% and the summer-autumn decrease was of 15.3%. According to ANOVA test, no annual and seasonal density variation proved significant.

Wild rabbit range appears slightly smaller as this species is present on 71.8% of Sardinia. Mean hunting bag densities were 8.4 rabbits/ Km^2 (min=0; max=164; SD=16.95). From spring to summer 2004 wild rabbit population density grew by 106.2% and then decreased by 43.3% in autumn-winter. If we take into account the data from all the study areas over the 3-year period, a progressive decrease by 80.6% in the spring population was recorded from spring to autumn. ANOVA test did not show significant variations between years and seasons.

Both species appeared to be distributed uniformly whereas the range of the mediterranean hare seemed to be larger than that of the wild rabbit. The population density of the Mediterranean hare resulted lower and more variable than the other mainland hare species, and the populations of Mediterranean hare seemed to be in decline. The population density of the Wild rabbit was more variable than that of the hare, and in some areas it was quite high, but on the whole appeared stable.

BANK VOLE *CLETHRIONOMYS GLAREOLUS* CMR ON THE TRANSECT LINES: HOME RANGE AND NONRESIDENT MOBILITY

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CMR is routine technique for studying space usage on grids. Being applied to line trapping the same efforts give at least six times more samples: one could get more data or investigate more area using transect lines instead of grids. The challenge is to reveal sustainable estimates correlative with a range and indicative for space usage. In this study we test the technique which was elaborated for shrews CMR. The technique imply using of the original live-traps, were installed 7.5 m each from the other, with oat flakes whetted with sunflower oil as bait, checked twice in 1.5 h, so that traps were operative 3 h per day. We use standard deviation (s) as analogies of the r2. Latter was shown a metric measure correlative with another estimations of a range. The number of revealing of individuals recaptured 3, 4 and more times within distances of +1, +2, and +3s were referred to the total number of recaptures. This gives us proportion of revealing of individuals in those zones. The portions of revealing of individuals within zones approached to the expected for normal distribution and the coincidence of empiric and expected portions were found for individuals with 8 and more recaptures. Mean s stabilizes after 6-th recapture and mean s for 3 recaptures made 0.8 from s for 6 and more recaptures. The position of center of activity - x3 (mean coordinate for 3 recaptures) deviate at distances less than 0.5s for P<0.05. We assume that 6s embrace over 99% of the home range revealed for border captures. In fact mean distance between border captures was slightly less comparing to 6s but gradually approached to the value till the 20-th recapture. Taking into account that accuracy of revealing of a center was +0.5s we used deviation from x3 less than 1.5s as a criterion for stable position, and greater than 3.5s for moved range. Replacement of the activity center correlate with the distance between the first and the last capture (d). The distance (L) greater than 3.5s between subsequent captures was used as a criterion for nonresident mobility. As result we could distinguished intensive space usage: L<3.5s, d<3.5s, x3<1.5s, extensive space usage: L<3.5s, d<3.5s, 3.5s <x3<1.5s, emigration: L<3.5s, d<3.5s, x3<3.5s, and excursion: L<3.5s, d<3.5s, x3<3.5s.

NESTBOX UTILIZATION AND SPATIAL DISTRIBUTION OF THE WOODLAND DORMOUSE, *GRAPHIURUS MURINUS*, IN THE RIVERINE FOREST AT THE GREAT FISH RIVER RESERVE (SOUTH AFRICA)

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Very little is known about African dormice and even their current classification and the number of species are matters for discussion. Whereas seven genera of dormice occur in Eurasia, only two are recognized in Africa: *Eliomys*, which is only represented by the North African, “Eastern Orchard Dormouse” (*E. melanurus*), and *Graphiurus*, with 14 species. Of the latter genus, only 4 species occur in Southern Africa. Two of them, *G. ocularis* and *G. platyops*, inhabit rocky hillsides and koppies, while the two others, *G. murinus* and *G. parvus*, are essentially arboreal. It is on one of these species, namely the Woodland Dormouse (*G. murinus*), that a study was recently conducted. From June 2006 to May 2007, I performed weekly nestbox checkings and monthly trapping sessions in order to gather preliminary information on this dormouse’s social and spatial organization. The use of nestboxes by dormice was highest during the active, breeding season. Dormice successfully reared young in the nestboxes. At the principal study site, more than 60% of the nestboxes were found with nest material or occupied by at least one dormouse, others had food remains or found empty. Communal nesting was obvious throughout the year, with up to 8 dormice sharing a single nestbox, and so could not only be explained as thermoregulatory huddling. Cases of communal nursing (each involving two suckling females) were also recorded. Male and female individuals were found occupying the same nestbox, both simultaneously and alternately. Further information on the spatial distribution of dormice (based on both nestbox utilization and trapping data) will also be presented.

DENTAL VARIATION AND MORPHOLOGICAL DIFFERENTIATION AMONG SIBLING SPECIES *MICROTUS ARVALIS* AND *M. ROSSIAEMERIDIONALIS* (ARVICOLINAE, RODENTIA)

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Dental variation in sibling species *M. arvalis* and *M. rossiaemeridionalis* was examined to determine the possible taxonomic value of molar teeth morphology and to assess the level of interspecific morphological differentiation. Patterns of ontogenetic, sex-related and geographic variation were studied in terms of multivariate analysis of linear measurements of the first lower molars in 959 karyologically dated individuals from 45 populations in Western and Eastern Europe, Caucasus, Ural Mountains, Siberia etc. Our results indicated that both species exhibited high degrees of ontogenetic and geographic variability of molar size and shape; sex-related variability in dental features might be regarded as negligible. Considering intraspecific patterns of age variation and morphological distinctiveness among sibling species within ontogenetic classes, the three groups of dental traits could be established (1 - species-specific characteristics showing no dependence on age; 2 - species-related characteristics showing different patterns of ontogenetic variability (could be detected within age classes); 3 - characteristics showing the same patterns of age variability in both species). An analysis of geographic variation indicated that *M. arvalis* exhibited differentiation within the species range coinciding with the pattern of distribution of two karyotypic forms, *M. arvalis 'arvalis'* and *M. arvalis 'obscurus'* whose taxonomic status could be regarded as debatable. The differences detectable within *M. arvalis* range were less pronounced than those found among *M. arvalis* and *M. rossiaemeridionalis*; however they should be taken into account when establishing diagnostic criteria. Considering the problem of taxonomic identification, it was shown that discriminant function analysis provided the highest number of correct classifications (up to 100%) when regional data were used. Discriminant functions derived from the data on the whole ranges could be regarded as less powerful providing 78-88% of correct classifications for *M. rossiaemeridionalis* and *M. arvalis*, and 71-76% for karyotypic forms within *M. arvalis*. The results were interpreted with respect to a problem of identification of fossil data on sibling species of common voles.

DISCORDANT EVOLUTION OF KARYOTYPE AND GENETIC DIVERGENCE IN *MICROTUS SUBTERRANEUS*

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European pine vole (*Microtus subterraneus*) exhibits the highest within-species genetic variability among the representatives of subgenus *Terricola* and two karyomorphs are known (2N = 52-54). Populations of voles with 52 chromosomes occur at the centre of the distribution, whereas those with 54 chromosomes are found at range peripheries. We sequenced genetic markers with maternal (mitochondrial DNA) and paternal inheritance (Y chromosome) as well as markers on the X chromosome that are inherited from both parents. We found deeply divergent evolutionary lineages congruent among molecular markers, which do not correspond to the distribution of the two karyomorphs. Divergence between Europe and Asia Minor is smaller than divergence within the Turkish part of the *M. subterraneus* distribution. The lineage that colonised the largest area is spread across Central and Western Europe. Our data indicate that *M. subterraneus* survived the last glaciation in multiple refugia in Turkey and Europe. These results are discussed in regard to the role of glacial cycles for the rapid speciation processes in the genus *Microtus*.

NEW DATA ON THE MORPHOLOGICAL VARIATION OF EXTANT AND FOSSIL EUROPEAN POPULATIONS OF *ARVICOLA* (RODENTIA)

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Fossil populations of the water vole (*Arvicola*) are matter of detailed analysis by small mammal palaeontologists dealing with Quaternary stratigraphy during the last four decades. Most of the available studies are based on dental morphology, in particular on morphometric characters of the first lower molar (M/1). *Arvicola* M/1s, indeed, show a consistent morphological variation related to geological time. One of the features, which show evident general trends, is SDQ Index (Enamel Differentiation Quotient, by Heinrich 1978). This index accounts for the different thickness of the enamel walls of dental triangles of the water vole M/1s.

In the present contribution four morphometric parameters measured on several samples of fossil (Middle to Late Pleistocene: 600 - 10 ka) and extant *Arvicola* populations from Southern (Italy, France) and Central Western Europe (Germany, France and other countries) have been examined based on original observations and data derived from the literature.

The results evidence that there are apparent differences between extant Italian samples and those from the other considered geographical areas; in addition, such differences can be traced through all time horizons back to 200 ka ago. The geographical pattern of morphometric data also point out the occurrence of remarkable differences in few Italian samples, located at the North Eastern and North Western side of the peninsula. This observation is a clue that these mammalian populations were influenced by faunal elements from the neighbouring (South-Western Mediterranean, Central- and Eastern European) sub-bioprovinces.

Eventually, the observed chrono-geographical pattern strongly supports that the Italian *Arvicola* represents a subspecies distinct from the other Central and Western water vole populations grouped within *Arvicola terrestris*. Such possibility is also supported by the results of molecular phylogenetic studies on extant *Arvicola* carried on by Wust-Saucy (1998) and opens up new prospects for further research on this topic.

HABITAT SELECTION OF COMMON DORMOUSE (*MUSCARDINUS AVELLANARIUS*) AT TWO SPATIAL SCALES IN A WOODLAND MOSAIC OF CENTRAL ITALY

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Common dormouse (*Muscardinus avellanarius*) is a vulnerable species in most of its geographic range. Woodland fragmentation is the major factor of its population decline. In order to plan adequate protection measures for this species, a basic knowledge of its habitat selection is required. In this study we gather detailed information about the habitat types selected by the species during its nocturnal activity. The study was carried out in the Natural Reserve "Castel di Guido" (near Rome, 41°54'N, 12°31'E), a mosaic of woodland types consisting of natural patches (thermophilous mixed oak woodland) and artificial patches (planted tree stands belonging to both deciduous and evergreen species). On the whole, 25 dormice (15 males and 10 females) were captured using nest-boxes and fitted with radio-collars. Radiotracking was performed in six sessions lasting three weeks each: three sessions in autumn (November - December 2003, 2004 and 2005) and three in spring (March - April 2004 and 2006, April - May 2005). Dormice were tracked every night. The position of the animals was established by observing them (homing-in method) or by cross-triangulation, receiving the radio signal on foot. The fixed-kernel method was used to calculate seasonal and weekly 90%, 50% and 70% home ranges. The use of different landscape elements by dormice was compared to their availability using compositional analysis at two spatial scales: (1) home range vs. study area, and (2) locations vs. home range. Compositional analysis showed that the habitat selection performed by dormice was influenced by the seasonal distribution of resources. In autumn, either for the study area or home ranges dormice preferred natural patches where they found food (acorns) and shelter (evergreen cover). In spring, pine stands played the most importat role, but also maple stands and natural patches were utilized by dormice. Moreover, during the spring, the ranking of habitat types changed throughout the weeks. It was probably due to the exploitation by dormice of different, patchily-distributed food sources as the season progressed. Because of the low mobility of the species and its small home ranges, we thought that the second scale (home ranges vs. study area) offered a more realistic information, respect to the first one (locations vs. home ranges). For example, the latter analysis assigned a high rank to open areas, while the second scale analysis recognized the lowest rank to the same habitat type.

THE ALPS AS AN INTERGLACIAL REFUGIUM FOR THE MOUNTAIN HARE *LEPUS TIMIDUS*

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The mountain hare, *Lepus timidus*, is a northern Palaearctic species that ranges from the Baltic countries to the Pacific Ocean, with several isolated populations in Ireland, Scotland, Poland, Alps and Japan. This distribution most probably resulted from a postglacial expansion to the north, following the deglaciation of the land. Recent analysis of mtDNA diversity suggests that it has a phylogeographic pattern typically ascribed to arctic species, with a general lack of geographic structure, except for the isolated populations, and a major population expansion possibly during a glacial period. Here, we analysed mitochondrial control region and cytochrome b sequence variation of 47 *L. timidus* from the Alps, one of the species' isolated populations, and compare it with that found among other Euro-Asiatic populations. Interestingly, we found in the Alpine population a genetic diversity of the same order of that of *L. timidus* over its range (1.9% and 2.3% respectively). The haplotype network shows that these haplotypes belong essentially to two highly differentiated groups (2.3% uncorrected net distance) which we found to have a correspondent geographic structure (group A in the East and group B in the West). The results suggest that the postglacial colonization of the Alps by *L. timidus* had multiple origins and this mountain chain can now be working as one, or multiple, interglacial refugium to this arctic species.

MITOCHONDRIAL PHYLOGEOGRAPHY OF THE STRIPED FIELD MOUSE (*APODEMUS AGRARIUS*) THROUGHOUT THE PALAEARCTIC REGION

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The phylogeography of the striped field mouse, *Apodemus agrarius* (N=164) has been studied throughout its distribution area from China and the Russian Far East in the East, to Western Europe in the West). The mitochondrial cytochrome b was sequenced for these animals and the obtained dataset was analysed using different phylogenetic reconstruction as well as other methods adapted to phylogeography.

We evidenced that animals from China are separated from the remaining populations since at least one million years. This can be attributed to the island character of this region caused by strong biogeographic barriers (Himalaya, Tibetan Plateau, Gobi desert.) preventing gene flow between Chinese field mice populations and those of the Palaearctic regions. The Russian Far Eastern populations appear strongly associated with populations from Central Russia as well as Western Europe. Moreover, the Far Eastern striped field mice are also characterised by a high level of genetic diversity as compared to the other ones. This result strongly suggests that the Russian Far East was the population of origin for the striped field mice and that it is from there that it colonised the entire Palaearctic region. In contrast, the extremely low levels of genetic diversity characterising contemporary European populations suggest that they derived from a very recent colonisation of Europe, probably during the Early Holocene.

POSSIBLE INVOLVEMENT OF A WHOLE ARM RECIPROCAL TRANSLOCATION (WART) IN THE EVOLUTION OF AN RB SYSTEM OF *MUS MUSCULUS DOMESTICUS* FROM GREECE

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It is now common knowledge that the Euro-Mediterranean natural populations of the house mouse *Mus musculus domesticus* are characterized by an extensive chromosomal variation, due to the appearance of Robertsonian fusions (Rb) in the karyotype. Thus Rb systems are formed, consisting of Rb races whose karyotype morphology deviates from the typical all-acrocentric form (2n=40) to as low as 2n=22.

In Greece, it has been established that there exist at least three Rb systems, one of which is among the oldest known, covers the area of NW-W Peloponnese and consists of at least three Rb races, with 2n=30, 28 and 24, respectively. It had been previously suggested that these races were formed, according to the "Multiple Succeeding Mutations" model. In that context, the two Rb races with 2n=28 and 2n=24, may have differentiated allopatrically in the past, since they are characterized by monobrachial homology: the former has Rb (3.6) and the latter Rb (1.3) and Rb (4.6). We hereby suggest that, alternatively, the two races may be connected through a type 'b' Whole Arm Reciprocal Translocation (WART). In that case, either race could be a potential precursor of the other. Apparently, was such a possibility true, it would modify the expected phylogenetic relationship among the Rb races of the system.

With this opportunity, a hypothesis is suggested on how the Rb system of NW-W Peloponnese may have achieved its current form, taking also into consideration the historical context of the area and the contribution of commensalism in the dynamics of the natural populations of the house mouse, as well as in the fixation of Rb fusions.

MULTIDISCIPLINARY APPROACH TO THE ECOLOGY OF EURASIAN RED SQUIRRELS (*SCIURUS VULGARIS*) IN AROLLA PINE (*PINUS CEMBRA*) FOREST

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Squirrels, caching cones or seeds in small holes in the forest floor, have an important role in conifer seedsdispersion and, therefore, contribute to the natural regeneration of forests. Seeds of arolla pine (*Pinus cembra*) do not have wings for wind dispersion but depend on caching by animals for germination the next summer. Moreover, squirrels are known to disperse spores after consumption of epigeous and hypogeous fungi, that in alpine forest habitats represent a considerable food source for squirrels from late spring to autumn. To investigate ecology of Eurasian red squirrel (Sciurus vulgaris) in alpine forests we started our studies in an arolla pine dominated area of 93ha in the southern Alps, Italy, in 2001. We monitored conifer seed production and consumption by counting cones on target trees every two weeks in order to to explore the extent of seed predation and caching by squirrels and other food competitors such as the nutcracker (Nucifraga caryocatactes). Two plots of 200 m^2 each, were used to monitor epigeous fungi production, and four circular plots of 3.14 m2 each, were established nearby each of the twenty trapping points and the ground was searched for epigeous fungi. Number of hidden seeds was counted in 80 plots of 2.5 m^2 from spring 2005 to autumn 2006. During capture-mark-recapture sessions carried out in spring, summer and autumn each year, we collected skin samples for genetical analysis and fecal samples to investigate the presence of fungal spores and to compare presence in the diet with availability of epigeus and hypogeus fungi on the study area. Coat polymorphism was investigated as well, to test whether one of the three morphs (red, black or intermediate) had a higher fitness then others under habitat-related environmental conditions. Seasonal sessions of radiotracking have been made in autumn 2002, spring and autumn 2003 and 2005 to analyze space use by squirrel related to previous year seed production. This poster illustrates some interesting characteristics of the ecology of squirrels in this particular forest habitat revealed by this multidiscplinary approach.

SPECIES RICHNESS IN RODENTS AS BIOINDICATOR OF CLIMATE CHANGES

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Geographical distribution and species richness in mammals, and in particular in rodents, seem to be highly dependant on climate. The geographical diversity of several rodent sub-families has been studied and is clearly not randomly distributed. The arvicolines have an holarctic distribution and are very well diversified in the most Northern areas. At the opposite, murines are only found in the old World and are particularly numerous in tropical and sub-tropical regions. Sigmodontines are distributed only in the New World. For these rodents, the correlations obtained between climatic parameters, as mean annual temperatures or precipitations and number of species, are high. They can be considered as good bioindicators of climate changes. These relationships yielded to quantification models based on linear regression that can be then applied on fossil faunas to estimate past temperatures.

Thus species richness has been compiled (1) in sigmodontines for 270 extant local faunas from North and South America, (2) in arvicolines for 250 extant local faunas from Old and New World and (3) in murines for about 180 extant local faunas from the old World with respectively the corresponding climatic data (mean annual, monthly minimum and monthly maximum for temperatures and precipitations). Local faunas represent homogeneous ecosystems and they cover surfaces ranging from 1 km^2 up to 50000 km^2, but they generally are less than 1000 km^2. Anyway, there is no correlation between areas of localities and numbers of species in the fauna. The relation between the number of species and the present day temperatures is high, ($R^2 = 0.848$ for sigmodontines and $R^2 = 0.828$ for arvicolines). This relationship means that more than 80% of the species richness and distribution is controlled by temperatures.

To compare and validate these temperature estimates, oxygen isotope composition of biogenic phosphates from vole teeth was used. An oxygen isotope fractionation equation was determined by using present-day European arvicoline tooth phosphate, and then applied to the Late Pleistocene karstic sequence of Gigny. The oxygen isotope compositions of arvicoline teeth record variations in mean air temperatures (from 0°C to 15°C) similar to those obtained with the species richness (from -2 to 12°C).

This relation to the climate is clearly higher for the small mammalian species, as rodents, than for the large ones, as ungulates, for which the determination coefficient is only equal to 0.3.

MORPHOLOGICAL VARIABILITY IN VOLES (RODENTIA, ARVICOLINAE) AND ENVIRONMENTAL CHANGES

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For a long time, morphological differentiation in size and shape has been related to many aspects of systematics, biogeography, ecological distribution or even biochronology. However the relationships between variability in size and shape on one side and the related changes occurring with time or climate are usually complex and difficult to understand and interpret. What kind of relationships can be described between shape and biotic/abiotic environments?

Morphological variability is here illustrated for different vole species on both extant (*Microtus arvalis*, *M.* (*Terricola*) *savii* and *Chionomys nivalis*) and fossil species: *M. (Terricola) grafi* from Bacho Kiro (Bulgaria, Pleistocene) and *Microtus arvalis* from Gigny (Jura, France, Pleistocene). Morphology is usually investigated using biometry or outline analysis on the first lower molar.

For the living species, the morphological analysis shows that (1) at a regional scale, morphological variability is clearly in relation to geography and consequently to climate and environment; and (2) at a local scale, the morphological variability can be due to the fragmentation of some particular areas leading to isolation of small populations characterised by different morphotypes. For example, in *M. arvalis*, a morphological analysis has been done on several French populations and shows that the variability is a function of continental gradient or altitude. In *M. (T.) savii*, the analysis has shown a clear morphological differentiation between north-central and south populations and the isolation of the populations from two regions of the Padana plain (Veneto and Emilia Romagna). Two hypotheses can be proposed to explain this divergence: 1 – the important change of this region due to human activity; 2 – the complex hydrography of this plain.

For fossils (*M. grafi* and *M. arvalis*), the morphometric analysis shows that the tooth shape is in relation to climatic and environmental conditions. But, for both fossil and living species, a direct relationship between the cause (climate) and the effect on tooth (morphological variability) is difficult to interpret. What is the significance of the response? Adaptation in a particular landscape? Or genetic answer, or phenotypic plasticity? In voles, one hypothesis can be that more the tooth has cusps, more the advantage is important in cold and dry landscapes with a better resistance to the abrasion.

POPULATIONS OF THE FIELD MOUSE (*APODEMUS AGRARIUS* PALLAS 1771) IN VARIOUS CONDITIONS OF URBAN ENVIRONMENT

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This reseach was devoted to study urban populations of the field mouse inhabiting two places (A, B) of Tomsk – one of the oldest Siberian cities. Some ecological characteristics (number of individuals, reproduction, demographic structure, mortality, helminth infestation), behavioral peculiarities and humoral immunity were studied. More than 600 specimens of *Apodemus agrarius* during 20 years period was investigated. In habitat A the field mouse was dominant (98-100%), while in habitat B varied from 10% up to 12% in different years. The number of the field mouse in site A was on average three times higher ($P < 0.05$) than in site B. The investigated populations differed by dynamics of demographic structure: males (60-65%) prevailed over females in population A as well as the percent of overwintered mice (40-50%). In population B the youngs-of-the year (80-90%) dominated that is typical for age structure of small rodents during the summer period; prevalence males here was more expressed (75 - 80 %). Both populations were infected by nematode *Heligmosomoides polygyrus* with a higher prevalence in A ($P<0.05$). Average fertility and scope of fluctuations of litter size in the population A was higher than in the population B. Smaller litter sizes (4.0 ± 0.35) bring overwintered females in the early spring. In summer their fertility considerably grows. In different years it changed from 8.6 ± 1.5 up to 9.5 ± 1.4. Humoral immunity estimated by the relation spleen antibody-forming cells to body weight of mature females in the population A was higher (319.5 ± 37.4) than in the population B (160.4 ± 23.2). As a whole the very high fertility of females can be caused by high mortality of the youngs-of-the year of summer generations. As we established early young mice in the age of till 40 days have the least immunoresistense. During this period most of them leave jacks and can be exposed significant mortality. On the other hand the large litter sizes in the population combined with the absence of interspecific competition and the weakened pressure of predators can be considered as some kind of the compromise (trade-off) the life cycle, allowing to direct a significant part of energy resources not only on reproduction but also on maintenance of high level of humoral immunity though a high level of population density, high fertility and significant helminth infestation assumes significant immunosupression. Experimental studying of behaviour has shown that adult males from the isolated population (A) have smaller locomotor and exploratory activity ($P<0.05$). Besides their behavior in the pair wise test was less aggressive ($P<0.05$). Thus synurbiziering population of the field mouse (A) has features characteristic for synanthropic species - the house mouse. It concerns spatial distribution of animals during the various periods of their life. Winter transition in the greenhouses provides the big survival rate, promotes, probably, to the reduction of the body sizes. The behavioural peculiarities of animals from this population testify to presence of the selection directed on preservation of less aggressive individuals.

SEASONAL AND AGE DYNAMICS OF REPRODUCTIVE ACTIVITY OF THE STEPPE VOLE

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A long-term keeping a steppe vole in the captivity revealed such a fact that a part of the animals do not breed (approximately 30-40% of females and males). The founders of the colony were caught in Kalmykia and since 1994 they have being kept in the laboratory of ethology. The aim of the present research was to evaluate the fertility of males of the steppe vole *Microtus socialis* and to find out the factors, which defines their reproductive success.

Males of the steppe vole are able to breed at the age from 3 to 12 months. Only several males breed at the age of 2 months, since their genital glands are not developed enough morphologically and functionally, it especially concerns seminal vesicles, which provide liquid environment of sperm. The intensity of spermatogenesis of males at this age is low, the developed spermatozoa are practically absent or there are very few of them. By 3-5 months, the genitals of 40% of males not only increase in size and mass, but also the spermatogenesis proceeds more actively, of what the increase in the quantity of active spermatozoa in the epididymis is evident (density 81.7%). Sequentially, 60% of males have a lowered level of the spermatogenesis already at this age (density 15.6%). At the age of 6-7 months, a part of the animals with the lowered reproductive qualities is decreasing and makes up only 30%, while the density and mobility of spermatozoa of voles remains rather high.

In the period from 8 to 12 months, natural selection according to the reproductive qualities takes place. A part of males with the lowered sperm density makes up from 15 to 30%. Beginning from the 10th month, the sexual activity is gradually fading. The spermatogenesis is gradually becoming slower, the density of spermatozoa is lower for 20% in comparison with young males, but the mobility remains at the same level. The data of the morphological showings of the reproductive organs of males correlate with the showings of sperm. The reasons of saving the males with the lowered reproductive abilities in culture are different: the genetic factor, deficient providing spermatozoa with nutritive materials. It can be supposed that in the conditions of the laboratory keeping, a slightly increased number of steppe voles can be pointed out which influences not only on the number of sexual contacts but also on a scent-signal field. As a result, the males' spermatogenesis can be destroyed because of destructive changes of the testes that leads to the decreasing of some developing spermatozoa as well as their mobility.

In culture, the steppe vole has an ability to breed during the whole year, nevertheless, the most successful breeding proceeds in spring and autumn. In summer and winter, the reproductive success decreases and only a part of voles breeds.

MORPHOMETRIC APPROACHES OF TWO SYNTOPIC SPECIES OF *APODEMUS* (RODENTIA) IN THE PYRENEAN REGION

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Apodemus is one of the most abundant components of rodent communities in south Western Europe. In some places of Southern France and Northern Spain, *A. flavicollis* and *A. sylvaticus* occur together in sympatry and are trapped in the same lines of captures (syntopy). Despite a clear genetic discrimination there are still some difficulties to separate the two species if we rely only on external morphology and it was interesting to study how syntopy may affect the morpho-anatomy of these species.

Consequently, we used a morphometrical approach in order to assess the population variability and study the impact of syntopy on the two species.

The material analysed here is composed of 134 *A. sylvaticus* and 30 *A. flavicollis* collected from 1994 to 1996 during four fieldworks in three localities from the Spanish and French Pyrenees (Eugi, Areu, Montseny). Skull and mandibular distances were used in multivariate analyses (PCA, DA) on genetically determined specimens.

Species are well separated by using PCA and DA and we found that both species could be discriminated by their form (size and conformation) with a notably larger size for *Apodemus flavicollis*.

Log shape ratio analyses displayed some differences of form between the two species. The age and sex effects were tested through ANOVA and MANOVA and are strong in these *taxa*. The locality effect was tested on mandibles and skull.

In the Pyrenean region the two species of *Apodemus* display an important variability. It seems that despite an old date of divergence between the two species they still keep globally very similar morphologies but morphometric analyses separate them easily. Is syntopy acting as a pressure on development and morphology? Other studies show that sympatric species generally display character displacements. Patterns that we observe here are consistent with a character displacement, nevertheless we need further study to confirm this hypothesis. Anyway at the population level, one notices form differences between species and changes in form between populations of the species *A. sylvaticus* in allo- or sympatry.

PRELIMINARY ANALYSIS OF SHAPE DIFFERENCES IN THE MANDIBLE OF *FUKOMYS* AND *CRYPTOMYS* MOLE-RATS (RODENTIA: BATHYERGIDAE)

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Bathyergids, commonly known as African mole-rats, are fossorial mammals distributed throughout sub-saharan Africa who use their teeth to dig the tunnels they live in. The family contains six genera. Primarily on the basis of molecular data the genus *Cryptomys* was split and the new genus *Fukomys* was erected for the mole-rats occupying the south-central African savannahs and the savannahs north of the equatorial rainforest belt. A landmark based geometric morphometrics approach has been used to investigate morphological divergence between *Fukomys* and *Cryptomys* and to look for possible adaptive trends in the mandibles. Preliminary principal component analysis and thin plate spline analysis reveals localised differences between the genera. Notably the shape of the coronoid process may be different between the taxa. Preliminary Canonical Variate analysis gives an indication of interspecific variation among *Fukomys* species.

SOME DATA ON THE PRESENCE OF SNOW VOLE *CHIONOMYS NIVALIS* (RODENTIA, ARVICOLIDAE) ON THE ITALIAN APENNINES

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The Italian range of the snow vole covers the Alps and Apennines. The northern and central Apennine ranges show to be separated. The more abundant records come form the Tuscan-Emilian Apennine and from the massifs of Gran Sasso and of Maiella to which further records are added, coming from other mountains such as the Apuan Alps, the Abruzzo National Park, the Mount Greco (30-07-1996, F. Conti, pers. obs.), the Duchessa, The Matese (the last record dating the 80s of the twentieth century). The species' real presence on the Sibillini and its persistence on the massif of Matese need to be confirmed. Its presence in Calabria - apart from literary records of uncertain reliability - is supported by one specimen caught in 1970 around the lake Cecita (Nat. Hist. Mus. La Specola, Florence, cat. n. 7448). Till now this is the most southern record for Italy and it is clearly separated by the remaining part of the Apennine areal distribution of the species. For 50 sites we were able to analyse altitudinal distribution that shows the snow vole living in a range between 805 e 2925 m a.s.l., mean 2051 m, SD=574. According to the altitudinal layers we had the following results (inside the parenthesis the number of records): 500-1000 (1); 1001-1500 (4); 1501-2000 (21); 2000-2500 (13); 2501-3000 (11).

HOME RANGE SIZE AND SOCIAL ORGANISATION OF MOUNTAIN HARES (*LEPUS TIMIDUS*) IN THE ITALIAN ALPS

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The mountain hare (*Lepus timidus*), is a palearctic species with a typical arctic-alpine distribution. In the Italian Alps, that constitute the southern edge of its range, it has a patchy distribution in suitable alpine habitats above elevations of 1500 m. These selected habitats, such as coniferous forests close to alpine pastures and coniferous and broad leaf shrubs, often occur as fragmented patches in the heterogeneous alpine landscape. There is very few information on the ecology of mountain hares in the Alps and the effects of habitat structure and composition on space use and distribution are unknown. We explored habitat-space use relationships by monitoring two populations occupying different habitat types (one composed of a homogeneous dwarf mountain pine (*Pinus mugo*) woodland, the other a mixed woodland of spruce (*Picea excelsa*), swiss stone pine (*Pinus cembra*), mugo pine (*Pinus mugo*) and larch (*Larix decidua*) in upper Valtellina, Sondrio province, using capture-mark-recapture and radiotracking.

During the first two years of the study, 34 hares were captured with live traps and long nets and individually marked with ear-tags and radio-collars. The average annual and seasonal home ranges were estimated with 100%, 95% MCP and 95% fixed kernel methods. We found no effects of sex, age (adults versus juveniles) and study site (habitat type) on mean annual home range size. Overall, annual home ranges in our alpine populations were smaller than the ranges documented for North Europe, where suitable habitats are contiguous and spread over larger areas in comparison with the fragmented alpine environments.Interestingly, and in contrast with many other small and medium sized mammals, mountain hares seem to have a homogeneous spatial behaviour pattern within the home range, since incremental cluster polygon analysis did not reveal the presence of a true core area. Finally, home ranges of individual hares of either sex overlapped considerably, suggesting absence of territorial behaviour.

THE EFFECT OF SEX, SOCIAL RANK AND POPULATION ON BASELINE GLUCOCORTICOID LEVELS IN SPINY MICE (*ACOMYS CAHIRINUS*)

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Spiny mice are social rodents living in family groups and aggressive interactions between members of family may occur. We assessed baseline levels of glucocorticoid metabolites (GCM) in two populations of spiny mice (*Acomys cahirinus*): commensal from Cairo and non-commensal from Abu Simbel (southern Egypt) that differ not only in appearance, but also in some behavioural traits.

To collect faecal samples, we constructed a special experimental cage with wire bottom (for collecting faecal samples). Family group lives inside the cage, during sampling are experimental individuals closed in lateral parts; they are allowed to olfactory and visually communicate with animals in the central part. This design allowed (1) regular faecal sampling from tested animal without any disturbance, (2) social communication among sampled animal and the other family members during sampling.

For the determination of the amounts of cortisol metabolites (CM), we used a 5α-pregnane-3β,11β,21-triol-20-one enzyme immunoassay (EIA), which recognises GCM with a 5α-3β,11β-diol structure. This method was physiologically validated by an ACTH challenge test. Administration of ACTH significantly elevated levels of GCM in faeces defecated 4 hours after injection.

The results showed no effect of rank and only a small effect of sex (higher levels found in females) on GCM concentrations. Thus, the hypothesis that dominant males are more stressed than other functional groups may be rejected. Surprisingly, there was a considerable difference among family groups. This may be interpreted as a substantial effect of social relationships within each particular group.

The commensal population exhibited much higher levels of GCM than the desert one. This is consistent with behavioural differences of the studied populations - commensals are more active, but simultaneously also more anxious. Evolutionary adaptation to living in buildings is suggested as the ultimate cause of these physiological and behavioural differences.

MORPHOLOGIC COMPARISON OF SARDINIAN AND CAPE HARES AND TAXONOMIC IMPLICATIONS

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The cranio-dental features of the Sardinian hare, *Lepus mediterraneus* Wagner 1841 today considered as a subspecies of *L. capensis*, have been compared with those of *L. capensis* from the type locality, in order to clarify the taxonomic status of this insular population.

Sardinian hares show unique cranial features, standing out the high protrusion of the frontal bone between nasals and the particular shape of supraorbital processes, which have oral parts diverging forwards and aboral parts converging backwards. When compared with *L. capensis*, Sardinian hares have a smaller skull size, as reflected by most measurements. However, Sardinian hares have a higher posterior zygomatic width, resulting in a wider braincase than *L. capensis*, and larger ventilation orifices and arterial foramina, e.g. higher values of anterior nasal width and postpalatal width variables.

Dental morphology differs as well in both species. In contrast to *L. capensis*, Sardinian hares show in most cases a p3 with a longer anterior lobe, a smaller hypoconid, no paraflexid or parafossettid, stronger crenulation depth in the hypoflexid enamel and no cement in the incisor groove.

The differences in cranial and dental features of Sardinian hares with respect to *L. capensis* clearly indicate its taxonomic status as a valid species independent of *L. capensis*, being *L. mediterraneus* the appropriate name to be used for this population.

FEEDING BEHAVIOUR IN FOSSIL RODENTS: NEW METHODOLOGICAL APPROACHES

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In the last few decades, new approaches have been developed to help defining the palaeo-autoecology and synecology of fossil mammalian *taxa* and to correlate structural change of environments and palaeocommunities with climatic variations. Invaluable information for palaeoclimatic and palaeoenvironmental reconstruction can be deduced by studies on trophic structure, and several attempts have been made for defining feeding behaviour of large mammals. There are several morphological features of the skull, mandible and dentition that are well correlated with dietary adaptations, and thus can be used for estimating the feeding ecology of extinct *taxa*.

Furthermore to defining trophic categories great importance got the analysis of the tooth wear defects produced by the attrition and abrasion (microwear). Indeed the alimentary habits of vertebrates (reptiles and mammals) can be deduced from microscopic scars on tooth enamel, result of direct contact between food and tooth or tooth and tooth, and influenced by masticatory dynamics, enamel structure and tooth morphology. Microwear can form or wear out quickly, even daily. Therefore a study of the microwear of a palaeocommunity can give significant information about the preferential diet in the considered time. Nonetheless, thus far very few or no study have been devoted to microwear analysis of molars in small mammals. For a sound reconstruction of dietary adaptation in fossil rodents it is imperative to known microwear patterns deriving from different feeding. For this purpose, 7 specimens of *Myodes glareolus* (both sexes) have been feeded with a controlled diet: the first one with fruit (apples), other two with cereals (respectively barley and oats) and the latter four with grass containing an high concentration of phytolithes (Gramineae spp.). Dietilic ether has been used to sacrifice the specimen. The skulls have been removed, skeletonized by larder beetles (Dermestidae) and washed with H2O2 (30 vol.). Successively, teeth surfaces have been observed by SEM (Scanning Electron Microscope) and by metallographic microscope to identify tooth microwears. This study will constitute the basis for any successive application to fossil specimens.

CHANGE IN SMALL MAMMAL MOVEMENT PATTERNS FOLLOWING FOREST ROAD CONSTRUCTION

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Movement patterns of the Korean field mouse (*Apodemus peninsulae*) were compared before and after forest road construction to investigate whether forest roads act as movement barriers for small mammals. Field mice were trapped in a deciduous forest in Jincheon, South Korea, with 200 Sherman live traps set in a 20x10 grid configuration with 10 m spacing between traps. The pre-road trapping grid was centered on the future location of the road. When constructed, the road bisected the trapping grid and resulted in a 10 x 10 grid of traps on either side of the road. Trapping was conducted for 2,000 trap nights in July and August both before (2005) and after (2006) forest road construction. No difference in home range sizes (100% minimum convex polygon) was found before and after construction ($P = 0.18$). Movement distances also did not differ ($P = 0.72$). However, parallel movements were longer ($P = 0.05$) and movements perpendicular to the road tended to be shorter ($P = 0.06$) after construction than before construction. Although field mice did not exhibit directional movement before road construction ($0.05 < P < 0.10$), after construction mouse movement paralleled the road ($0.025 < P < 0.05$). No mice appear to have crossed the road. These results support the hypothesis that forest roads may act as barriers that alter movement patterns of small mammals.

COMPARISON OF HOME RANGE SHAPE OF SMALL MAMMALS WITHIN FOREST ROAD EDGE AND INTERIOR FOREST

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Home range shape of the Korean field mouse (*Apodemus peninsulae*) was studied to investigate a barrier effect of forest roads on small mammals. Five ‘edge’ field mice were captured within 10 m of a deciduous forest road in Jincheon, South Korea; an additional five ‘interior’ mice were captured >50 m from the road. All 10 mice were fitted with radio transmitters and located by telemetry between 14 and 65 times (mean = 45.3) over a period of 4 to 18 days (mean = 14.7) in October and November 2006. Home range shape of the two mouse groups, as determined from point locations, was analyzed with the Jennrich-Turner method, a comparison of the minor and major axes of an oval-shaped home range. The analysis demonstrated that the mean ratio of major and minor home range axes of edge mice was smaller than that of interior mice (0.2583 ± 0.0425 and 0.4804 ± 0.0901, respectively), i.e., mice along roads had elongated home ranges while interior mice had more rounded home ranges. These results support the hypothesis that forest roads may impact small mammal movement patterns and home range shape through a barrier effect.

PATERNITY AND RELATEDNESS IN THE NATURAL POPULATION OF THE SOLITARY BATHYERGID, THE SILVERY MOLE-RAT *HELIOPHOBIUS ARGENTEOCINEREUS*

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The African mole-rats (family Bathyergidae) are subterranean rodents that form a wide range of social systems varying from solitary to eusocial species. Based on the spatial distribution of burrow systems, low population density, absence of sexual dimorphism and expected limited aboveground movement, it was assumed that solitary silvery mole-rat has monogamous mating system, but until now no genetic data were available. The aim of this study was (1) to check the litters containing at least three embryos for the occurrence of multiple paternity (2) to analyse in detail the paternity and relatedness in one population living in miombo (Brachystegia woodland) in Malawi.

Ten litters with three or more offspring originating from five localities were examined by using eight polymorphic microsatellite loci to identify the number of fathers siring the litter. Furthermore, 54 specimens from one population (8 ha, Mpalanganga estate, Zomba, Malawi) were captured and sampled for relatedness analyses (four adult and three subadult males, twenty-four adult and seven subadult females and sixteen offspring in eight litters). By using Cervus 3.0, we identified the most likely parents for each offspring.

No multiple paternity in larger (3 offspring) litters, i.e. maximum of two paternal alleles in one litter was observed. We identified the father of three litters from the Mpalanganga locality - all these litters were sired by the same male. In seven subadult mole-rats born in previous season, we revealed the mother and in four cases we identified the father. Again, it was the only one male who fathered these subadults (but different of the male that sired the offspring one year later) indicating variation in male reproductive success. The distances between burrow systems of mates were up to 370 m, indicating the importance of the aboveground movement of the Silvery mole-rat, at least in the breeding season. If mole-rats return into their burrow systems, they have to possess (previously unexpected) excellent homing and navigation skills.

The pairwise relatedness was calculated for all adult and subadult individuals to determine if there is any correlation between distance of burrows and the relationship of their inhabitants. We haven't found any correlation between distances of burrows and pairwise relatedness suggesting important dispersal behaviour.

THE MOUNTAIN HARE IN THE EASTERN ITALIAN ALPS: EVIDENCE OF STRONG GENETIC STRUCTURE AND HYBRIDIZATION WITH THE EUROPEAN BROWN HARE

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The ecology of the mountain hare, *Lepus timidus*, is poorly known, but the conservation status of this boreal species is likely to be strongly affected by land use changes, habitat fragmentation, over-hunting, climate change and competition with the brown hare (*L. europaeus*). Previous genetic studies have indicated a lack of phylogeographic genetic structure in this lagomorph, suggesting that it once formed a large panmictic population. The present study focuses on the pattern of genetic variation of the mountain hare in the Eastern Italian Alps. The analysis of mtDNA sequences of 77 individuals from five valleys reveals a surprisingly strong genetic structure: the haplotypes from the alpine individuals are clearly divergent from those from other Euroasiatic sites, and they can also be divided into two highly distinct and monophyletic groups corresponding to mountain ranges east and west of the Adige Valley. However, this result is only partially confirmed by the analysis of eight autosomal STR loci, and the effects of differences in sex-specific dispersal and climatic oscillations on these genetic patterns are discussed. In addition, the analysis of 119 European brown hares from the same area demonstrates that hybridization occurs between the mountain and brown hares in our study area, resulting in bidirectional genetic introgression. We conclude that the relict alpine populations of the mountain hare could preserve a considerable fraction of the overall genetic variation in this species; however, climate change is likely to result in a dramatic loss of habitat and increasing competition with the brown hare. Therefore, these results emphasize the urgent need for management plans specific to alpine populations.

EFFECTS OF POPULATION DENSITY AND HABITAT ON SURVIVAL AND DISPERSAL OF BROWN HARES (*LEPUS EUROPAEUS*, PALLAS, 1778) ON INTENSIVE FARMLAND IN NORTHERN ITALY

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Survival and dispersal of the Brown hare in two protected area of Northern Italy were evaluated by tracking 36 radiocollared individuals. The land use of the first study area, called "Vistarino", was predominantly monocultures of rize and maize (44.7%) and poplar groves (13.7%). The second study area, called "Portalbera", was characterized by smaller field sizes and by rotational farming (winter weath and barley and lucerne) (40.9%). Spontaneous vegetation was limited to the riversides (3.40% in Vistarino and 3.5% in Portalbera). We live trapped 16 brown hares in the "Vistarino" area and 20 in the "Portalbera" area; we equipped them with necklace tree-stage radio-transmitters (25g). A portable receiver (IDS Scout 200) and a hand-held four-element Yagi antenna were used for radio tracking. Each hare was located using triangulation once a day during the first two weeks and then once-twice a week. Home ranges and core areas were defined by MCP and Kernel Analysis, at 95% and 50% respectively; home ranges sizes and dispersal measures were calculated for winter and spring seasons. Mean home range size was 86.5 ha (SE=20.915) in "Vistarino" and 78.5 ha (SE=12.960) in "Portalbera", where the spring home ranges (95% Kernel) were significantly larger for young hares than for adults (F=5.304; P=0.0035). The average survival rate was 0.66 (SE=0.126) in "Vistarino" and 0.11 (SE=0.100) in "Portalbera". In "Vistarino" survival was positively correlated with: (1) the maximum distance between subsequent radiolocations (r=0.68; P=0.004); (2) the distance between capture point and furthest radiolocation (r=0.796; P<0.000); (3) the mean distance between capture point and radiolocations (r=0.511; P=0.043); (4) the 100% MCP (r=0.581; P=0.018). In "Portabera" the minimum distance between subsequent radiolocations was negatively correlated with survival (r=-0.597; P=0.005). The lower survival in "Portalbera" was probably linked with high density of hare population. In "Vistarino" the survival rate was high, even though the landscape is less heterogeneous; the hares had large home ranges, probably in order to include a wider diversity of habitats.

HABITAT USE OF BROWN HARES (*LEPUS EUROPAEUS*, PALLAS, 1778) ON INTENSIVE FARMLAND IN NORTHERN ITALY

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Agricultural intensification has dramatic effects on farmland biodiversity, and hare is one of the species that can be influenced by reduction of landscape heterogeneity. Seasonal home range sizes and habitat selection were evaluated in two protected areas in Northern Italy by tracking 36 radiocollared individuals. The land use of the first study area, called "Vistarino", was predominantly maize and rize (44.7%) and poplar groves (13.7%); the second study area called "Portalbera", is characterized by rotational farming (winter weath and barley and lucerne) (40.9%). Spontaneous vegetation is limited to the riversides (3.40% in Vistarino and 3.5% in Portalbera); the arboreus stratum is characterized by poplars (*Populus nigra* and *Populus alba*), alder (*Alnus glutinosa*), willows (*Salix* spp.) and *Robinia pseudoacacia*; in riverside vegetation many herbaceous families are present, such as Leguminosae, Papaveraceae, Compositae. We live trapped 16 brown hares in the "Vistarino" area and 20 in the "Portalbera" area; we equipped them with necklace tree-stage radio-transmitters (25g). A portable receiver (IDS Scout 200) and a hand-held four-element Yagi antenna were used for radio tracking. Each hare was located using triangulation once a day during the first two weeks and then once-twice a week. Home ranges (95%) and core area (50%) were defined by the Kernel Analysis. Compositional Analysis was used to compare utilized and available habitats at three levels: (i) home range (95% Kernel) versus study area availability, (ii) core area (50% Kernel) versus study area and (iii) radiolocations versus home ranges. In "Vistarino" hares selected poplar groves both in winter and in spring, margins, natural vegetation along streams and canals. In "Portalbera" habitats with presence of herbaceous cover were selected both in winter and in spring: the hares selected cartroads, fallow fields, vineyards and margins; in winter the first variable selected was lucerne; the first variable during the winter became crops characterized by rotational farming. In "Vistarino" study area the hares selected poplar plantations with a high canopy cover and food resources. In "Portalbera"study area the high presence of vineyards, lucerne, cereals and the network of cartroads guaranteed food availability, but poor cover.

MONITORING RODENT RESISTANCE TO ANTICOAGULANT RODENTICIDES USING FAECAL SAMPLING

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Resistance to anticoagulant rodenticides, the most common and indispensable means for the control of commensal rodents (*Rattus norvegicus* and *Mus musculus*), has developed under high selection pressure in restricted areas of many countries. Due to the natural mobility of the species or incidental translocation of individuals, resistance is spreading out from the initial areas. Therefore, specific compounds lose efficacy and may even become totally ineffective. Anticoagulants inhibit blood coagulation by repression of the vitamin K reductase reaction (VKOR).

Recent studies identified VKORC1 as the target protein of the anticoagulants. New investigations into resistant brown rats and mice originating from various localities in several European countries identified eight different missense mutations in the VKORC1 gene conferring resistance, suggesting at least seven independent and mostly region-specific mutation events in brown rats and two in mice. These results establish mutations in VKORC1 as the genetic basis of anticoagulant resistance in wild populations of rodents. The identification of the basic anticoagulant resistance gene provided new opportunities for resistance testing by molecular-biological techniques. A PCR-based genetic test for mutations in the VKORC1 gene can successfully identify resistant rats trapped in the field. This test can not only be applied to rodent tissue but also to faecal pellets, allowing for a totally non-invasive sampling and testing procedure. The results suggest that in cases where resistance is suspected to occur, a sample of only a few faecal pellets should be sufficient to confirm or exclude resistance as the major cause of failures to control rodent populations. An ongoing monitoring project on rat resistance in Northwest Germany, based on faecal pellet collection, already revealed that the resistance area is rapidly extending and reaching considerably further East than mapped earlier. Genetic tests using faecal analysis provide a simpler, non-invasive and more efficient methodology for monitoring the distribution of resistance in rats and mice than previous methods, thus supporting both registration authorities and users of rodenticides in their efforts to develop resistance management strategies, and to avoid animal experiments as well as to burden the environment with ineffective pesticides.

INFLUENCE OF POPULATION DENSITY ON GENETIC VARIABILITY AND KINSHIP STRUCTURE IN A LOCAL POPULATION OF THE ROOT VOLE *MICROTUS OECONOMUS*

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Population demography, population genetic variability and kinship structure are connected by a mutually dependent relationship. Our study is aimed at analysing changes in genetic variability and kinship structure in a local population of the root vole, *Microtus oeconomus*, that underwent substantial density changes during 7 subsequent years. Intensive live-trapping was performed each year, aimed at sampling most individuals from the studied population. At the first stage of the study, we compared genetic variability and kinship structure in this population in the years of high (2000) and low (2003) population density. Individuals sampled during these two years (113 and 47, respectively) have been genotyped at 20 microsatellite loci, originally developed for *M. oeconomus* (7), *M. montebelli* (7), *Clethrionomys rufocanus* (2) and *Arvicola terrestris* (4). The number of alleles per locus (13.0 and 13.2) and expected heterozygosity (0.77 and 0.78) were similar in the two years. Deviation from Hardy-Weinberg equilibrium towards heterozygote deficit ($P<0.01$ in both years) and positive Fis values (0.06 and 0.07) suggested moderate inbreeding. However, mean relatedness within population did not substantially differ from zero in both years. Sex-biased dispersal, with females being more phylopatric, was revealed by significant differences in frequency distribution of different assignment index AIc classes between sexes ($P<0.05$ in both years).

Populations from the two years substantially differed in kinship structure. In 2000, 21% of individuals were identified as parents, and for 28% of individuals at least one parent was assigned. In 2003, 13% of individuals were identified as parents, for 34% of individuals at least one parent was assigned. These preliminary results suggest that population size did not substantially influence genetic variability, but strongly influenced kinship structure in the studied population. This conclusion will be verified by the analysis of samples collected in

INTROGRESSION OF MITOHODRIAL DNA FROM THE RUDDY VOLES TO THE BANK VOLES IN POPULATIONS OF THE EUROPEAN RUSSIA

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Recently it was shown, that interspecific hybridization at mammals does not represent the unique phenomenon. Of special interest is a question on possible hybridization of closely related simpatric living species, such as bank (*Clethrionomys glareolus* Schreber) and ruddy (*Clethrionomys rutilus* Pallas) voles. Introgression of mitochondrial DNA of one species to another is a consequence of the process of interspecific hybridization in natural populations of voles.

We used sequences of the mitochondrial DNA cytochrome b gene (1143 base pairs) isolated from 80 bank voles collected at 34 localities on the territory of Russian Federation (the Arkhangelsk, Belgorod, Volgograd, Voronezh, Kursk, Novgorod, Novosibirsk, Moscow, Murmansk, Samara, Saratov, Sverdlovsk, Tver and Tambov areas, republics Belarus, Kareliya, Komi and Udmurtiya) and from 16 ruddy voles collected at 8 simpatric localities.

The patterns of DNA fragments were used as nuclear genetic markers, which were obtained by means of RAPD PCR. The Neighbor-Joining (NJ) and the minimal evolution (ME) phylogenetic trees of haplotypes of cytochrome b gene, constructed on the basis of Kimura 2-parameter model, had similar topology. Both of them contain two clusters with very high bootstrap support (99%) and a genetic distance between them of 8.5%. One of them consists of ruddy voles representatives of some populations together with bank voles from northwest region of Russia (Kareliya - the Kandalaksha reserve and Kem; the Arkhangelsk area - reserve Pinezhsky and village Small Korely; Murmansk area - Lappish reserve) and Novgorod areas (reserve Rdejsky). The second cluster is formed by bank vole haplotypes from more southern regions, including a territory of European part of Russia, Ural Mountains and Siberia.

Presence of the mitochondrial DNA of another related vole species at bank vole genome can be consequence of ancient and/or modern interspecific hybridization and possible selective advantage of the mitochondrial genome of ruddy voles on the border of the area of bank voles. The phenomenon of transferring of mitochondrial DNA of ruddy voles to bank voles for the Novgorod area and Northwest region of Russia is shown for the first time and if in the Northwest region of Russia this phenomenon has a mass character, for the Novgorod area this phenomenon is unique (one haplotype from 16 studied).

EVOLUTION OF *PHODOPUS* MILLER, 1910 (CRICETINAE, RODENTIA) FROM MORPHOLOGICAL VIEWPOINT

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The monophyly of the genus of dwarf hamsters (*Phodopus*) as well as its basal position within Palearctic hamsters (Cricetinae) is well supported by genetic data. However, scarce paleontologic record available at present is insufficient to provide an insight into its evolutionary history. In our study we tried to examine the pattern of evolution of the genus on the basis of morphological data. Species-specific morphological characteristics are discussed in relation to adaptive specialization and level of structural complexity of several functional systems including masticatory apparatus and osseous middle-ear.

Morphological synapomorphies for *Phodopus* include derived pattern of dental morphology (more pronounced in *P. roborovskii*) and rostral displacement of diminutive stapedial foramen. In contrast to that the shape of tympanic bullae as well as their relatively small size often regarded as the diagnostic feature for the group is treated as plesiomorphy. Since size reduction was an important factor in evolution of the group additional test for the role of allometric coordination in skull shape evolutionary transformations characteristic for Phodopus is warranted.

Morphological divergence between *P. roborovskii* and closely related *P. sungorus* and *P. campbell*i is substantial and exceeds the average level of intergeneric differentiation for Palearctic hamsters. *P. roborovskii* being a specialized psammophilic form is also one of the most morphologically advanced species within Cricetinae. Contrary to the tendency observed in many desert rodents its bullae tympani are not inflated but instead appear disproportionately small. At the same time, ear ossicles are relatively more specialized than in *P. sungorus* and *P. campbelli*. Other specific traits include the molar crown pattern which is non typical for cricetines being intermediate between prismatic and bunodont, paedomorphic skull shape, elongated palatinum, extremely narrow opistodont upper incisors, unusual position and size of coronoid process, transformation of anterior part of zygomatic arch which is featured by reduced zygomatic spine thus demonstrating tendency to pseudosciuromorphy. The overall pattern of morphological variation fully corresponds to the existing phylogenetic hypothesis suggesting that Phodopus is one of the earliest offshoot of cricetine radiation represented by two deeply divergent lineages.

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PHYLOGENETIC RELATIONSHIPS WITHIN THE GENUS *ACOMYS*

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To the present day, a great number of species of spiny mice belonging to the genus *Acomys* have been described from Africa and East Mediterranean regions. The aim of this research project is to improve the current knowledge of the phylogeny of this genus by the genetic analysis of a series of samples collected during our expeditions to Jordan, Egypt, Kenya, Libya, Malawi, Yemen, Cyprus, Iran and Turkey. We sequenced part of the mitochondrial DNA: a segment of about 550 bp of the Mitochondrial Control Region and, subsequently, most of the Cytochrome b (1141 bp).Our results confirmed the close kinship of various morphological types all belonging to the *dimidiatus-cahirinus* group. Within this group, it is possible to distinguish three main clades: 1) *A. dimidiatus* from Jordan and the Sinai Peninsula; 2) *A. cahirinus*, obviously paraphyletic with respect to *A. minous*, *A. nesiotes* and *A. cilicicus*; to this line belongs also the sample from central Sahara (Akakus Mts); 3) haplotypes originating from Yemen and Iran. The origin of the last mentioned clade can be explained by the existence of a land bridge in place of the Persian Gulf (during the last ice age), which allowed the dispersion of spiny mice from the South of the Arabian Peninsula toward North-East.

The analysis of samples of *A. lewisi* confirmed that this species is, in fact, just a color race of *A. russatus*. Populations from East and Central Africa belong to lines that originated at the base of the phylogenetic tree of the genus *Acomys*. Their specific collocation is discussed.

HUNTING STATISTICS REVEAL INFLUENCE OF CLIMATIC OSCILLATIONS AND DENSITY DEPENDENCE ON HARE POPULATIONS

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Gamebag records for Irish hares (*Lepus timidus hibernicus*) from throughout Ireland for the period 1846-1970 were analysed to assess long-term historical trends. Prior to 1914, bag indices fluctuated markedly but there was no overall trend. Thereafter, the annual hare index declined markedly (-88%), consistent with declines in hare bags elsewhere in Europe, reflecting a major decline in the number of hares shot in Ireland. Time-series analysis suggests that the Irish population exhibited periodicity both before and after the initiation of the population decline. Prior to 1914 a significant decadal anti-phase and a 16 year positive phase were detected. Further analysis suggests that population growth rate was regulated by both intrinsic delayed density dependence, principally determined by the abundance of hares in the previous year, and extrinsic climatic factors, specifically the weather in autumn, described by the Northern Atlantic Oscillation (NAO) index. The NAO also exhibits a decadal periodicity and we suggest that the interaction of density dependent processes and the autumn NAO gives rise to the significant decadal periodicity observed in the Irish hare population prior to the major population decline. After 1914, there was a reduction in the amplitude and frequency of periodicity and the relative importance of the long term decline in accounting for variance in abundance increased markedly. There is no reason to discount the marked influence of climate and related periodicity in contemporary hare population dynamics but the decline of game shooting has removed one tool for detecting this influence.

NEW KARYOTYPE OF *CALOMYSCUS* (RODENTIA) IN KHORASAN PROVINCE OF IRAN

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Calomyscidae are a group of rodents which are distributed in West Pakistan, throughout of Iran and Afghanistan to south western Syria and north of Torkamanistan to south of it. Information obtained from 10 specimens of *Calomyscus* collected from two areas in Khorasan province has been used to demonstrate new Karyotype in this genus. In this study chromosomes of the *Calomyscus* from Khorasan province were examined by conventional staining and C-banding techniques. The diploid chromosome number (2n) and the fundamental autosomal arm number (FN) were 44 and 62, respectively. In comparative with to other studies in this case we found that this karyotype is different from other that recognized. In old report see the karyotypic list of including: the diploid number and the number of autosomal arms (FNa): (2n = 30, FNa = 44; 2n = 32, FNa = 42; 2n = 44, FNa = 46; 2n = 44, FNa = 58; 2n = 37, FNa = 44; 2n = 50, FNa = 50; 2n = 52, FNa = 56). Subsequently with comparision morphological, cranial and dentary characters to become distinguished the great variations between Khorasan and Geno (sourth Iran) *Calomyscus* populations. In morphometric studies, 8 cranial and dental characters were showed significant difference between populations that involved Width of Molar 1(M1) up, Width of Molar 2 (M2) up, Width of Molar 2 (M2) down, Nasal Length, Occipitonasal Length, Foramina incisive Width, Interparietal Width and Maxillary toothrow length. Notice to this information we can say that probably this population is a new species but it is needed to more studies.

PROBLEMS OF PARALLELISMS IN THE EVOLUTION OF THE ARVICOLIDAE *TAXA* (RODENTIA)

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The Arvicolidae family has originated from the advanced Cricetinae forms in the upper Miocene (c. 4 ml. years ago). Since that time the evolution of this family was closely linked with regularly periodic appearance of morphological parallelisms, especially in the structure of teeth. The teeth structure was characteristic for the more advanced Cricetinae (*Trilophomys*, *Ishymomys*, B*aranomys*) and even some Muridae (Microtia).

The first Arvicolidae (*Baranarviomys*, *Polonomys*) from the early Miocene have undergone rapid adaptative and taxonomic radiation, based the variations and parallelisms. Almost in the same, such genera as *Promimomys*, *Dolomys*, *Pliomys*, *Villanyia*, had appeared as various filogenic lineages. Each of them had particularities of morphological transformations, e.g.: reduction or retain of root, appearance or lack of the cement, presence of absence (reduction) of mimomys lineage (kante) and enamel island, anteroconid elongation and a degree of its complexity, inversion and differentiations of the enamel and others. Such evolution was preceded on the basis of constant harmonization process (correlating or adjusting) of alternative morphological features. The contrast in development of features in certain environmental conditions takes a stand as important factor of evolution of the group, based on natural selections.

The second wave of intensive divergention of Arvicolidae was in the early Pleistocene; it was a period of a formation of recent genera, such as *Clethrionomys*, *Chionomys*, *Microtus*, *Dicrostonyx* and *Eolagurus*. These groups helped to prove the biggest parallelisms in transformation of morphological feature for Rodentia. We can explain such a phenomenon in evolution of Arvicolidae by such factors as: wide range of teeth variability; local adaptation; limited range of direction changes in teeth morphology; general cooling of climate in the Pleistocene.

MORPHOLOGICAL VARIABILITY AND MODULARITY IN VOLES

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Quaternary climatic cycles had a large impact on flora and fauna populations. At this time, the explosive radiation of arvicoline (voles and lemmings) was recorded on fossil material leading to the occurrence and the diversification of modern voles. Morphological analyses in voles are essentially made with first lower molar (M1) for two main reasons: first, strong systematic determinations are made on this tooth and second, it is the most abundant fossil material. A great morphological variability on M1 was demonstrated by some authors on recent but also on fossil voles populations. Most of the observations and quantitative analyses show an increase of the triangle number in the M1 anterior part.

Is tooth pattern corresponds to wide dispersion success of arvicoline in time and space? Some authors pointed out correlations between tooth pattern variability and climatic variations. However, direct causality links are difficult to demonstrate. Modularity approach might be a helpful concept to understand developmental processes involved in observed phenotypic tooth variations. Modularity is a concept pointing out modules, which are half-autonomous units of strong interactions at genetic and phenotypic level. Integrity and coherence of those modules are maintained by developmental direct interactions. From a recent morphometrical method on modularity at a phenotypic level, different modular hypothesis in tooth were tested: first, is there several developmental modules inside one tooth? Second, are the inferior molars independent modules? The first results made on recent and fossil M1 (*Microtus arvalis* and *Microtus* (*Allophaiomys*) *plioceanicus*), with an antero-posterior partition test, show that a better modular partition is possible: antero-lingual/postero-jugal. This modular pattern on the M1 seems to be robust through time. However, a cusp partition might be more congruent with works on tooth morphogenesis postulated that cusps are the result of reiterative signalling module. The robustness of this partition is tested through time and on different tooth pattern of voles.

FIRST ECOLOGICAL DATA ON THE HELMINTH COMMUNITY OF THE LUSITANIAN PINE VOLE *MICROTUS LUSITANICUS*

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The lusitanian pine vole *Microtus lusitanicus* (Rodentia, Muridae) is one the most scarcely known murid species from western Europe. Its geographic distribution area is restricted to the west of the Iberian Peninsula and soutwestern France. Although this rodent has a certain economical interest because in high population density conditions it can cause severe damages on crops and gardens, surprisingly several of their life histories have never been studied. One of these subjects concerns its parasitological characteristics. In this study, we analysed the helminths detected in a sample of *M. lusitanicus* formed by 227 specimens from Matarrosa de Sil (León, northern Spain), obtained between 1994 and 2005. These animals were captured by farmers of this region during trapping sessions undertaken to control the population density of this vole. Animals were criopreserved and donated to us for study. Analysis of the viscera allowed us to determine and quantify their helminths. This includes adult cestodes (two species) and nematodes (three species) and larval stages of cestodes. The lusitanian pine vole was not parasitised by trematodes and acantocephalans. The general prevalence was 60%. For helminth species, larval stages of cestodes showed the lowest prevalence. Males had higher prevalence than females (64% *vs* 56%) and juveniles showed for this variable lower value (11%) than subadults (57%) and adults (63%). Analysis of the annual variation of the structure of the helmintofauna revealed that the prevalence was highest in winter (68%) and lowest in autumn (50%).

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TWO CASES OF XXY ANEUPLOIDY IN THE 'ATTICUS' CHROMOSOMAL RACE OF THE UNDERGROUND VOLE *MICROTUS THOMASI* FROM GREECE

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Two cases of XXY aneuploidy (2n=45, FN=48 instead of the normal 2n=44, FN=46) from different localities of NW Peloponnisos, Greece were recently recorded, as a result of an ongoing extensive cytological study in natural populations of the underground vole *Microtus thomasi* (Rodentia, Arvicolinae). In a large sample of 366 individuals from 89 localities of Greece, these two instances constitute the first report of sex chromosome aneuploidy for this species. Both individuals appeared with a male phenotype and normal morphology, however measurements and histological examination in the testes of one of the two individuals imply a severely impaired fertility. The above findings translate to a relatively high rate of sex chromosome aneuploidy (0.55%) for the natural populations of *Microtus thomasi* and possible reasons for this finding are analyzed.

REPRODUCTION AND FERTILITY STUDIES BETWEEN TWO CHROMOSOMAL RACES OF *MICROTUS THOMASI* FROM GREECE

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The underground vole *Microtus thomasi* (Rodentia, Arvicolinae), a Balkan endemic species with a wide distribution in Greece, is characterized by an extensive chromosomal polymorphism, which has resulted in at least four chromosomal races. Laboratory crosses between wildly caught individuals of the chromosomal races "*thomasi*" and "*atticus*", were performed to analyze the degree of interracial reproductive isolation. According to G- and C- banding pattern, the two chromosomal races appear to have a similar autosome set, but differ in the morphology and the heterochromatin content of the sex chromosomes. Based on chromosome preparations obtained from bone marrow and right testes, all sacrificed individuals were attributed to either of the two chromosomal races. The fertility of the studied specimens was evaluated by taking into consideration the reproductive success, the litter size and the testis size (weight and volume). Furthermore, testicular histology on the left testes of the parental, backcross, F1 and F2 hybrid groups, was used to calculate the number of spermatogonia and primary spermatocytes per 100 Sertoli cells. The results gathered during this study, provide new insights to the potential phylogenetic relationships and the taxonomical status of the two chromosomal races.

THE STUDY OF MEIOSIS IN WOOD MICE OF THREE SPECIES OF THE GENUS *APODEMUS* (RODENTIA, MURIDAE)

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The meiosis in wood mice species *Apodemus* (*Sylvaemus*) *flavicollis*, *A*. (*S*.) *ponticus* and *A*. (*S*.) *uralensis* has been studied by means of light and electronic microscopy. A correlation between relative length of chromosomes in the mitotic karyotype and the relative length of synaptonemal complex (SC) of chromosomes in the meiotic karyotype has been noted in *A. flavicollis*. In all three species the axes of chromosomes X and Y form synapsis practically along the whole Y chromosome length at middle pachytene stage; at diakinesis-metaphase I stage the sex chromosomes associate end-to-end. Synaptical behaviour of sex chromosomes of these species is very similar. No significant difference in meiotic process has been revealed between studied species.

THE STUDY OF THE MICROSATELLITES LOCATED WITHIN T-COMPLEX REGION FROM WILD POPULATIONS AND LABORATORY STOCKS IN HOUSE MICE (*MUS MUSCULUS*)

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The proximal region of the chromosome 17 in house mouse (*Mus musculus*) includes the complex system of genes which charactereterized by four non-overlapping paracentric inversions span a 20cM region. The microsatellite analysis of mice from wild populations of Russia (Volgograd, Rostov, Saratov regions), Iran and Bulgaria and also of laboratory stocks of house mice carrying t-haplotypes in our collection (t12,tw5,tw12 ,tw73) has been carried out using PCR method with primers of D17Mit (17, 167, 214, 28, 31, 57, 62). The microsatellite amplificated are DNA sequences that located at the chromosome 17 in the region from 7.6 till 18.8 cM. Each pair of primers recognized from 3 to 6 nucleotide sequence variants of different size at range from 90-120 bp (D17Mit 16) till 300-330 bp. The patterns of microsatellite DNA fragments were specific for each specimen, and in the most of cases two variants of nucleotide sequences of different size have been detected. The most of the spesimens under study were heterozygous for the microsatellite loci. It has been shown that the best similarity of patterns of microsatellite DNA fragments occurred in laboratory stocks of house mice carrying variation t-haplotypes t12, w12 and tw5, tw73. The variants of patterns of microsatellite nucleotide sequences from the laboratory stocks were the most similar to Volgograd and Rostov regions while those from Bulgaria and Saratov region were similar to each other. Interestingly, microsatellite specimens from Iran significantly differ from all other patterns. Thus microsatellite variants of nucleotide sequences located in t-complex region can be used as markers for identification of *Mus* representatives from wild populations.

A MITOCHONDRIAL PHYLOGEOGRAPHY OF SIX *APODEMUS* SPECIES IN FAR EAST RUSSIA AND CHINA

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The phylogeography of six *Apodemus* species. (*A. agrarius, A. peninsulae, A. latronum, A. draco, A. chevrieri* and *A. ilex*) have been studied in Far East Russia and China using cytochrome b gene sequences. Our analyses indicate a higher genetic diversity in some regions such as the Yunnan, Sichuan and Eastern Russia suggesting the existence of multiple refugia in these regions for these species. Several genetic lineages were observed within each of these species, evidencing a strong intraspecific differentiation for them, particularly for *A. draco*. This phenomenon is probably the result of past allopatric isolations associated to the existence of strong biogeographic barriers such as mountains and deserts which are frequent in China and Far East Russia. The presence of such barriers prevented the colonisation of these *Apodemus* species in other regions, at the exception of *A. agrarius* and *A. peninsulae* which were able to colonize more occidental areas, through the South of Siberia.

EFFECT OF LAND USE ON WINTER BROWN HARE (*LEPUS EUROPAEUS*) DENSITY IN SOUTHERN TUSCANY (ITALY): CONSIDERATIONS FOR FARMLAND MANAGEMENT

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Winter Brown hare (*Lepus europaeus*) density was surveyed in 23 sample sites of about 1 km^2 each selected in 11 protected areas (managed for small game species) located in a Hunting District of the Grosseto province (Southern Tuscany).

At any site two successive counts were carried out at night using spotligths in December 2006 - January 2007. Moreover 13 habitat variables were measured in each study area using a GIS software.

We performed a Linear Multiple Regression Analysis (LMRA) by stepwise selection in order to evaluate the effect of the habitat variables on the hare density.

Hay fields in rotation with winter cereals and mixed-crops (field crops edged by olive trees, typical of Mediterranean landscape) were positive associated with hare abundance, whereas permanent pastures seemed to have a negative effect.

Surprising, we found a negative relationship between habitat heterogeneity and the hare density.

It is possible that sampled areas with higher heterogeneity index had a higher incidence of habitats less suitable for hares as pastures or ploughed fields.

The relationships between hare density and rotation hay fields shows that also a relative low incidence of this crop (between 5 to 10%) can be very beneficial in a landscape dominated by winter cereals.

The permanent grassy bank wich is usually present in the field edged by olive trees (mixed-crops) probably provides year round food and cover favouring higher hare density.

The analysis of relationships between habitat variables and hare abundance carried out at local scale can allow us to establish more effective habitat improvement programs. In particularly, the results of present study suggest that even small patches of grasses and rotation hay crops can improve hare density.

A PHYLOGENETIC STUDY OF IBERIAN HARE SPECIES BY MTDNA ANALYSIS: *LEPUS CASTROVIEJOI*, *L. EUROPAEUS* AND *L. GRANATENSIS*

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In Europe, five hare species are present. Three of them coexist in the Iberian Peninsula, *Lepus europaeus*, *L. granatensis* and *L. castroviejoi*, and their genetic relationship is uncertain. To provide a phylogenetic framework, 141 individuals from the three species were analysed using mitochondrial DNA cytochrome b (1140 bp) and control region (400 bp) sequences. Due to problems of saturation between ingroups and outgroups (*Oryctolagus* and *Sylvilagus*), rooted trees were generated discarding the control region and the third position of codons in cytochrome b. We found two distinct evolutionary lineages which may correspond to an African-Asian and an European origin. The lineage with an African-Asian origin comprises *L. granatensis* and *L. europaeus*, and the estimated time of separation of these two species was dated back to 4.5-2.2 Myr ago. The lineage with an European origin comprises *L. timidus*, *L. castroviejoi* and *L. corsicanus*. In this case, the separation of *L. timidus* and the common ancestor of *L. castroviejoi* and *L. corsicanus* was valued in 1.3 - 0.64 Myr, while, *L. castroviejoi* and *L. corsicanus* diverged more recently, 0.65 - 0.33 Myr ago. Finally, we observed that the estimated time of mitochondrial DNA introgression from *L. timidus* into *L. castroviejoi*, *L. europaeus,* and *L. granatensis* was concordant with the glaciation of the Pyrenees.

THE EFFECT OF WILDFIRES ON GLIRIDS (*MUSCARDINUS AVELLANARIUS* AND *GLIS GLIS*) LIVING IN MEDITERRANEAN ECOSYSTEMS

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Human-induced fires periodically hit the Mediterranean belt of the Madonie Regional Park, about 1200 ha of such vegetation, struck by fire on November 2001, and defined our study area. In this territory, a sample-area with nest-boxes for common dormouse, already active from 1999, burned almost completely and represented one of our controls. This latter had a post-fire age of 26-27 years and hosted a common dormouse population in the re-growth stage of young forest. To reconstruct, at least partially, the post-fire secondary succession, we checked natural nests and mounted 175 artificial nest-boxes in burned areas of age 2-3 years and in intermediate re-growth stages of 4 and 9 years. In addition, 55 cassettes were mounted in 10 forest fragments (FF) left after the passage of fire. A similar but smaller design was used to investigate the effect of fire on *Glis glis*.

The study evidenced the role of FFs in maintaining small nuclei of individuals of both species. For the common dormouse, the total occupation rate of nest-boxes and the frequency of occupied FFs, were quite high 2 and 3 years after fire. The parameters of presence dropped down 4 years after fire, probably due to dispersion in the nearby recovering vegetation. For the fat dormouse, the rescue effect of FFs was smaller, only 1 out 8 FFs hosted survivors; they reproduced and stayed in the FF forming a small population. Analysis of the FFs' vegetation structure says that fat dormouse needs much larger and wooded fragments. The relative occurrence of the two species along the secondary succession was quite different also. The common dormouse was present with a fluctuating index of presence all along the post-fire succession. Population first peaked in the high-maquis of 10 years, and later in the young forest of 26 years. Mature open forest (50 years post-fire) was scarcely frequented. A GLM analysis showed that several factors predict the species' presence. In conclusion, areas likely with different ecological conditions and past fire histories seem accounting for the species occurrence in the secondary succession, together with the age of fire and the presence of a well-developed understorey around the nest-boxes. The fat dormouse requires certain tree canopy coverage (30-40%) left available after fire. It started frequenting again parcels of such recovering woodlands at 60 months of age, when chestnuts and oaks produced fruits; however, the highest abundances were in the control mature wood.

MASSETER ARCHITECTURE IN A MURINE MURID, *RATTUS RATTUS*, AND ITS EVOLUTIONAL ADVANTAGE

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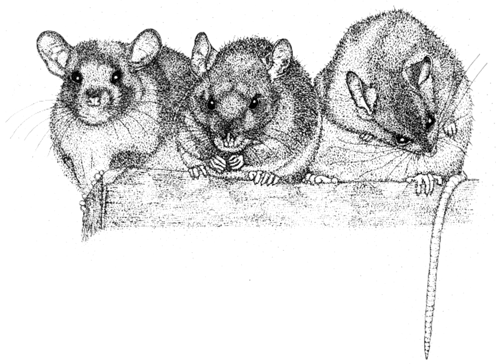
The murine murid is the largest subfamily of the muroid rodent and contains over 100 genera. To clarify the key to their evolutional success, the internal architecture of the masticatory muscles in a murine murid, *Rattus rattus*, was examined and compared with that of *Peromyscus maniculatus*, which retains unspecialized dental morphology for muroid rodents. There were remarkable differences mainly in the masseter muscle and corresponding aponeurosis. In *Peromyscus*, both the origin and insertion of the anterior part of the masseter deep layer lie on the aponeurosis. In *Rattus*, however, the deep fibers of the anterior part are long and form a muscular attachment to the bone surface at either end. This characteristic suggests that the maximum angle of the gape is increased in murine murids, which allows them to ingest various-sized foods. Murine murids appeared in the middle Miocene period, and have replaced several primitive murid groups with *Peromyscus*-type molars in Asia and Europe. The masseter structure of murines would be advantageous when competing with other murid lineages for food resources.



FACTORS AFFECTING THE DISTRIBUTION OF EUROPEAN WILD RABBIT (*ORYCTOLAGUS CUNICULUS*) IN NORTHERN ITALY

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The European wild rabbit (*Oryctolagus cuniculus*) is an important keystone species of the Mediterranean ecosystems and a "landscape modeller" with an important impact on plant communities. In northern Italy the species is present mainly in the Po Plain at low density and it shows a clustered distribution; populations show dramatic fluctuations in relation to the epidemiological events of myxomatosis. The aim of this research was to investigate the relationships between wild rabbit presence and vegetation and soil characteristics. The study area (1871 km^2) is located in western Po Plain and is characterized by irrigated arable lands (81.5%; mainly maize and rice). Natural vegetation (scrubland and other uncultivated lands) covers the 1.2% of the total area, while broad-leaved woods are the 4.6%, and grasslands and poplar groves are 0.5% and 1.0% respectively. Climate is sub-continental with temperate winters and hot summers, and precipitation concentrated in spring and autumn. The presence of wild rabbits was assessed by direct surveys in 60 1-km^2 sample squares of the UTM grid superimposed on the study areas. In these squares we measured by the software ArcView 3.2, 8 variables concerning the main land use classes and 15 variables relative to soil types. The same variables were measured also in 60 randomly selected control squares. Then we compared the squares of presence with the control ones by one-way ANOVA and binary Logistic Regression Analysis (LRA, stepwise procedure, Log-Likelihood method). The presence squares were characterized by greater percentages of woods ($P=0.007$), natural vegetation ($P=0.038$), grasslands ($P=0.056$), and sandy banks ($P=0.022$) than the control ones; whereas the percentages of arable lands, and areas periodically flooded were greater in control squares ($P=0.033$ and $P=0.030$ respectively). Logistic regression model ($P<0.001$) correctly classified 74.5% of total squares, 80.4% of control squares, and 68.8% of presence squares; the percentages of woods and natural vegetation influenced positively the probability of the species presence. The presence of the species seems to be well related to natural vegetation, woods and grasslands, consequently changes of the landscape due to intensification of agricultural practices could act negatively on the population abundance; moreover the species could be considered a good indicator of the landscape naturality.

RODENTS DIVERSITY OF CENTRAL DESERT OF IRANIAN PLATEAU

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The purpose of this study is to identify the faunistic, systematic, distributional, and ecological characteristics of the rodents of central desert of Iran and also to direct the attention of the international scientific community to the vast fauna of the area. This region, which is surrounded by different mountainous areas, is of many biogeographical interests, because it has limited the distribution of animals from east to west and vice versa. Besides, the existence of the Shirkuh Mountains in the middle of this area has created a microclimatic condition quite similar to the extended Zagros mountain chain in the west. In this study samplings were undertaken in the area during two years (2004-2006). A new species, *Apodemus avicennicus*, some new records for *Allactaga hotsoni* and *Gerbillus* cfr. *henleyi*, as well as two unknown species (*Meriones* sp. and *Gerbillus* sp.) were reported. The other recorded species consist of: *Dryomys nitedula* from family Gliridae, *Gerbillus nanus*, *Meriones libycus*, *Meriones persicus*, *Meriones crassus*, *Rhombomys opimus* and *Mus musculus* from family Muridae, *Allactaga elater* and *Jaculus blanfordi* from Dipodidae, and finally *Cricetulus migratorius* from Cricetidae. Standard external characters as well as cranial ones were measured and statistically analyzed. Karyotypes of the all live specimens were prepared and compared with the reported ones of the same species from different localities. A preliminary zoogeographical analysis is presented, considering the distribution of the recorded species in the other parts of the Iranian plateau. The photos of the all species, which were taken from live specimens, as well as the photos of their habitats are given.

CHROMOSOMAL EVOLUTION OF THE HOUSE MOUSE, *MUS MUSCULUS DOMESTICUS*, IN THE AEOLIAN ARCHIPELAGO (SICILY, ITALY): AN INSTRUMENT OF PHYLOGEOGRAPHICAL RECONSTRUCTION FOR THE STUDY OF THE COLONIZATION PATTERN

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* this contribution is dedicate to our friend and guide Marco

The western house mouse, *Mus musculus domesticus*, is widespread in Western Europe and in the entire Central and Western Mediterranean basin. This species is characterized by a standard karyotype of 40 telocentric chromosomes. Many populations show a reduction of diploid number due to Robertsonian (Rb) translocation. This produced many chromosomal races scattered in several parts of the subspecies range. In this study we characterized the karyotype of mice from the Aeolian Archipelago, a group of seven volcanic islands in the Tyrrhenian Sea to the north of Sicily. The chromosomal analysis was performed on a sample of 92 specimens collected all over these islands. For the 48 specimens with Rb translocation the G-banding was performed to identify the fusion. The results show the presence of four Rb races in five different islands. Three of these races share a subset of two metacentrics: the Alicudi race 2n=34, the Lipari race 2n=26 (described by Gropp in 1977, that we found also in Stromboli) and the Vulcano race (2n=26). The two latter races differ for two metacentrics. The fourth chromosomal race in Panarea is characterized by two different Rb fusions, not found in the other islands of the Archipelago. The remaining two islands, Salina and Filicudi, are characterized by populations with a standard karyotype (2n=40). The most parsimonious pattern of chromosomal evolution involves the appearance in an ancestral 2n=40 populations of the two shared fusions to obtain the 2n=34 Alicudi race. An additional reduction of the diploid number should be occurred in the Lipari race. The Vulcano race could be easily derived from the latter, following a Whole-Arm Reciprocal Translocation. In this scenario, the Panarea race must be originated independently. However, it should be mentioned that the Lipari race shares three metacentrics with the ACR race (2n=24) localised in Central Italian Appennine. This is a remarkable fact because the colonization history of the major Aeolian islands was characterized by a long period of Appennine Culture influence during the middle Neolithic. For this reason the allochthonous origin of some metacentrics cannot be ruled out. Molecular analysis by mean of mtDNA and nuclear loci are in progress in order to elucidate the relationships between the populations within the Archipelago and between them and the mainland Robertsonian races.

ECOLOGY AND EPIDEMIOLOGICAL IMPORTANCE OF THE MARGINAL POPULATION OF *MUS SPICILEGUS* (RODENTIA)

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The results of comprehensive study over the biodiversity, ecology and epidemiological importance of the marginal population of mound-building mouse (*Mus spicilegus* Petényi, 1882) are presented. Nearly 370 specimens and 14 winter nests of *M. spicilegus* at the northernmost part of its area (eastern Slovakia, 15 km southern of Kosice town; 21,14 E, 48,33 N) during several years (2003-2006) were sampled and investigated. The population structure, the somatic and craniometrical parameters of different age and sex groups of population were analysed. The emphasis of material collection was put on overwintering population. This population characterizes by a considerable predominance of young mice (more than 70 %), while sexual index in subadults group is balanced, males among adults significantly dominated. The comparison of biometrical and craniometrical parameters shows significant differences. Adult females are greater than males in mostly biometrical marks, probably their growths continue longer than males. About one-third of mice were positive on mites (Mesostigmata), among them nine parasitic species were found. The specific parasite - *Laelaps algericus* - evidently dominated (73 % of mites collected). Four flea species (Siphonaptera) and three sucking lice species (Anoplura) were confirmed on the host, infestation parameters were very low. *Ctenophthalmus assimilis* (flea) and *Hoplopleura captiosa* (louse) dominated. The presence of antibodies against *Chlamydophilla* (*Chlamydia*) *psittaci* and *Toxocara* spp. were confirmed at the first time in this species. Sporadic occurrence and very low infection on some other endoparasites in blood were confirmed - *Trypanosoma* sp., *Babesia* sp. and *Hemobartonella* sp. Analysis of *M. spicilegus* winter nests confirmed very rich arthropod communities - 56 mites (7 parasitic) and 6 flea species, mean number of arthropods was high (almost 2 thousand per nest).

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MATING SYSTEM VARIATION IN FOUR EUROPEAN SPECIES OF *APODEMUS* MICE

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Promiscuity and monogamy are two extremes of fitness optimisation. Direct evidence for both extremes is documented in numerous studies where a measure of promiscuity / monogamy is often the number of fathers in individual litters. Fitness benefits of multiple paternity (i.e. multiply-sired litters) mainly accrue from the increased survivorship among offspring that results from increased genetic diversity within litters. Other benefits to females from multiple mating could include for example assurance of conception, fresh sperm for fertilization, promotion of sperm competition, and larger litters. Recently, the differences in the occurrence of multiple paternity between different mice species of the genus *Apodemus*, have been described. These initial results together with known interspecific differences in some other behavioural traits (e.g. aggressive behaviour) make this genus suitable for comparative analysis of mating systems in mammals.

By using eight polymorphic microsatellites we identified number of fathers within embryos of 98 snap-trapped females of four *Apodemus* species. The paternal alleles on each locus were assessed by comparing mother’s and offspring’ genotypes and multiple paternity was assumed if the minimal number of paternal alleles at a locus within litter was greater than two.

Multiple paternity was found in all analysed species of the genus *Apodemus*. In *A. microps* and *A. flavicollis*, a maximum of two males sired a litter, while three males per litter were regularly found in *A. sylvaticus* (9.1% of analysed litters) and *A. agrarius* (20.6%). Number of males that sired one litter increased significantly from spring to autumn. This fact may be caused by low numbers of available males in early spring. To analyse non-biased factors influencing the occurrence of female promiscuity, we restricted the analyses only to litters obtained after mid-May, when young of the year males can be reproductively active in the populations (i.e. the opportunity for promiscuity is high enough). In that period pronounced variation in the proportion of multiply-sired litters was found among species (Am - 45.0%, Af - 56.3%, As - 68.8%, Aa - 69.2%), especially *A. agrarius* showed significantly higher numbers of multiply-sired litters than *A. microps* ($P < 0.005$). This study unequivocally demonstrates important within-genus variation in the promiscuity level which predestines the Apodemus mice for further comparative behavioural and ecological studies.

SEX-BIASED RANGING BEHAVIOUR OF YELLOW-NECKED MOUSE *APODEMUS FLAVICOLLIS* AT HIGH POPULATION DENSITY

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Apodemus flavicollis is the most abundant rodent species in woodland of eastern Italian Alps and a relevant reservoir of zoonotic pathogens. We analyzed radio-tracking data collected from adult individuals during the breeding season in a year of high population density and low seed production to determine sexual differences on use of space, nesting behaviour and dispersal. The field trial was based on CMR and radio-tracking (homing-in) techniques. We fitted collars to 20 male and 12 female adult resident individuals. From July to October 2005, we completed 4 radio-tracking sessions of 3 weeks. Fixes were recorded from dusk to dawn; additional daylight fixes allowed to localise burrows. The mean number of nocturnal fixes/ animal/session was 65.7 ± 2.2 and 12.4 ± 0.8 for diurnal fixes. We calculated home ranges as MCP 100% and Kernel utilisation distributions (UD), from which we derived 95% and 50% probability polygons. We could estimate home ranges for 13 males and 7 females. We quantified static overlap between individuals by a range of indexes, including UD overlap and distance between centres of maximum activity. We calculated successive distances at 24 hours interval to assess ranging movements and dispersion. We assessed the effect of sex on the behavioural parameters listed above by GLM or GLMM. All statistical analysis were carried out by R and spatial analyses by ArcGis 9.0.

Male home ranges and core areas were larger than those of females, as well as daily ranging movements. Spatial range of individual males overlapped both with that of males and females. In turn, female spatial ranges never overlapped one to each other. Similarly, we never detected more than one female in the same nest. From the end of September to early October, 9 individuals, of both sexes, dispersed to new sites (from 1 km to 2.5 km apart) suddenly and quickly.

Our results indicated that spatial behaviour of *A. flavicollis* is affected by sex. During mating season, males may maximize their probability of meeting sexually active females by covering large areas, while females may compete for food, thus defending core areas from conspecific of the same sex. The food scarcity, exasperated by the high population density, seemed to drive individual dispersal towards habitat spot of better quality.

Sex biased ranging behaviour may exert a central role in disease transmission, leading to greater exposure of males to pathogens, thus cumulating to hormonal effects.

DISCRIMINATION OF THE CLOSELY-RELATED GENOMES IN THE ALLOTETRAPLOID RED VIZCACHA RAT *TYMPANOCTOMYS BARRERAE* (RODENTIA, OCTODONTIDAE)

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The tetraploid rodent *Tympanoctomys barrerae* (2n = 102) has a diploid-like meiosis that suggests allotetraploidy. This notion is further supported by the matching combination of chromosome numbers between two closely-related species, *Octomys mimax* (2n = 56) and tetraploid *Pipanacoctomys aureus* (2n = 92). To test this hypothesis, genomic in situ hybridization (GISH) was used to examine the genomic constitution of *T. barrerae*. GISH was conducted with biotin-labelled genomic DNA from O. mimax (the probe), mixed with an excess (30 x) of *P. aureus´* unlabelled genomic DNA (the blocker). These DNAs were hybridized to in situ metaphase chromosomes of *T. barrerae*. The probe mix together with the blocking DNA was denaturated, applied to each slide, covered with a coverslip, and hybridized for 72 hrs. Hybridization signals were detected with avidin-FITC. Mitotic plates were counterstained with DAPI before examination by epifluorescence light microscopy.

GISH results indicate that approximately 30 chromosomes differing in size and shape exhibit enterely greenish-yellow hybridization signals. These chromosomes belong to *O. mimax*. Approximately 30 chromosomes, derived from *P. aureus*, did not fluoresced green, but were DAPI-stained. Approximately 42 rearranged chromosomes were labelled greenish-yellow in one arm and blue in the other, indicating a high rate of chromatin rearrangement through reciprocal translocations. It is worth mentioning that after the formation of a new allopolyploid, several genetic and epigenetic mechanisms stabilize the species´ genome dynamics and lead to cytological and functional diploidization. This stabilization can explain the diploid-like meiotic configuration and selective silencing of ribosomal genes reported previously in the red vizcacha rat. From an evolutionary point of view, this instance of allotetraploidy is suggestive of instantaneous speciation in mammals. Our results have demonstrated once again the usefulness of GISH methods for monitoring chromatin transfer and introgression in organisms having complex genomes.

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EVOLUTION OF SOCIALITY IN TREE AND GROUND SQUIRRELS: DOES VISIBILITY MATTER?

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Habitat structure in terms of obstructive/protective properties of vegetation cover affects conspicuity of prey species and their predators on the one hand, and ability to monitor surroundings and to detect prey or predator, on the other hand. In open habitats (grasslands or deserts) where rodent size is comparable with vegetation height, an increase in body size extends the lateral view of these prey species, allowing long-distance monitoring of surroundings and, at the same time, making individuals conspicuous to conspecifics, competitors and predators. I hypothesized that in ground squirrels, open-dwelling sciurids, an increase of perceptional scope and conspicuity due to the combined effect of large body size and habitat openness would allow and enforce social interdependence of individuals, thus promoting sociality. In contrast, I expected the forest-dwelling tree squirrels to be less social, and to have less pronounced variation in their sociality due to lower effect of body size on visibility and conspicuity in closed obstructed forest habitats. To test this hypothesis, I studied the relationship between sociality, body size, degree of habitat openness and type of habitat in 16 species of North American and Eurasian ground squirrels and in 4 species of tree squirrels. I introduced 14 variables that described the degree of territoriality, natal philopatry, reproduction suppression, nepotism, and duration and strength of male-female associations. Next, multi-dimensional scaling was used to ordinate species within the space of these variables. The primary axis was interpreted as a quantitative measure of sociality. As predicted, sociality appeared to increase both with increase in body size and habitat openness in ground squirrels. Moreover, species inhabiting open areas were more social, whereas species of closed habitats tended to be less social than what was predicted by body size alone. Thus, the single effect of extended lateral view, rather than body size and habitat openness as separate factors, stimulates development of sociality in open-dwelling ground squirrels. In accord with expectations, no effect of body size on sociality was observed in tree squirrels, which proved to be less social and varied less in degree of sociality than ground squirrels. Thus, the obstructed view weakens the effect of body size on sociality of sciurids due to poor visibility and conspicuity in closed forest habitats.

EUROPEAN BEAVER'S POPULATION AT THE NORTH-EASTERN UKRAINE AND FACTORS INFLUENCING ITS EXPANSION

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The European Beaver (*Castor fiber*) in a forest-steppe zone of Ukraine was considered as extinct species. Now in the Northern-East and East Ukraine the beaver population increases and extends. There was reacclimatization of animals in Poltava and Lugansk regions (in 1972-1974). On the north of Kharkiv region beavers were observed at first in 1982. A draining was an only factor which opens the way for Beaver's expansion to the south-east. The beavers have gone 93 km for 12 years. In 2000, European Beaver got over the border between Dnepr and Don Basins.

Since that time of acclimatization (70-years, Lugansk region), the beaver settled the majority of tributaries of Severskiy Donets River. In 1998 the first beaver settlements were found in the centre of the region (more than 300 km from the place when beaver was let out). From the beginning of 2000 the species became to settle by the tributaries in the steppe part of Kharkiv, Donetsk and Lugansk regions having gone to present time near 400 km. There are beavers settlements at the tributaries of Severskiy Donets in Lugansk region (161 km and more 250 km from Severskiy Donets), in Donetsk region (88 km from Severskiy Donets) that are situated at the steppe area. The intensive developing of new territory is continuing. Since 1991 the most colony of beavers on Northern-East Ukraine (1993 - 23, 2000 - 34 settlements) was situated within drainage flood-land of the Merla River. In 1999-2000 the project was carried out by financial supporting of British Ecological Society, the main of it was the detection of environmental factors, which determine the beaver's dispersion. Such factor as poaching is a single significant factor from human activities. Sometime anthropogenious factor becomes apparent, - even the plot has well other conditions (high productivity of forage resources, sufficient depth). In some cases beaver's plots situated near the human settlements. The most density of beavers (ind./1 km of watercourse) was determined on canals (5.23), rivers (2.38) and lakes (2.2). In 1993 and 2000 beaver's settlements within these waterbodies were following: river 43.4% and 38 % correspondingly from all settlements, lakes 8% and 3% and canals 48.9% and 59%.

KEY FACTORS PROVIDING PRESENCE OF MARMOTA BOBAK IN STEPPE ECOSYSTEMS IN UKRAINE

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Contrary to the researchers, who directly connect fluctuations of mammal number with global climatic processes (global warming etc.), we develop and confirm the idea of key factor. Key factor is a guarantor of existence of the given mammal species as functional component of a present ecosystem. The model object for such an approach in our investigation is European subspecies of the steppe marmot (*Marmota bobak bobak* Muller (1776), Rodentia, Sciuridae). In the beginning of the XX century it was under threat of full disappearance in Ukraine. Then, to early 60-s, its rapid revival had happened. The number of the steppe marmot was increasing till the beginning of the 80-s. After the short period of stabilization (to the end of the 80-s), the decrease of its number begins. Since the end of the XX century, the number of marmot individuals has been decreasing, but the area of *M. b. bobak* continues to be extending. The steppe marmot is evolutionally connected with pasturable type of phytocenosis. Such type of phytocenosis existed and had been maintained in the past by herds of large herbivorous ungulate. Today it is formed by agricultural activity by means of cattle grazing. We have traced and analyzed the dynamic of both the steppe marmot number and grazing pressure of its habitats. The direct correlation between both processes is doubtless. Our investigations in one of the steppe marmot historical refuges located in Kharkov region /Ukraine/ have shown the influence of progressive increasing of cattle grazing pressure on potential habitats of the steppe marmot during the XX century. We consider that this process stipulates the restoration of pasturable ecosystems with the steppe marmot as one of the basic components. Since the end of the XX century, the depression of livestock farming begins. It means the extinction of grazing as ecological factor and progressive increasing of a proportion of ungrazed sites. The lack of grazing pressure causes a reverse succession of phytocenosis; therefore the foraging base of the steppe marmot changes for the worse. This fact leads to decrease of both young viability and population density that means the decreasing of the steppe marmot number in whole. However, there are heavy grazed sites that support the high density of the marmot population. At the edge of the area such sites provide further expansion of *M. b. bobak*. Thus, the cattle grazing is a key factor providing existence of *M. b. bobak* in modern steppe ecosystems.

EVOLUTION OF P53: HYPOXIA-STRESSED *SPALAX* MIMICS HUMAN TUMORS

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The mole rat, *Spalax,* a model organism for hypoxia tolerance, spends its entire life cycle underground at decidedly lower oxygen tensions than any other mammal studied. We suggested that because a wide range of respiratory adaptations to hypoxic stress evolved in *Spalax,* it might also have developed hypoxia adaptation mechanisms analogous to the genetic/epigenetic alterations acquired during human tumor progression. We studied the tumor suppressor gene p53 that controls cellular response to a variety of stress conditions, including DNA damage and hypoxia. Inactivation of p53, found in 40-50% of human cancers, confers selective advantage under hypoxic microenvironment during tumor progression. We demonstrated that in *Spalax* the p53 DNA-binding domain contains a specific Arg174Lys amino acid substitution identical to known tumor associated mutations. This mutation reduces the p53 effect on the transcription of both human and *Spalax* apoptosis genes (apaf1, puma, pten and noxa) and enhances it on cell cycle arrest and p53 stabilization/homeostasis genes (mdm2, pten, p21 and cycG). Similar neighboring mutations found in human tumors favor growth arrest rather than apoptosis. We conclude that *Spalax* evolved hypoxia adaptive mechanisms, analogous to the alterations acquired by cancer cells during tumor development, with a bias against apoptosis while favoring cell arrest and DNA repair.

PREDATOR MEDIATED EFFECTS ON TWO VOLE SPECIES

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The interaction between boreal voles and the specialist predator, the least weasel is a model case in predator-prey relationship. As the prey community includes voles with different characteristics and ability to escape predation, focusing on changes in vole community provide an excellent case to study predator mediated effects on behaviour of the prey community. We conducted an experiment in large indoor arena divided into risky and less-risky area. We looked at the effect of predation risk expressed by the least weasel *Mustela nivalis nivalis* on space use, foraging and activity of two competing vole species *Myodes rufocanus* and *Myodes glareolus*. Our results suggest the effect of the weasel presence on the vole community: generally voles shifted their activity from risky to less risky area, climbed trees more and were less active. However, foraging was not affected by the weasel presence. In general, grey-sided voles were dominant over bank voles in horizontal, but not in vertical, space use. Males were more exposed to predation risk, i.e. spent more time and foraged more in risky area. When related to risky area, the use of area, trees and food stations was sex-dependent. Activity, and also the use of trees, was species-dependent. We conclude that in horizontal space use both species showed anti-predatory responses to weasel presence as a community, but did not respond as the species. It seems that it is the sex, which is playing a crucial role in the response to predation.

INFLUENCE OF VARIOUS ODOURS ON THE FORAGING BEHAVIOUR OF BANK VOLES (*CLETHRIONOMYS GLAREOLUS*)

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Rodents represent 43% of the mammalian class. They overtake all the other orders with their abundance and number of species and genera.

Bank voles (*Clethrionomys glareolus*) are small forest rodents, largely distributed in Europe. They represent a potential prey for many predators like mustelids, canids, raptors or even snakes. Bank voles are not fast runners, so predation escape thus rather relies upon anticipating the presence of predators in their neighbourhood. We carried out an experiment to test whether bank voles modify their foraging behaviour in response to olfactory cues of predation. Indeed, olfaction is very well developed and known to play a major role in intraspecific relationships in bank voles. A group of 8 male and 8 females was installed in an outdoor 5x5 m enclosure in a prime bank vole habitat. On each day, 40g of food (wheat and corn) were equally distributed in two feeding trays; in one of them the food was impregnated with a test odour. Tested odours were extracted from faeces of predators (fox, weasel, cat), from pellets of raptors (tawny howl and peregrine falcon) and from bank voles. We also included a control with the extracting substance (methanol). After 24h, the trays were replaced by new ones with fresh food and another test odour, and the food consumption of each tray was measured. Both trays were filmed in order to record the foraging behaviour. The whole set of odours was replicated three times (during the fall, the spring and the summer).

The results obtained with ANOVA and orthogonal complexes, show that bank voles strongly modify their foraging behaviour depending on the cues of predation risks. Bank voles clearly avoid risky foraging places marked by odours of predators.

In perspective, information obtains with these results may help in a conservatory context program to prevent over-dispersion by blocking bank voles with odour lines containing these predators odours.

THE ROLE OF HORMONAL STATUS OF SIGNAL RECIPIENT IN RECEPTION OF PHEROMONES IN HOUSE MOUSE

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It is well known that exposure of male mice to the urine from receptive females produce considerable increase of plasma testosterone. We studied the influence of steroid hormones: testosterone and corticosterone (in plasma and urine) of males on reception of female chemical cues in vomeronasal organ. Test subjects were adult male mice of different social status. Hormone assay was performed using ELISA technique. Plasma testosterone ranged from 0.1 ng/ml to 12ng/ml. Corticosterone ranged from 120ng/ml to 640 ng/ml. Patterns of c-fos expression were recorded in receptor tissue in response to stimulation with urine from receptive females. We observed activated cells in basal and apical zone of receptor tissue regardless of differences in plasma testosterone level of males. Another group of males was exposed to predator urine (*Felis catus*) for three days in environmental chamber. Monitoring of steroid hormones showed that testosterone ranged from 1 ng/ml to 2 ng/ml, corticosterone - from 840 to 1050 ng/ml. We did not observe pattern of activation in receptor tissue in stressed males with high corticosterone levels (over 800 ng/ml). The data obtained indicate that glucocorticoids may play an important role in pheromone reception in vomeronasal organ.

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EFFECTS OF ENVIRONMENTAL FACTORS ON THE SPATIAL DISTRIBUTION OF COMMON VOLE (*MICROTUS ARVALIS*)

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Common voles live in groups in large burrows that pattern of their spatial distribution is affected by several factors.

In this research spatial distribution of population of common vole (*Microtus arvalis*) and its correlation with several environmental factors was studied in an approximately isolated plot that is located around of Louvan-la-Neuve city in Belgium.

In order to preparation of burrows map distribution, a permanent 1/4-ha grid for two consecutive years was utilized as a reference for location determining of each burrows entrance in the grid.

The research plot where characterized based on soil, phytosocialology and hydrologic measurements.

For years 2005 and 2006, two step cluster analysis has indicated 4 clusters that are distinct from each other (p values are highly significant).

The result has shown that 70% of variance of number of burrows is explained by five variables that means of them are not; t homogenous in the clusters of the burrows entrance and among of soil variables that some of them has shown an important and power correlation with distribution of burrows. The Limon variable of soil was the most important environmental variable that was affected burrows entrance distribution of common voles and in the other words the cluster with low burrows number was associated with high mean of the Limon in the soil.

LEARNING, IDIOTHETIC NAVIGATION AND SWIMMING PATTERNS IN SMALL TERRESTRIAL RODENTS IN THE MORRIS WATER MAZE

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We compared learning, idiothetic navigation and swimming patterns in four wild rodent species *Microtus arvalis, M. brandti, Acomys dimidiatus, Mus musculus*, and in laboratory mouse (outbred CD-1 strain) in the Morris water maze (MWM). After handling the animals underwent classical MWM training in a pool which was surrounded with a non-transparent and non-translucent tent. So they did not see any visual landmarks and they had to use idiothetic navigation for locating a hidden platform. The observed swimming patterns were evaluated for the first, third and fifth days of tests. The semicircular swimming was the most used navigation strategy in the environment with restricted landmarks. According their performances we can divide species into two groups: *M. arvalis, M. musculus,* and CD-1 strain searched better than *A. dimidiatus* and *M. brandti*. However the latter two species improved their navigation markedly after they had been able to delete the ineffective navigation strategies at the end of the test. Probably there is a relation between their natural environment and ability of the species to orientate with or without visual landmarks.

DIGGING ENERGETICS IN TWO MOLE-RATS (BATHYERGIDAE) WITH DIFFERENT SOCIAL SYSTEMS

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For subterranean rodents, searching for food by hard digging through the tunnel systems is the most important factor affecting their life underground. There are only few studies on energetics of subterranean rodents dealing with the energetic cost of burrowing in respect to soil type, ambient temperature and body mass. However, none of them have concentrated on comparison of digging energetics in related species with different social systems.

In this study we investigated and compared resting and digging energetics between two mole-rats (Bathyergidae), solitary silvery mole-rat (*Heliophobius argenteocinereus*) and social giant mole-rat (*Fucomys mechowii*). Both species live in sealed burrow systems in similar habitats, where they face similar microenvironmental conditions. They differ in body mass slightly. However, they differ significantly in their ways of life, the giant mole-rat is a social species but the silvery mole-rat is a strictly solitary one. Social giant mole-rat can form cooperative "digging chains" and then burrowing can be more economical than that of solitary digging.

The resting (RMR) and digging metabolic rate (DMR) were measured through open flow respirometry. DMR was measured in both species exposed to both types (soft and hard) of soil. We focused on questions if i) the cost of burrowing in individual species varies with soil type; ii) differences between sex occur within species; iii) the cost of burrowing, in respect to soil type, varies between species and if expected interspecific differences could be explained by different social systems. Finally, we compared the energetics data with those reported for other subterranean and fossorial rodents.

KIN RECOGNITION IN VOLES: INCEST AVOIDANCE IN FAMILY GROUPS OF SOME SPECIES OF VOLES ARVICOLINAE

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The ability of animals to recognise relatives has great value for the formation of population structure. The purpose of this work was to study the probability of the formation of mating pairs among close relatives of voles in the same family as well as the mechanisms of inbreeding avoidance. This research deals with three vole forms - Steppe (*Microtus socialis astrachanensis*), Gorian (*M. s. goriensis*) and Brandt (*Lasiopodomys brandtii*). The hypothesis is that the interbreeding ability differs in species with different reproductive strategy: the more polygamy is expressed in the species the higher the probability of inbreeding, but mechanisms of incest-taboo avoidance are less developed.

Four versions of experiments were carried out (mother and son; father and daughter, brother and sister from one litter, and for the control – unrelated individuals). Experiments have shown that all three studied forms of voles differently react to inbreeding. Steppe vole avoids copulation with kin. Gorian voles more often give offspring when pairing with kin, and Brandt's voles copulate with family members or related individuals almost without restriction. The revealed differences correspond to variations in incest-taboo mechanism and correlate with different types of social relations.

Apparently, the taboo mechanism is formed in voles, in early ontogenesis by imprinting of a related smell that during the reproductive period determines an opportunity to avoid inbreeding. To investigate reaction formation to a related smell among animals with a different degree of the relationship, voles have been taken from a family group, from a group of distant relatives, unrelated individuals. Observations have shown that recognition and preference of a family smell is necessary for the period of the opening of the eyes and active behaviour formation of the young (at the 9-12th day). At the age of 45-60 days steppe voles avoid contact with potential sexual partners bearing a related smell, preferring a smell of distant relatives and unrelated individuals. In Brandt voles the preference of an unrelated smell is expressed considerably less than in steppe voles.

The author found out that all three forms are able to recognise and discriminate kin odour from non-kin odour and that there are two kin recognition mechanisms - learning of kin odour and genetically determined kin recognition. The data shows that the Steppe vole form monogamous family; it is a dominant reproductive relations' type of *M. s. astrachanensis*. However with *M. s. goriensis*, facultative monogamy is possible with transformation into polyginous relations. Brandt's vole has typical polyginous reproduction strategy.

GATHERING BEHAVIOURAL INFORMATION ON THE ENDANGERED HUNGARIAN MOLE RAT (*SPALAX LEUCODON*) BY MEANS OF AN ACOUSTIC METHOD

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Mole rats (Rodentia: Spalacidae: Spalacinae) are extremely adapted to fossorial way of life and spend their whole life underground which makes their monitoring and ethological study very difficult. The blind mole rat (*Spalax leucodon*) is a strictly protected species in Hungary with limited distribution and probably less than 800 individuals. The chromosome number of this population differs from those of the neighbouring countries thus they represent a separate evolutionary unit. The species is on the verge of extinction in Hungary but the information necessary to appropriate conservation measures are very limited.

A specimen was kept in an artificial tunnel system under laboratory circumstances where signs of its activity were collected by a geofon and recorded in a computerized data logger system. The records were analysed by a sound analysing program developed by our group. By means of this program we were able to distinguish different types of activities (moving, eating, sleeping, communication) and to investigate their daily patterns. Based on these preliminary results a system is under developement which - without the slightest disturbance - makes possible the monitoring of populations, determination of population size and gathering of behavioural information in the natural habitats of mole rats.