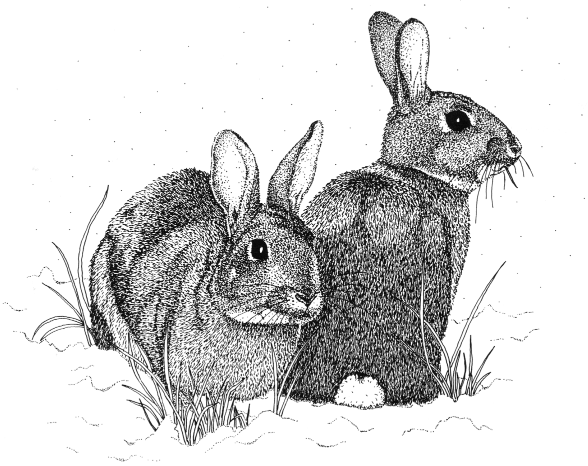
WORKSHOP

Competition in Lagomorph species: a multidisciplinary approach



DISTRIBUTION OF APENNINE HARE (*LEPUS CORSICANUS*) IN LATIUM, CENTRAL ITALY: COMPARISON/VALIDATION WITH A PROPOSED MODEL OF HABITAT SUITABILITY, AND WITH AN EUROPEAN HARE (*LEPUS EUROPAEUS*) MODEL

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The Apennine hare (*Lepus corsicanus*) is an Italian endemic species widespread in Central and Southern Apennine, and in Sicily. Although this species is often confused with the European hare (*Lepus europaeus*) and it is in way to extinction, it is still present in Latium region (Central Italy), probably with small populations, often both geographically and ecologically isolated.

Starting from 1981-1982 one of the authors (FMA) collected information on this species (firstly considered as an Italian subspecies of *L. europaeus*), more organically from 1990. From this date till today, information of captured specimens during hunting season or killed accidentally, were recorded. Every record was reported on a geographic map using a GIS software (ArcView 3.2). Moreover, always using the same software, and independently, we have constructed a habitat suitability model for this species, and this one was compared with an already proposed model of habitat suitability made by University of Rome "La Sapienza". This latter model is used by the Regional Park Agency (ARP) of Latium (2004). Some differences concerning habitat suitability can be noticed comparing the two models. In fact, our proposed model seems more likely, considering all records collected till now.

Analysing the distribution of Apennine hare in Latium, it seems clearly a taxon adaptable to different habitat and altitudes. In fact it was found from the sea level, in Mediterranean environment, until at the Apennine pastures (the highest record was at 1,700 m a.s.l.). A right model of habitat suitability must be taken with serious consideration for future conservation and/or restocking projects of this species.

Moreover, the habitat suitability model of *Lepus corsicanus* proposed in this study was critically compared with a similar proposed model, in the same region, concerning the European hare *Lepus europaeus*. This latter species is continuously restocked in Latium for hunting purpose even if it is not certain to be autochthonous in Central Italy.

POPULATION DENSITIES AND HABITAT SELECTION OF BROWN HARE (*LEPUS EUROPAEUS*) AND INTRODUCED EASTERN COTTONTAIL (*SYLVILAGUS FLORIDANUS*) IN NORTHERN ITALY

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The eastern cottontail (*Sylvilagus floridanus*) is a lagomorph native to America that was introduced into Italy for hunting purposes. A concomitant dramatic drop in the brown hare (*Lepus europaeus*) presence in the same area, allowed us speculation about a possible competitive interaction between the two species. In 2002 we started a research to investigate habitat characteristics and population abundances, and to explore the mechanism that allows local coexistence or competition between the two species.

We used night counts to evaluate population densities; subsequently, we started a study with capture and recapture (cottontail) and radiotracking (both species).

Average density of hare populations (7.1±10.5 ind./km^2, up to 29.9/km^2) was lower in respect to cottontail populations (24.3±27.1./km^2, up to 110.4/km^2; $t = -3.58$, $P = 0.001$). A positive correlation between the abundance of cottontails and hares ($R = 0.76$, $P < 0.002$) suggested a dependence of both species from habitat characteristics and food availability and did not support a competition between them. Fox population indexes increased with the density of hares ($R = 0.80$, $P < 0.0006$) and cottontails ($R = 0.59$, $P < 0.05$).

Mean home ranges in cottontails were similar between sexes but differed according to season, with smaller areas in autumn-winter (means 1.07-2.16 ha) compared to spring-summer (2.50-3.60 ha). Home ranges in hares were generally between 30-40 ha, without differences according to sex and seasons.

Cottontails used for daily resting sites shrubby areas along the river, avoiding other habitats. Hares selected more habitats, with some seasonal preferences (wheat in spring, maize in spring and summer, woodlands and stubbles in autumn).

During the nocturnal activity the cottontails selected crops, uncultivated fields and shrubs, while hares used herbaceous habitats (crops and meadows) and ploughs.

The result of this study show that cottontails and hares use, at least partially, different habitats as daily resting places and for feeding activity. However this divergence seems related to different ecological and behavioural adaptations and not to competitive exclusion. Overall, hares used more habitats than cottontails, both natural and cultivated. Nevertheless, the change in landscape use toward a more intensive agriculture, the presence of large areas covered by rice fields, and of natural areas with a good ligneous cover, made many censused sites not suitable for hares.

LATE MIOCENE-RECENT OCHOTONIDS OF EURASIA WITH EMPHASIS ON EUROPEAN: SOME CASE-STUDIES OF COEXISTENCE AND COMPETITION AMONG EXTINCT AND EXTANT FORMS

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Family Ochotonidae consisting of two subfamilies – Sinolagomyinae Gureev, 1960 and Ochotoninae Thomas, 1897 includes 17 extinct genera and one extant genus *Ochotona* with 34 extinct and 30 extant species. The earliest record of ochotonids is known from the Middle Oligocene of Asia. Ochotonids flourished throughout the world during Early Miocene, invading Europe for the first time. In Early Miocene European lagomorphs, besides ochotonids, were represented by leporids, amphilagins and prolagins. The latter two taxa are morphologically close to ochotonids and show evolutionary trends similar to pika-lineage. It is possible to assume that they could occupy similar landscapes. Since Late Miocene lagomorph diversity decreased in the Europe, and no Amphilagins and scarce fossils of Leporids are known in the region, while Prolagins still flourished, even if they showed a more limited geographical distribution than in Middle Miocene. In Late Miocene ochotonids are represented by the genus *Proochotona*, while the genera *Pliolagomys*, *Ochotonoma* and *Ochotona* appeared in Early Pliocene; they occupied the easternmost regions of Europe. It is possible to suggest that Prolagins were one of the main ecological and nourishmental competitors of Ochotonids at that time. During Pliocene and Early Pleistocene Prolagins decreased in their number and diversity, pikas of the genus *Ochotona* were present in Central Europe. In Late Pleistocene *Ochotona pusilla* occupied vast plain periglacial territories of Europe as well as the Prebalkalian region in the east; Prolagins only survived insular areas in the Western Mediterranean islands of Sardinia and Corse.

As for recent Ochotonid species, they are mainly distributed in Asia. Mongolia and China (especially Tibet and Himalaya mountains) are heavily populated areas. The distribution areas of several modern Ochotonid species overlap: *Ochotona alpina* with *Ochotona hyperborea* in Sayan mountains, *Ochotona pusilla* with *Ochotona pallasi* in Kazakhstan, *Ochotona daurica* with *Ochotona pallasi* in Mongolia, *Ochotona roylei* with *Ochotona macrotis* in Nepal, etc.

It is known that *Ochotona alpina* and *Ochotona hyperborea* in Sayan mountains, in their zone of sympatry segregate altitudinally: the former occupies rock and talus, the latter inhabits rocky terrain in dark coniferous forests (Arakcha L., personal communication).

The same evidence is mentioned by T. Kawamichi for *Ochotona roylei* and *Ochotona macrotis* from the Nepal ranges. The large-eared pika *O.macrotis* is a rock-dwelling form and its distribution area covers higher altitudes than *O. roylei*, which lives at lower elevation, in forests.

The distribution areas of *O. pusilla* and *O. pallasi* in some regions of Kazakhstan overlap, however these species are not competitors because they prefer different habitats. *O. pusilla* is burrowing steppe-dwelling species in contrast to Pallas's pika which is talus-dwelling at low elevations and burrowing in steep cliff faces, and may inhabit dry steppes or deserts.

GENETIC DISTINCTION AND ASSESSMENT OF INTERSPECIFIC HYBRIDISATION AMONG THREE SPECIES OF HARES (*LEPUS*) IN ITALY

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The distribution and population dynamics of three species of hares (*Lepus*) in the Italian peninsula (*L. corsicanus*, *L. europeaus* and *L. timidus*) have been strongly affected during the last few decades by deep habitat changes, hunting and massive restocking of some over-hunted populations. In particular, the distribution range and global population size of the recently rediscovered endemic Italian hare (*L. corsicanus*) has shrunk in central and southern Italy and Sicily due to over-hunting and restocking with non-indigenous brown hares. Presence of released brown hares in central and southern Italy and in Sicily thus raised risks of hybridisation and introgression of the scanty surviving populations of Italian hares. It is well known that populations of *L. timidus,* widely distributed in alpine areas, hybridised naturally with brown hares in the past. This study was planned to describe species distinction among *Lepus* in Italy, and assess events of interspecific hybridisation, using a panel of DNA markers. We collected about 200 samples of *L. corsicanus*, *L. europeaus* and *L. timidus* from Northern, Central and Southern Italy, which were analysed using 10 microsatellite loci, three nuclear genes and mitochondrial DNA sequences. All these markers showed sharp differences among the three species, and allowed to: 1) describe their phylogenetic relationships; 2) infer their recent evolutionary history and phylogeographic structure; 3) estimate both inter-population divergence and intra-population genetic diversity; and 4) identify cases of inter-specific hybridisation in Italy.

HABITAT SELECTION AND OVERLAP OF EUROPEAN HARE (*LEPUS EUROPAEUS*) AND EASTERN COTTONTAIL (*SYLVILAGUS FLORIDANUS*) IN NORTHERN ITALY

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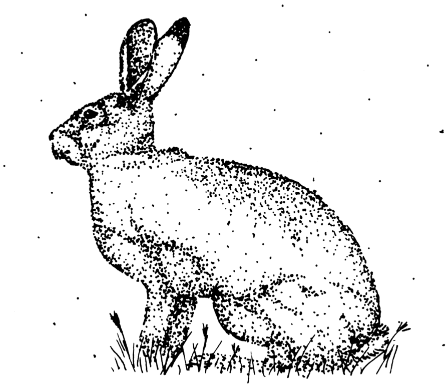
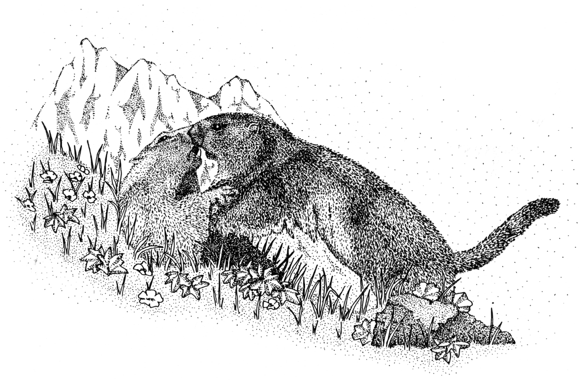
The Eastern cottontail (*Sylvilagus floridanus*) was introduced in 1966 in the western part of the Po Plain (N-Italy), to increase the potential for small game harvesting. Presently, the range of the species is expanding to the central and eastern Po Plain as a consequence of population growth and additional releases. There is some concern that Eastern cottontails may compete with the native *Lepus europaeus*, especially in marginal habitats and in limiting seasons. We studied resource selection and exploitation (macro- and micro-habitat) of both species in three study areas of the Po Plain in 2006-2007 winter (the most limiting season in northern Italy). We chose two areas of allopatry for hares and for cottontails (areas A and C) and one of sympatry for the two species (area B); in this way, niche shifts observed in sympatry should reflect the response to interspecific competition. In each area we assessed the presence/absence of both species based on faecal pellets in 1 m - radius random plots (150 in area A, 150 in area B and 200 in area C). Each plots was assigned to one type of habitat and at each plots we measured the percentages of habitat types in a radius of 100 m (11 macro-habitat variables) and 12 micro-habitat variables in a radius of 1 m. Then we compared in each area the use (proportion of positive points) and availability (proportion of total points) of the habitat types by Bonferroni Confidence Interval Analyses (BCIA) and carried out Discriminant Function Analyses (DFA) between positive and negative points with the macro and micro-habitat variables. We also performed BCIA and DFA comparing directly the two species in area B. BCIAs showed that both species used the habitats in proportion to their availability in each study area with few exceptions, and in area B only the use of crops was different between hares and cottontails ($P<0.05$). From DFAs cottontails were more selective than hares at the micro-habitat level, and in area B the plots with cottontails were characterized by greater percentage of woods, short and long rotation coppices, farmsteads, streams, field margins, and were nearer to permanent cover ($P<0.01$). Probably the key factor allowing the coexistence of the two species is the selection at micro-habitat level, as both species seem to be generalist at the macro-habitat level.



WORKSHOP

Genes, chromosomes and populations: a Symposium in honour of Nicolai N. Vorontsov



PHYLOGENY OF THE SUBFAMILY MURINAE (MUROIDEA: MURIDAE) INFERRED FROM THE COMBINED ANALYSIS OF CYTOGENETIC AND MOLECULAR DATA

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Despite considerable progress during last two decades, numerous aspects of the systematics and phylogeny of muroid rodents remain poorly studied a situation that is further compounded by the likely underestimation of species richness given the high occurrence of sibling species among murids. On the other hand, the existing molecular phylogenetic hypothesis concerning relationships at both intra- and intergeneric levels are often contradictory depending on type and/or size of molecular markers used. In earlier studies of three rodent sibling species complexes by cytogenetic and molecular approaches, we demonstrated that by combining data sets a more detailed understanding of a group's evolution could be inferred. In addition, the frequent finding of low sequence divergences among karyotypically distinct sibling species clearly emphasized the power of the combined approach in detecting unrecognized species diversity. In the present investigation we extended this advance to the subfamily level by analysing chromosomal and molecular data from 21 species comprising 10 genera and 6 suprageneric groupings (divisions) of the subfamily Murinae, the largest taxonomic assemblage in all Placentalia.

Comparison of G-banding patterns and incorporation of available ZOO-FISH data allowed us to identify all the species-specific chromosomal segments and their associations among species. The analysis of a chromosomal character matrix by maximum parsimony resulted in a single phylogenetic tree which was compared with that one obtained from phylogenetic analysis of molecular sequences of both mitochondrial and nuclear genes. Our aims were to evaluate contribution of chromosomal changes in cladogenetic events, to investigate the nature of cytogenetic signatures at the species, genus and suprageneric levels, and to critically compare the support of nodes obtained by the cytogenetic and molecular phylogenetic reconstructions. The analysis of the combined data sets resulted in a phylogenetic tree that is examined for concordance with existing phylogenetic hypotheses on the subfamily Murinae.

CHROMOSOMAL SPECIATION IN *ELLOBIUS* (RODENTIA): NONRANDOM SEGREGATION OF ROBERTSONIAN TRANSLOCATIONS IN NATURE AND EXPERIMENT

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Genus *Ellobius* is one of most interesting and perspective group for study chromosomal speciation. Long-term research of Robertsonian fan in mole-vole *Ellobius tancrei* was initiated by Prof. N. Vorontsov. Wide chromosome variability was described from local zone in Vakhsh-Surkhob valley (Pamiro-Alai). We made a comparative analysis of karyotype structure for natural and experimental populations (hybrids of crossing forms 2n=34 and 36 with original form 2n=54, six hybrid generations and backcrosses). Level of heterogeneity of chromosome sets is different in nature and experiment. In nature we found animals heterozygous for not more than four translocations. Experimental hybrids should be and they really are much more heterogeneous. Because of these we were surprised to discover hybrids homozygous for translocations in second generation. The combination of metacentrics in sets are non random. In nature the mainstream in structural patterns of karyotypes is fixation of large metacentrics II-VI. In experiment, apparently because of short time for stabilizing genomes, different tendencies were revealed. Fixation is trustworthy for one of the largest metacentric III. But in case of breeding forms 2n=50 and 2n=48 large metacentic V was eliminated from hybrid sets. As we showed by cluster analysis for natural samplings of these forms, animals from populations situated on opposite banks of Surkhob River have different combinations of translocations in their chromosome sets. On the northern bank population is more low-chromosomal and metacentric V is common for chromosome sets (2n=48-37). Animals inhabited the southern bank have chromosome sets without this metacentric (2n=50), the translocation appears only in hybrid zone with form 2n=34. In experimental crossing of low-chromosomal 2n=32 and 2n=34 forms we got data proving fixation of small metacentric X. This fact corroborates our hypotheses of chain process in formation of low-chromosomal part of Rb fan. The prevalence of certain combinations of translocations is possible due to meiotic drive.

GENETIC AND CHROMOSOMAL MECHANISMS OF HYBRID INCOMPATIBILITY IN MAMMALS

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We analyzed a relative contribution of chromosomal and genetic divergence into reproductive isolation and speciation in three different taxa of mammals. We demonstrated that male sterility in hybrids between different subspecies of South American rodent *Thrichomys* and hybrids between geographically isolated population of the house musk shrew *Suncus murinus* was determined solely by genetic incompatibility, and chromosomal changes played minor if any role in the speciation. The genetic incompatibility in these two taxa was controlled by a very small number of loci affecting the early stages of meiosis of the hybrids, while the viability of the hybrids was not affected. The analysis of the hybrid zone between two chromosome races of the common shrew *Sorex araneus* revealed more complex picture. Their genetic divergence for habitat preferences led to formation of ecological pre-mating isolation. Divergence for the genes controlling morphological traits affected the development of the hybrids and, apparently, their viability, thus contributing into post-mating isolation. Meiosis in the hybrid males was also affected. In the hybrids we observed a high frequency of synaptic aberrations, which were apparently determined by chromosomal incompatibility. Thus, we may conclude that the fixation of different selectively neutral chromosomal rearrangements in geographically isolated populations does not drive these populations to speciation; however in some cases chromosomal differences may reinforce post-mating isolation already established by the divergence of the genes controlling development and chromosome pairing and recombination at meiosis.

MOLECULAR PHYLOGENY AND SYSTEMATICS OF MARMOTS (*MARMOTA*, SCIURIDAE, RODENTIA)

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The Holarctic genus *Marmota* is used as a model group for long-term evolutionary studies. Using of molecular approach in phylogeny and systematics of marmots was started by comparative sequencing of cyt b mtDNA gene (Steppan et al, 1999; Kruckenhauser et al, 1999). For testing their results multilocus IS-PCR analysis of nDNA was used. IS-PCR data divide marmot species in two parts with strongly geographical Nearctic and Palearctic distribution in contrast with cyt b data. Single event of marmot migration through Beringian Bridge is supported. Close similarity of *M. menzbieri* and *M. caudata* mtDNA markers and high genetic distances between their nDNA markers support a view on remote hybridization of these species. *M. kastschenkoi* featured by unique chromosomal characters (Brandler, 2003) diverges as a sister species to *M. bobak* and *M. baibacina*. One more mtDNA gene D-loop sequences were used for analysis of intraspecies structure and sister species relationships in bobak group. Evident divergence of *M.b. centralis* into *M. baibacina* clade was showed. A population structure of wide distributed species *M. bobak* was investigated. Using some nDNA genes sequences as markers in phylogenetic and systematic studies of marmots is discussed.

SEX CHROMOSOMES VARIATION IN RODENTS

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Mammalian sex chromosomes are characterized by independent evolution with respect to the autosomes. In placental mammals, the diversification between X and Y chromosomes has determined the maintenance of few functional genes in the Y chromosome, and a larger and highly conserved gene content in the X chromosome. We describe several patterns of variation of sex chromosomes that we have come across during cytotaxonomic studies of numerous Rodent genera performed by means of G- and C- banding and fluorescence in situ hybridization (FISH) with telomeric probes. In the African rodents *Grammomys sp*. and in different species of *Arvicanthis* and *Lemniscomys* it has been observed an intra-population polymorphism for sex chromosomes due to different amount of heterochromatin. Pairs of species with similar autosomal sets and differences in shape and size of sex chromosomes have been observed in *Aethomys* and *Microtus*. Translocations between sex chromosomes and autosomes are present in different African population of *Nannomys minutoides*. In this species sex-reversed XY females were also observed in one Zambian population. Finally, in *Acomys sp*. from Tanzania aneuploidy that manifests in the presence of a single giant X chromosome in female, and mosaics for Y chromosome in male, is described.

The trend of sex chromosomal changes is supported by phylogenetic analysis based on mitochondrial cyt-b gene sequences. The overall data provide evidence of chromosomal plasticity of sex chromosomes in rodents. We discuss now whether the sex chromosome variation in rodents can be subjected to natural selection and involved in chromosomal speciation events.

THE LEADING EDGE MODEL AS A POSSIBLE EXPLANATION FOR THE FIXATION OF ALIEN MTDNA AS THE RESULT OF ANCIENT HYBRIDIZATION

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Widespread mtDNA introgression involves a paradox: if we assume that all carriers of mixed nuclear genomes become extinct as the result of their low adaptability, then what accounts for the broad distribution of alien mtDNA? After all, in the first stages (F_1 and crossbreedings) alien mtDNA carriers are inevitably also carriers of mixed nuclear genomes. That is, massed introgression of mtDNA seems to need a radical change in the direction of selection in relation to hybrids - from positive to negative. From our point of view, this paradox may be explained with the help of Godfrey Hewitt's leading edge model. According to Hewitt's model, the rapid expansion of a species will be accompanied by homozygosity of peripheral populations. Thus peripheral populations, given expansion of the range, repeatedly pass through a "bottleneck". One should note that for most species sharp differences in philopatry according to sex are typical. Therefore in peripheral local colonies of one species, when it occupies the range of another species, the 1-to-1 sex ratio is generally violated. This results in an increase in the frequency of hybridization on the edge of the range - this is a widespread and well-known phenomenon. F_1 hybrids, given a low density of the expanding parent species, may successfully use the parent species' free ecological niche. In the first stages of expansion this determines their greater adaptability and compensates the negative selection of carriers of mixed nuclear genomes. With an increase in density the niche turns out to be occupied and this produces a change in the direction of selection of hybrids - from positive to negative. Thus the application of the leading edge model allows us to explain the paradox of mtDNA introgression. The fixation of alien mtDNA occurs as a result of the same mechanism - repeated "bottlenecks" - and we need not assume an increased adaptability of alien mtDNA, for example "northern" mtDNA of *Clethrionomys rutilus* given an expansion to the north of *C. glareolus*, or mtDNA of *Tamias ruficaudus* in *T. amoenus*. Conclusions: 1) Introgression is, as a rule, asymmetrical since the simultaneous expansion of two species into each other's ranges is extremely rare; 2) The direction of introgression goes in the opposite direction of expansion. Following this logic, the distribution of alien mtDNA 600 km to the north from the ranges of their original carriers in the Volga populations of *Spermophilus major* suggests a distinctly different picture of the ranges of these species during the Pleistocene.

KARYOTYPES OF COLLARED LEMMINGS, *DICROSTONYX* SPP.

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Collared lemmings have a circumpolar distribution in arctic regions. There are four species, *Dicrostonyx torquatus* in Eurasia and *D. groenlandicus, D. hudsonius* and *D. richardsoni* in North America. The two first mentioned have an extensive distribution, the other two a relatively limited distribution on both sides of Hudson Bay. During two tundra expeditions lemmings were collected for genetic studies. In 1994 chromosome preparations were made from 161 collared lemmings collected in 13 localities along the Siberian coast, from Kanin Peninsula to Wrangel Island. In 1999 preparations were made from 86 collared lemmings trapped in 15 localities in the Canadian Arctic (unfortunately 1999 was a poor lemming year).

The two species with a wide distribution exhibits extensive chromosomal polymorphism, both within and between populations. The polymorphism in *Dicrostonyx torquatus* concerns primarily the sex chromosomes and number of B chromosomes. Robertsonian translocations between autosomes and sex chromosomes (A-X and A-Y) characterize four chromosome races. In *D. groenlandicus* from the Canadian Arctic the chromosome number varies between 38 and 50 due to Robertsonian translocations and 0-4 B chromosomes of variable size and morphology. In Wrangel Island (collected in 1994) the collared lemmings belong to the species *D. groenlandicus.* They have only 28 chromosomes and neither polymorphism nor B chromosomes.

Collared lemmings, like wood lemmings, have an exceptional mechanism for sex determination. Fertile females with XY sex chromosomes occur together with XX females; males have the normal XY sex chromosome constitution. XY females seem to be more common in *D. torquatus* than in *D. groenlandicus*.

The karyotypes of all species of the genus *Dicrostonyx* will be presented and discussed in connection with karyotype evolution and speciation.

ISOLATION EFFECT ON GENETIC DIVERGENCE OF PALAEARCTIC GROUND SQUIRRELS *(SPERMOPHILUS,* SCIURIDAE, RODENTIA*)*

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Genetic research on Palaearctic ground squirrels was initiated and developed and headed by N.N. Vorontsov since the sixties of last century. The results extensive studies allow to examine into details of *Spermophilus* systematics and evolution history of the genus.

Although *Spermophilus* is intensively studied genus, the common view about number and limits of Palaearctic species does not exist up to now. Based on morphological data from six to therteen species have been distinguished. Karyological data add another two species. The starch gel electrophoresys of 9 enzymes and 8 other proteins coded by 26 hypothetical loci from all Palaearctic species with exception of *S. alaschanicus* was performed in order to determine both intraspecific and interspecific differentiation. As a rule, intraspecific differentiation was insignificant. Nei´s (1978) genetic distances (D) =0.015±0,008. No locus exhibited alternatively fixed alleles. But three loci exhibited alternatively fixed alleles between western (*S.u.eversmanni*, *S.u.stramineus*) and eastern (*S.u intercedens, S.u.menzbieri, S.u jacutensis*) geographical forms of S. *undulatus* (D = 0.19). The hybrid zone between these forms was found near south part of the lake of Baikal. The interspecific level in Palaearctic *Spermophilus* characterized by a wide range of genetic differentiation. D ranged from 0.06 (*S. pygmaeus, S. musicus*) to 0.71 and number of loci with alternatively fixed alleles from 0 (between two adjacent forms of major-group brevicauda, (2n=36) and pallidicauda, (2n=34) to 13 (between *S. relictus* and *S .undulatus*). A low level of genetic differentiation was found in a group of adjacent species *S. odessanus, S. suslicus* and *S. musicus, S. pygmaeus*, and of the major-group. Species of the groups are known to hybridize along contact zones. Allopatric species have shown more significant distinction as among themselves, and compare to above mentioned. Perhaps that existing structure of Palaearctic *Spermopthilus* is a result of several speciation flashes. The separations of *S. odessanus, S. suslicus* and *S. pygmaeus, S. musicus* and major-group species as well as of geographical forms of *S. undulatus* perhaps came about during the last glacial period.

CHROMOSOME EVOLUTION AND HYBRID ZONES IN MEDITERRANEAN SPALACIDAE

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Here we present comparative cytogenetic studies based on C-, G-banding, Ag NORs, fluorochrome staining and fluorescence in situ hybridization (FISH) with telomeric and rDNA (45S) probes of nine *Nannospalax leucodon* cytotypes from 21 localities in northern and northwestern Turkey, four *N. ehrenbergi* cytotypes and their hybrids from Israel, and *N. ehrenbergi* cytotype of 2n=60 from Jordan.

Comparative analyses of C-banded chromosomes shown, that *N. leucodon* cytotypes had lesser amount of heterochromatin than *N. ehrenbergi*. The heterochromatin in *N. ehrenbergi* cytotypes was largely GC-rich, while heterochromatin in *N. leucodon* cytotypes was defined both as AT- and GC-rich.

According to the results of FISH, telomeric sites of most chromosomes in *N. leucodon* cytotypes were characterized by symmetrical signals contrary to enlarged above-centromeric hybridization signals in acrocentric chromosomes in *N. ehrenbergi* cytotypes. Most biarmed chromosomes (including the X-chromosomes) possessed interstitial (near centromeric) telomeric signals in both *Nannospalax* groups.

In contrast to *N. ehrenbergi* cytotypes which were not differed in the number and localization of rDNA sites, *N. leucodon* cytotypes shown great variability both in the number (from 4 in the cytotype of 2n=50 to 10 in the cytotypes of 2n=60) and in the localization of rDNA sites including translocation of rDNA clusters from an autosome to the Y-chromosome.

Different arm combination in biarmed chromosomes in the cytotypes with low chromosome numbers and remains of telomeric sequences at centromeric regions argue in favor of Robertsonian fusions responsible for the chromosome number changing in the genus *Spalax*. Shift of centromeric positions and reorganization of heterochromatin structure accompanied by deletion (or amplification) were responsible for the arm chromosome number variation in the studied Mediterranean mole rats.

A series of homoplastic events took place in the course *Nannospalax* chromosome evolution.

Cytogenetic analysis of hybrid zones between *N. ehrenbergi* cytotypes gave us significant additional information on the process of *Nannospalax* chromosome evolution.

The analysis of chromosome divergence between *N. leucodon* cytotypes and the pattern of their distribution predict existence of hybrid zones yet to be studied.

ROBERT MATTHEY, A HUMANIST WHO BRIDGED THE GAP BETWEEN CHROMOSOMES AND TAXONOMY: AN HISTORICAL PERSPECTIVE

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The scientific work of Robert Matthey (1900-1982) comprises a legacy of methodological innovations, experimental and theoretical studies and, not least, the first artistically executed karyotypic descriptions of a large number of vertebrate and insect taxa. Acknowledged by the international scientific community as a champion of comparative vertebrate karyology, his enthusiasm, dedication and patient tutoring inspired over three generations of researches. Given the context of this symposium one case is worth special mention.

During the mid-fifties, Nikolai N. Vorontsov (1934-2000), a recently fledged PhD in evolutionary morpho-anatomy, read a series of Matthey's papers. Impressed by the scale and importance of karyological studies for mammalian systematics, he became Matthey's strongest advocate, as well as a proponent in his own right, of the value of chromosomal investigations. In his seminal paper "Importance of chromosomal studies for systematics of mammals" (1958), he attempted a synthesis of Robert Matthey's life's work, introducing him as the founder of mammalian karyosytematics. Some years later Vorontsov set up the first laboratory in the former URSS and organized numerous field expeditions directed at karyologically characterizing the Russian mammalian fauna. His numerous pupils (and in turn, their graduates) continue today with mammoth task.

The aim of our communication is to present an analytical assessment of Matthey's published work and to consider some of the problems highlighten by his endeavours but which still remain the focus of modern comparative cytogenetics investigations such as determining ancestral karyotypes, characterizing karyotypic evolution, chromosomal changes and phylogeny, the irregularity of occurrence of chromosomal mutation, cryptic species and hidden biodiversity. Special attention will be paid to the progressive conceptual deepening of Matthey's ideas on chromosomal changes and possible sympatric speciation, and their interaction with those developed by M.J.D. White and N.N. Vorontsov on chromosomal speciation.

GENETICS OF SPECIATION. DEVELOPMENT OF EVOLUTIONARY IDEAS OF NIKOLAY N. VORONTSOV

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Nikolai Vorontsov (1934-2000), eminent scientist, educationist, political figure, and bright and charming individual had exceptional talents in different areas. He was a naturalist and innovator, combining wide interests with deep erudition. Being a classical zoologist, he also was interested in ideas and approaches to genetics, cytology, evolution and molecular biology to which he made important contributions. He authored more than 550 publications (including 34 books written and edited).

Influenced by R. Matthey, his papers and personal communication, N. Vorontsov in his review “The significance of chromosomal studies for mammalian taxonomy” (1958), defined area of scientific interest over the following 40 years of intense research. In “*Cricetidae* species of Palaearctic in statu nascendi” (1960), he formulated principles of genetic speciation. Working as classical zoologist he described the phenomenon of unevenness of evolutionary changes in organs and traits of the same system, and the principle of compensation of functions in monograph “Evolution of the Digestive System of Rodents” (1967). He and his followers organized a lot of expeditions to many regions of the former Soviet Union. Abundant new zoological and cytological material was obtained especially important for identifying problematic species by cytogenetic methods, and providing a basis for collections and inventories. In 1999, he published his last book “The Development of Evolutionary Ideas in Biology”, which in a way was a summary of his scientific interests.

A tremendous success of the scientific school he created is due to a broad intrusion to classical zoology of modern molecular biology. A current research of his followers is a continuation of such approaches. Speciation is a very complicated and diversified process hardly learnable by experimental way; our task comes down to decode facts getting from nature model cases. Early stages of species differentiation are explored by detailed analysis of species structure for wide-ranged species (*Sylvaemus uralensis*, *Ursus arctos*), and intensive study of chromosome speciation in *Ellobius*. Such inmost species relations as phylogenetic relationships, Beringian connections, history of species distribution are studied on *Marmota* and *Spermophilus*. Karyosystematical investigations are continued, new species were described recently (*Marmota kastschenkoi* 2n=36; *Spermophilus suslicus* 2n=36 and 2n=34). Other recent studies are also discussed.

COMPARATIVE ANALYSES OF HOLARCTIC VOLES AND LEMMINGS USING G-BANDS AND HIGHLY REPEATED DNA FAMILIES

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G-banded karyotypes from 41 species representing 12 genera, with diploid numbers ranging from 17-62, have have been prepared and analyzed. Based upon outgroup comparisons a primitive karyotype of 2n=56 is proposed. Interspecific comparisons document numerous rearrangements including centric and tandem fusion, pericentric inversions, and apparent centormere repositioning. Certain chromosomes are involved in rearrangements more often than are other chromosomes, suggesting that mutation 'hot-spots ' for chromosomal rearrangements exist. Phylogenetic analyses indicate that certain Eurasian species are more similar to North American taxa than to other Eurasian species. In addition, fluorescence *in situ* hybridization documents the distribution of six highly repeated DNA families in the chromosomes of nine species of *Microtus*. Both autosomal centromeric heterochromatin and large C-band positive blocks on the sex chromosomes contain different repeated families in different species. Interspecific variation in the chromosomal distribution and copy number of the repeats suggests that a common ancestor to modern species contained most of the repetitive families, and that descendant species selectively amplified or deleted different repeats on different chromosomes. The characterization of genetic variation within and between species defines management units and assists in implementing conservation and reintroduction programs.

WORKSHOP

Rodent-borne viruses: from field to genes

VIRUS DYNAMICS IN RODENT POPULATIONS: FIFTEEN YEARS OF COWPOX

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Cowpox virus is endemic in many rodent populations in Europe, but causes no obvious symptoms of disease. As such it is almost certainly typical of many pathogens in wildlife populations. A number of questions naturally arise. Are there subtle effects on the fitness of infected hosts in spite of the absence of overt symptoms? May these translate into effects on the dynamics of whole populations? What are the characteristics of the dynamics of the virus itself, and how might these influence its effect on its host? These questions will be addressed by reviewing studies on wood mice, bank voles and (cyclic) field voles in the UK. Neither the dynamics of the virus, nor its effects on individual hosts, nor its effects on whole populations are what might initially be imagined. Cowpox virus appears to be deceptively important - as no doubt other endemic pathogens are.

RELEVANCE OF IMMUNOGENETICS TO ASSESS THE RISKS OF RODENT-BORNE VIRUS EMERGENCE

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Since ca. 20 years, the study of immune defences has included the concepts of population biology and evolutionary ecology to explain the variation observed across individuals, species and situations. Immunogenetics, the analysis of genetic polymorphisms in specific recognition and immune regulation, is now at the core of the study of host-parasite coevolution.

One of the leading goals of immunogenetics has been to understand the genetic basis of susceptibility to diseases. The profound influence of the host genetics on resistance to infections has yet been established in numerous human infections. In wild animal populations, immunogenetics may provide essential information to assess the risks of disease (re)-emergence. A number of new viral infections have emerged or re-emerged during the past 15 years. The majority of these infections are transmitted to humans by animals and thus called zoonoses. Immunogenetics may be useful in two ways. First, the reasons why hosts differ in their susceptibility to different parasites could rely on the degree of matching between immune genes and parasite antigens. Immunogenetics may thus contribute to the identification of unidentified zoonotic agents. Second, natural population studies of immune gene polymorphism may provide key insight into the factors determining the appearance, spread and distribution of resistance/immuno-modulating alleles within populations and across geographical landscapes. This information is essential to study the spatial and temporal variations in disease risk or incidence.

Most of the empirical immunogenetic studies focusing on natural populations consider the genes of the major histocompatibility complex (MHC), which is a central component of the vertebrate immune system. The genes encode cell-surface glycoproteins that are responsible for the recognition and presentation of antigens to T cells [40].

During this talk, I will briefly review some evidence of the implication of MHC genes in rodent borne diseases. I will then focus on Puumala virus, the causative agent of mild hemorrhagic fever with renal syndrome (HFRS), and its wild reservoir, the bank vole *Clethrionomys* (*Myodes*) *glareolus* to illustrate the relevance of immunogenetics in the understanding of coevolution and HFRS emergence in Europe.

FUTURE NEEDS IN THE STUDIES ON HOST RESERVOIRS OF RODENT-BORNE VIRUSES

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In this summary talk I will review several topics on rodent-borne viruses (robos) - host interactions. The emphasis will be on hantaviruses. I wish to emphasize that there is a considerable diversity of patterns in these interactions.

Hantaviruses have been found in the rodent families Muridae (subfamily Murinae) and Cricetidae (subfamilies Arvicolinae, Sigmodontinae and Neotominae), and very recently in several species of insectivores, still mostly unpublished. Is this distribution in only a few rodent families and subfamilies, and some shrew species real, is there a hidden diversity ahead of us. If yes, it would shed interesting implications on hanta phylogeny.

Our knowledge of hantaviruses in regions with high rodent diversity, e.g. in tropical regions, is not too good. If the diversity of tropical hantas reflects that of murine rodents, why hanta diseases are not more common in the tropics? Are tropical hantas less infectious or do they survive poorly in high temperatures impairing the transmission.

Density-dependence (dd) is a crucial phenonmenon in host-pathogen interactions, and both direct and delayed dd's have been reported. In the latter ones, the time lag seems to be often related to the time interval between sampling events, and could depend on the trapping design, i.e. some of reported long time lags are artefacts. Prevalence alone is not a good parameter to describe hanta dynamics and consequent human infections, because hanta prevalence in rodents seems to be seasonal, and can be high even in low host densities. The number/density of infected, virus shedding rodents seems to be the relevant parameter to understand the infection risk to humans.

Other topics to be covered are e.g. the impact of robos on heir hosts, are robos only directly transmitted, how large are the differences among hantavirus species in their infectivity and other characteristics, what are the roles of direct and indirect (via environment) transmission dynamics, the role of maternal antibodies, the role environmental variation (seasonality, snow cover, community structure, landscape homo/heterogeneity) on host and consequently robo dynamics.

NEW AND REDISCOVERED ARENAVIRUSES IN EUROPE

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In this presentation we briefly overview the novel and rediscovered arenaviruses in Europe, and pinpoint priorities for future arenavirus research. Until recently, the only arenavirus in Europe was thought to be *the Lymphocytic choriomeningitis* virus (LCMV), which circulates in the house mouse, *Mus musculus*/*Mus domesticus*. Our recent screenings of rodent serum samples from various parts of Europe and elsewhere with immunofluorescent assays (IFA) have shown that arenavirus antibodies occur in many rodent species including voles. The characterization of these viruses by animal experiments, virus isolation and PCR analyses is in progress. Along with the identification and description of these viruses, studies on the ecology and effects of these viruses on humans are high priorities for future research. Antibody surveys of general human populations have rarely been done in Europe but analyses of risk groups (e.g. forestry workers) indicate that seroprevalence may be relatively high (2-10%).

The recently intensified research on various rodent-borne viruses (ROBO) in Europe has demonstrated that in addition to the relatively well-known hantaviruses, there are other significant rodent-borne virus groups in Europe which could have considerable impact on human health issues in changing environments and climatic conditions. Due to the differences in the nature of the infections and transmission patterns of the various rodent-borne viruses, each virus group may react differently to changing global conditions, creating challenges for the surveillance, modelling, and prevention of these virus infections in humans.

THE FOCAL DISTRIBUTION OF PUUMALA HANTAVIRUS INFECTION IN EUROPE

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Nephropathia Epidemica (Puumala hantavirus disease) is widespread throughout Europe, but there is a strong geographical variation in incidence of the disease, with areas where it is a fairly common health problem and other areas where it is rarely or never seen. In Fennoscandia, the disease is endemic in large contiguous areas, whereas in the rest of Europe it is distributed over much smaller foci. It is almost certainly underreported in some areas. The natural reservoir for this infection is the bank vole *Myodes [Clethrionomys] glareolus* and since there is no person-to-person transmission, we are looking for ecological factors to explain the spatial variation in the occurrence of the disease.

Within the EU-funded EDEN-ROBO project, we are approaching this question at two different levels. At a large geographical scale, the occurrence of human cases is related to spatially low-resolution environmental variables so that areas with an increased risk for hantavirus disease can be predicted. At a fine resolution spatial scale, in a more mechanistic approach, the epidemiology of the infection in the natural host is related to detailed information about local biotic and abiotic conditions and landscape. The latter approach should then assist in spatially modelling the R0 of the infection and identify the patches that ensure persistence of the infection within areas where hantavirus disease occurs.

The preliminary low-resolution results show risk maps for Fennoscandia that correspond fairly well to areas with known occurrence of Nephropathia Epidemica. For Western Europe, the patterns are complex, but there is considerable variation on the risk maps. These are currently being evaluated.

At the fine scale resolution in Belgium, we also observed complex relations. There seems to be a minimum threshold abundance that vole populations must have reached for hantavirus infection to persist (at least outside outbreak years) and hantavirus abundance is related to forest patch size, greenness of the vegetation and rainfall. However, threshold abundance is not a sufficient condition for hantavirus presence. Long-term prevalence is negatively related to average winter temperatures. Also the proportion of other rodents in the community is negatively related to occurrence of Puumala hantavirus. These data certainly need further analysis.

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OLD WORLD HANTAVIRUSES - 2007

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Currently, 22 hantavirus species are officially recognized by the International Committee on Taxonomy of Viruses (Nichol et al., Bunyaviridae; in the VIIIth ICTV Report, 2005) and the list of candidates is almost as long. In recent years new genetic variants of known hantavirus species of the Old World have been described: for instance, novel Puumala virus strains from Austria, France, Russia, and Slovenia, and new Thailand virus strains from Thailand and Cambodia. New variants of “cosmopolitan” Seoul virus have been discovered in Indonesia, France, and Belgium. Most intriguingly, sequences of potentially new hantavirus species have been recovered from, e.g., *Hylomyscus sinus* captured in Guinea, *Myodes spp*. trapped in Korea, Russia and China, and *Rattus rattus* captured in Cambodia. These findings, and also the latest taxonomy of rodents belonging to Cricetidae and Muridae families of *Muroidea* superfamily strenthen positions of the hantavirus-host co-evolution theory.

MODELLING PUUMALA HANTAVIRUS (PUUV) DYNAMICS

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Our previous modelling work emphasized the role of the bank vole demography coupled to the PUUV shedding dynamics by infected rodents, to explain the occurrence and the geographic distribution of *Nephropathia epidemica* (NE). Bank voles exhibit multi-annual fluctuations in northern Europe with the largest NE epidemics and the highest human incidence, and rather seasonal patterns in central and southern Europe. In addition, the PUUV shedding by infected voles is highest during the first month of infection.

Hence, the model suggested that the virus may persist in the seasonally fluctuating and hence more stable bank vole populations although the large and rapid increase of the multi-annually fluctuating populations appeared necessary to obtain the high number of acute-infected voles required to provoke the peak of viral concentration in the environment that leads to the human infections.

New experimental data from Kallio *et al.* (2006) revealed the role of transient protection through maternal antibodies against PUUV for offspring born from infected mothers. In addition, Kallio *et al.* (2007) have highlighted an additive mortality of infected voles during winter. To explore how these new features affect the predictions of our previous models, we considered the protection from maternal antibodies and the additional winter mortality for infected voles. All other hypotheses and parameters remained the same between previous and new models. Sensibility analyses were performed to explore how the infection dynamics are affected by realistic modifications in the protection period's length, ranging from 50 to 90 days, or in the additional mortality, ranging from a rate of 0 to 0.5.

Despite differences in the amplitude of several features, the predicted patterns remained similar between previous and new models. The proposed mechanism underlying the dynamics of the host-parasite system appears supported by its robustness to these new data. However, the additional mortality of infected rodents during winter may affect the local persistence of PUUV; the delay in the contamination of voles protected by the maternal antibodies may decrease or increase the global persistence probability whether it synchronizes or desynchronizes the infection in connected populations. This is currently under investigation in stochastic models of a bank vole metapopulation and will be presented here as perspectives.

TRANSMISSION DYNAMICS OF PUUMALA HANTAVIRUS IN CYCLIC BANK VOLE POPULATIONS IN NORTHERN TAIGA

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The most common rodent-borne zoonosis in Europe is Nephropathia epidemica (NE), a mild form of hemorrhagic fever with renal syndrome (HFRS). NE is caused by Puumala hantavirus (PUUV), carried by the bank vole (*Myodes* (earlier *Clethrionomys*) *glareolus*). Most of the human NE cases occur in Northern Fennoscandia and Western Russia, where the epidemiology is driven by the cyclic density fluctuations of bank voles, whereas in Central Europe the occurrence of NE depends more on the mast-driven fluctuations in bank vole abundance. Also the greater landscape homogeneity obviously promotes the commonness of NE in the north.

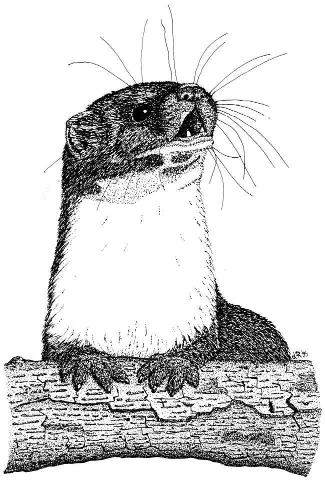
In bank vole, PUUV infection is asymptomatic and chronic, and the virus is shed to the environment basically throughout the host individual’s life span. Transmission occurs both via direct contact and indirectly via aerosolized excretions.

Since the spring 2002, we have carried out a longitudinal capture-mark-recapture study on a bank vole population in the highly PUUV endemic area in Central Finland. Bank voles are captured monthly on a 5.8 ha study area on a year-round basis, with smaller surrounding “satellite” areas of 0.36 ha, within 5 x 5 km area, trapped three times per year serving as replicates. Since it is possible to determine the time of PUUV infection for each individual, we are able to examine the impact of different vole population characteristics on the virus transmission dynamics, such as density, phase of vole cycle and demographic structure. Furthermore, the role of different functional groups in the PUUV transmission dynamics can be investigated.

The results show a high landscape level synchrony both in bank vole density and prevalence of PUUV in continuous boreal forest landscapes. The prevalence of PUUV in bank voles is strongly seasonal, being highest in spring, even in low densities. As bank vole populations increase after the cyclic decline phase, PUUV accompanies the increase with a very short time lag. The abundance of infected animals is density dependent.

WORKSHOP

Phylogeography in Southern Europe: the role of glacial refuges in shaping mammalian genetic diversity



MOLECULAR PHYLOGENY OF THE EUROPEAN MOLES OF THE GENUS *TALPA* LINNAEUS, 1758: SYSTEMATIC AND BIOGEOGRAPHIC IMPLICATIONS

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The genus *Talpa* is widely distributed throughout the Western Palaeartic region with nine species recognized, six of which occurring in Europe. Due to the subterranean life adaptations all the species are very similar and show high degree of morphological convergence. The phenotipic similarity led to some uncertainness on the taxonomic status and systematic relationships of some taxa and only genetic investigations allowed the evaluation of the specific status of the European species *T. stankovici*, formerly included in *T. romana*, and *T. occidentalis*, formerly considered a subspecies of *T. caeca*.

The distribution pattern of *Talpa* species in Europe is characteristic. *T. europea* is widespread throughout the continent from the Urals to the Pyrenees. The blind mole, *T. caeca*, shows an apparent discontinuous distribution in southern Europe being reported both in Italian and Balkan Peninsulas. The three species *T. romana*, *T. occidentalis* and *T. stankovici* are endemic of the three European Peninsulas (respectively Italian, Iberian and Balkan). Finally, *T. levantis* is restricted to the south-easter Bulgaria and Turkey. The phylogenetic relationships among these taxa and the taxonomical status of some isolated population are still uncertain.

We present results of molecular phylogeny of the six European species (*T. romana*, *T. europea*, *T. occidentalis*, *T. caeca*, *T. stankovici* and *T. levantis*) discuss their systematic relationships. Results shed some light on the evolutionary relationships among these species and suggest a monophyletic origin of the other western European moles, i.e. *T. romana*, *T. europea*, *T. occidentalis*, and *T. caeca*, with *T. stankovici* and *T. levantis* as sister species. Results also allow to hypothesize two different colonization route starting from Asia. A tentative of molecular clock is proposed to correlate the biogeographic pattern suggested by molecular data with available fossil records.

PHYLOGEOGRAPHY OF THE WEASEL (*MUSTELA NIVALIS*) IN THE WESTERN PALAEARCTIC REGION AND COLONIZATION OF MEDITERRANEAN ISLANDS

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The weasel (*Mustela nivalis*, Linnaeus 1766) is distributed throughout the entire Holarctic region (North America, Asia and Europe with the exception of several Atlantic islands). Phylogeographic structure of *Mustela nivalis* is here investigated in the western Palaearctic area by sequencing the first 550 bp of the mitochondrial control region and the entire cytochrome b gene (1140bp). Our taxomonic sampling includes a total of 84 animals covering 13 countries from Morocco to Finland as well as five Mediterranean islands (Minorca, Corsica, Sardinia, Sicilia and Crete). Phylogenetic trees were reconstructed in maximum likelihood and using partitioned bayesian analyses on separate and combined genes. Population structure was assessed through a parsimony network on the combined dataset and estimation of different population genetic parameters. These analyses reveal the existence of two groups. The first clade is well-supported but shows little genetic diversity and contains all samples from Western Europe. This genetic structure is interpreted as resulting from a glacial refuge located in South-Western Europe, followed by an expansion in all Western Europe. The second grouping includes several highly structured groups corresponding to Mediterranean islands, North Africa and Balkan area. The interpretation of a second glacial refugia somewhere in Eastern Europe appears more conjectural. The observed sub-groups would rather trace different colonization events that would have happened later (North Africa, Mediterranean islands). These results will be discussed in a broad phylogeographic context by (i) comparing genetic structures between weasel and other mammals shaped by Quaternary glaciations, (ii) analysing palaeontological and ecological factors that could allow identification of potential glacial refugia, (iii) reviewing morphological and anatomical characters that lead to recognize several subspecies in Europe, and (iv), considering the impact of human migrations on the roads of colonisation of Mediterranean islands by this species.

FROM PYLOGEOGRAPHY TO LANDSCAPE GENETICS. DESCRIBING THE ORIGIN AND STRUCTURE OF ITALIAN ROE DEER (*CAPREOLUS C. ITALICUS*) POPULATIONS

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During the last glacial periods, European roe deer (*Capreolus capreolus*) populations survived in southern refuge areas around the Mediterranean. Fragmented populations, isolated in the central-southern Italian Apennine, evolved unique genetic traits (and probably peculiar local adaptations to Mediterranean climate and habitats), and were recently recognized as a distinct endemic Italian roe deer subspecies (*C. c. italicus*). Nowadays, only a few small, fragmented and geographically isolated Italian roe deer populations still survive in central-southern Italy. All those populations are threatened by hybridisation with rapidly expanding populations of reintroduced non-local European roe deer. Aiming to define the genetic structure of the Italian roe deer populations, and identify areas of introgressive hybridisation with European roe deer, in this study we analysed 540 samples collected throughout the species' distribution range in Italy. These samples were genotyped using 11 unlinked microsatellite loci and mtDNA control-region sequences. Mitochondrial DNA sequences showed a unique haplotype clade, which was identified in samples collected within the historical range of the Italian roe deer, and in samples collected in southern Tuscany, thus contributing to delineate the subspecies' distribution range. Multilocus microsatellite genotypes further supported a genetic distinction between Italian and European roe deer, and showed instances of genetic admixture between them in parts of Tuscany. GIS mapping and landscape genetics modelling of composite mtDNA and microsatellite genotypes allowed reconstructing a fine-scale distribution of Italian and European roe deer populations, and of their hybridisation areas. These data are being used to implement a national action plan for the conservation of the Italian roe deer.

MORPHOMETRIC VARIABILITY OF HOLOCENE - LATE PLEISTOCENE SAVI VOLE (*MICROTUS* (*TERRICOLA*) EX *GR. SAVII*; RODENTIA) FROM SICILY

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During the last two decades the fossil record of the Savi vole, *Microtus* (*Terricola*) *savii* (Sélys Longchamps, 1838) is becoming more and more consistent in Sicily. Descriptions of these fossils, however, are still limited to the site of Contrada Pianetti (Late Pleistocene, Ragusa).

In the present contribution new fossil samples from karstic deposits (Holocene - Late Pleistocene in age) from North Western Sicily and the Nebrodi area are considered. Samples have been described by means of morphological features relative to two dental elements which are considered as the most diagnostic for the taxonomy of *Microtus* voles (first lower Molar - M/1; third upper molar). A morphometric analysis has been carried on M/1s using rough measurements and morphological indexes. The data have been compared with extant *M.* (*Terricola*) *savii* nebrodensis samples from diverse locations in the island and with extant and fossil samples from the Southern Italian Peninsula.

The results show that the Sicilian fossil and extant savi voles are characterized by a great range of variation, particularly for what concerns size. It is remarkable that some of the fossil samples display very large size, beyond what is observed in the available samples from the Peninsula. The morphological features also display a wide variation which is, however, fairly consistent with that of the fossil and extant savi populations from the Southern Italian Peninsula. Size variation in the island is also related to different geographic locations, being the voles (extant and fossil) from South-Eastern Sicily smaller than the others. Variation in size and morphology is also observable among the Sicilian samples in relation to their different geological age.

Such fairly complex pattern opens up new prospects for further research on the dispersal history and microevolution of this vole in the Sicilian Archipelago. The occurrence in the Island of Malta of a fossil endemic species (*Microtus* (*Terricola*) *melitensis*, Late Pleistocene) which displays some peculiar morphological features not observed even in the oldest Sicilian fossils, is a further piece of information which evidences the complexity of the paleo-biogeographical pattern. These results highlight the opportunity of a compared approach between palaeontological and phylogeographical data to unravel the history of these insular voles.

MITOCHONDRIAL DNA PHYLOGEOGRAPHY OF EUROPEAN WOLVES

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Isolation in different refugia during the Pleistocene glaciations strongly influenced genetic differentiation patterns of many species. However, in highly mobile mammals with long dispersal distances, traces of postglacial history may be blurred by subsequent intensive admixture. We addressed this question based on an example of a highly mobile carnivore, the grey wolf. We analysed mtDNA control region sequences of 643 individuals representing most of the continuous wolf range in Eastern Europe, and found 21 different haplotypes. The nested clade analysis (NCA) provided no evidence of past fragmentation in the Eastern European wolf population, suggesting its origin from only one, Balkan refugium. A decrease of haplotype and nucleotide diversity with the increasing latitude was revealed, which is likely to be a result of post-glacial recolonisation from one southern refugium. We then extended our dataset by incorporating published data on wolf mtDNA haplotypes from different parts of the continent, including isolated populations from the Apennine and Iberian Peninsulas. Among 947 individuals analysed altogether, we found 27 haplotypes, 24 of which occurred in Eastern Europe. Geographic distribution of haplotypes was characterised by a high frequency of unique haplotypes in southern populations. Two main haplotype clades, 4-1 and 4-2, had overlapping ranges in Eastern Europe. However, all wolves from the Iberian Peninsula and 87% of wolves from Eastern Europe carried haplotypes from the clade 4-1, while the only, unique haplotype carried by wolves from the Apennine Peninsula belonged to the clade 4-2. The NCA results were consistent with the results of an earlier study, which suggested long-term isolation of the Apennine population. The NCA also suggested past gene flow between the Iberian and Eastern European wolf populations, followed by extinction of intermediate populations from Western Europe. The fact that traces of this admixture were not detected when Eastern European population alone was analysed, could possibly result from the asymmetric gene flow with the prevailing westward direction. To test this hypothesis, the analysis of ancient wolf samples would be necessary. Our results show that even in highly mobile mammals such as wolves, genetic traces of historical events can still be detected in contemporary populations. However, the reliable reconstruction of postglacial history is impossible without ancient DNA analysis.

PHYLOGEOGRAPHY OF THE EUROPEAN WILD BOAR: POSSIBLE EFFECTS OF A POST-GLACIAL EXPANSION

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The Eurasian wild boar *(Sus scrofa)* is a widely distributed and intensively managed large mammal, for which up to four different subspecies have been described. Several populations in Europe have experienced in the last century demographic explosions, which were favoured at some extent by human-mediated translocations.

Here, we present molecular data resulting from the analyses of 252 wild boars from 15 different localities across Europe and 40 Italian pigs. All of them were typed by 10 polymorphic microsatellites and partial mtDNA control regions of a subset of 160 individuals were sequenced. The mtDNA dataset was enlarged with 257 published homologous sequences available in GenBank and belonging to other European wild boars and to different domestic pig breeds.

Three major mitochondrial haplogroups are found across wild populations in Europe: clade E1, widespread in Europe, clade E2, occurring only in Italy, and clade A, which is of Asian origin and was seemingly introgressed from domestic stocks. Only clades E1 and A are observed in European pigs. Divergence time between such lineages largely predate domestication. European pig breeds are only slightly differentiated from their wild conspecifics, supporting the hypothesis that independent domestication events took place in Europe.

Outside the Italian peninsula, European wild boars show the signature of a post-glacial demographic expansion, which possibly spread from a southern glacial refugium. This is consistent with the absence of a strong phylogeographic structure across the continent. Wild boars from mainland Italy and Sardinia show high levels of genetic variation, which cannot be only ascribed to recent dynamics but are likely to represent a residual of the pre-glaciation diversity occurring in the peninsular population. Overall, signs of man-mediated gene flow among populations are weak, although in some regions the effects of translocations are detectable and a low degree of pig introgression can be identified. Finally, subspecies designations proposed in the past do not reflect the present genetic differentiation observed in Europe.

LATE QUATERNARY DISTRIBUTION DYNAMICS AND PHYLOGEOGRAPHY OF THE RED DEER (*CERVUS ELAPHUS*) IN EUROPE

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We present spatial-temporal patterns for European late Quaternary red deer (*Cervus elaphus*), based on radiocarbon-supported evidence derived mainly from archaeological sites. This is followed by an overview of the recent phylogeography of this species using haplogroup studies of recent molecular data. The implications of the synthesis of palaeontological and genetic data are discussed and we propose that present day European red deer haplogroup distributions are best explained against the history of late Quaternary population contractions into and expansions from glacial refugia. We suggest that this argument can be tested by a systematic study of ancient DNA (aDNA) from critically selected material. Around 800 records of *Cervus elaphus* were assigned to the period covering the later part of the Last Glacial and the Early to Middle Holocene. Red deer becomes increasingly visible in faunal assemblages dated to late OIS-3 (<40.0 ka 14C BP). The species persisted throughout the LGM on the Iberian Peninsula, in adjacent regions of south-western France (Gascony, Dordogne, Languedoc), on the Italian Peninsula, in the Balkans and Greece, and east of the Carpathians in Moldavia. We suggest that genetic exchange between the populations of the Balkans and the East of the Carpathians remained uninterrupted during the LGM. The expansion of red deer from its southern refugia into Central and Northern Europe begins rapidly at 12,500 14C BP. The expansion of red deer coincides with the sudden rise in temperature at the onset of Greenland Interstadial 1e and the dispersion of open birch woodland into the northern half of Europe. Radiocarbon supported records show a more or less universal distribution of *Cervus elaphus* across Europe following the Pleistocene / Holocene climatic change at 10.0 ka 14C BP for the first time. Molecular data and fossil record combined provide a clearer temporal and spatial pattern for the Late Glacial recolonisation process of the northern part of Europe.

GLACIAL REFUGIA AND COLONIZATION PROCESSES OF THE COMMON VOLE (*MICROTUS ARVALIS*): EVIDENCE FROM MOLECULAR DATA

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The influence of Quaternary cold periods on composition and distribution of European fauna and flora is unquestioned. Some general trends of postglacial expansions have been identified for several species of plants and animals: (1) postglacial recolonization of northern regions generally from southern peninsulas (Iberia and Balkans) acting as refugia; (2) isolation of the Italian lineage due to the Alpine barrier; (3) occurrence of four main suture-zones where populations from different refugia meet (Taberlet et al., 1998; Hewitt, 2004). In the case of the common vole (*Microtus arvalis*), Haynes et al. (2003) agree with these general trends of colonization, whereas Fink et al. (2004) and Heckel et al. (2005) bring an other vision of the evolutionary history in Western Europe. According to these latter authors, the genetic diversity in European populations of the common vole suggests a glacial survival of the common vole outside the classical refugial areas and a potentially more ancient colonization (ante-Last Glacial Maximum) from the northeast to the southwest of Europe.

We investigated the genetic diversity of about 20 common vole populations in France (local scale) from mitochondrial sequences (the 5' peripheral domain of the control region and the cytochrome b gene) in order to clarify the evolutionary history of the western lineage and its hypothetic implication in postglacial recolonization of Western Europe. In Europe, five main evolutionary lineages (western, central, eastern, Italian and "Freiburg") were defined. Our study brings to the fore a genetic structure of common vole populations with the occurrence of at least three French sub-lineages. The French northeast populations look like a part of the second suture-zone as defined by Taberlet et al. (1998), between the central and western European lineages, but also as a spreading centre for the French populations after the penultimate glaciation. Our study corroborates the hypothesis of Fink et al. (2004) and Heckel et al. (2005) about *M. arvalis*, and the occurrence of futher north European glacial refugia.

WORKSHOP

Remote sensing in mammalian studies: aims, methods and results

THE LYNX, THE ROE DEER AND THE MAN. HABITAT SELECTION IN A 3-COMPONENTS SYSTEM

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With the generalization of GIS (Geographic information system) and more powerful computing abilities, we have been able to describe and analyse the use of space by wildlife more in details, including always more complex data (environmental or localization data). Spatial ecology in general and habitat selection in particular are especially confronted to this new situation. To integrate this incredible amount of data, many multivariate methods have been developed. Here I will focus on the ecological niche, an old concept (dating from 1957 with the formulation of Hutchinson) that can be fully analysed nowadays. The ecological niche can be seen as the geometrical representation of the study area in the ecological space (i.e., the geometrical space composed of the different environmental variables). I will present some methods based on the concept of niche, for instance the ENFA (Ecological-Niche Factor Analysis) and the MADIFA (Mahalanobis Distance Factor Analysis). The niche concept and the related methods will be applied to the study of the lynx in Norway, as an illustration of habitat selection by a flag species in a system with 3 linked compartments: the predator (the lynx), the prey (the roe deer) and overall, human. The idea behind this study is to integrate as tightly as possible the different species into one study of habitat selection of the lynx. For this purpose, we will investigate the ecological niche of the lynx in South Norway, related to its environment as well as roe deer density and human activities. We aim to demonstrate that both roe deer density and human disturbances are key factors for the distribution of the lynx, each with different constraints. For instance, we showed with this methodology that the lynx is looking closely for roe deer by actively selecting areas with higher roe deer densities. As a consequence, the lynx habitat encloses relatively disturbed areas, with many roads, isolated houses and fields, as roe deer is often distributed over fragmented landscapes. We show however that there is a threshold on the level of disturbances that the lynx can afford, over which the lynx stops is quest for roe deers.

REMOTE SENSING OF LARGE MAMMAL HABITAT DISTRIBUTION. A CASE STUDY OF BROWN BEARS IN EUROPEAN RUSSIA

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With remote sensing we can characterize environmental factors working on large territories and hardly can be evaluated by other methods. Remote sensing is particularly valuable in regions where land use and land cover is changing rapidly, and for species with large home ranges. European Russia has experienced substantial changes in its rural landscape after the breakdown of the Soviet Union, and anecdotal evidence suggested that brown bears are expanding their range southward, and reclaim area where they had been extirpated during the 20th Century. Our goal was thus to conduct a study of brown bear distribution in European Russia and to identify measures of habitat quality that can be derived from remotely sensed imagery. Field studies demonstrated that single brown bears need approximately 90 km^2 of forest, three bears need at least 155 km^2, and 5-8 bears need 300-350 km^2. We used 1-km resolution MODIS land cover data to assess forest abundance, and we measured forest fragmentation using indexes proposed by Riitters to distinguish interior forests from forest edges and isolate forest fragments. The measures of forest pattern were complemented by data on road density, human settlement, and rural population density. Regression analysis showed that bear density in 529 districts was significantly positively correlated with forest abundance, and even more so with the abundance of interior forests. On the contrary, measures of human disturbance were all negative correlates of bear densities. The strongest negative correlate was 'travel cost', i.e., a distance measure between bear source populations in the North, and forests in the South, which is weighted according to land cover (forest cover entails low travel cost, agricultural areas are medium, and urban areas are high). Multiple regression analysis explained almost two-thirds of the variation in bear density (R-squared 0.62). Our analysis shows that relatively coarse remote sensing measures of habitat availability and human disturbance can successfully model patterns of bear densities, and presumable other species as well. Both scientific understanding of habitat use patterns and the conservation of large mammals may thus be enhanced by satellite image analysis.

COMPLEX MODEL OF EVALUATION OF FORAGE OPPORTUNITIES OF THE FOREST PHYTOCENOSIS, OPTIMAL DENSITY AND NUMBER OF UNGULATE ANIMALS IN RUSSIA USING GROUND AND REMOTE SENSING DATA

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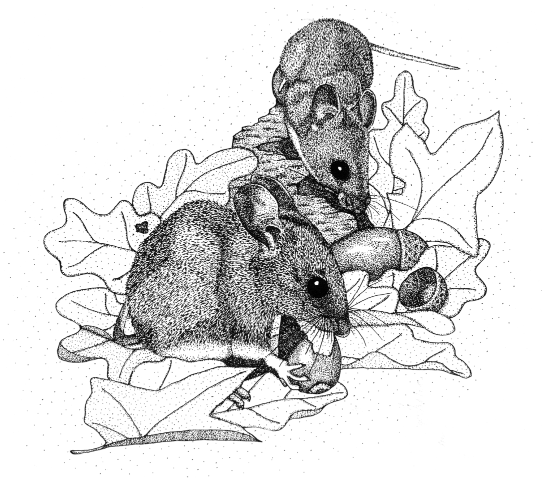
Complex of interrelated simulation models for evaluation of the forage opportunities of forest phytocenosis, the optimal density and number of ungulate animals at the local, regional and federal levels by the example of moose are presented.

The first block of models is based on long-term (1965 – 2005) monitoring data and is intended for the determination of dynamic number, sexual and age structure of population taking into account the functional factors (parameters of fertility, viability, death-rate, official hunting, role of predators and poachers, capacities of habitats, accessibility of forage and others), influencing the current state and population dynamics. The results of computing experiment using the special software (Game Species Information System - GSIS) for understanding of the basic factors determining a low number of mosses in Russia are presented.

The second block of models is intended for the determination of forage phytomass of the main forestation species using the forest taxation data. In the information system GSIS, the program utilities were designed for the evaluation of a forage capacity of habitats for the ungulate game species at the local, regional and federal levels. The functional relations obtained allowed transformation of the phytoproductivity of the basic tree species (coniferous, hard and soft deciduous) at different hierarchical levels (timber stand, underwood, underbrush) into the available forage phytomass. The threshold value of forage resources used by animals and the optimal animal density within the studied area were realized by means of an auxiliary simulation module.

Major principles of the data syntheses on ground forest taxation and of remote multichannel images got from the Landsat satellite, for determination of the forest phytocenosis forage opportunities are given. The analysis of the main blocks of the complex model, including assessment of optimal animal density, evaluation of forage opportunities of the forest phytocenosis and simulation models for a moose population, is carried out by the example of the Visimsky Biosphere Nature Reserve.



WORKSHOP

Mammals and their metazoan parasites: are there general rules?

EXTRINSIC MORTALITY, ANTIOXYDANT DEFENCES AND LONGEVITY IN MICROMAMMALS

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According to classical evolutionary theories, lower rate of mortality resulting from environmental factors (extrinsic mortality) should translate into a later onset of senescence. Thus, a lower mortality rate on one sex should select for lower senescence and higher maximum lifespan compared to the other sex. In this talk I will present some observations and experiments that we are currently conducting in our laboratory. I will first present data on sex-biased predation rate in rodent species that we obtained by taking advantage of the peculiar prey caching behaviour of owls during reproduction. I will then present data on sex-biased parasitism in bat species as well as results on the effects of parasitism on survival prospect in the common vole *Microtus arvalis*. In the last part of this talk, I will compare the effects of the observed sex-biased extrinsic mortality on the level of antioxydant defences which are supposed to play an important role in aging processes.

CONSTRAINTS OF AN HEMATOPHAGEOUS PARASITE ON PHYSIOLOGY OF ITS MICROTINE HOST

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To respond to resource withdrawals by parasites, hosts have to trade off investments between defences against parasites and compensation of damages. Although rodent-flea host-parasite systems are very common, very few studies have evaluated the costs imposed by fleas on their rodent hosts. In this study, we measured costs of parasitism for common vole *Microtus arvalis* parasitized in a long term experimental design by rat flea *Nosopsyllus fasciatus*. We compared growth, body condition, resting metabolism rate and humoral immune responses of 26 experimentally parasitized captive young male voles with 25 deparasitized ones.

We found that parasitized voles were smaller and had lower haematocrit than deparasitized individuals. Moreover, voles with fleas had lower immune response and higher resting metabolic rate than parasite-free individuals. During immune challenge, haematocrit of parasitized individuals also decreased.

Our results suggest that parasitism by fleas induce high physiological and metabolic costs. These findings are in accordance with previous studies which showed either cellular immuno-depression or increase in daily metabolic rate in gerbils parasitized by fleas. Parasitized animals may have to deal with trade-offs between immune response and compensation of fleas exhaustion. By modifying physiology and decreasing the ability to mount humoral immune response, parasitism by fleas can have strong effects on reproductive value and population dynamic of voles.

COMPARATIVE PHYLOGEOGRAPHY OF CESTODES (*ANOPLOCEPHALIDAE*) OF ARVICOLINE RODENTS

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We review the molecular phylogenetic analyses of four monophyletic groups of anoplocephalid cestodes and their arvicoline rodent hosts (voles and lemmings) in the Holarctic region. Cytochrome oxidase I (mtDNA) sequences were the basic tool in the analysis of cestode phylogenetics, accompanied in some assemblages by 28S or ITS1. The host phylogenies, based mainly on cyt *b* sequences (mtDNA), were extracted from published sources. **i)** The sister species *Paranoplocephala arctica* and *P. alternata* are common host-specific parasites of collared lemmings (*Dicrostonyx* spp.). The main phylogenetic and distributional split of hosts at the Bering Strait (ca. 1 mya), as well as the subsequent splits in the Palearctic, are reflected in the phylogeographic structure of the parasite. However, in the Canadian Arctic and on the Wrangel Island there is no strict congruence between the host and parasite phylogenies.
ii) *Paranoplocephala omphalodes* and related species (i.e. *Paranoplocephala s. str.)* are primarily parasites of *Microtus* voles. For the whole assemblage, no strict correspondence between parasite and host phylogenies was observed; instead, an obvious case of speciation by host shift was observed. An intraspecific comparison of the phylogeographies of *Paranoplocephala jarrelli* and its main host *Microtus oeconomus* also did not reveal shared histories; the main splits of the parasite did not correspond with those of the hosts and a distinct subclade of *P. jarrelli* occurred in northern Alaska, where *M. oeconomus* is not known (so far) to show significant phylogeographic structure. **iii)** *Anoplocephaloides dentata* and related species (i.e. *Anoplocephaloides s. str.*) are ubiquitous parasites of *Microtus*- and *Chionomys*-voles, true lemmings (*Lemmus* spp.) and bog lemmings (*Synaptomys borealis*). The interspecific phylogeny lacks evidence of coevolution between parasites and hosts, and suggests a sequential colonization among host species and genera as the main source of parasite divergence. In intraspecific comparisons, *Anoplocephaloides lemmi* shows a deep phylogeographic split corresponding to the main split of its hosts (*Lemmus* spp.) (ca. 2 mya, at Kolyma), but no congruence is evident in the phylogeographies of *Anoplocephaloides septemtrionalis* and its primary host *M. oeconomus.* **iv)** *Anoplocephaloides variabilis*-like species and *Paranoplocephala krebsi* are rare parasites of *Microtus*- and *Chionomys*-voles and collared lemmings (*Dicrostonyx* spp.). The molecular phylogenetic analysis of this assemblage is not yet completed, but it also suggests a high cryptic diversity and absence of clear evidence for cophylogeny. Thus, among arvicoline-carried anoplocephaline cestode species, colonization of new lineages has been the predominant mode of diversification. There is some evidence for allopatric divergence following host shifts, particularly in *Anoplocephaloides s. str.* Within species or between closely related species, parasite divergence may or may not correspond to that of the hosts. High host specificity may have enhanced strict phyletic coevolution in some of the assemblages. Finally, the presence of phylogeographic structure in a parasite in the absence of corresponding host divergence may reflect "cryptic" divergence or inadequate sampling (or both) of the latter. Each anoplocephaline taxon in arvicolines shows an independent response to the host phylogeography, and there is no concerted common response. The two main cestode families in arvicoline rodents, Anoplocephalidae and Hymenolepididae, show different species diversity and host specificity in the same host species and genera, which may have affected the evolutionary pathways of these parasite assemblages.

ARE THERE GENERAL RULES GOVERNING PARASITE DIVERSITY IN SMALL MAMMALIAN HOSTS?

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Parasite biodiversity varies on several scales, and in particular among different host species. We examined the potential of several host characteristics (host body mass, basal metabolic rate, size and position of the geographic range, and diversity of co-occuring hosts) as determinants of diversity in two groups of ectoparasites, fleas and gamasid mites (superfamily *Dermanyssoidea*). Our analyses used one measure of diversity for fleas (species richness) and three measures of diversity (species richness, the Shannon diversity index, and average taxonomic distinctness) for mites, and controlled for sampling effort and phylogenetic influences. None of the host body parameters (body size, basal and average daily metabolic rates) correlated with species richness of flea assemblages. Flea species richness increased with an increase in latitude of the geographic range center of a host as well as with an increase in a composite variable that described the size of the geographic range. In rodent and lagomorph hosts, the species richness of mite assemblages correlated negatively with host body mass and was not affected by either of the two other host parameters. Shannon diversity of mite assemblages significantly increased with an increase of host BMR. The taxonomic distinctness of mite assemblages significantly decreased with an increase of either host geographic range or its BMR. In addition, in insectivores, the Shannon diversity of mite assemblages increased with an increase of body mass and the variance in taxonomic distinctness. Thus, although several significant relationships were observed, they depended entirely on which diversity measure was used, or on which host (insectivores versus rodents and lagomorphs) or parasite (fleas versus mites) taxon was investigated. Thus, there appears to be no universal determinant of parasite diversity, and associations between host features and parasite diversity probably evolve independently in different host-parasite systems.

ALLOMETRIES IN MAMMAL-PARASITE INTERACTIONS

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The search of patterns, rules, and laws is central in ecology since its foundation to the recent development of macroecology and macroevolution. Kleiber’s law, Bergman’s rule, Rapoport’s rule, Cope’s rule are, among others, some well-known examples.

The use of ecological laws, or rules, can also fruitfully irrigate parasitology and epidemiology. First, I show several examples of the applications of some rules and/or laws to parasite (pathogen) - mammal interactions. Most of these laws or rules are based on allometric relationships. Second, I develop one example, the Taylor’s power law that has been applied recently to epidemiology and evolutionary ecology of parasites and pathogens. The Taylor’s power law takes the form of a power relationship $s^2 = a\ m^b$, where s^2 is the variance in population abundance and m is mean abundance of the population, and a represents a constant parameter and b an index of spatial heterogeneity. If the Taylor’s power law reflects the aggregation of parasite (or pathogen) individuals among host population, since the values of b may reflect various processes from epidemics to regulation in host-parasite (or pathogen) systems.

INFLUENCE OF RODENT DENSITY AND CLIMATIC VARIABLES ON TICK POPULATION DYNAMICS IN NORTHERN ITALY

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The risk to humans of contracting tick-borne zoonotic diseases depends on the risk of a bite from an infected tick, which can be broken down into its component parts as the number of host-seeking ticks in the environment, in particular nymphs, and the prevalence of tick-borne pathogens they are carrying. In this study, we analyse tick biting intensity on rodents in a known tick-borne encephalitis (TBE) focus in Trentino (Northern Italy). We examine patterns of tick demography and the influence of host densities and climate on ticks' generation time, development rates, tick density and intensity. During the period 2000-2004 a population of the yellow-necked mouse, *Apodemus flavicollis*, the most important TBE transmission host, was intensively monitored. Ticks feeding on individual rodents were counted, distinguishing between the larval and nymph life-stages. Local temperature and relative humidity was calculated using both dataloggers in the field site and regional weather stations. We investigated which factors had a predictive value both on feeding tick intensity and on the overall density of larvae or nymphs feeding on rodents in a year. We observed a negative effect of rodent density on tick intensity, while temperature influenced positively both larvae and nymph intensity. Overall larval density was higher in the years and trapping grids where rodent density was higher, while for nymphs no such effect was observed. The best explanatory variable for nymph density was the larval density in the previous year, confirming the discrete nature of tick demography. This gives us a useful framework on which to build future models and provides important information in terms of monitoring the risk of tick-borne pathogens to humans.

HOST DIVERSITY, ENVIRONMENT AND HISTORY AS DETERMINANTS OF ECTOPARASITE SPECIES RICHNESS: A CASE STUDY OF *AMPHIPSYLLA* FLEAS

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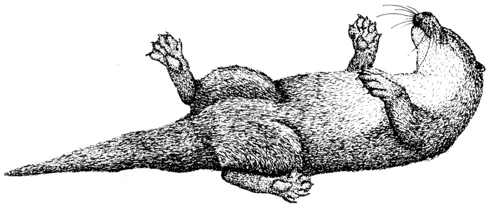
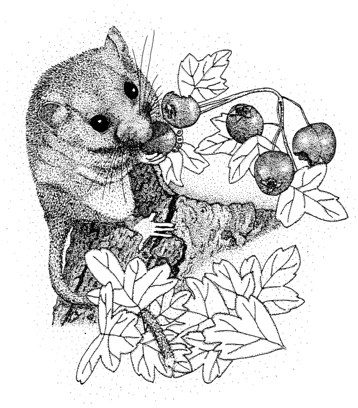
Species richness of ectoparasites is known to be positively correlated with species richness of hosts. However, patterns of this relationship were found to vary geographically and mediated by environmental conditions. We analyzed how species richness of fleas genus *Amphipsylla* is related with species richness of their hosts and climatic and topographic variables. Geographic ranges of 41 *Amphipsylla* species and 173 species of their potential rodent hosts belonging to families Calomyscidae, Cricetidae (subfamilies Arvicolinae and Cricetinae) and Spalacidae (subfamily Myospalacinae) were modelled using GARP algorithm. Species richness was estimated by overlapping geographic ranges of individual species. Step-wise multiple regression analysis was used to estimate relationships between species richness of *Amphipsylla* fleas (independent variable) and species richness of potential hosts, altitude, slope, mean annual, summer and winter temperatures and precipitation (independent variables). Results of analysis demonstrated that species richness of *Amphipsylla* fleas was positively correlated with species richness of potential hosts, altitude, annual precipitation and mean annual temperature and negatively with winter temperature and winter and summer precipitation. Combination of these variables explained about 40% of variation in *Amphipsylla* species richness. Mapping of the residual variation revealed several areas where observed *Amphipsylla* species richness was significantly higher than that of predicted by regression (Central Kazakhstan, Tien-Shan, Altai, Trans-Baikal and Eastern Tibet). These regions can be considered as historical centres of diversification of the genus.



WORKSHOP

Island mammals



BODY SIZE IN ISLAND *APODEMUS* POPULATIONS

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The general pattern in body size is that *Apodemus* mice show larger body sizes on islands compared to on mainland. This could be due to many factors. However, by comparing body size in *Apodemus sylvaticus* and *A. flavicollis* between islands it is possible to test specific hypotheses where a general island effect is constant. On some islands important competitive species are absent. This mostly confers an increase in body size of both *A. sylvaticus* and *A. flavicollis*. On other islands important predator species are absent. This confers a larger body size in *A. flavicollis* and other morphological changes. On the island of Gotland in the Baltic Sea, for example, *A. flavicollis* were larger but had relatively smaller brains and shorter tails. This suggests a habitat shift from a more arboreal life to a life on the ground. The results show that the faunistic perturbations on islands result in lower competition and predation and that this can explain at least part of the gigantism of *Apodemus* mice on islands.

PHYLOGEOGRAPHIC STUDY OF THE MAGHREBIAN BAT, *MYOTIS PUNICUS*, AND ITS PARASITE, *SPINTURNIX MYOTI*, IN CORSICA AND SARDINIA

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Recent studies highlighted the utility of parasites as a tool to better understand the phylogeographic history of their hosts. In this study, we compared the genetic patterns of one parasitic mite, *Spinturnix myoti*, with its two hosts, the Maghrebian and the Greater mouse-eared bats. The Maghrebian bat, *Myotis punicus*, is widespread in North Africa and in some Mediterranean Islands (Corsica, Sardinia and Malta), whereas its sister-species, *Myotis myotis*, is only present in Europe. Here we focused on Corsica and Sardinia to assess the importance of intercolonial movements both inside and between these two close islands. Microsatellites and mtDNA analyses revealed the absence of structure between colonies within the islands whereas a high genetic structure between islands was found. Thus, despite the high flight ability of *M. punicus*, 15 km of open water between the 2 islands seem to hamper gene flow between Corsica and Sardinia. Furthermore, mtDNA analyses of its specific mites, *S. myoti*, confirmed the isolation between colonies of Corsica and Sardinia. Indeed, *M. punicus* from Corsica hosted mites genetically distinct from Sardinian ones. More surprisingly, genetic analyses revealed that contrary to Sardinian mites, Corsican mites are identical to mites found on the greater mouse-eared bat, *M. myotis*, from continental Europe. As *M. myotis* is restricted to continental Europe and no contact zone between both species is currently known, this result suggests a host switch between *M. punicus* and *M. myotis* in the past. Then, bat mites give clues for a former contact between both species and for an ancient presence of *M. myotis* on these islands.

COMPARATIVE DEMOGRAPHY OF *MASTOMYS ERYTHROLEUCUS* (*RODENTIA*) BETWEEN AN INSULAR AND A MAINLAND SITE IN SENEGAL

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Mastomys are among the most common rodents in West Africa. Because some species in this genus are considered as pest species for agriculture, most of the studies on demography have focused on populations in anthropogenic ecosystems. Here we will compare the demographic characteristics of *Mastomys erythroleucus* at two less man-modified ecosystems in Senegal: an insular site, Madeleine Island, and a mainland site, Bandia. Both sites were sampled over ten primary trapping sessions, from 1984 to 1986, using large trapping grids (ca. 400 traps over 4 ha). At each primary trapping session we collected capture-recapture data during five days on individually marked individuals. Each individual was weighted, sexed and its reproductive condition was assessed. More than 750 and 250 individuals were respectively marked at Madeleine Island and Bandia. Using up-to-date methods of capture-recapture, we have carried out comparative analyses between both sites on several demographic parameters (survival, recruitment.). In accordance with the island syndrome, preliminary results showed that survival was markedly higher at Madeleine Island than at Bandia.

ISLANDS IN ENCLOSURES: AN EXPERIMENTAL STUDY ON MAMMALIAN PREDATOR-PREY INTERACTION IN A FRAGMENTED LANDSCAPE

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Habitat fragmentation by human disturbance has been recognised as a major threat for species persistence. The habitat fragmentation can potentially affect also the predator-prey interaction, but that has been seldom studied experimentally. We have approached this problem by conducting a series of experiments in experimentally manipulated habitat in large outdoor enclosures using bank voles (*Myodes glareolus*) and weasels (*Mustela nivalis*) as model species. Breeding habitat of voles was experimentally fragmented into one large (continuous) or four small habitat (fragmented) patches. For both voles and weasels the habitat patches provided safe habitat and open matrix a risky one. In the first experiment we focused on the effects of indirect cues of the predator presence on spacing behaviour and breeding success of voles, while in the second experiment we concentrated on survival of voles and hunting efficiency of weasels in different habitat configurations. In the first experiment, we did not detect any effects of predation risk on the behavior of voles or their breeding success. The second experiment was conducted during two seasons, spring and autumn. In spring voles survived better in the continuous habitat than in fragmented habitat but during autumn trend was opposite. This is tentatively explained by significantly higher avian predation pressure during autumn, which has probably restricted the movements of weasels between habitat patches. In continuous landscape weasels can move freely, but in fragmented landscape it is better to stay inside the patch until it is empty before moving over the risky matrix. In addition, cold weather during autumn increase energy needs of weasels and they are also more likely to "surplus kill" voles for storage, which may have also contributed the observed high mortality of voles in continuous habitat. In spring weather was hot and energy requirements of weasels were low. In continuous habitat voles could avoid predation by going further away from the weasel and survive better, whereas in fragmented enclosures voles were not willing to leave small fragments and cross matrix area and were therefore caught by a weasel more easily.

ISLAND SYNDROME': COMPARATIVE STUDIES ON INSULAR POPULATIONS OF BANK VOLES, *MYODES GLAREOLUS*

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Frequently, animals on islands show different morphological and behavioural traits to their mainland counterparts. This has been well documented in rodents, with individuals showing increased body size, increased density, changes in reproductive behaviour and, sometimes, different habitat use and food sources. If such traits are evolved adaptive mechanisms, 'island syndrome' is predicted to increase with isolation from the mainland and decrease with island size because of a corresponding decrease in species diversity and habitat complexity. Several adaptive theories seek to explain island syndrome (e.g. decreased risk of predation, dispersal limitations, increased intraspecific competition) but other possible mechanisms through which these changes could occur include founder effects and genetic drift. From extensive studies on island populations of bank voles (*Myodes glareolus*) around the British Isles and intensive studies on bank voles on Skomer Island, off the south west coast of Wales, We will provide data on genetics, ecology and behaviour, and relate these to possible explanations for the evolution of 'island syndrome'.

BANK VOLES ON THE ISLANDS OF SKOMER AND RAMSEY, OFF THE COAST OF WALES, UK

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This paper presents the results of studies of the Skomer bank vole (*Myodes glareolus skomerensis*) that have been undertaken since 1971.

The vole is a large variety of the bank vole found on Skomer Island, Pembrokeshire, off the west coast of Wales, UK. It is larger than animals caught on the nearby mainland (the mean weight for males in the breeding season is ca 35g and females ca 36g) with a coat that is bright red above and a cream belly.

The animals can live at high densities with numbers of up to 475 ha being recorded. The breeding biology of the animals differs from that of bank voles on the nearby mainland in that the breeding season is shorter (lactating females are not usually detected before the end of May and most young are produced between July and the middle of September) and few animals breed in the year of their birth so most young are produced by overwintered animals.

The animals occupy a habitat that is rich in bracken (*Pteridium aquilinum*), the highest densities being found in areas where the bracken is dense with little understory. The diet of the animals includes a large proportion of bracken.

The animals are easy to handle and show an apparent tameness in the hand.

A population of bank voles is also found on the nearby island of Ramsey. These animals have not been studied as intensively as the Skomer voles and less is known about their biology. The Ramsey bank voles are smaller than the Skomer voles and have a darker coat (their appearance is much closer to that of the bank vole found on mainland Britain). They live at much lower densities. Nevertheless they occupy a similar habitat to the Skomer voles and also show an apparent tameness when handled. The results of a series of trapping programmes over the last ten years will be reported.

GENETIC AND MORPHOLOGICAL VARIATION OF FIELD VOLES FROM THE BRITISH ISLES

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Field voles (*Microtus agrestis*) are common and widespread throughout mainland Britain but are found on very few of the smaller surrounding islands. Their sporadic distribution among the Hebridean islands has been attributed to Neolithic or subsequent human traffic. Seven subspecies of field vole have been described from the species' range in the British Isles, based on apparent morphological differences. An intraspecific phylogeny, using the mitochondrial cytochrome b gene, is presented here and morphological variation in field voles from the mainland and other islands of Britain is re-examined against this background.

THE EVOLUTION OF DWARF ELEPHANTS IN THE MEDITERRANEAN

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The most dramatic examples of 'island dwarfing' are found among the extinct elephant species from Mediterranean islands, where dwarfs estimated at less than 150kg have evolved from a 10,000 kg mainland ancestor, *Palaeoloxodon antiquus*. Consequently, dwarf elephant fossils have been highly influential on research into body size change on islands, and yet their own evolution remains little understood. New data collected from western and eastern Mediterranean elephant assemblages challenges accepted theories of dwarf elephant evolution and adaptation. Here we present an overview of our new findings regarding dwarf elephant evolution across the Mediterranean, and discuss its importance to wider questions of insular vertebrate evolution and the 'Island Rule'.

ISOLATION, CLIMATE CHANGE, AND ECOLOGICAL TRAPS: CHALLENGES FOR MAMMAL CONSERVATION IN TERRESTRIAL ARCHIPELAGOES

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Due to their significant isolation, island ecosystems are notoriously sensitive to disturbance, in particular to biological invasions by non-native species and humans. Terrestrial islands of habitat are also similarly isolated and are hypothesized to be equally sensitive to change. High-elevation montane ecosystems are often isolated from similar habitats by intervening low-elevation zones of increased temperature, decreased humidity, and concomitant changes in vegetation. Montane islands are often valued by humans for these cool climes, increased water availability, timber resources, recreation, and aesthetics in addition to endemic flora and fauna, which results in conflicts in land management and conservation strategies. The Madrean Archipelago that extends through northern Mexico and southwestern United States of America represents an extensive chain of montane environments. Endemism is common in this region and it represents the greatest diversity of tree squirrels in North America. Introduced species (*Sciurus aberti* and *S. carolinensis*), forest management practices, and climate change interact to threaten these sensitive environments and in some cases appear to result in ecological traps for several species of Sciurus and Tamiasciurus. Forest structure, composition, and fuel loads have resulted in increased frequency and intensity of wildfire that is likely facilitated by climate change-related heating and drying. In addition, insect damage has also increased in relation to these factors further degrading forest quality. Nearly all endemic tree squirrels (*Sciurus*, *Tamiasciurus*) in the region are of precarious conservation status as a result. Given current trends in global climate and human population growth, such challenges are likely to be faced worldwide in terrestrial archipelagoes.

THE ORIGIN OF THE ORKNEY VOLE

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The common vole (*Microtus arvalis*) is a widespread and abundant species in Europe. It is absent from Great Britain and Ireland, but occurs on seven islands of the Orkney archipelago where it is distinguished as a separate subspecies. Orkney voles (*M. a. orcadensis*) were probably transported by humans from continental Europe to Orkney in the Neolithic. We sequenced the mitochondrial gene for cytochrome b to identify better the source area of Orkney voles. They originated from northern France/Belgium, not from Spain or the Pyrenees region as has been proposed previously. Voles from other lineages occur in the Netherlands and Denmark. No recent introduction between Orkney and continental Europe has been detected. We will describe how phylogenetics and molecular diversity indices may be used to study the pattern of colonisation within the Orkney archipelago.

CONCERNING THE MAMMALIAN SPECIES CURRENTLY REGARDED AS ENDEMIC TO THE MEDITERRANEAN ISLANDS

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In the light of current knowledge, less than about one-fourth of the mammalian species found in the continental Mediterranean region have been described as endemic to the area. Moreover, the number of endemics decreases drastically if we consider the composition of the extant mammalian fauna on islands. This is almost exclusively characterised by continental taxa, whose appearance on the island appears to be directly related to human activity.

The insular endemics are exclusively limited to two species of shrew, the Sicilian, *Crocidura sicula* Miller, 1900, and the Cretan white-toothed shrew, *C. zimmermanni* Wettstein, 1953; the recently discovered Cypriot mouse, *Mus cypriacus* Cucchi et al., 2006; and, perhaps, one gerbil, *Dipodillus zachariai* Cockrum, Vaughan & Vaughan, 1976, reported from the Tunisian archipelago of Kerkennah. Further studies are required for a better understanding of the taxonomic status of the lesser white-toothed shrew, *C. suaveolens* (Pallas, 1811), from the small island of Tilos, in the Dodecanese (Greece). Although, in fact, the external size and colour of its coat fall within the variability range for the species, this shrew reveals an unexpected white tail tip, a characteristic which up to now has only been reported for the endemic *C. sicula*.

In any case, it is interesting to note that none of the above-mentioned species displays the most common trend of endemisation reputed to affect micromammals on islands: the well-known increase in size characteristic of fossil and/or subfossil shrews and rodents.

This fact, together with their almost total absence from the Quaternary fossil horizons of the islands from which they are now reported, raises a series of intriguing questions that are still far from being answered. The invitation is to further study which, if conducted in the correct manner, integrating the information to be derived from the palaeontological, archeozoological, neontological and genetic ambits, will be bound to make an ulterior illuminating contribution to a better understanding of the significance of the extant occurrence of these species on the Mediterranean islands.

SIZE EVOLUTION ON ISLANDS

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Size evolution is thought to follow predictable patterns in insular mammals with larger species getting smaller and small ones evolving larger size. I examine empirical patterns and mechanistic explanations in mammals and other insular vertebrates, and show that:

a. patterns are generally weak
b. phylogenetic comparative methods - no patterns emerge
c. different selection pressures affect different taxa based on their diets and body sizes
d. even within species different autecological conditions can result in very different rajectories of size evolution

MOSAIC INSULAR EVOLUTION: THE EXAMPLE OF THE WOODMOUSE *(APODEMUS SYLVATICUS*) IN THE ATLANTIC AND MEDITERRANEAN ISLANDS

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The distinct nature of island populations has traditionally been attributed either to adaptation to particular insular conditions or to random genetic effects. In order to assess the relative importance of these two disparate processes, insular effects were addressed in the European wood mouse, *Apodemus sylvaticus*.

Populations coming from 33 localities on both mainland and various Atlantic and western Mediterranean islands were considered. The insular syndrome primarily invokes variations in body size, but ecological factors such as release from competition, niche widening and food availability should also influence other characters related to diet. In the present study, the morphology of the wood mice was quantified based on two characters involved in feeding: the size and shape of the mandibles and first upper molars. The size of the mandible is also a proxy for the body size of the animals. Patterns of morphological differentiation of both features were estimated using two-dimensional outline analyses based on Fourier methods.

Significant differences between mainland and island populations were observed in most cases for both the mandibles and molars. Mandible shape diverged mostly on islands of intermediate remoteness and competition levels, whereas molars exhibited the greatest shape differentiation on small islands (Port Cros and Porquerolles). A mosaic pattern was also displayed for size. Body and mandible size increased on Ibiza, but molar size remained similar to mainland populations.

In conclusion, the pattern of insular variation of size and shape on various characters appears to be the consequences of a complex interplay of factors including ecology, physical environment and genetic determinism. Morphological differentiation on islands might thus appear as a collection of distinctive cases, mosaic evolution characterising insular divergence. Finally, the molar seems to be more prone to change with reduced population size on small islands, whereas the mandible could be more sensitive to peculiar environmental conditions on large and remote islands.

ISLAND AREA AND RATES OF MORPHOLOGICAL EVOLUTION IN MAMMALS

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In a recent paper, I showed that the rates of morphological evolution in mammals were larger in island species when compared to their mainland relatives (Millien 2006). This was the first empirical demonstration of a long standing hypothesis of accelerated evolution on islands.

According to the theory, evolution on islands is supposed to be the most marked on the smallest islands. The island area is correlated with many factors, including the elevation (a reflection of the habitat complexity on the island), and the diversity of species on an island (a reflection of the force of competition and predation pressures on the species).

Here I used a dataset of 82 evolutionary rates calculated for 29 mammal species from 51 different islands, evolving over time intervals ranging from 21 years to 2.8 Ma. I show that there is no effect of island area for rates of evolution calculated over the smallest time intervals (i.e. below 120 years). However, when considering only those points for which the time interval is larger than 600 years, there is a significant negative relation between the evolutionary rates in darwin and island area; this finding is in agreement with the theory of island evolution. In contrast, there is no significant relation between the magnitude of morphological change and island area, which suggests that the amount of morphological evolution in island mammals is not dependent upon the island on which the species evolved.

"ISLAND RULE" AND BODY SIZE EVOLUTION IN INSULAR PLEISTOCENE MAMMALS

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Islands have been regarded by scientists as living laboratories of evolution and an optimal context for the study of forces influencing evolution and diversification. Two main issues have been attentively scrutinized: the loss of biodiversity and the peculiar changes undergone by island settlers, above all changes in size. Over time plenty of hypotheses have been formulated to explain causal mechanism of body size modification and the debate continues today, with a diversity of alternative explanations, confirming or rejecting the soundness of island rule. Large mammals undoubtedly derive some advantages from reducing their size because: 1) larger-sized mammals generally require more food, and need larger home ranges; 2) reducing body size and increasing metabolic rate lead to a higher reproduction rate which, in turn, increases population density and may preserve heterozygosis, thereby avoiding the threat of extinction; 3) reducing their size, large herbivores increase exploiting environmental opportunities and optimising energy costs;4) small mammals by enlarging their size should reduce their metabolic rate and food requirements, and thus increase their life expectancy. But, what are the main factors driving these changes? To contribute to the debate Pleistocene mammalian faunas have been analysed and compared with the coeval mainland faunas. Results obtained provide evidence that: 1) size evolution on islands is not directly dependent on abiotic characteristics such as area; 2) evolution and size of endemic species might be indirectly affected by isolation (constraining colonization from mainland) and physiography (sometimes permitting adaptive radiation); 3) in unbalanced insular communities, the shift in size of non carnivorous species largely depends on the nature of vacant species; 4) body size of carnivorous species mainly depend of the size of the most available species and adaptive strategy for more efficient energy use under the special environmental conditions of insular ecosystems. Accordingly, we can suppose that, given the intrinsic characteristics connected with their bau-plan, and removing biotic and abiotic environmental constraints, the body size of non carnivorous insular species could converge towards a taxon-specific "optimal size" allowing the best energetic balance and maybe developing evolutionary novelties.

CONSERVATION GENETICS OF ISOLATED GAZELLE POPULATIONS ON THE DAHLAK ARCHIPELAGO, RED SEA

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The Dahlak archipelago in southern Red Sea consists of more than 200 islands and islets of which only the two largest are inhabited. Despite the location of these islands on one of the world's busiest shipping lanes, there is limited contact with the outside world as a result of the harsh climate and long running armed conflicts in the region. This insularity of the Dahlak islands is reflected in their fauna too, the ungulates (gazelles) being a good example. Early visitors considered Dahlak gazelles *Gazella dorcas*, a small antelope whose range extends from the Levant to North Africa. More recent reports considered them a dwarf subspecies of the much larger *Gazzella soemmerringii*. A third possibility, that they are more closely related to the Arabian gazelle (*Gazella saudia*), a species originally endemic to the western parts of the Arabian peninsula but currently extirpated in the wild can not be excluded, although unlikely. We have gathered baseline data on the gazelles of the Dahlak archipelago focussing on population size and movement. Through non-invasive genetic sampling using fecal pellets, we have gathered data on 8 microsatellite loci in 50 animals from the biggest island in the archipelago. Thirty more animals from two mainland coastal populations are also being genotyped for comparative purposes. Mitochondrial DNA sequence data (cytb) are also being acquired. Our aim is to ascertain whether Dahlak gazelles represent a dwarf subspecies of *Gazella soemmerringii* or belong to *Gazella dorcas*, to characterize their population genetic structure and obtain estimates of their divergence from mainland populations, and, to assess the conservation policy implications of the findings.

WORKSHOP

Mammal conservation in Europe: status and priorities

EUROPEAN NON VOLANT MAMMAL DIVERSITY: CONSERVATION PRIORITIES INFERRED FROM MITOCHONDRIAL DNA

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The increasing of nuclear and mitochondrial DNA (mtDNA) studies on European mammals provides more accurate information on the genetic structure of the populations. Such information can be used not only for a reconstruction of the phylogeographic history of each taxon but are useful in identifying cryptic species and areas that may represent conservation priorities from an evolutionary perspective.

The aim of this paper is to identify, by mean of a DNA taxonomy approach, populations representing putative species, non yet formally described, among European mammal species belonging to all orders, with the exception of Chiroptera.

For each European not flying species, reported in the last edition of Mammals Species of the World (Wilson and Reeder 2005), we review the published data (about 100 articles) reporting sequences of the mtDNA gene for cytochrome b (cyt-b). As expected many species revealed to be composed by two or more cyt-b phylogroups. To identify those phylogroups having an high probability to represent true species, we considered the criteria presented by Baker and Bradley (2006, J. Mamm., 87: 643-662) for the identification of mammals species under a genetic species concept. Thus we identified, for each species, the number of cyt-b phylogroups, their geographic localisation and calculated the genetic distance among them. Then we compared the genetic distances among phylogroups, with the distribution of pairwise genetic distance between sister species belonging to the same genus or family. We identified a putative species when the genetic distance between allopatric or parapatric phylogroups is equal or greater to the mean value found for sister species. When available, also data from others mtDNA genes and data from nuclear DNA has been used for the taxonomic evaluation of phylogroups.

Mammal species in Europe are often lacking in comprehensive taxonomic revision that take into account the results of genetic studies, as, instead, is the case in North America. As a consequence, lists of protected taxa such as those of the Habitat Directive, based on current taxonomy, may fail to protect a large amount of mammal diversity in Europe.

PHYLOGEOGRAPHIC HISTORY OF THE IRISH LEISLER'S BAT (*NYCTALUS LEISLERI*) - THE AZOREAN LINK

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While the Leisler's bat (*Nyctalus leisleri*) is rare and vulnerable across most of its range, which extents over the British Islands and most of Europe, the species is very common in Ireland. Indeed, Ireland is considered to be the European stronghold for the species and is thus internationally important from a conservation viewpoint. Although very little is still known about Leisler's in Ireland, some relevant ecological differences have been reported in comparison to their European counterparts. For instance, in Europe Leisler's bats are known to be highly migratory, covering distances up to 1000km² between summer and winter roost sites. However, this does not occur in Ireland, except perhaps on a small scale. In trying to understand the origin, the genetic relationships, and the differences in migratory behaviour of Irish Leisler's bats in relation to their European counterparts, we undertook a comprehensive phylogeographic investigation of the species throughout most of its range. Thus, we analysed genetic variability at a highly informative region (320bp) of the D-loop mitochondrial DNA (mtDNA) for a sample comprised of 120 individuals from 38 widespread localities throughout Europe. Resulting sequencing data were analysed in comparison to analogous data, available in the GeneBank, consisting of sequences from 165 individuals of the closely related species *N. azoreum*, which is endemic from the Azores Islands. Analysis of combined data set reveals the existence of two very distinct mtDNA lineages, which probably diverged in separate refugia during the last glacial maxima. Surprisingly, one lineage (*azoreum*) is entirely restricted to Ireland and the Azores. The second lineage (*leisleri*) has widespread distribution in Europe also occurring in Ireland albeit at lower frequency. Results indicate that Irish Leisler's bats, contrary to their European counterparts, share an unexpected phylogeographic history with *N. azoreum*. Thus, Ireland represents a zone of secondary contact between two distinct genetic lineages. The absence of *azoreum* haplotypes in Europe is indicative of unidirectional gene flow and suggests a genetic basis for the limited migratory behaviour of the Irish Leisler's bat in relation to their European counterparts. These findings have important implications for the conservation of this species in Ireland.

POLYMORPHIC MICROSATELLITE MARKERS CONFIRM EXTENSIVE POPULATION FRAGMENTATION OF ENDANGERED BALKAN PALEOENDEMIC MARTINO'S VOLE

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Martino's vole *Dinaromys bogdanovi* is the only living member of the Tertiary genus *Dinaromys* and likely also the only surviving member of the *Pliomys* lineage. The species shows all three attributes of rarity in accordance with Rabinowitz's seven forms of rarity model. Historical range exceeded the recent one and its shrinkage continued into the recent times. The species has frequently been reported as being rare throughout its range, but very little is actually known about it. Martino's vole depends on isolated rocky habitats which are rare and widely separated even in those regions where the species is relatively common. The persistence of a species in patchy habitats, as it is typical of Martino's vole, may vary as a result of habitat complexity and quality, spatial organization of patches, dispersal frequency, population size, and life-history characteristics. The yearly extinctions of fragmented populations can be frequent but they are normally balanced by recolonization events. By using cross-amplification approach, we have optimized a set of eight polymorphic microsatellite loci to analyze metapopulation dynamics in Martino's vole population on Mt. Zelengora (eastern Bosnia). Sixth of them were originally developed for the common vole (*Microtus arvalis*) and two for the water vole (*Arvicola terrestris*). Preliminary results confirm very extensive fragmentation of populations of this rare rodent species.

ITALIAN HARES (*LEPUS CORSICANUS*) IN CILENTO AND VALLO DI DIANO NATIONAL PARK: STATUS AND CONSERVATION

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Italian hare is an endemic species of central and southern Italy. At present, in Cilento and Vallo di Diano National Park lives a population showing the higher density among Italian peninsular ones, so to manage it represents a focal point of conservation strategy on the entire species. Park Managers start in the 1998 a conservation plan in collaboration with zoologists from Istituto di Gestione della Fauna and Universities of Naples. This contribution reports the results of population monitoring and shows the status of conservation activities carried out in the Park. In fact, during these years population density, habitat structure (with particular attention to the patchiness structure), foraging and population genetic have been studied. Nocturnal transects allowed us to estimate the hares density, founding individuals ranging from 2 to 12 /km^2. Habitat suitability was built using ENFA by means of software Biomapper. We considered eco-geographical variables in buffer areas of 300 m radius around each territory. A GIS software was used to select habitat structure in each buffer areas, by means of overlay functions among buffer areas and habitat maps. The eco-geographical variables were: land cover, elevation, slope, aspect, man-made structures. Moreover, food availability is described in each feeding habitat by means of phytosociological survey. Finally, we use microsatellite and mitochondrial markers in order to describe genetic variability within population. Genetic data suggest a recent bottleneck occurred to population in the Park: the levels of variability are worrying. Conservation activities, follow-on our study, concern direct habitat protection and a translocation program of hares in suitable areas where species is not else present.

MODERN STATUS OF SAIGA ANTELOPE POPULATION IN KAZAKHSTAN

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Saiga antelope is a migratory gregarious animal of Eurasian deserts and semi-deserts. It is the most ancient reprehensive of the fauna, unique and valuable property of the Republic of Kazakhstan. The largest part of present-day natural habitat of Saiga antelope lies within the territory of Kazakhstan. Present-day natural habitat of saiga antelope for the most part covers desert and semi-desert areas of 10 administrative oblasts. They are: West-Kazakhstan; Atyrau; Mangistau; Aktyubinsk; Karagandy; Kyzylorda; South-Kazakhstan; Zhambyl; and partially Akmolink and Almaty. The natural habitat areas also include neighboring oblasts of Uzbekistan (Karakalpakya), and to a lesser extent (in certain years) - the oblasts of Turkmenistan and Russia. Three separate populations of Saiga antelope inhabit Kazakhstan. They are betpakdalinsk, usturtsk, and uralsk populations.

Saiga antelope historically undergoes abrupt population waves. Main reasons of that may be divided into two categories: the first is large volume of snow, ice-covered ground, and diseases, in lesser extent - predators (wolves); the second is anthropogenic character factors, such as illegal hunting (poaching). The quantity of animals had heavy decrease during last decade. Thus in 1991-1994 Kazakhstan had 976-810 thousands of Saiga antelopes, but in 2001-2004 - 79.4-30.7 thousands (Bekenov and other., 2002, Bekenov, Grachev, 2003; Meldebekov and other, 2005). Beginning with 1999 there is prohibition on bag of Saiga antelopes. Mass loss of Saiga antelopes caused by the diseases was not observed. Heat and coupling of Saiga antelopes goes in December, at winter habitat places. Calves are born in may, during spring migration to the North. During calving period Saiga antelopes form large gatherings on a small area, so called "maternity hospitals". Sexual ratio (buck : cow) among new-born calves is close to 1 : 1, among grown-ups with normal population structure it is 1:2 - 1:3. Depending on structural failure extent, the quantity of gown-up bucks of exploited population lately was 3-10%. Grown-up cows give birth to 1,8 calves as average. Juvenile (yearling) cows have 1,0. Average quantity of calves for a cow is 1,5. Today Kazakhstan works on quantity recovery of Saiga antelopes. Creation of special forms of keeping and rearing of Saiga antelopes is one of the main directions of this work.

CONSERVATION STATUS OF WALIA IBEX USING GENETIC MARKERS AND ENVIRONMENTAL DATA

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The Walia ibex (*Capra walie*) belongs to the *Caprinae* - a family where numbers and status of the different taxa are still under debate. This flagship species in Ethiopia has been recorded as critically endangered by the IUCN. It represents the most southerly distributed taxon of its genus, confined to a small area in the Simien Mountains. The total population size is estimated to be about 400 animals, with recent slight increase. Habitat loss, poaching, and potential inbreeding have become major issues of concern in its conservation. Unfortunately, the Walia ibex has never been included in the several papers dealing with the phylogeny of the *Capra* genus. Moreover, despite having the status of critically endangered species, the level of genetic polymorphism has never been assessed. The goal of this study is to assess the conservation status of the Walia ibex (i) by estimating its position within the *Capra* genus by sequencing the cytochrome *b* of the mitochondrial genome for a few individuals, (ii) by comparing its realized ecological niche with that of the Nubian ibex (*Capra nubiana*), and (iii) by estimating the level of inbreeding by analyzing the polymorphism of a few microsatellite loci. Preliminary cytochrome *b* results show that the Walia ibex and the Nubian ibex form a monophyletic group, and that the Walia ibex is a sister species of the Nubian ibex. The genetic distance between Walia ibex and Nubian ibex is comparable to the genetic distance between Spanish and Alpine ibex (*C. pyrenaica* and *C. ibex*). The realized niche of the Walia ibex is completely disjoint from that of the Nubian ibex for many parameters such as annual precipitation, elevation, and temperature of the coldest month. The microsatellite analysis is ongoing, but we expect a higher level of polymorphism than in the Alpine ibex, because the mitochondrial polymorphism is still high (up to now four haplotypes for five individuals analyzed in Walia ibex). All together, these results indicate that the specific status of Walia ibex is not questionable, and that the remaining population, despite being small, has not suffered from a strong bottleneck in the past.

ENDEMISM, RARITY AND CONSERVATION ISSUES ON SMALL TERRESTRIAL MAMMALS FROM THE BALKANS AND ANATOLIA

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Small mammals are just as likely to become extinct as larger species, although the latter receive disproportionate attention with respect to conservation activity and research. Nonetheless, the majority of mammalian extinctions, both those recorded over the last 400 years and those likely to happen during the next few decades are of smaller-bodied species. Rodents, as the most specious mammalian order, contribute most to this number in absolute terms and proportionally. Species that are very rare according to all three criteria of Rabinowitz's seven forms of rarity model are more common among mammals than would be expected in a random process, and rodents comprise the majority of these rare species in absolute terms. Also, species displaying both restricted distribution and low density, i.e. two of the criteria of Rabinowitz's rarity model which are common in rodents, are those most at risk of extinction. Even though rarity does not necessarily indicate threat of extinction, species generally become rare before they go extinct. Although the number of small mammals listed in the IUCN Red List of Threatened Animals increased dramatically in 1996, the conservation status of many species remains only tentatively known because of poor taxonomic knowledge of various groups and a lack of information on population status. With these issues in mind we approached the assessment of rarity and conservation status of small terrestrial mammals in southeastern Europe (the Balkans) and adjacent southwestern Asia (Anatolia). Within the western Palaearctic both these regions are biodiversity hot spots in mammalian species richness and contain a substantial number of small range endemics. A shortage of information frequently hampers risk assessment of rare and little-known species and endemics from the Balkans and Anatolia are no exception in this respect. Although a significant historical shrink in range is documented for several species (*Talpa davidiana*, *Dinaromys bogdanovi*, *Myomimus roachi*) it is unclear whether threats are immediate enough to require elevation of conservation status and implementation of measures.

A POSSIBLE APPROACH TO THE "CONSERVATION" OF THE MAMMAL POPULATIONS OF ANCIENT ANTHROPOCHOROUS ORIGIN ON THE MEDITERRANEAN ISLANDS

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If we consider the existing non-flying terrestrial mammals of the Mediterranean islands, we can find very few of the endemic elements that characterised the late Quaternary faunal structures. These refer exclusively to two species of white-toothed shrew, respectively from the Siculo-Maltese archipelago and Crete, the recently discovered Cypriot mouse, and, perhaps, one gerbil endemic to the Tunisian archipelago of Kerkennah. Instead, at present, the existing populations of non-flying terrestrial mammals of the Mediterranean islands are almost exclusively dominated by continental taxa, as a rule regionally specific in relation to the nearest mainland, and whose appearance on the islands appears to be essentially related to human intervention.

The legacy of this global redefinition of the original ecological equilibrium brought about by man since prehistoric times - and continued possibly without interruption throughout historical times - raises not inconsiderable problems of conservation and management. First of all because, in the vast majority of cases, it is impossible to reconstruct the natural ecosystems of the past, which have been destroyed for millennia. However, this leaves the question of how to treat the allochthonous populations of certified ancient origin. Several of these anthropochorous populations, in fact, represent invaluable historic documents: images which remain fixed in time and history. This could be the case, for example, of the genets of the Balearic islands, the wild boars and the red deer of Sardinia, the wild goats of Montecristo and Crete, the fallow deer of Rhodes, the mouflons of Cyprus, and so on.

Unlike the case of artistic monuments, however, here we are dealing with living organisms which interact with an environment, originally extraneous to their natural distribution, in which they have survived since ancient times.

Frequently, they may also represent the last survivors of continental populations which vanished many millennia ago.

Their protection and their study can provide an opportunity for testing a range of different evolutionary theories. Therefore, they deserve to be protected and considered as an authentic "cultural heritage".

A REVIEW OF PRIORITIES IN MAMMAL CONSERVATION IN GERMANY: DO BLACK BOXES HIDE URGENT PROBLEMS?

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Factors which have a negative impact on mammal populations are reviewed for all 83 native species occurring in Germany today. Forest management affects most species of the mammal fauna as well as of the sub-groups of red list species and of species, which were assessed to give Germany a special responsibility for their conservation. This is because of the current forestry practice of a large scale selective harvesting of ancient trees. The review also highlights habitat fragmentation, agriculture and direct taking of mammals (legal, illegal or accidental) as major problems for species conservation. There is the risk of a faster decline in mammal species and populations within the next years, because of the composition of crops grown in agriculture, are going to change once again. Areas now set aside with financial support by the EU will be used for the production of so called bio-fuels with highest intensity.

The results of the analysis of factors threatening mammal species in Germany correspond to intuitive experts´ assessments and underline the importance of ongoing "traditional" conservation measures. However, very few German mammal species seem to be affected by climate change or invasive alien species, but we distrust this part of our analysis. To our minds impacts of these two factors are underestimated by a general lack of data. There is no reliable mammal monitoring programme operating in Germany so far, not even for most species protected by the EU Habitats Directive, and research capacities in mammal population ecology are limited. So changes in mammal occurrence and abundance may be overlooked even if they were significant. To prove that urgent problem can be identified and appropriate priorities are set in species conservation in Germany, the implementation of a mammal monitoring programme and specific research projects on the effects of climate change and alien species on mammal populations are needed.

MAMMALIAN FAUNA INVESTIGATIONS ON CONTIGUOUS PROTECTED TERRITORIES OF RUSSIA AND UKRAINE (PROBLEMS AND PERSPECTIVES)

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In the course of inventory of protected areas of Bryansk region in 2000-2006, the materials on current species composition of mammalian fauna were collected. The complex faunistic investigations permit to make recommendations concerning establishment of new preserves as well as reorganization and enlargement of existent ones.

We compile the List of Mammals of Bryansk region on the basis of original data as well as reliable sources of information. It includes 81 mammalian species (73 animals undoubtedly occur on studied territory; 5 species occur only presumably, i.e. no contemporary findings; 3 species unlikely occur). From this number 4 species are adventive (*Nyctereutes procyonoides*, *Ondatra zibethicus*, *Cervus nippon* and *Mustela nivalis*) and 3 ones - reacclimatized (*Bison bonasus*, *Cervus elaphus* and *Desmana moschata*).

Mammalian fauna of Bryansk region in a whole is presented by 21 families and 6 orders (Insectivora - 10 species, Chiroptera - 14, Carnivora - 15, Lagomorpha - 2, Rodentia - 26 and Artyodactyla - 6). From the total number 4 representatives (Rodentia) are in IUCN Red List; 3 species are listed in the Red Data Book of Russian Federation (Insectivora -1, Chiroptera - 1, Artyodactyla - 1), 19 species - in the Red Data Book of Bryansk region (Insectivora -1, Chiroptera - 6, Carnivora - 4, Rodentia - 7, Artyodactyla - 1); 10 species - in the Red Data Book of Ukraine (Insectivora -1, Chiroptera - 2, Carnivora - 4, Rodentia - 2, Artyodactyla - 1) and 55 species are under protection of Bern Convention (at that 23 ones listed in Annex II: Insectivora -1, Chiroptera - 12, Carnivora - 6, Rodentia - 4) .

The peculiarities of mammalian fauna of Briansky Les National Reserve (Russia) and Desnyansko-Starogutsky National Nature Park (Ukraine) are analyzed. These natural reserves are situated on either side of Russian-Ukrainian frontier but represent the part of common natural unit - edge of boreal coniferous forest.

Scientific and nature-conservation programs which have been carried out on contiguous protected territories are reviewed. Benefits of the establishment of international Russian-Ukrainian Biosphere Reserve are discussed. It will promote both the enrichment of Ukrainian fauna with rare wildlife elements, which are still preserved in Bryansk forests, and also the improvement of international collaboration in the field of nature conservation.

ASSESSING THE PATTERNS OF GENETIC DIVERSITY IN OTTER (*LUTRA LUTRA*) POPULATIONS

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During the 20th century otter (*Lutra lutra*) populations in central and western Europe strongly declined and eventually disappeared due over-hunting, destruction of riparian habitats and chemical pollution. In some regions, from where the species completely disappeared, reintroduction projects were carried out, and wild or captive-reproduced otters have been released in the wild. In this study we aimed to describe the main patterns of genetic diversity and the structure of otter populations throughout Europe. We used 11 unlinked microsatellite loci and mitochondrial DNA sequences (mtDNA) to genotype 745 individual otter samples collected from 20 natural, reintroduced or restocked populations in Europe. Most of these samples were georeferenced. Most of the mtDNA sequences showed low divergence and were closely related, producing a star-like network that suggests a recent postglacial origin of all European populations from a single ancestral source. However, two mtDNA haplotypes identified in otters that originated in the UK captive stock (Otter Trust) were sharply distinct from the others and could be of non-European origin. Microsatellites results showed that otters in Europe are genetically variable, but not strongly differentiated, although some populations (Iberian Peninsula, Germany, Scandinavian Peninsula and Southern Italy) showed instances of recent population subdivision. In contrast, otters of non-European (Israel) or captive (Otter Trust) origins showed distinct genotypes. Captive individuals showed some distinct private alleles and can be genetically identified if released in wild. Population structure and landscape genetics model allow to describe the fine-scale structure of local populations and infer the origin of the individuals (either if natural migrants or translocated). These data can be used to implement global and local otter conservation programmes.

GENETIC DIFFERENTIATION AND HYBRIDISATION IN WILD AND DOMESTIC CAT POPULATIONS IN EUROPE

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The conservation of wildcat (*Felis silvestris*) populations in Europe is threatened by habitat destruction and fragmentation, and, locally, by risks of hybridisation with widespread free-ranging domestic cats. Here we summarize results of a long-term project aimed to describe the genetic structure of wildcats sampled in Europe, and develop a cost-effective procedure to assess hybridisation rates in natural populations. Wild and domestic cats were genotyped at 27 unlinked and linked microsatellite loci, and analysed using Bayesian admixture models. Results indicate that habitat fragmentation and demographic decline led to detectable genetic diversification among wildcat populations. The gene pools of wild and domestic cats are sharply distinct in several countries (Fst = 0.10-0.14), indicating reproductive isolation and low admixture rates. However, hybridisation rates are very different locally, being limited in central Europe and in Italy, but widespread in Hungarian wildcats. Different historical, demographic and ecological conditions can lead to extensive crossbreeding between wild and domestic cats, thus threatening the genetic integrity of wildcat populations in Europe. Genetic monitoring and assessment of admixture should be used to identify critical areas of introgression and implement the appropriate conservation strategies.

THE USE OF PVA AND HABITAT SUITABILITY MODELS IN THE CONSERVATION OF MAMMALS: A CRITICAL APPROACH

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The assessment of threat levels usually involve the use of Population Viability Analysis to obtain threshold values and prioritise conservation actions. User-friendly software allow the easy implementation of complex analyses, but these require reliable estimates of ecological parameters. PVA and habitat suitability models have been extensively used to deliver conservation strategies for endangered Mammals. However, detailed estimates are only available for a few well studied taxa, penalising threatened species in developing countries and remote areas. Besides, ecological adaptations can vary locally (values from a habitat and a time may not be applicable to other contexts). Some authors have used vicariant data from common species phylogenetically related to threatened ones, in the ungranted assumption that parameters estimated for a common taxon were comparable to those of a rare one. Thus, unreliable results may follow, possibly compromising conservation efforts. Furthermore, viability simulations often span several decades of years, making it difficult or impossible to test hypotheses and assumptions. Viability analyses without high quality data are only theoretic exercises, with little relevance to actual conservation. The use of habitat suitability and distribution models is also popular in the conservation biology of Mammals. Suggestions from these models are often accepted without adequate evaluation. Many critical issues may arise when a model is examined: errors affect model building from remote sensing to evaluation stages and circularity can occur during the training procedures. New instruments and techniques need continued reappraisal and critique to make them actual tools for conservation. Funding should be directed to collection of field data (a relatively slow action, but just unavoidable), rather than to theoretic exercises, when reliable estimates of population parameters are missing. Meanwhile, a conservative management approach should be used.

MAMMALS IN EUROPE: RED LIST STATUS, TRENDS AND CONSERVATION PRIORITIES

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The threatened status of plants and animals is one of the most widely used indicators for assessing the condition of ecosystems and their biodiversity. It also provides an important tool in priority-setting exercises for species conservation. In May 2007 IUCN completed the European Mammal Assessment (EMA), the first review of the threatened status of all wild mammals in Europe and the EU according to IUCN regional Red Listing guidelines. In our presentation we report the key findings of the EMA, and discuss how the EMA data can be used to support biodiversity monitoring and conservation planning in Europe.

Nearly one in six (15%) of Europe's mammal species are threatened, and a further 9% are close to qualifying for threatened status. By comparison, 13% of European birds are threatened. No other groups have yet been comprehensively assessed at the European level according to IUCN regional Red List guidelines. A higher proportion of marine mammals are threatened than terrestrial mammals (22% versus 14%). Two European mammal species, the aurochs *Bos primigenius* and the Sardinian pika *Prolagus sardus* have become globally extinct since 1500, and a third species, the grey whale *Eschrichtius robustus*, is regionally extinct. More than a quarter (27%) of European mammals have declining populations. A further 32% are stable, and 33% are of unknown population trend. Only 8% of species populations are increasing. A number of these increases are due to successful species-specific conservation action.

MONITORING OF THREE BOVIDAE SPECIES POPULATIONS INTRODUCED IN THE BOU HEDMA NATIONAL PARK (CENTRAL TUNISIA)

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In order to evaluate the results of the introduction of three Bovidae species (Scimitar-horned Oryx (*Oryx dammah*), Addax (*Addax nasomaculatus*) and Dama Gazelle (*Nanger dama*) in the Bou Hedma National Park (Central Tunisia) after completely disappearing from Northern Africa, the males, females, adults, youngs, new-borns, deads and total monthly numbers of the species mentioned above, collected during ten years approximately, have been submitted to statistical analyses.

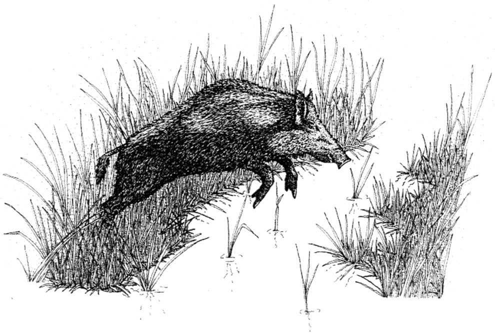
Those analyses with field observations have revealed the existence of a competition between Oryx and Addax at this last Bovid's expense which numbers are generally decreasing while those of its competitor species is increasing. The Dama Gazelle population is still presenting a low and constant number. Mating and birth of the three species occur in any time of the year.

If the environmental conditions still globally constant, the present tendencies of the three species populations will continue for approximately one year more, before reversing.

The statistical analyses have also revealed the existence of a certain intrinsic rhythm in the population of each studied species. The species numbers show consecutive periods of decrease and increase independently of the environmental conditions (especially rainfalls).

WORKSHOP

Non-lethal methods to manage wildlife



DOES SCAT MORPHOLOGICAL MISIDENTIFICATION INFLUENCE ECOLOGICAL STUDIES? A CASE STUDY WITH THE EUROPEAN WILDCAT (*FELIS SILVESTRIS*) AND RED FOX (*VULPES VULPES*) IN PORTUGAL

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The majority of the Iberian terrestrial carnivores occurs in low densities and presents elusive behaviour. These characteristics make them difficult to study in the field, whereas indirect methods based on scat identification are often applied, where species are identified using scats' morphological characteristics. The wildcat (*Felis silvestris*) and the red fox (*Vulpes vulpes*) are two mammalian carnivores autochthonous to the Iberian Peninsula, where they are frequently sympatric. The scat morphology of these two carnivores has common characteristics making species distinction hard. Moreover, although the wildcat is generally characterized as a facultative specialist species, the red foxes' plasticity regarding habitat selection and feeding ecology is well known. In Mediterranean regions, such as in the Iberian Peninsula, the wild rabbit reaches particularly high densities and thus resource segregation becomes more relaxed. The high dietary overlap makes the morphological scat identification even more difficult, and may lead to significant bias in field studies. However, the potential identification error rates are not quantified, nor the resulting implications in subsequent studies. The recent development of DNA based techniques provides more accurate species identification, avoiding the inherent subjectivity of the traditional ones. In this study, we determined the error rates on morphological identification of wildcat and red fox scats to evaluate the consequent bias in habitat selection. The scats were collected in three geographically distinct areas in Portugal and were identified based on morphological characteristics by three trained researchers. Habitat composition was analysed in a 4km^2 area surrounding the scats' locations. A total of 75 and 65 potential wild cat and red fox scats, respectively, were collected and a subset of 58 wild cat and 41 red fox were genetically identified using a SSCP technique. The results revealed that 37% of the wild cat scats were correctly identified and that misidentified scats belonged to red foxes (52%) and dogs (11%). Most of the red fox scats were correctly identified (89%). These results indicate that the morphological error rates should be considered in future ecological approaches, mainly in wildcat studies. In this work, despite the high error rates observed, first results did not show significant differences between habitat selection analysis based on scat genetic and morphologic identifications but the high detected bias suggests that other biological aspects, such as species diagnosis, distribution and diet may be misinterpreted.

IMPACTS OF SUPPLEMENTAL FEEDING ON WILD BOAR *SUS SCROFA*

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Wild boar are an important component of the indigenous Eurasian fauna and an important game species. In addition, they impact significantly on agriculture via crop damage and disease transmission. Although the cause of the increase in population size since the 1950s is likely to be complex, one possible factor is the widespread practice, mainly by hunters, of providing food for wild boar. Little is known, however, about the importance of supplemental food in the diet of wild boar and its possible impact on the species.
I investigated the quantitative importance of supplemental feeding in wild boar diet in Luxembourg, and its impact on reproduction, by analysing the contents of 1200 stomach samples and 740 female reproductive tracts collected over 27 months. Food from supplemental feeding occurred in 70% of stomachs and contributed 40% of total volume consumed. Supplemental food was consumed all year round over the whole of Luxembourg, but varied in quantity depending on the availability of other foods. Females started to reproduce early and although the sample was composed mainly of animals <2 years old, mean litter size was 5.3. The live weight of yearlings at age 12 months was 50 kg. Comparing these results to previous studies, it seems likely that year-round supplemental feeding has contributed to the drastic increase in the size of the Luxembourg wild boar population.

THE EFFECT OF SCENT-MARKING, FOREST CLEARING, AND SUPPLEMENTAL FEEDING ON MOOSE–TRAIN COLLISIONS

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We analyzed how the application of scent-marking, forest clearing, and supplemental feeding correlated with the number of moose (*Alces alces*)–train collisions along the most vulnerable railroad stretch in Norway. Data on 1,045 collisions has been compiled for 18 years since 1985, and remedial actions have occurred during various periods since 1990. We used sections of the rail line where remedies had never been applied as control sections to estimate the expected number of collisions per year and per km. In this way, we took into account the yearly variation in the number of accidents by using the difference between the actual number of accidents and the expected number of accidents as our response variable. We compared the difference between periods when remedies were applied to periods without any remedy. We found a general 46% decrease in the number of accidents during years with a remedy compared to what would have been expected the same years without any remedy. Forest clearing and supplemental feeding seem to be reliable ways of reducing the number of collisions. Scent was only applied for short distances in a few years, and the beneficial effects we observed were questionable. We conclude that mitigative effects may substantially reduce accidental mortality in moose populations if applied for long distances. We discuss the economics of game-vehicle collisions by performing a simple calculation to visualize the need for a bioeconomic approach to the problem.

THE ROLE OF LONG-ACTING CONTRACEPTIVE IMPLANTS TO MANAGE HIGHLY-VALUED MARSUPIALS IN AUSTRALIA: THE CASE OF KOALAS AND KANGAROOS

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Over the last decade, wildlife management agencies in Australia have been faced with a new challenge; to manage overabundant native marsupial species within a socio-political climate which demands the use of non-lethal control methods. This changing social ethos has driven research and development of new bio-technological approaches to wildlife management which aim to reduce/regulate population size by reducing the reproductive capacity of the population (i.e. fertility control). To date, large-scale fertility control operations have predominantly utilised laparoscopic surgical sterilisation techniques, particularly in the case of overabundant koala populations. In addition, ongoing research aims to evaluate the efficacy of using long-acting hormonal contraceptive implants for marsupial population management.

Long-acting contraceptive implants, based on the gonadotrophin-releasing hormone agonist deslorelin (Suprelorin®) or the synthetic progestin levonorgestrel, successfully inhibit reproduction in females from a range of marsupial species including koalas (*Phascolarctos cinereus*), eastern grey kangaroos (*Macropus giganteus*) and tammar wallabies (*Macropus eugenii*) and the effects on their reproductive physiology have been well documented. Current research aims to investigate the use of these agents in field situations by examining the effects on individual health, reproduction and home range and the resultant changes in population structure. A parallel line of research aims to develop methods of remotely delivering Suprelorin contraceptive implants to animals in the field, thereby enhancing the potential practicality of this form of fertility control. We will also discuss questions of cost efficiency.

FERTILITY CONTROL TO MANAGE WILDLIFE IN EUROPE

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Worldwide, current trends of human population growth and landscape development indicate that conflicts between wildlife and human interests are likely to increase in the near future. This is particularly apparent in European countries characterised by highly developed landscapes and increasing urbanisation.

In parallel, increasing public antipathy towards lethal methods has placed major constraints on management options and has fostered research into alternative, non-lethal options to mitigate the impact caused by wildlife to human interests.

Fertility control has the potential to offer benign, long-term, effective and humane approaches to reducing the size and growth of problem wildlife populations. Significant progress has been made in recent years on the development of fertility control agents, culminating in the availability of single-dose immunocontraceptive vaccines that inhibit the fertility of individual animals for several years. This represents a major technological breakthrough and further developments, such as orally delivered agents, can be expected in due course. The emergence of these vaccines makes the prospect of practical wildlife applications credible. However, in order to realise this potential, further research is required which needs to be focussed on approaches suited to European contexts.

This talk will aim to 1. identify European contexts in which fertility control of wildlife could be used to mitigate human-wildlife conflicts, 2. illustrate a case study on the effectiveness and potential side-effects of a GnRH vaccine on wild boar (*Sus scrofa*) and 3. discuss future research requirements and priorities to drive the fertility control approach towards practical applications.

GOOD FENCES MAKE GOOD NEIGHBOURS - PROSPECTS OF NON-LETHAL PLANT PROTECTION MEASURES TO PREVENT VOLE DAMAGE

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Cyclic vole species like *Microtus agrestis*, *Microtus arvalis*, *Microtus subterraneus* and *Arvicola terrestris* cause significant damage throughout their wide geographical range during peak years of abundance. Besides taking grain from fields, voles debark trunks of young trees and destroy their root system by gnawing. Fruit trees in orchards and afforestations in forestry mostly suffer this type of damage. Furthermore huge areas of grassland may be devastated when voles occur in high numbers (more than 1,000 per ha in *Arvicola terrestris* and up to 5,000 in *Microtus* species).

In conventional agriculture and forestry voles are usually controlled by distributing anticoagulant or zinc-phosphide baits. Due to restrictions in the use of pesticides, these poison baits cannot always be applied, they are costly and the application is time consuming. As practicable forecasting methods are not available, they are usually applied during peak densities when their effect is very limited. These pesticides are mostly non-specific and effects on non-target species may occur. Thus farmers are in bad need of alternative means of reducing damage to crops.

During recent years we developed and tested a mechanical barrier system to stop recurrent immigration of voles into apple orchards and a repellent from globe thistles (*Echinops sphaerocephalus*) to prevent voles from girdling young forest trees. The mechanical barrier system consisting of a 10 mm wire mesh fence reaching 50 cm below and 30 cm above the soil surface was found to provide excellent protection against vole immigration and damage in laboratory and field experiments, once the voles inside the fence had been removed. However, where moles were common in medium to light soils, extra arrangements at the lower side of the fence proved to be necessary to prevent undermining. The wire-mesh fence included flexible doors for easy access with machinery. To prevent voles from climbing the fence, the top 10 cm were bent rectangularly to the outside.

Application of an extract from globe thistles reduced debarking of treated twigs or young trees by 75 % and 85 % in cage and pen trials respectively, but was clearly dependent on available feed ressources. Such results show that there is indeed some potential in non-lethal methods to prevent vole damage which should be further explored and reduced to practice.

LIVESTOCK GUARDING DOG BREEDS AND COEXISTENCE WITH WOLVES: THE CASE OF ANATOLIA

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Anatolia, the Asian part of Turkey, had been occupied by Palaeolithic man and there are evidences of early agricultural life, including goat and sheep domestication, dating back to 7040 B.C. This suggests a long coexistence history of wolves and man on this land. Nevertheless, today, the human-wolf conflict is the biggest threat to survival of this carnivore in Turkey as in other parts of the world.

The wolf is still one of the least studied wildlife species in Turkey, contrary to its notoriety as "canavar", the beast. Its notoriety is due to it still being a major cause of damage on the large flocks of sheep that are kept in Central Anatolia under a semi-extensive production system. Traditional sheep husbandry systems involve grazing of open landscapes during the summer months when flocks are most vulnerable to wolf depredation. We present our findings on traditional husbandry practices, depredation rate and the role of the livestock guarding dogs (LGDs) in Bozdağ (Konya) and Haymana (Ankara). Through interviews with shepherds and livestock holders, we also assess their perception of wolves.

Traditionally, indigenous LGD breeds are kept by shepherds to protect the flock against attack. We show that the quality, not the quantity, of the LGDs accompanying a flock is important for significantly decreasing sheep losses. The most preferred dog breed is Kangal because these dogs are famous for pursuing the wolf and even killing it when possible. However, this is not concordant with the principles of coexistence. On the other hand, the Akbash breed, which tends the flock by always staying with the sheep and not going after the wolf, seems to provide more reasonable protection against depredation. We suggest a rethinking of LGD breed preferences and selection in order to promote coexistence of humans and wolves.

A NEW NON-INVASIVE METHOD FOR DIET ANALYSIS OF VEGETARIAN ANIMALS

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The development of DNA barcoding (species identification using a standardized DNA sequence), and the availability of new DNA sequencing techniques offers new possibilities in diet analysis. Our approach is based on the fact that short DNA fragments, shorter than 150 bp, are usually very slowly degraded and can be recovered from faeces. As a consequence, by using universal primers to amplify a very short but informative DNA fragment, it is possible to reliably identify the plant species that have been eaten.
We developed such an approach by using the chloroplast trnL(UAA) intron P6 loop as a target for plant barcoding. We demonstrated that this new method is efficient by studying two species in the Deosai National Park in Pakistan, the Himalayan brown bear (*Ursus arctos isabellinus)* and the long-tailed marmot (*Marmota caudata*). Brown bears in this region are predominantly vegetarian with very low dietary meat. Long-tailed marmots were analyzed to compare the diet of two species living in the same habitat. The plant species that were identified from faeces showed that the diets of the two species were different. These differences were related to differences in the foraging behaviour. Most of the bears mainly eat a single plant species, with a maximum of four different species found in single scat while marmots have a more diverse diet. This new technique appears to be very robust and can be applied at large scales. It opens new perspectives for determining the diet of wild animals under field conditions.

MANAGING HUMAN-WILD MAMMAL CONFLICTS BY EXCLUSION: VISIBLE AND INVISIBLE BARRIERS

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Public antipathy towards lethal control of wildlife necessitates the development of novel approaches. Here we present studies on two non-lethal control methods, which have been used to exclude wild mammals with varying degrees of success.

In urban areas sett excavation by European badgers (*Meles meles*) can undermine property. Mitigation efforts usually employ one-way gates, under licence, to exclude badgers from the target sett.

We studied 11 licensed exclusion operations involving 28 badgers to assess their success and effects in order to develop new and improved methods for resolving human-urban badger conflicts. Only 21% of badgers were fully excluded from target setts. However, all badgers altered their movement patterns in response to action against the sett, sometimes resulting in new licence applications. Subsequent research indicated the inability of ultrasonic deterrents and water sprinklers to reduce badger presence at baited plots. Other novel methods, which may provide a higher rate of conflict resolution, have yet to be tested.

Physical barriers clearly have limitations. Invisible, non-physical barriers may overcome some of these. We reviewed literature on the use of electronic shock collars for wildlife management purposes. Shock collars deliver an auditory alarm when a collared animal approaches the invisible barrier and a static electric shock if the animal does not retreat. Broadly speaking, these collars can be used in two ways. Firstly, collars may be fitted to wild animals, which are excluded from an area by signals delivered to the collars via radio beacons. Using this approach Schultz et al. (2005) significantly reduced gray wolf (*Canis lupus*) predation on domestic sheep. With the second method, collars are attached to dogs, which are kept within an area enclosed by a buried wire from which a radio signal is transmitted to the collar. Dogs then exclude wildlife from the area. Using this approach Curtis & Rieckenberg (2005) significantly reduced white tailed deer (*Odocoileus virginianus*) browsing in apple orchards. These systems hold potential for a diversity of human-wildlife conflicts, but consideration must be given to animal welfare, good training methods, responses of different species and strategies for successful use. These issues and the effectiveness of invisible barriers will be discussed.

WORKSHOP

Mammal conservation in Europe: strategies and delivery

A FIVE-YEARS ANALYSIS OF PREDATION ON LIVESTOCK: CHARACTERISTICS OF PHENOMENON RELATED TO WOLF POPULATION STATUS IN THE MAJELLA NATIONAL PARK

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In the Majella National Park the assessments of livestock damages caused by predators are analysed following a standardized procedure, which includes information concerning environmental context, livestock management and also the report of the necropsies analysis carried out by the veterinary of the Park.

The utilization of this procedure had allowed collecting information about the most critical periods of the years, moments of the day, recurrent weather conditions and husbandry methods or management situations observed at the moment of wolf attacks.

Data have also been related with the actual knowledge on the wolf population status inside the study area.

LIMITED GENETIC VARIABILITY OF WESTERN POPULATIONS OF THE ENDANGERED CARNIVORE SPECIES EUROPEAN MINK (*MUSTELA LUTREOLA*). IMPLICATIONS FOR MANAGEMENT AND CONSERVATION

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Loss of genetic diversity in populations of threatened species is often associated with inbreeding, reduction of reproductive fitness, population fragmentation and a decrease of gene flow. The present study is focused on the endangered carnivore species European mink (*Mustela lutreola*), whose populations have suffered a drastic decline in the last century due to different factors as habitat loss, hunting, and competition with farm-released American minks. The extant populations of European mink comprise three genetically distinct demes, Western (restricted to south-western France and northern Spain), South-eastern (limited to Romania) and North-eastern Europe (distributed into different parts of Estonia, Belarus and Russia). In this study, the control region of mitochondrial DNA and eight newly isolated polymorphic microsatellites were analyzed in the Western population to determine its genetic structure , as well as to assess potential genetic bottlenecks and to elucidate its origin and colonization history. Phylogenetic reconstructions and population genetic analyses showed that the Western population constitutes a monophyletic group, with extremely low mtDNA control region sequence, and microsatellite allele variation. This genetic information will be decisive for improving conservation of this population in the wild and for monitoring breeding programs in captivity.

DO LANDSCAPE PROPERTIES MATTER FOR DENSITIES OF THE GREY-SIDED VOLE? A COMPARISON AMONG MANAGED AND PRISTINE FOREST LANDSCAPES

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In northern Sweden, there has been a pronounced long-term decline in the numbers of grey-sided voles (*Chlethrionomys rufocanus*) in managed lowland forests in 1971-2005. In three pristine mountain forest landscapes, recent monitoring (2001-2004) indicated density indices that were similar to and even higher than the pre-decline densities in the managed landscape. We here evaluated the importance of landscape properties in the two landscape types, i.e. managed versus pristine, for densities of the grey-sided vole. First, we tested the hypotheses that the pristine landscapes had a higher cover of preferred habitats and a lower cover of avoided habitats (clear-cuts) compared with the managed lowland forest landscape. As expected, the pristine landscapes had a significantly higher cover of preferred habitat and a lower cover of clear-cuts than the managed landscape. We also tested the hypothesis that fragmentation and proximity of preferred habitat were of major importance for the grey-sided vole in landscapes poor in preferred habitat (here managed landscape) but of minor importance in landscapes rich in preferred habitat (here pristine landscapes). Previous studies in the managed landscape showed correlations of the cumulated trapping indices 1980-1999 with landscape structure of preferred habitats (proximity and fragmentation). We compared these correlations with those between the cumulative trapping indices 2001-2004 and fragmentation and proximity of preferred habitats in the pristine landscapes. Most correlations were non-significant in the pristine landscapes compared with the managed landscape. The current results support our hypotheses. They also indicate the importance of landscape properties for the persistence of the grey-sided vole in managed landscapes that suffer from decreasing preferred habitat.

IS THE LONG-TERM DECLINE OF THE GREY-SIDED VOLE IN BOREAL SWEDEN CAUSED BY GRADUAL HABITAT DESTRUCTION AT THE LANDSCAPE LEVEL?

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There has been a long-term decline of cyclic grey-sided voles (*Clethrionomys rufocanus*) in boreal Sweden since the 1970's with local extinction on permanent sampling plots, almost without exception. A cluster classification of 29 of the long-term time-series previously revealed that two groups (C1 and C2) were high quality sites (HQS:s), and three groups (C3-C5) low quality sites (LQS:s), characterized by high and intermediate to low cumulated density indices and persistence's, respectively. Previous studies, based on cumulated vole time series data and static landscape structure, also supported the hypothesis that altered landscape structure, especially in terms of decrease of forest patch sizes and increased amount of clear-cuts, has contributed to the decline. In this study, we investigated whether the long-term decline has been related to a gradual change of the landscape. We used digitized land-cover types (>0.25 ha) from aerial photographs within 6.25 km2 squares centred on each of 29 sampling sites with 5 year intervals (1970-2005) to spot landscape changes, the cumulated area of clear-cuts in the surrounding landscapes of the sampling-plots. This disturbance measure was low and did not differ between HQS:s and LQS:s in 1970 and 1975. However, the main decline in vole numbers in 1980-1985 coincided with the LQS:s having a much higher cumulated area of clear-cuts in the surrounding landscape than the HQS:s. This is in line with our earlier studies and strongly indicates that long-term habitat fragmentation is involved in the current decline of the grey-sided vole. However, this does not exclude that other factors have been involved. The previously reported decreased wintering success in the grey-sided vole from the 1980's and onwards, also suggests some additional disturbance, perhaps from the warmer winter climate. Any such negative effects of climate change could then reinforce the negative effects from increased forestry, via habitat destruction, and vice versa.

PRESERVATION OF THE BIODIVERSITY OF MAMMALS IN KAZAKHSTAN

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Kazakhstan has 178 species of mammals. This diverse and rich zoological potential of the Republic is determined in many respects by its geographical location, amplitude of territories and different natural conditions. Preservation of mammal's diversity of greatly depends on the status of environment. Anthropogenic press with its present scale, overcoming the influence of natural factors, has more influence on nature and the animal world of Kazakhstan. Many areas with high density of different animals are ecologically destabilized. Strategic plan of the Republic development provides the series of measures aimed at protection, reproduction and rational usage of animal world resources. It has the provisions for data bank, taking of the stocks and cadastre of animal, development of international cooperation.

Today certain problems became very urgent. They are: Kazakhstan mammals' fauna stock-taking, the evaluation of the status of species, biology and ecology peculiarities study, the issue of regional Red Book, based upon these assessments. The species that have particular local distribution and low ecological plasticity are the most sensitive to anthropogenic influence. The following ways are considered to be important anthropogenic influence neutralization measures: creation of reserves and other closely guarded areas; revegetation of developed landscapes; closed rearing of rare and disappearing species of animals; and in some cases domestication of previously wild animals. The protection of a species not only within the Republic, but if possible, within whole area of natural habitat plays an important role in protection of mammals. It requires Kazakhstan to take part in international actions aimed at the protection of mammals. Certain measures have already been assumed. Other essential measures of biodiversity protection are: laying down and following the rules and standards for protection, usage, and reproduction of animals; prevention of animal loss during different industrial processes in all sectors of the national economy; limitation of requisitioning of animals for zoological collections; rendering assistance to animals in case of natural disaster threats. We suppose that the problem of acclimatization and reclimatization of animals worth special attention. Ecological education takes special significance for youth and growing up generation.

THE EFFECTS OF ROADS AND VEHICLES ON VERTEBRATES, ESPECIALLY ON MAMMALS IN NATURAL LANDSCAPES, HUNGARY

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The effects of roads have been turned out more and more obvious. In Europe, annually, more than 10 billion vertebrates are hit by vehicles. The roads imply especially serious danger for those animals, which live in small, isolated populations. Since these populations are more sensitive for disturbance, that can easily lead to their extinction. The Hungarian road network is quite dense comparing to other countries worldwide, therefore its impact on the adjacent flora and fauna is larger than the average. During our research we compared areas, where there is a conflict between the roads or their traffic and the wildlife, especially mammals to those, where rate of the conflict was tried to be reduced with the aid of technical structures. The goal of our research was to estimate the scale of usage of the existing corridors by the studied species and to reveal those sites, where the construction of new corridors is required. Our results show, that the individuals of the studies species used the different types of corridors in most cases. However, the factors affecting the use of wildlife passages are different for the different vertebrates.

A COMMUNITY-BASED CONSERVATION PROJECT TO PROTECT A STRONGHOLD FOR WATER VOLES AGAINST THE SPREAD OF AMERICAN MINK

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As the impact of invasive species on native fauna becomes apparent, there is a growing realisation of the need for active management to minimise their impact. As even limited immigration of invasives precludes their eradication from non-insular areas, control must be sustained in perpetuity. Close involvement of local communities is one way to achieve sustainability.

The American mink is established as an alien species in much of Europe and responsible for a conservation crisis with numerous native species badly affected. British water voles have experienced an accelerating decline of no less than 96 % since 1950, largely attributable to mink predation. While water voles have disappeared from the majority of lowland waterways, widespread but small water vole colonies still persist in upland moorland. A new cooperative community-based project has been established in the Cairngorms National Park (CNP) in Scotland to conserve water vole populations. The CNP area (3800 km^2) still holds substantial water vole populations and its mountainous geography, low prey biomass and high gamekeeper density make the area a defensible stronghold for this priority conservation species. One aim of the project is to secure existing, nationally significant water vole populations rather than restore populations already decimated, by controlling mink in the surrounding area, which should then facilitate the expansion of these populations into previously occupied areas. The aims are being achieved through coordinating and stepping-up mink control by the local community, including gamekeepers, water-bailiffs, estate rangers, fishing ghillies and volunteers to deliver maximum conservation benefit.

Convergent interests between conservationists and a local community have the potential to ensure long term sustainable mink control with limited input of additional resources. Education is a crucial element of the programme, both for the general public and the active participants. Management of the project will be adaptive, so that data collected in the early stages can be used to optimise the project’s conservation benefit, sustainability and cost effectiveness. The project is a showcase, which will be the first water vole conservation project to be undertaken in a very large, defensible geographic area. It will also serve as an example of how to fund and manage such action as a community project, which can be maintained in the long term.

AN ECOLOGICAL NETWORK FOR THE CONSERVATION OF THE OTTER *LUTRA LUTRA* IN ITALY

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The otter *Lutra lutra* is one of the most endangered mammals in Italy. A viable population is found in the southern regions of Campania, Basilicata and Puglia, while fragmented nuclei occur in Molise and Abruzzo. Among priorities for conservation of the species is the assessment of distribution, consistency and connectivity of suitable habitats, in order to evaluate potentialities for its future expansion and recolonization of vacant areas. Following this need the Italian Ministry of Environment funded a research project to set up a fine scale ecological network for the otter in Italy, as a complementary tool for the national action plan now in progress. The network is derived from an habitat suitability map produced for a 300 m buffer around all rivers were the otter is actually present and for neighbouring rivers, based on a fine scale GIS-based habitat suitability index. The index is derived from twenty environmental variables related to the availability of water, food resources and riparian vegetation cover. Different algorithms are used to spatialize point and linear data according to biological, hydrogeological and landscape considerations. Different suitability indices based on an inductive approach are tested to evaluate their predictive power, and compared to deductive indices produced at different scales. The habitat suitability map is validated using presence and absence data. The resulting ecological network is evaluated for connectivity and permeability to otters using a landscape approach.

USING REINTRODUCTIONS TO RECLAIM THE LOST RANGE OF THE DORMOUSE *MUSCARDINUS AVELLANARIUS* IN ENGLAND

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The common dormouse *Muscardinus avellanarius* lost almost half its range in England during the 20th century. Important factors in this loss were inappropriate woodland management and habitat fragmentation. Since 1993, a reintroduction programme has attempted to restore populations to some of these areas and by 2006 fifteen reintroductions had been carried out.

Reintroductions to single woods can be seen as the start of a process to produce wider populations in suitable areas, but needs to be supplemented by habitat improvements to restore lost connections between woods and manage existing woods in a suitable way. We provide an update of the success of the reintroductions project and the way in which habitat improvements are being targeted to assist with the natural spread of introduced populations.

CONSERVATION OF SHREWS IN FRAGMENTED LANDSCAPES: THE ROLE OF FOREST MANAGEMENT AND SMALL WOODLAND PATCHES

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A considerable amount of literature exists on the effects of habitat loss, fragmentation and forest management, on biodiversity; however few studies have investigated the distribution of shrews (Insectivora, Soricidae) in fragmented landscapes (none with European species), despite their important role in ecosystem functioning as predators and preys. Moreover basic species-habitat relationships in coppiced Mediterranean woodlands are still unknown.

The aim of our research is to determine the effects of habitat fragmentation and woodland management on the distribution of 5 species of shrews (*Sorex samniticus*, *Sorex minutus*, *Crocidura leucodon*, *Crocidura suaveolens*, *Suncus etruscus*) and on their community structure.

We studied the distribution of shrews in 35 woodland patches plus 2 control areas, in the Province of Siena, central Italy. Patches varied in size range 0,3- 80 ha) isolation, shape and vegetational structure; shrews were trapped with 250 permanent pitfall traps activated for 1 year.

The reliability of the observed distribution was evaluated with occupancy models using the software PRESENCE, in order to detect false absences. Data were tested for spatial autocorrelation; according to the degree of autocorrelation, multivariate logistic or autologistic models were fitted to presence/absence data. Patch geometry and landscape configuration characteristics, as well as patch internal structure variables were used as predictors. Models were ranked according to Akaike Information Criteria; we followed a multimodel inference approach to account for model-selection uncertainty.

Insectivores were widely distributed in the sampled patches, showing a strong capacity of colonisation/persistence even in extremely small and isolated woodlots. The community structure was strongly affected by forest management regimes: *Sorex samniticus* and *Crocidura suaveolens* were associated with recently logged forests, while distribution of *Crocidura leucodon* and *Sorex minutus* was associated with more mature forests. Landscape fragmentation plays a secondary but still important role in shaping the species' distribution, removing less abundant species in the community.

We interpret these results providing key-guidelines for the conservation of shrews in fragmented landscapes: in particular we will focus on forest management and on it's effects, and on the conservation value of small forest patches in an agricultural matrix.

CONSERVATION BIOLOGICAL ASPECTS OF CYTOGENETICS OF HUNGARIAN MOLE-RATS (*SPALAX LEUCODON*)

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Hungary is the northwestern limit of the blind mole-rat (*Spalax leucodon*) distribution area. The populations of this typical steppe species are decreasing and now probably less than 800 animals live in Hungary. Based on Israeli scientific researches it has been proven that active speciation process is under way on the populations of mole-rats. They are characterised by different chromosomal numbers and could not breed with each other. We have hardly any information about Hungarian mole-rats and until very recently we knew nothing about the chromosomal types we have. Since the species is strictly protected in Hungary we have to solve the problem of catching animals alive, work out a non-invasive sampling method and find the proper laboratory process. After two years of extensive field work and laboratory experiments we are able to catch live specimens and found the way how to determine karyotype from 0.5 ml of blood. According to the first results two populations are characterised by 2n=50 chromosome number, and another by 2n=52, which are differ from other populations studied near our borders. The evolutionary background and taxonomic significance of this chromosome polymorphism still need to be investigated but in the light of this finding it is clear that the different and isolated populations of mole-rats should be treated as separate units in the management plans.

CHANGES IN POLISH PUBLIC ATTITUDES TOWARD CARNIVORES

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In the Polish Carpathians wolves, Eurasian lynx and brown bears have always coexisted with each other and with humans. In the 1990s carnivore conservation policy in Poland radically changed and both species were declared "strictly protected". This change in management direction occurred without any consultation with key interest groups.

In 1998/1999 we completed a study on attitudes toward wolves and Eurasian lynx among four social groups (hunters, foresters, farmers and teenagers) in four regions of Poland (NE and SE - both carnivores constantly present; central PL - wolves absent, lynx reintroduced in the early 1990s; W PL - migratory wolves appear, no evidence of lynx). We used a self-administered questionnaire to assess the attitudes, knowledge and opinions on management. Sample sizes were: 580 hunters, 363 foresters, 356 farmers and 1211 teenagers.

In 2006/2007, the study was repeated using the same research instrument in the same study scheme. By comparing these two time periods we wanted to examine whether attitudes toward carnivores changed, if the current management policy was accepted and if the legal protection of the wolf and lynx influenced attitudes toward carnivores.

To define the attitudinal spectrum and check knowledge and opinions about management, mean attitude, knowledge and management scores were calculated for each interest group, by each study zone. To identify the types of attitudes measured by individual items, factor analysis was used. To compare interest groups' attitudes within and between study zones analysis of variance was used. Tukey's honestly significant difference was used to test for pair-wise comparisons. Reliability estimates for our scores were acceptable, except for knowledge suggesting the multidimensional nature of knowledge. To evaluate which factors influenced attitudes and opinions about management, we performed regression analyses. To compare attitude, knowledge and opinions about management between two species we used pair-wise t-tests for each interest group in each region.

In both time-periods, the wolf attitudinal spectrum was more clearly defined while attitudes toward lynx were more positive and not so extreme. Foresters held the most positive attitudes, while farmers and teenagers were least positive. The strongest predictor of attitude for each respondent group was fear. Knowledge scores were low amongst all interest groups, however knowledge was important in predicting attitude.

WHEN REINTRODUCTIONS TURN TO HAVE BAD CONSEQUENCES: THE CARPATHIAN AND THE BALKAN LYNX IN THE BALKAN PENINSULA

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European biodiversity bears strong footprints inflicted by the Quaternary glacial-interglacial climatic cycles which caused a pronounced peripheral diversification in the southern refugia. One among such neoendemics is also the Balkan lynx (*Lynx lynx martinoi*), a subspecies which survived human persecutions only in southern Serbia (Kosovo), eastern-most Montenegro, western Macedonia, northern Albania and northwestern Greece. This endemic subspecies is highly endangered, largely due to its excessively small numbers. Following extirpation of the autochthonous lynx from the northern parts of the Balkans Peninsula already in the 19th century, Carpathian lynx has been introduced to Slovenia in 1973. Their descendants spread rapidly across Croatia and Bosnia and Herzegovina into Montenegro and possibly already reached the range of the Balkan subspecies. We provide evidence from the probably zone of contact between the two taxa and discuss possible measures to preserve the identity of the Balkan endemic.

ALPINE IBEX OR THE DUTY OF RE-INTRODUCTION. RECOVERY HISTORY, STATUS, AND FUTURE MANAGEMENT IN THE ITALIAN ALPS

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At the beginning of XIX century, ibex became extinct all over the Alps with the exception of a small group surviving in the Gran Paradiso Massif. After the first protection attempts in Italy, dating back to 1821, in 1836 King Carlo Alberto issued the "Regie Patenti" and established the Gran Paradiso Royal Hunting Preserve, supplied with 150 gamekeepers: this is the beginning of history of ibex conservation.

In Italy the first ibex re-introduction program, performed with animals coming from Gran Paradiso, occurred in 1921 in the former Royal Hunting Preserve of Valdieri (Cuneo), now Alpi Marittime Natural Park. After decades of stagnation, a new thrust for ibex conservation took place from the 60's and the 70's with the creation of some new colonies in Valle d'Aosta and Stelvio National Park. The culmination of re-introduction programs was nevertheless reached in the last 30 years in which a great number of releases was planned, helped and stimulated by natural colonization from bordering areas of Swiss and Austria. According to updated information contained in the Ungulate database of the Wildlife National Institute (INFS), that will be presented, Alpine ibex is currently widespread in the whole Italian Alps, from Marittime Alps (Piedmont) to Giulie Alps (Friuli – Venezia Giulia). Total abundance is estimated in about 14.000 ibex split into about 60 different colonies. Distribution can be still considered extremely patched, with the exception of few populations characterized by large numbers (36% of Italian ibex live in Gran Paradiso, Stelvio and Alpi Marittime Parks). Despite connections and exchange of individuals between populations are more frequent, the gap between present and potential distribution is still substantial, especially for Central and Eastern Alps. In Italy Alpine ibex is protected by law and not subjected to hunting (L. 157/92), however it is subjected to culling plans only in the Autonomous Province of Bolzano.

In the present work a reconstruction of the evolution of ibex distribution and abundance, from the beginning of the last century up to present days, is presented. Information about re-introduction and re-stocking programs performed are showed. A synthetic analysis outlines how the number of founders and the occurrence of suitable feasibility studies and programming affect the success of re-introduction projects and a more rapid growth of the new colonies. At last, possible solutions for improving future conservation and management of ibex in the Italian Alps will be discussed.

SOME BIOLOGICAL AND POLITICAL ASPECTS FOR BROWN BEAR CONSERVATION IN PYRENEES MOUNTAINS, FRANCE

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Brown bear (*Ursus Arctos*) population in Pyrenees mountains is considered as one of the most endangered population in West Europe. During the 20th century, the intensive persecution by human led this species near extinction. The first step of the conservation strategy for the brown bear in France has been the suppression of hunting (1958), the compensation for livestock damages and a legal status of protected species in 1973. From 1983 to 2006, the management and the conservation policy of the French authorities relied on at least 5 plans based on different objectives and using different strategies. Simultaneously, during this period, scientific monitoring and applied research was carried out by a state establishment (Office Nationale de la Chasse et de la Faune Sauvage) to get accurate knowledge of this population. The main components of ecology and behaviour of this population were investigated (distribution, population size, reproduction, diet, habitat and home range, livestock depredation) using both classical methods (survey of presence signs, radiotelemetry) and more recent technologies (remote camera, GPS/GSM collar, genetical analyses of hair and scats samples). Data gathered on the field are also used to build models useful for management of the population and its habitat (viability population model, habitat suitability model). The main lesson from brown bear management in France is that it is a complex process with many stakeholders where biology of conservation is only a small part of the process. Ten years after the first reintroductions, the second phase of re-introductions, which occurred in 2006, confirmed the biological success of this action plan, but also shows that the conflicts with the majority of farmers (mainly sheep breeders) are not yet resolved.

ROBUST DATA ON BAT POPULATION TRENDS AND DISTRIBUTIONS IN IRELAND FROM A CAR-BASED BAT MONITORING SCHEME

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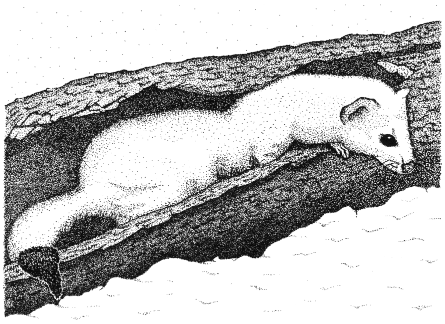
The first systematic car-based bat monitoring system in Europe was devised for the Republic of Ireland (ROI) in 2003 by the Bat Conservation Trust (UK), funded by the Heritage Council, ROI. The scheme is ongoing and has been administered by Bat Conservation Ireland (BCIreland) since 2004. The scheme is now undertaken throughout the island of Ireland and is funded by the National Parks and Wildlife Service (NPWS - ROI), The Heritage Council and the Environment and Heritage Service (EHS), Northern Ireland. The scheme aims to monitor roadside populations of common pipistrelle, soprano pipistrelles and Leisler's bat and to collect sufficient data to act as an early warning system for Amber or Red Alert declines in these bat populations. Known survey routes are driven with a time expansion bat detector clamped to an open window. Sounds are recorded to minidisk and recordings are analysed using Bat Sound software. Coverage across the country has been increasing yearly and by 2006, routes had been mapped in 26 of the 94, 30km squares across the island (i.e. 28% of the surveyable land mass). Surveys are carried out in July and August. As the first systematic, island-wide monitoring scheme for any Irish bat species much new information on relative abundance and distributions has come to light. The common pipistrelle is the most frequently encountered species. From 2003 to 2005 the soprano pipistrelle was the second most frequently encountered species, with Leisler's bat the third. In 2006, Leisler's bat was recorded more often than soprano pipistrelle. No discernible patterns for common or soprano pipistrelle populations are evident yet; both show large year to year variation. The Leisler's bat may, however, be increasing. The Nathusius pipistrelle dramatically increased in abundance and distribution in 2006. Abundance of the common pipistrelle is greatest in the south east of the country. The soprano pipistrelle is most frequent in the west and the Leisler's bat in the east. Power analysis indicates 90% Power can be achieved for detecting Red and Amber Alert declines of the three target bat species within 20 years, if up to 24 squares are surveyed twice annually. From initial examination of air temperature data and bat activity some of the potential impacts of climate change on the Irish bat fauna will be discussed. Given its cost effectiveness, and the robustness of the data collected, this methodology has potential for use in many other countries.

WORKSHOP

Role of long-term studies and experimentation in mammalian life histories



THE IMPORTANCE OF A LONG-TERM EPIDEMIOLOGICAL STUDY OF *M. BOVIS* INFECTION IN A BADGER POPULATION TO UNDERSTANDING THE FUNDAMENTAL BIOLOGY OF THE EURASIAN BADGER *MELES MELES*

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Studies on mammalian life histories are generally restricted to the duration of the research funding, which may be much shorter than the individual life expectancy of many larger mammals. Some form of manipulation or experimentation is often employed to obtain meaningful results in a relatively short study period, but this approach is usually only feasible with smaller taxa that have shorter generation times. Consequently, comprehensive life history data for larger mammals is often lacking. The Eurasian badger *Meles meles* has been implicated in the transmission of *Mycobacterium bovis* (the causative agent of bovine tuberculosis) infection to cattle in the UK and the Republic of Ireland since the early 1970s. Since 1976 a population of wild badgers at Woodchester Park in Gloucestershire, England have been the subject of research on the dynamics of *M. bovis* infection. The Woodchester database represents over 12,000 badger captures from 2,300 individuals and is unique in providing a 30-year dataset on badger life histories, genetics, and disease status. Longitudinal analyses already conducted on this database have contributed enormously to our current understanding of badger ecology and epidemiology. Important epidemiological findings include the observations that there is no simple linear relationship between badger density and the incidence of disease, TB does not spread rapidly through the population and is not a major cause of mortality for badgers, the distribution of infection in badger groups is spatially and temporally aggregated and the incidence of disease is strongly correlated with badger movements. From the beginning of the project in the late 1970s to the early 1990s the badger population at Woodchester grew steadily, but since then numbers have fluctuated or even declined. An analysis of the factors that influence population growth and decline has never been carried out on this dataset. We are currently exploring the relative importance of the key processes that contribute to population size, growth and decline using techniques such as structured demographic accounting, and we will present results of these analyses at this workshop.

WHY DO MANY EUSOCIAL ORGANISMS ENJOY A BENEFIT OF REPRODUCTION INSTEAD OF A COST?

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Most theories on the evolution of life histories and ageing assume that sexual reproduction is inevitably costly. Eusocial insects (e.g. ants or bees) challenge this view because the reproductive queens usually live much longer than the non-reproductive workers. In mammals, eusociality has been described hitherto only in the African mole-rat genera *Fukomys* and *Heterocephalus* (*Bathyergida*e, *Rodentia*). We have recently shown that at least in *Fukomys*, sexual activity and reproduction increase life-expectancy significantly, too. Here we discuss why the classical trade-off between reproductive investment and longevity is so often reversed in eusocial organisms irrespective of their phylogenetic background, and the implications of this phenomenon.

LIFETIME BREEDING SUCCESS IN SOUTHERN ELEPHANT SEALS (*MIROUNGA LEONINA*)

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Reproduction is a key feature in the evolution of life-history strategies and quantifying variation in lifetime breeding success (LBS) of individuals is essential for determining the potential for sexual selection in a population. Here, we present preliminary results of a long-term study on southern elephant seals (*Mirounga leonina*) from Falkland Islands. Elephant seals are among the most sexually dimorphic species of all mammals and their mating system is probably the most extreme example of polygyny observed in mammals and vertebrate at large. Females haul out and gather in large groups to give birth, while males establish dominance hierarchies that regulate the access to the females. As a result, male breeding success is exceptionally skewed. Variance in LBS is much higher in males than in females and most life history traits are different between the two sexes. When breeding effort is large, reproductive theories predict a negative effect between reproductive success and survival to the following breeding seasons (i.e., future reproductive success). Although demonstrated for many species, this negative correlation is not always verified, and in some species reproductive success does not decline with age and there are no clear signs of reproductive senescence. In elephant seals, the reproductive history of a successful male seems to follow an increasing trend, as his success increases with his age and experience, and he is able to hold larger harems with the passing seasons. In a previous study of the authors, behavioural and demographic indices were found to accurately predict individual paternities, as genetic estimates confirmed the extreme level of polygyny in the population. In this long-term study, behavioural and demographic estimates indicated that males southern elephant seals from the Falklands can have a high seasonal success for many consecutive years; as a result, some individuals gained an exceptional lifetime success while other only bred with few or no females. Given this evidence, we also tested the hypothesis that the variance in male LBS is larger than the variance in seasonal success, as a result of the exceptional qualities (i.e., resource holding potential, feeding and mating strategies, etc.) shown by the most successful males. Finally, male LBS in *M. leonina* proved to be much higher than that reported for either the northern elephant seals or for other polygynous or lekking species, often believed to be the most 'extreme' mating systems in term of reproductive success variance and potential action of sexual selection.

ROLE OF HUNTING AS A LONG-TERM EXPERIMENTATION IN HARVESTED MAMMALIAN LIFE HISTORIES

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The detailed analysis of long-term account data for population size of the main hunting mammal species is carried out. The population size dynamics of the following hunting animal species is analyzed: predators - the brown bear (*Ursus arctos*), wolf (*Canis lupus*), fox (*Vulpes vulpes*), sable (*Martes zibellina*), Siberian weasel (*Mustela sibirica*), otter (*Lutra lutra*); herbivores - the elk (*Alces alces*), Manchurian deer (*Cervus elaphus xanthopigus*), roe (*Capreolus capreolus*); the wild boar (*Sus scrofa*); the squirrel (*Sciurus vulgaris mantchuricus*), and hares *(Lepus timidus*, *L. mantschuricus*).

The approach based on mathematical modeling is used for the description of the population size dynamics tendencies. General mathematical model of the population number dynamics for harvested species is developed. It reflects periodicity of reproduction process (model with discrete time) and is focused on the description and research of the trade influence results. Model parameters are estimated on the basis of the harvest statistics of the hunting facilities in the Middle Priamurye. Modeling retrospective forecasts have allowed to show the adequacy of the model for the majority of harvested species.

Analytical and numerical researches of this model have led to the following conclusions:

Without hunting the character of population dynamics is determined by reproductive potential and food stocks. In case the reproductive potential is not big, the population dynamics actually reflect (with some delay) fluctuations of food stocks. This kind of dynamics is observed with the wild boar, wapiti and some other species. If the reproductive potential is great then the fluctuations of population number become sharper and are basically determined by density-dependent factors. Fluctuations of the forage stocks are also very important. Both the squirrel and weasel are the typical examples.

Harvesting reduces the fluctuations intensity connected with a higher density, but it preserves the fluctuations connected with a change in food stocks. Moreover, as harvesting intensity depends on the population size, hunting can strengthen the compelled fluctuations, as well as result in population size abrupt fall, as far as its full degeneration (some herbivores populations). The obtained results give a qualitatively new picture of mechanisms and a character of some harvesting species dynamics; they make it possible to estimate influence of hunting from new positions.

CHOOSY FEMALES BOOST MALE DISPERSAL IN A SOCIAL MAMMAL

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We investigated whether in a social mammal patterns of male dispersal and reproductive activity in the natal group were best explained by avoidance of male mating competition, resource competition, inbreeding or by female mate choice. For this purpose, we analysed long-term demographic data from eight social groups ('clans') of spotted hyenas (*Crocuta crocuta*), and determined female mate preferences and fitness benefits of decisions made by males using microsatellite profiling of 426 offspring. Females avoided males that were members of their group when they were born and preferably chose sires that immigrated or were born into their group after their birth. Furthermore, young females preferred short-tenured sires and older females preferred longer-tenured sires. Given these female mate preferences, males would be expected to initiate their reproductive career in the group containing the highest number of young females. Males conformed to this expectation and, as a consequence, 11% of males started their reproductive career in their natal group and 89% of males dispersed. Males that initiated their reproductive career in the group containing the highest number of young females had a higher long-term reproductive success than males that did not. Contrary to predictions from the male competition hypothesis, the number of reproductively active males or the ratio of such males to adult females did not influence clan selection. The level of resource competition also did not influence clan selection, and there was no evidence that males dispersed to avoid breeding with close relatives. Our results show that simple female mate choice rules may lead to a high level of male dispersal and represent a sufficient cause for the evolution of sex-biased dispersal in social mammals.

DENSITY DEPENDENCE IN LIFE HISTORY EVOLUTION OF BANK VOLES

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Density of conspecifics affects the reproductive success and survival of individuals, thus modifying the life history evolution of the species. Large seasonal and annual density fluctuations that characterize the life histories of Microtine rodents have received a vast amount of research, however, data that examine the effects at the individual level are surprisingly scarce. Here we use both long-term (1995-2006) correlational live-trapping field data and enclosure experiments to study density dependence in morphological and reproductive traits of the bank vole *Myodes glareolus*. Moreover, potential genetic shifts that may occur with density changes were examined by screening individuals with 30 polymorphic microsatellite markers between two peak and two increase phases of the population cycle. The bank vole population showed a three-year cycle with three-fold and more than ten-fold changes in density within years and between different cycle phases, respectively. The size of individuals was phase dependent with individuals at their largest at the peak phase, whereas offspring number and size seemed to differ only between seasons. In enclosure experiments, reproductive success of females was clearly density dependent but females did not seem to adjust the characteristics of their litters with density. The data on genetic diversity in different cycle phases is currently under analysis. Our results confirm the important role of density both as a proximate factor affecting reproductive success of individuals as well as a selective agent in the evolution of life history traits.

MOBILITY AS AN ELEMENT OF BREEDING STRATEGY OF INDIVIDUALS IN SMALL RODENT POPULATIONS

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According to the common view, breeding colonies of many small rodent species include separate territories of a few adult females and home ranges of a few males monopolising females within their own breeding colony. Such a system would provide males with constant and reliable access to a small number of sexual partners ("stay and watch" strategy), and females with a high chance of being fertilised ("wait for a familiar one" strategy). However, the most recent studies suggest that breeding systems in small rodent populations are of much more dynamic character. Males may achieve maximum breeding successes also through wandering and mating with a large number or females representing various breeding colonies ("run and search" strategy), and females could achieve maximum breeding success through accepting stranger males "accept a stranger" strategy). Field studies show that individuals apply various breeding strategies during the breeding season depending on population density. Basing on the results of studies on the bank vole, the breeding strategies described above are discussed and their significance in optimisation of breeding success of both sexes and the role of those strategies in maintaining population genetic diversity. A model is presented in which all the parameters describing the population subjected to modelling, such as pregnancy length, individual maturation time, home range size, etc. are actual parameters characterising natural populations. In the model effectiveness of both male breeding strategies was assessed at various population densities, taking into consideration diversified mortality and breeding success. The obtained modelling results show that at low densities the offspring number in males applying the "run and search" strategy is higher than that in males applying the "stay and watch" strategy whereas at high densities the opposite is true. Assuming that males optimise their breeding strategy in real populations, seasonal changes in frequency of males applying different strategies should be expected and such changes were actually recorded. Thus, "stay and watch" or "run and search" strategies correspond to the evolutionarily stable strategy (ESS) and are discussed in this light.

LIFE-HISTORY STRATEGIES, SEX-RATIO ADJUSTMENT AND ENERGY ALLOCATION IN ROE DEER: AN EXPERIMENTAL APPROACH

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The study of life-history strategies in mammals is a challenging task, especially in long-living species giving birth only once a year. European roe deer (*Capreolus capreolus*) are the smallest ungulates in Europe and they present an excellent model to study evolutionary adaptations to seasonality, in particular the timing of reproduction, energy allocation, maternal investment and nutrition. Roe deer are income-breeders and a constant energy supply is required to fuel reproduction demands. They rut in July/August and following a five-month diapause, fawns are born in May or June. Roe deer can successfully rear up to three fawns per litter, which is exceptional for ungulates.

Litter size, birth mass as well as sex ratio are supposed to depend on the females condition, which in addition is affected by energy supply. Offspring sex ratio adjustment of roe deer is discussed controversially. Whereas some results of previous studies are in accordance with the Trivers and Willard model, others support the local resource competition hypothesis. However, up to now, most results derive from culled or captured animals lacking information about previous energy constraints. Here we present data from a long-term feeding-experiment which we conducted under semi-natural conditions with captive roe deer, and where we experimentally manipulated energy supply. The aim of our study is to investigate energy allocation to traits like reproduction (litter size, birth weight, sex ratio), maintenance or immune function in energy restricted as well as in *ad libitum* fed roe deer.

The long-term experiment started in 2003 and lasted four reproductive cycles (2003-2007). One group (AL) of roe deer was fed *ad libitum*, whereas a second group was fed energy restricted (ER, ~ 75% of AL's intake) from shortly after the rutting season (October) to parturition (May of the following year). To control for the individual effects, the groups were switched after two years.

Our preliminary results show a significant effect of severe energy restriction on sex ratio ($p<0.01$, Binominal Test). Energy restricted does delivered male biased litters (84 % of offspring were males) in contrast to *ad libitum* fed does. Since males disperse and females are the philopatric sex, our finding supports the local resource competition hypothesis. Furthermore, severe energy restriction decreased birth masses ($p<0.01$, ANOVA) of litters from ER does, irrespective of the fawns` sex. However, litter size was not effected by diet. Our experimental set-up provide a powerful tool to investigate mechanisms and consequences of energy allocation as well as reproduction adjustment to energy supply in captive roe deer.

POPULATION DEMOGRAPHY OF INDIVIDUALS: LINKING EVOLUTIONARY AND ECOLOGICAL PROCESSES IN WILD POPULATIONS

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Individual variation in life-history traits is linked to population dynamics and evolutionary change by the fundamental processes of birth and death. For example, in several mammalian groups, larger individuals usually survive better and are more likely to reproduce than smaller ones. Observational studies of marked animals are therefore invaluable tools to link individual-level demography to population-level dynamics and to estimate selection and responses to selection on life-history traits. I will present results from two detailed longitudinal studies, on Red deer and on Soay sheep from the Scottish islands of Rum and Hirta, to illustrate how long-term monitoring of marked individuals can provide insights from both ecological and evolutionary processes in the field. Specifically, I will described how the decomposition of population growth rate into contributions from different demographic rates can be used to quantify the relative importance of different ecological processes (such as climate and density) for population dynamic and how variability in individual contribution to population growth can elucidate the interplay between ecological and evolutionary processes.

LIVING IN AN UNPREDICTABLE WORLD: LONG-TERM STUDIES OF TREE SQUIRRELS TO EXPLORE PRODUCER-CONSUMER DYNAMICS

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Herbivorous or granivorous mammals are primary consumers in producer-consumer systems. Their reproductive output is constrained by the added energy requirements necessary for offspring production. As a consequence, reproductive rates, and related demographic processes, are often correlated with resources available prior to and during parental care. However, in systems characterised by intermittent resource pulses, consumers take advantage of these pulses only after they become available, creating a lagged population response that leads to consumer numbers increasing and crashing after the resource pulse has come and gone. A typical example is tree masting, the 'unpredictable' production of large seed crops in one year followed by several years of poor or medium seed production, which is widely cited as an evolutionary mechanism of predator satiation. In ecosystems where food supplies are less variable over time (and space), relationships between food production and consumer dynamics may be confounded by density-dependent processes that can results in population regulation in so-called stable habitats. The species' space use and social organisation offer the behavioural mechanisms that determine the observed patterns of density dependence. Here we illustrate how longterm studies of different Eurasian red squirrels (and other tree squirrels) occurring in a variety of habitat types that differ in spatio-temporal variation in food production, have revealed complex, and unexpected relationships between fluctuating food resources, social organisation and population demography.

DETERMINANTS OF OVERWINTERING SUCCESS IN BOREAL VOLES AND IMPLICATIONS FOR POPULATION DYNAMICS

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In the Holarctic region, strong seasonality divides the year into a short intensive breeding season and a long non-breeding season. Boreal rodents are iteroparous, but a major proportion of females breed in one summer only. Thus the large pool of next season breeders has to survive winter and breed successfully the following spring. Winter survival and determinants of the variability in the onset of reproduction are major factors shaping life histories in boreal rodents. During the long, harsh, non-breeding season and unpredictability of quantity and quality of food, social factors and predation pressure are major constraints determining the onset of reproduction.

Over the last 20 years we have been studying overwintering success and onset of reproduction in boreal rodents, especially in the bank vole, *Clethrionomys glareolus*. During winter, bank voles nest communally. Studies on food supplementation demonstrate the importance of food in determining the onset of breeding. However, strong predation pressure, especially by the least weasel, might counter the food effect and delay the onset of reproduction. Although the bank vole is mainly granivorous, the timing of spring reproduction may depend on availability of animal protein under the snow in the form of insects, pupae and possibly carcasses of mammals and birds.

In terms of population ecology onset of reproduction may affect the number of cohorts produced during the breeding season. Besides food and predation constraints, the onset of reproduction may be strongly density-dependent. Under favourable conditions and release of predation, early onset of breeding helps to create high summer densities, which are commonly followed by high winter densities, but poor overwintering success.

WORKSHOP

Patterns and processes in fluctuations of small mammal populations

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 60th 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.

LONG-TERM PATTERNS IN ARVICOLINE DYNAMICS AT PALLASJÄRVI AND KILPISJÄRVI, NORTHERN FINNISH LAPLAND

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Dynamics of voles and lemmings in northern Finnish Lapland have been monitored at Kilpisjärvi since late 1940's and at Pallasjärvi since 1970. Basic work consists both of spring and autumn monitoring on permanent study sites and various experimental field approaches on the role of interspecific competition in shaping community patterns and of supplemental food in modifying seasonal and long-term dynamics. A drastic change in population dynamics took place in the mid and late 1980's. Earlier "beautiful" cycles have turned to primarily seasonal dynamics. In the cyclic times, vole dynamics were characterized by synchronous cycles, particularly the deepest crash phase was synchronous in all sympatric species, though in the increase and peak phases some moderate inverse density changes were observed among competing species. In the long-term time series, linear delayed density dependence (dd) was a dominating factor, suggesting trophic interactions as a cause of cycles. Synchronous crashes in all sympatric species, with different food repertoires, speak for predation by weasels. Still, non-linear direct dd was also observed. The change in the dynamics was first observed at Pallasjärvi, where the deviating patterns were reported from 1982-84 (Henttonen et al. 1987). Since 1985-86 the earlier cyclic patterns has turned to seasonal. This has also included drastic changes in the species composition of rodent communities. The dynamic change took place a bit later, around 1990, at more northern and altitudinally higher Kilpisjärvi. The species with larger body size have become more uncommon. Also some demographic features have changed. The two main hypothesis put forward to explain the change are based on the role of intensive forestry (decline in arboreal lichens as winter food for *Myodes glareolus*, and consequences for *Microtus agrestis* through shared predation), and climate change affecting the snow structure and subnivean space. The decline in clumsy species with large body size refers to predation effects. This decline has taken place both in *Myodes rufocanu,s* and *Microtus agrestis* and *M. oeconomus.* It has taken place in all habitats, also far (more than 100 km) from any forest management, possibly suggesting for the role of mobile predators and /or climate change.

TRANSITIONS BETWEEN SEASONAL AND CYCLICAL DYNAMICS OF VOLES AND LEMMINGS CLOSE IN SPACE AND TIME

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Snap-trapping near Umeå, Västerbotten, in boreal Sweden since 1971 has revealed an unexpected long-term decline of sympatric vole populations, especially of the grey-sided vole (*Clethrionomys rufocanus*), as has also been observed elsewhere at northern European latitudes. The good-old-days- (GOD-) cycles of the 1970's were replaced by disturbed (DIS-) cycles in the 1980's with a strong seasonal element. The main feature of the decline has been an increased frequency and severity of winter declines, i.e. between fall and spring trappings. This shift has been most pronounced in the field vole, *Microtus agrestis*, but has also been observed in *C. rufocanus*. These over winter declines have led to a general levelling of spring densities and have given the characteristic "saw-tooth"-pattern to graphs over the vole's dynamics. In the GOD-cycles of the 1970's this was only seen in the bank vole, *Clethrionomys glareolus*. The start of parallel monitoring in the mountains in Ammarnäs, southern Lapland, in the mid 1990's revealed a similar, very strong seasonal dynamics in the same species for a few years, and as it seemed also in the Norwegian lemming, *Lemmus lemmus*, and wood lemming, *Myopus schisticolor*. However, in the early 2000's there has been two GOD-cycles in at least *M. agrestis* and *C. rufocanus*, and perhaps also in the two lemmings. In contrast, near Umeå only the latest cycle was GOD-like in *M. agrestis*, and it was still only of moderate density, and the dynamics of *C. rufocanus* remained seasonal and at a very low density. As it is mainly the winter dynamics and spring densities that have been affected negatively, the main hypothesis is that the warmer winter climate in later years has been causative. However, in the case of *C. rufocanus* in boreal Sweden, habitat destruction is hypothesized to be another important contributing factor.

DENSITY DEPENDENCE DURING WINTER - ROLE OF FOOD RESOURCES IN VOLE CYCLES

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Time series analyses have shown that cyclic vole populations exhibit direct and delayed density dependence in growth, in particular during winter seasons. It has been suggested that predation or other natural enemies are the source of delayed density dependence while direct density dependence might arise from food resource depletion. During peak phases of the cycle, vole population growth typically ceases during late autumn or early winter, and is followed by a decrease in density over the winter. To investigate whether this decrease is due to increased mortality induced by a depletion of food resources, we studied overwinter food consumption and physiological condition of field voles (*Microtus agrestis*) in western Finland in both an increase and a decrease phase of a three year population cycle. The growth rate of vole populations was negatively related both to prevailing vole densities and to densities six months earlier. Multiple indices of physiology and immunology revealed that the overall physiological condition of voles was lower in the winter of the decrease phase as compared to the increase phase and dependent upon population growth rates. Almost 90% of all green vegetation shoots were consumed by voles during the winter of the decrease phase while only two thirds were eaten in the increase phase. Our results suggest that the winter decrease phase of cyclic vole populations is associated with both a deterioration in the physiological condition of voles and a significant depletion of winter food resources. This implies that malnutrition induces poor physiological condition in voles, which in turn may increase mortality either directly through starvation or indirectly through increased susceptibility to predators and pathogens.

COINCIDENT CHANGES IN SPATIAL AND TEMPORAL DYNAMICS IN CYCLIC BRITISH FIELD VOLE POPULATIONS AND FENNOSCANDIA

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As with many small mammal populations, in Fennoscandia, the spatial and temporal dynamics of field vole populations in Kielder Forest, northern England, have undergone marked changes since ca 1985. Population cycles with a 3 year period have first become longer, with 4 and 5 years intervals between most recent peaks, and then characterized by stronger direct density dependence operating in winter. As a result, the amplitude of the fluctuations in spring has decreased with a noticeable impact on the breeding strategies of avian vole predators. In addition, the spatially organized pattern resembling a traveling wave that prevailed in the 1980ies has been replaced by nearly complete asynchrony. Consequently, very steep spatial gradients in density now exist over distances will within the foraging and dispersal range of vole predators (e.g. <5 voles/ha to 300 voles/ha over 5 km). The striking similarity in the syndrome of change and the near coincidence in its timing between Kielder Forest and Fennoscandia strongly suggest that a common cause is responsible for these changes, despite the subtle differences in the underlying cyclical patterns. We discuss how variation in vole demographic parameters may account for the observed dynamics in the light of our work on the role in relation to specialist predators, pathogens and vegetation dynamics.

DEMOGRAPHY AND POPULATION DYNAMICS OF THE MULTIMAMMATE MOUSE (*MASTOMYS NATALENSIS*) OVER A RANGE OF RAINFALL REGIMES IN EASTERN AFRICA

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The multimammate mouse (*Mastomys natalensis*) is the most widespread African rodent species, occurring from Senegal to Ethiopia and south to South Africa. Its numbers vary seasonally and between years with irregular population outbreaks. Earlier studies in Morogoro, Tanzania, showed that both density-dependent and density-independent factors (rainfall) affect demography and hence population dynamics. The wet season in Morogoro on average shows two rainfall peaks, a first and highly variable one between October and December and a second more predictable one between March and May. The main reproductive season in *M.natalensis* starts after the March rains and continues until September with several consecutive litters. Juveniles normally do not reach maturity in the year they were born but delay reproduction until the following breeding season. If rainfall during the first peak is abundant, however, breeding may start already in January and the juveniles that are born then quickly mature and reproduce already in the main breeding season of the same year, effectively inserting an additional generation and multiplying population size up to tenfold. A population matrix model was developed earlier to investigate demography and carry out simulations of rodent control interventions.

Here we investigate whether the same density-dependent and density-independent demographic relations also operate in regions with different rainfall regimes. We are using 21 monthly capture-recapture sets of 2-3 years each that were collected in 6 different eastern African countries over the past years, representing categories of rainfall distributions: unimodal, bimodal with a variable first peak, bimodal with a reliable first peak and non-seasonal rainfall. We compared the degree of reproductive seasonality and the patterns that can be seen in the survival of females. We compared the observed dynamics with simulations that were obtained by changing the rainfall seasonality in the Morogoro model.

Breeding is seasonal everywhere and related to rainfall, and where rainfall is distributed throughout the year, there is also no distinct reproductive season. Survival analysis (for sites with sufficient data) confirms the effects of density and rainfall. The simulated population dynamics patterns of the Morogoro-model run with alternative rainfall series match fairly well with the dynamics that were observed in the corresponding sites.

So far, our studies confirm that *M.natalensis* follows the same demographic mechanisms in all the studied sites and the differences in population dynamics can be largely explained by different rainfall regimes, rather than changes or adaptations in how the rodents react to the rainfall.

COMPARING POPULATION DYNAMICS OF SMALL MAMMALS IN OLD GROWTH AND MANAGED FORESTS IN THE AUSTRIAN ALPS AFTER A MASTING OF EUROPEAN BEECH (*FAGUS SYLVATICA*)

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Small mammals are common in all forest types influencing forest development as seed dispersers, seed and seedling predators or vectors of ectomycorrhizal fungi. Their impact on forest regeneration varies with fluctuating population densities. In particular tree masting can trigger rapid increases in small mammal abundances. We conducted this study after a mast year of *Fagus sylvatica* (2003) in the Wilderness area “Dürrenstein” in Lower Austria, which comprises the largest remaining old-growth forest in Central Europe, and the Limestone Alps National Park in Upper Austria. In both areas, small mammal populations have been investigated from 2004 to 2006 in two different types of mountainous forests (old growth forests and managed forests). Periodical live trapping and individual marking were used to analyse population performances over years, addressing the following questions: 1)Does species composition in small mammal communities vary between different types of mountainous forests and geographic regions? 2) Does a mast year lead to changes in small mammal abundance in all habitats and do the species show the same reaction? 3) Do population dynamics after a mast year vary in different habitats over time?

Species composition varied with time and was unique on each study plot. In general we found a higher species diversity of Soricidae and lower overall small mammal abundances on managed forest sites whereas old growth forests had higher small-mammal abundances, a higher overall species diversity but a lower species diversity of Soricidae.

The mast year in 2003 influenced the population densities of *Apodemus flavicollis* and *Myodes glareolus* on all study plots in 2004. In this year, *A.f.* and *M.g*. reached extremely high population densities and inhabited also suboptimal habitats like grasslands. All other species did not respond to the mast year in terms of population densities and were only found in marginal densities and never on grassland. Not all species were able to benefit (directly or indirectly) from the mast year in the same way. Mast years are likely to influence the population densities of euryoecious rodent species, thereby even effecting the composition of small mammal communities in adjacent habitats without masting trees.

All study plots showed the highest species diversity and population density in 2004. In 2005, populations crashed on all study sites. Trapping success was rather low on all forest types and most of the captured species a year before were missing in 2005. Unlike the year before, both diversity and density in general were now slightly higher on the managed forest sites. In 2006, population densities and species diversity were again increasing but small mammal communities were still different in terms of species composition compared to 2004. Again managed forests and old growth forests differed concerning species composition and population density. Comparing the densities of each study plot over years regeneration of rodent populations was faster on old growth forest sites, whereas Soricidae did not show as distinctive population fluctuations as rodents did.

WHAT CAN COUNTRY-WIDE PREDATOR DATA TELL US ABOUT THE POPULATION DYNAMICS OF VOLES?

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In this work I use country-wide data on predator abundances, small Mustelids and vole-eating avian predators, to reveal and predict patterns in population dynamics of voles. Although there are data on vole abundances from different areas of Finland, they are spatially relatively sparse compared to data on their predators. Keen amateur and professional ornithologists monitor abundance and breeding success of raptors and owls, while hunters count annually snow tracks of mammalian predators for management purposes. Bird ringing data is available from 1973 and data on snow tracking from 1989. Data organized in 50 x 50 km^2 grid is used for evaluating the previously observed patterns in vole population dynamics such as large-scale spatial synchrony, cycle length, amplitude, geographical gradients and temporal trends in abundance. Outcome of the two different predator data sets is also compared and their applicability to correctly reveal vole dynamics is discussed. Despite some sources of errors most of the previously observed patterns in vole data are also observable in predator data suggesting that predator data can be used as a proxy of vole abundances.

FLUCTUATIONS OF SMALL MAMMAL POPULATIONS IN NORTH NORWEGIAN BIRCH FORESTS: PATTERNS AND ECOSYSTEM CONSEQUENCES

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Fluctuation patterns in populations of small mammals in Fennoscandia have changed since the 1980s. To better understand the present temporal and spatial patterns, we have live-trapped more than 100 grids spread over three spatial scales (1 km, 10 km and 100 km). All grids were located in the dominant forest habitat of northern Norway, mountain birch forest. Trapping started in 1998 and is still going on. Two *Clethrionomys* species, the red and the grey-sided voles, were by far the most abundant small rodents. Temporal fluctuation patterns of *Clethrionomys* exhibited a wide variability: from non-cyclic to cyclic patterns with a 3 to 5 years period. Continental areas to the northeast were dominated by 5-years cycles whereas coastal areas in the southwest were either non-cyclic or had shorter periods. Spatial fluctuation patterns were correspondingly variable, with large-scale synchrony in the northeast, and asynchrony in the southwest. We discuss possible causes for such variability in spatial and temporal patterns, and the consequences of present fluctuation patterns on ecosystem functioning.

WORKSHOP

Alien mammals

IMPACTS OF ALIEN MINK PREDATION ON BIRDS, MAMMALS AND AMPHIBIANS OF THE FINNISH ARCHIPELAGO: A LONG-TERM EXPERIMENTAL

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Feral American mink (*Mustela vison*) are emerging as one of the biggest threats to biodiversity in northern Europe and quantification of their effects on wildlife is essential to managing long term impacts. Here we summarize responses of migratory seabirds, island small mammals and amphibians to a long-term, large-scale experimental mink removal in the outer Finnish archipelago. Mink were removed during spring and autumn from two large study areas since 1992 (R1) and 1998 (R2), while two other areas remained as controls; each area covered 72120 km and comprised 6070 small isolated islands, most less than 2 ha. Mink control led to increases in breeding populations of 14 of 22 species of seabirds. These species were generally of smaller body size and later breeders compared to those species which showed no responses. Mink also suppressed the natural summer increases of bank vole (*Clethrionomys glareolus*) and field vole (*Microtus agrestis*) populations but only during years of good rainfall, and ongoing research is investigating how this alters vole dispersal patterns that are vital to metapopulation processes. Impacts on common frogs *(Rana temporaria*) were similarly cryptic, with the biggest response taking seven breeding seasons to appear probably because of delayed maturation of frogs; the less palatable common toads *(Bufo bufo*) seem unaffected. It appears then that mink impacts are complex but its detrimental and disruptive effects may cover the entire island vertebrate community with cascading consequences to the whole archipelago ecosystem.

BALANCING COSTS AGAINST BENEFITS OF BLACK RAT MANAGEMENT ON MEDITERRANEAN ISLANDS

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Modern restoration programs should be evaluated in terms of ecological impact and benefits for native ecosystems. Furthermore, economic aspects (i.e. cost-effectiveness) should be also considered. The Black rat (*Rattus rattus*) has been worldwide introduced in island ecosystems. The detrimental impact of this species on native ecosystems has been well documented in last decades, especially on seabird populations, and a considerable effort has been put into practice in order to remove or mitigate it. Here we present results from an eight-year study on nine Tyrrhenian islands, with area ranging from 0.5 to 239 ha, where rat control was carried out by using second-generation anticoagulants. In this study we aim at: (*i*) assessing the impact of the Black rat on colonial seabird species, especially on Cory’s shearwater (*Calonectris diomedea*), (*ii*) comparing the results of two alternative management strategies, such as eradication, i.e. the removal of each individual from the island, and containing, i.e. temporary removal of rats only in close proximity to bird colonies, (*iii*) assessing benefits of local populations (especially to seabirds and endemic lizards) deriving from temporary or permanent rats removal, (*iv*) estimating non-target effects on seabird populations deriving from use of toxic baits and (*v*) evaluating the cost-effectiveness of the two control strategies.

Rats were successfully eradicated in all but one the islands, where the eradication project is still in progress. Containing was performed in two islands, in order to protect seabird colonies. Both eradication and containing positively affected Cory’s shearwater’s reproductive success (χ^2 test, at least $P<0.05$). Non target effects at population level, investigated for two bird species (i.e. *Larus michahellis* and *Falco peregrinus*), were not significant, as for none of the two target species was recorded a numeric decline in the year following the rat eradication, but incidental loss of individuals were recorded for some bird species.

Finally, cost-effectiveness analysis (CEA) suggested that eradication is especially suitable for islands with small area and with a widespread distribution of colonies or scattered pairs, while containing could be considered for larger islands.

THE ERADICATION OF INVASIVE MAMMALS FROM NEW ZEALAND ISLANDS: IMPLICATIONS FOR EUROPE

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Invasive alien mammals have now been eradicated from many islands in the New Zealand archipelago, with a substantial increase over the past 30 years in the number of successful eradications. Perhaps the most significant advance has been in the ability to eradicate invasive rodents from increasingly large islands. Based on the New Zealand experience, there are good prospects for further eradications of invasive mammals from islands in Europe and elsewhere, thereby facilitating ecological restoration and the recovery of threatened species.

ALIEN MAMMALS IN EUROPE: PATTERNS OF INVASION, TRENDS AND MAJOR IMPACTS

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DAISIE (http://www.europe-aliens.org/) is a 3-years project funded within the European Commission 6th Framework Programme, aimed at creating an inventory of invasive alien species that threaten European biological diversity. A consortium of teams and collaborators from 19 European states has collected and verified all known cases of introductions, in all taxonomic groups and environments.

The resulting European alien species database is structured in updated and peer-reviewed national and regional inventories for all European countries (including Russia and Israel) and major island systems, covering all taxonomic groups and environments. For each species introduced into a European state or region, the database reports a range of relevant information , such as ecological features, vectors of introduction, patterns of spread and impacts, etc.

In the present paper we present an overview of the Daisie data on alien mammals in Europe, based on information excerpted from over 200 literature sources and many unpublished data. The Daisie mammal dataset also covers ancient introductions and introduced populations that have been eradicated or got extinct.

In total, ca 800 known cases of introductions by over 100 alien mammal species have been recorded. On the basis of this dataset we assess and summarise the main patterns of invasions by alien mammals, and discuss the main environmental, social and economic factors involved.

A major aim of the inventory is to provide the basis for prevention and control of the threats posed by invasive alien species through the understanding of the main patterns of introduction, establishment, spread and impact. Therefore the data are discussed in respect to possible future responses to alien mammal invasions.

WHAT MAKES A RODENT SPECIES SUCCESSFUL IN EUROPE: A TALE OF NATIVES AND ALIENS

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We examine the association between the success of European Rodent species and a range of life history and niche breadth parameters with a view to assessing if these factors determine the likely success of invasive species.. Data on eight life history trait and forty niche breadth variables of each species were derived from literature for native and invasive species. The niche breadth variables were matched to the CORINE land cover classification. We derived a measure of success from the Atlas of European Mammals, based on species density and geographic spread. A series of multivariate ordinations were carried out to summarize the major patterns of variation within the data matrices for the native species which were subsequently compared using procrustes rotation and partial mantel tests. The results of the procrustes analysis showed a strong correlation between the habitat and the life history matrices. Similarly partial mantel tests indicated a strong relationship between the niche breadth and the success matrices when controlling for life history. We superimpose the introduced alien species on the life history and habitat ordinations and analyses the risk of expansion of the invasives. We conclude that species specific variables and life history characteristics play an important role in determining the success of a rodent species in Europe.

A REVIEW OF THE DIET AND IMPACT OF FERALCAT ON ISLANDS

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Feral cats predate on distinct type of prey in the different islands depending on their respective prey availability. So, in some of them, and apart of the native and endemic species, are nowadays present invasive non-native species, suitable as prey for cats and which are rather abundant. We review more than 60 feral cat diet studies on islands all over the world in order to analyze the overall biogeographical and ecological patterns in the diversity and type of preys, and subsequently the feeding habits, the success and impact of this introduced predator. Data set were homogenized with meta-analyses procedures and several questions were addressed about trends in feral cat preys, island characteristics, diversity of biogeographic areas with more favorable and abundant resources for feral cat establishment, etc.

On the other hand, no review has been carried out on the impact of feral cats since a species/prey conservation perspective despite of the great biodiversity that harbor the islands. Therefore, this is the main objective of this review which can be useful for scientist and conservation practitioners who work in these particular, fragile and threatened environments. We reviewed more than 150 studies on feral cat impacts on island worldwide with the aim to evaluate the main groups and species deleteriously affected, to know what characteristics make island natives more vulnerable than others, and to prioritize future conservation actions. We compiled data from published and gray literature covering most of the world's insular regions and considering only feral cats and not domestic or stray ones. Due to the high number of prey/species affected by feral cats in the different islands, we only included those species which show a deleteriously conservation status and that has been considered among the five most critical categories of the IUCN Red List of Threatened Species of the World. We consider impact any contrasted evidence that cats have caused a decline in the population abundance or geographical distribution of any native species.

ERADICATING RATS FROM THE ISLAND OF CANNA WITHOUT IMPACTING NON-TARGET SPECIES

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The Scottish island of Canna is a Special Protection Area for its important seabird colony. Monitoring by the Highland Ringing Group had shown that seabird populations had been declining since the 1980s including the elimination of a colony of an estimated 1000 pairs Manx shearwater *Puffinus puffinus* but other species, notably Eurasian Shag *Phalacrocorax aristotelis* and Razorbill *Alca torda* had also been impacted. Overall, the colony had declined by 40% since 1995. Investigations carried out by the National Trust for Scotland (NTS), who own the island, showed that there was a large, introduced population of brown rats *Rattus norvegicus* and that this was responsible for the decline in seabirds. A feasibility study showed that eradication of the rats with rodenticies should be possible and funds were obtained from the LIFE Nature Programme, Scottish Natural Heritage and NTS. The presence of both golden eagle *Aquilla chrysaetos* and white-tailed eagle *Haliaeetus albicilla* and a locally distinctive race of field mouse *Apodemus sylvaticus* necessitated careful mitigation plans. The main danger to eagles was secondary poisoning through ingestion of rat carcases. This was mitigated by the use of a first generation poison, Diphacinone, which has a very low toxicity to birds but is highly effective against rodents. As heavy mouse mortality was inevitable, it was decided to capture and remove an assurance population of mice which were maintained at Edinburgh Zoo and Highland Wildlife Park. The eradication programme was carried out under contract by Wildlife Management International from Sept 2005 - March 2006. 4300 bait stations were installed: in areas of high rat density, around the coast, they were spaced at 50m intervals, with a spacing of 100m elsewhere. Blocks of poison were placed in the stations from November onwards and each was visited twice a week by a team of 14 staff and volunteers. Bait take was monitored and most had stopped by January; the last sign of a rat being detected on 20 Feb 2006. Following this, the poison was removed and replaced with monitoring blocks manufactured from candle wax impregnated with cocoa powder. This was attractive to rodents and allowed easy distinction between the teeth marks of rats and mice. Additional blocks were placed outside the bait stations to ensure detection of rats reluctant to enter the stations. Each monitoring block was checked at monthly intervals, with an intensive period from Oct-Dec 2007. No further sign of rats has been detected. Teeth imprints on the blocks have shown that the populations of mice have built up rapidly throughout most of the coastal parts of the island. It is believed that the 50-m spacing between the poison bait stations has allowed sufficient mice to survive and no release from the assurance population has been necessary. No mortality of birds of prey has been detected.

A QUESTIONNAIRE SURVEY AND REVIEW OF INVASIVE ALIEN MAMMALS AND THEIR MANAGEMENT IN EUROPE

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A questionnaire survey was sent to researchers working on mammals in Europe. The questionnaire focussed on the following main areas:

1. Impacts: The top 5 most invasive alien mammal species in their country in terms of impacts; the impacts they were having, socially, economically, ecologically; and if the impacts were ecological, the most affected species/ecosystems.
2. Management: The survey then went on to look at ways the species and their impacts were managed either through lethal control techniques (i.e. hunting, trapping or poisoning) or non-lethal control techniques (i.e. fertility control, management of the species behaviour, barrier control such as fencing).
3. Eradication versus ongoing control: From the species listed in section 1. participants in the survey were asked to list the number of projects they had knowledge of where the species have been eradicated successfully from a region, or if there was no option other than long term control.
4. Monitoring and preventing spread: From the species listed in section 1. participants were asked to list the measures being used to prevent their spread into new areas and what techniques were used to monitor the presence or absence of these species. They were questioned about the effectiveness of these techniques.
5. New invaders: Participants were also asked to list the species, which would be the next invaders into their countries.

The results of this survey have been presented in order to initiate general discussion and to explore how they relate to data presented in recently established web based databases on invasive species, DAISIE, NOBANIS and SEBI.

HOW ALIENS CAN REPLACE NATIVE SPECIES: MECHANISMS OF REPLACEMENT OF THE NATIVE RED SQUIRREL BY THE INTRODUCED GREY SQUIRREL

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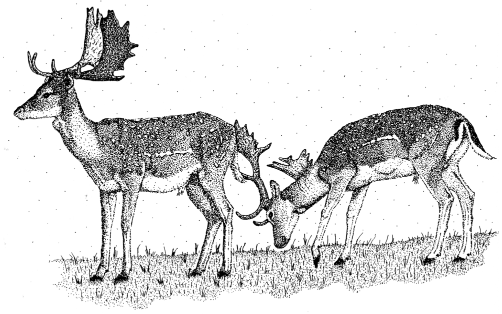
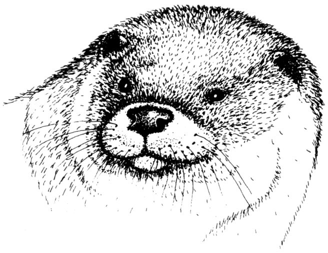
One of the best documented examples where an invasive introduced mammal species occupies the niche of an ecologically similar native species, causing its extinction in most areas where distributions overlap, is that of the replacement of the Eurasian Red squirrel (*Sciurus vulgaris*) by the alien grey squirrel (*Sciurus carolinensis*). Grey squirrels from North America, have been introduced in different sites in Great Britain, including Ireland, and Italy in the 19th and 20th century, causing wide-scale extinction of native red squirrels. The first evidence came from distribution maps showing that, in most cases, range expansion of greys was, after a short period of time, followed by a reduction of the range of red squirrels in the region. These trends were later confirmed by spatially explicit population dynamics models (SEPM), developed to make predictions of how the dynamics and distribution of both species change over time under different scenarios. These scenarios can model interspecific competition for resources, shown to be the most relevant mechanism of replacement in Italy, and/or infection rates of red by grey squirrels of a squirrelpox virus, lethal to the native species. It has been demonstrated that the transmission of this virus has caused local extinction of red squirrel populations in many areas on the British Isles. Here we discuss how a multi-disciplinary approach is essential to study/understand mechanisms of inter-specific competition between reds and greys and the relative role of competition and virus transmission in replacement dynamics. We show how experiments of virus transmission, studies on behaviour and interspecific competition in areas of co-occurrence, and applications of SEPM models in different geographic regions have produced a broad knowledge on the red-grey squirrel system. SEPM models have also produced predictions of future demographics and distribution of both species and of the effects of possible management scenarios, in particular the efficiency of different control methods. Our final questions are: what should be the next steps; and how close (or far?) are we of an efficient control of grey squirrels, the key-issue for conservation of native red squirrels in Britain and Italy.



WORKSHOP

Non-invasive genetic methods for monitoring populations of elusive mammalian species



NON-INVASIVE GENETIC METHODS FOR WOLF POPULATION MONITORING

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Individual genotypes determined from non-invasive DNA samples (typically extracted from shed hairs or scats) are used to estimate population size and other demographic and genetic parameters in monitoring projects of elusive species. However, PCR success rates usually are lower, and genotyping errors higher than in standard population genetic surveys, due to DNA degradation or contamination in aged field samples. In this study we evaluated the results obtained in long-term non-invasive genetic monitoring projects of wolf populations in Italy. We compared the results obtained using standard multilocus multitube microsatellite genotyping and novel SNPs genotyping methodologies: Real-Time PCR, Pyrosequencing and SnapShot. Performances, error rates and costs of these different approaches are evaluated.

NON-INVASIVE GENETIC SAMPLING OF THE ABRUZZO BROWN BEAR (*URSUS ARCTOS MARSICANUS*) POPULATION

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A small isolated brown bear population (*Ursus arctos marsicanus*) is surviving in the central Italian Apennines (Abruzzo, Lazio and Molise National Park and surroundings). Aiming to obtain empirical data that could be used to estimate brown bear population size and structure, a long-term non-invasive genetic monitoring project has been carried out during the last five years, lead by the Italian Forest Service (CFS), and thanks to the scientific coordination and collaboration of several institutions (University of Rome "La Sapienza", Istituto Nazionale per la Fauna Selvatica, Abruzzo, Lazio and Molise National Park and other national and regional parks in Abruzzo Region). A few invasive (tissues from found-dead bears) and ca. 2000 non-invasive hair and scat samples were collected from 2002 to 2005 and analysed at the Laboratory of genetics of INFS. Field sampling included systematic hair collection through baited traps, opportunistic collection of scats along trails, occasional sampling and intensive surveys in *Rhamnus alpinus* patches, which represent seasonal foraging areas for bears. Laboratory protocols were implemented to obtain reliable individual genotypes and molecular sexing. Genotyping replicates were used to assess the occurrence of PCR failures and errors, i.e. false alleles (FA) and allelic dropout (ADO), per sample and locus. Reliable genotypes were used to estimate genetic and demographic parameters. Results indicate that: 1) PCR success rate was significantly higher in hair than in scat DNA samples; 2) PCR errors were in the lower range of typical bear non-invasive genetic sampling; 3) laboratory performances and genotype reliability significantly improved across the years. These results suggest that false genotypes and "shadow effect" should be negligible in this data-set, despite the low genetic variability of the Abruzzo brown bear population. Those results have been used to define a panel of markers and a standard multitube procedure allowing the identification of individual genotypes with high reliability at the lowest possible cost. Individual genotypes identified so far are being used to obtain estimates of population genetic variability, to evaluate the performances of various population size estimators, sex ratio and individual displacements in the study area.

A RELIABLE METHOD FOR SPECIES IDENTIFICATION OF THE ENDANGERED *MAZAMA BORORO* DUARTE, 1996 USING NON INVASIVE SAMPLING METHODS

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The small red brocket deer *Mazama bororo* is one of the most endangered Neotropical deer that inhabits the Atlantic forest. In their area of distribution there are three other species of brocket deer that are sympatric such as the red brocket *Mazama americana*, the Brazilian dwarf brocket deer *Mazama nana*, and also the grey brocket deer *Mazama gouazoubira*. In order to obtain estimates of population size and conduct assessment of conservation status it is imperative to determine the area of distribution of this species. In this project we developed a method that improves the detection of this endangered small red brocket deer among the other brocket deer species that are sympatric, and therefore will enhance the conservation and management strategies aimed at this species. We designed a new set of primers that amplify a short (224 bp) fragment of the mitochondrial cytochrome b region with a system of restriction enzyme digestion that specifically target broket deer and that results in a fast and reliable method for *Mazama* species identification from faeces. For primer and enzyme optimization, we utilized 30 tissue samples from individuals representing all the potential broket species in the area. In the small red brocket deer (*M. bororo*) we found that the PCR fragment contains the ECORII digestion site which is unique for this species. Successful PCR products showed a clear single band 164 bp long in a 2% agarose gels. Another two diagnostic sites were identified for *M. gouazoubira* (SspI) and *M. americana* and *M. nana* (AflIII). In the field, 246 scat samples were collected with the help of trained dogs. We successfully amplified 95 % of the scats. The PCR-RFLP method determined that 43% were *M. bororo*. The RFLP reaction failed in 23 cases (9%). The remaining sample was distributed among grey brocket deer (30%), red brocket deer (10%) and the Brazilian dwarf brocket deer (8%). In conclusion the designed molecular tool showed to be efficient for performing the species identification of the four brocket deer that are sympatric. Furthermore the sampling strategy used proved to be effective and we were able to map the distribution of the small red brocket deer in the area.

THE DUTCH OTTER REINTRODUCTION PROJECT: WHAT NON-INVASIVE GENETIC SAMPLING TOLD US ABOUT SOCIAL STRUCTURE AND BEHAVIOUR IN A LOW DENSITY POPULATION

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The otter (*Lutra lutra*) went extinct in The Netherlands in 1988. In 2002 16 otters, originating from Eastern-Europe, were re-introduced in a large wetlands area in the north of The Netherlands (Weerribben- Wieden). In subsequent years another 10 individuals were added. From all these individuals a genetic fingerprint, based on 12 microsatellites, was collected. Because otters are elusive animals they are hard to observe during daylight. Therefore, a non-invasive genetic sampling protocol was developed based on extracting DNA from freshly collected sprainst (droppings) in the field. During the period 2002-2006 we collected a DNA profile from 205 sprainst (out of 558 collected sprainst). These genotyped sprainst revealed information on: 1) territory use of adult males and females; 2) social structure and mating behaviour; 3) detection of newborns and their subsequent fate; 4) dispersal within and out of the original release area; 5) dynamics of genetic diversity in a small isolated population; and 6) density estimates of the population. Moreover, because we are working with a small isolated population that was fully genotyped on beforehand we could evaluate the technical protocols and problems related to non-invasive genetic sampling (allele dropout; incomplete profiles because of low DNA quality; the need for repeated PCR (multiple tube) and the trade-off between replication and number of microsatellites that could be used).

MONITORING WOLF POPULATION SIZE AND SURVIVAL BY NON-INVASIVE CMR TECHNIQUES IN THE WESTERN ALPS

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Population size and survival rate estimates are fundamental for the conservation of species but are often difficult to obtain, especially for rare and elusive species. Wolves began recolonizing the south-western Alps of Italy and France in the early 1990s through dispersal from source populations in central Italy. We monitored this recolonization process and the increase in population size using non-invasive genetic capture-mark-recapture (CMR) analysis from 1999 to 2005. The overall process of using non-invasive genetic techniques to estimate population parameters involved three main steps: 1) designing the appropriate sampling scheme, and executing the study in the field, 2) conducting the laboratory analysis and interpreting the genetic results, and 3) using the molecular tags in a CMR framework to estimate population parameters. We analyzed ten microsatellite markers for 1,372 scat samples, of which 46.1% produced reliable genotypes. We used an open mark-recapture model to estimate survival and population size using these genotypes. Juvenile survival (0.36) was lower than adult survival (0.83) and individual heterogeneity was not a problem, although genetic recaptures were low. Different levels of sampling effort explained part of the recaptures probabilities. On our 7,000 km2 study area in the western Alps, population size estimates ranged from 9 to 40 wolves from 1999 to 2005, depending on the season. Population estimates are fundamental for proper management of the expansion of the wolves in the Alps, however, precision must be improved, and limits and pitfalls of the non-invasive techniques need to be properly addressed.

GENETIC IDENTIFICATION OF FELID EXCREMENTAL DNA FROM SAGARMATHA NATIONAL PARK (NEPAL)

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In the 60s the snow leopard *Uncia uncia* was extirpated from what is now the Sagarmatha (Mt. Everest, Nepal) National Park. However, recently signs of presence have indicated that the snow leopard has made a comeback to the Park. Presence records are difficult to obtain for elusive carnivores and non-invasive genetic sampling has became a valid alternative to obtain information on these species. We collected and analysed 31 faecal samples in the Sagarmatha National Park to estimate the minimum number of felids ranging in this area. We analysed the samples using mtDNA sequences to identify the species and 10 microsatellite loci to characterize individual genotypes. Preliminary results indicate the presence of seven distinct individuals belonging to three different species (*U. uncia*, *Panthera pardus* and *Prionailurus bengalensis*). The local community of wild cats can probably exist through ecological separation either by habitat (*U. uncia*: open areas above the forest tree-line, from 3700 m a.s.l. up; *P. pardus*: forested and bushy areas) or by trophic niche *(P. pardus*: meso-mammals, large birds; *P. bengalensis*: small mammals, middle-size/small birds, in forested areas).

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NON-INVASIVE GENETICS OF OTTER (*LUTRA LUTRA*) POPULATIONS IN ITALY

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Non-invasive genetic methods are being used to identify individuals and estimate population size in many elusive carnivore species. Non-invasive methods are particularly promising for monitoring presence, individual ranges and population size in otters (*Lutra lutra*). In Italy, the species distribution is currently limited to a few southern regions, and its population size is just roughly guessed. Therefore, more accurate genetic and demographic monitoring in these areas is important for sound management and conservation of the species. In this study we analysed 187 scat samples collected from the Pollino National Park, using 11 microsatellite loci and mitocondrial DNA sequences. The aim of this study is to develop a reliable method useful for monitoring otter populations, minimizing the occurrence of the genetic errors (allelic drop-out and false alleles), which are caused by low concentration of degraded DNA in the samples, and that can produce false genotypes. PCR success rate was low (around 40%), as well as low was in data reported in other studies. All these samples showed the same mtDNA haplotype, that is unique for the Italian otter population. Microsatellite genetic variation was slightly lower than in other otter population in Europe. However, the probability of identity and PCR error rates were low enough to allow reliable genotyping.

AN EVALUATION OF THE RELIABILITY OF ESTIMATING POPULATION ABUNDANCE WITH FAECAL AND HAIR DNA FOR THE AUSTRALIAN ENDANGERED SPECIES THE SPOTTED-TAILED QUOLL (*DASYURUS MACULATUS*)

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Despite its potential as a tool for enumerating populations non-invasive DNA sampling has only been applied successfully to a few mammal species. We assessed the feasibility of identifying individuals and estimating population abundance of the endangered species the spotted-tailed quoll (*Dasyurus maculatus*) using remotely collected faeces and hair from a well-studied population in Kosiuszko National Park, Australia. The reliability of the faecal and hair genetic profiles and population estimates were evaluated against genetic and capture data derived by live-trapping. Population estimates were directly comparable as the datasets were equal in temporal and geographical scales and in sampling effort. Faecal sampling and trapping were carried out for 28 days in 2005, and hair tubing and trapping over 17 days in 2006. Microsatellite profiles were derived from 209 faeces, 55 hair-traps and trapped individuals of each year. Allelic dropout and false alleles were present in the 10-locus faecal and hair profiles, however using a multiple tubes approach and with comprehensive error checking individuals could be reliably identified. Faecal DNA sampling detected 16 of the 22 trapped individuals and identified three individuals not known from trapping in 2005. Hair-tubing methods detected 11 of the 20-trapped individuals in 2006. Both faecal and hair DNA sampling methods provided unbiased sampling methods detecting males, females, adults and juveniles. Extended faecal and hair tubing sampling periods were able to improve the population estimates substantially. Over four months of faecal sampling a further 10 individuals were detected bringing the total to 28 animals. With three additional periods of hair tubing of 7-9 consecutive days a further five individuals were detected; hence a total 16 individuals were observed. In conclusion, this study has demonstrated that non-invasive DNA sampling offers an unbiased method for sampling individuals and is able to provide meaningful estimates of population abundance. However when compared with live-trapping efforts a longer sampling period is required to detect equivalent numbers to that detected by trapping. The need for longer sampling periods may limit the use of the non-invasive methods as a stand-alone management tool.

MITOCHONDRIAL VARIABILITY SUGGESTS POPULATION STRUCTURE IN BENGAL TIGER (*PANTHERA TIGRIS TIGRIS*)

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The Bengal tiger (*Panthera tigris tigris*) is highly endangered throughout its distribution range therefore, the Project Tiger was initiated by Government of India to provide special protection to this flagship species as well as conservation of other associated species. This study aims at developing highly sensitive genetic markers to monitor wild populations by sampling scats. The genetic structure of particular tiger populations from Northern, Western, Central, North Eastern and Southern parts of India is investigated along with captive animals as reference. We preferred analyzing the control region variability and by investigating previously discovered polymorphisms within coding genes of the mitochondrial genome. The study analyses haplotype distribution in the Indian tiger population to estimate genetic differences between major population of different tiger reserves. Taken together, these results of the first genetic investigation of wild Indian tiger populations will be important to develop conservation strategies and provides a methodological basis for long term genetic monitoring of wild tiger populations in India.

ESTIMATION OF WILDCAT (*FELIS SILVESTRIS SILVESTRIS*) POPULATION SIZE WITH NONINVASIVE GENETIC METHODS AND CAMERA TRAPPING

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Population size of European wildcats (*Felis silvestris silvestris*) was estimated by genetic typing of hair samples collected in an area of approximately 100 km2 in the northernmost chain of the Jura Mountains near Basel, Switzerland. Systematic hair sampling was accomplished by means of lure sticks, sprayed with valerian tincture. Valerian tincture urges wildcats to rub against the lure sticks. Two luresticks per square kilometer were placed at pre-determined locations and hair samples were collected every two weeks during one year. Polymorphic microsatellites DNA markers were used to differentiate the individuals genetically. A second dataset was provided by camera traps placed in the same area during the same observation period. Capture-recapture techniques are applied for both the genetic and the camera trap dataset. The results allow not only to estimate the population size, but also to assess the precision of this estimation.