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been discovered near Fürstenu, (north-western Germany) in shark tooth-rich conglomerates of a coastal delta environment north-west of the European Rhenish Massif. Whereas the oldest seals indicate a cold upwelling water adaptation and main habitat in the Pre-North-Sea, instead for *Protosiren* it is the most northern of its genus whose global distribution was generally restricted to warm waters. Its presence can be explained by seasonal inflow of warm Tethys surface water. The old models of evolution of seals must be dated back into the Paleocene, whereas possibly in both upwelling influenced marine coastal regions of North America (north Atlantic) and Europe (Pre-Northsea Basin) those were already present within the Middle Eocene by well-developed species, recently known only from Europe. Also the siren evolution seems to be polyphyletic with an existence of two centers of sirenian evolution, that can be explained by the opening of the Atlantic and by upwelling that separated the warm water faunal province of North America from those of Africa and Eurasia. A modified evolutionary model was recently presented in which oldest Early Eocene manatee sirenians developed in the Caribbean of Central America. *Protosiren*, instead, appears to have developed polyphyletically along the African coastline of the Tethys, as the oldest dugong ancestor. Several up to eight cm large teeth of the megatooth shark ancestor *Carcharocles sokolovi* have been found in northern Germany, suggesting a spatial correlation with their prey, the sirenians (and probably also whales), correlating with their presence in warm waters only. In contrast, the smaller white shark ancestor *Carcharodon auriculatus*, from which some thousands of teeth have been found in the Middle Eocene gravels in northern Germany, was adapted to cold water, as were its main prey, the seals, which dates back the oldest seal hunt specialization over 50 Million years ago.

Genetic structure and range expansion of reintroduced roe deer populations in Great Britain

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Roe deer (*Capreolus capreolus*) were nearly extinct in Great Britain around 1700, with refuge populations surviving only in woodlands in Central and Northwestern Scotland. However, they are currently widespread throughout the country, having spread from the Scottish refugia and populations reintroduced to England from Continental Europe. Roe deer have a high capacity for demographic and spatial expansion, and they presently have the widest distribution of all British deer. We find that the rate of range expansion varies between the reintroduced populations. The scenario of rapid range expansion following reintroduction enables an examination of the population genetic diversity and structure of spatially expanding populations influenced by contemporary processes following a documented bottleneck. Additionally, geographically peripheral populations are expected to exhibit lower genetic diversity and higher differentiation than core populations because of their smaller size and greater spatial isolation. We test the hypothesis that genetic diversity within populations is lower at the range limits than at the geographic centre. Over 300 tissue samples were collected from 18 locations in Great Britain, spanning the core and periphery of the expanding populations. Using genotype data from AFLP markers, we assess the population genetic structure of the reintroduced populations, and compare levels of diversity at the core and periphery of their ranges. Gaining a better understanding of the landscape and genetic factors influencing the range expansion of roe deer may help with prediction of their movement into new areas.

Reintroduced red deer and threatened Apennine chamois: Can restoration of biodiversity elicit concern?

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In mountain ungulates, environmental conditions and access to high quality forage in the short warm season can influence the winter survival of offspring, in turn population dynamics. In a seasonal environment, in the warm months, interspecific overlap in resource use, i.e. potential for competition, may be a threat for rare taxa. In Abruzzo, Lazio and Molise National Park (ALMNP, central Apennines, Italy), a 30% decrease of numbers of Apennine chamois *Rupicapra pyrenaica ornata* (vulnerable, IUCN; ALMNP: from c. 650 to c. 450 individuals, in 2005–2010) has been recorded, whereas red deer *Cervus elaphus* (reintroduced in 1972–1987: 81 individuals) have greatly increased (2010: >2000 individuals, ALMNP archive), partly overlapping with summer ranges of chamois. Pellet group counts, micro-histological analyses of faeces, vegetation sampling and behavioural observations indicate: (1) a great space/diet overlap between deer and chamois; (2) an increase of unpalatable plant species and an apparent decreasing trend of the most grazed species by chamois, with a reduction of area available to grazing, with respect to 1982–1984; (3) irrespective from vegetation type, a reduced bite rate of adult female chamois in patches used also by deer, with respect to areas with no overlap. Our results suggest a negative effect of red deer on the quality of Apennine grasslands, in the warm season. We suggest that reintroductions of potentially competing species may be avoided in areas where small populations of rare taxa survive. The conservation of rare taxa should be locally prioritized, rather than the re-establishment of pristine assemblies.

Applying conservation genetics in Bulgaria and Romania to protect one of Europe's last brown bear (*Ursus arctos*) refugia

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While most areas of Western and Central Europe are intensively used by means of agriculture, timber production, and human settlement, some eastern regions, such as the Balkans and parts of the Carpathians still comprise large, near-natural areas. Especially in vast, forested mountainous landscapes, large carnivores, such as brown bears still persist in considerable population sizes and provide a valuable genetic reservoir for the long-term persistence of this species in Europe. Bears as well as other wildlife in these regions, however, face increasing anthropogenic pressure due to the intensification of land-use. Here we present data from ongoing genetic bear monitoring activities in Bulgaria and the Carpathians

(including their foothills) in Romania. Genetic data were obtained through noninvasive collection of scat and hair or tissue from killed animals and subsequent molecular analysis (14 microsatellite loci, mitochondrial haplotype analysis, sex determination). The obtained genotypic data will help assessing the general level of genetic diversity, identifying functional ecological corridors used by bears and determine the numbers of populations and their sizes. Knowledge about the presence or absence of brown bears, the genetic diversity in and between populations and the actual number of individuals in every area, for instance, is a basis for refining management plans for hunting, steer tourist activity in, e.g., ski resorts, and for the coexistence of large carnivores and livestock. We here demonstrate the effectiveness of embedding genetic research methods in broad regional conservation projects.

Neogene and Quaternary Eulipotyphlan fossil assemblages in Spain: Synopsis of the last 23 Ma. of Erinaceomorpha and Soricomorpha evolution in Southwestern Europe

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We present for the first time a calibrated biostratigraphic chart with the Neogene and Quaternary insectivore assemblages from Spain. Our database is based on almost 400 fossil associations, some directly studied by the authors, the rest taken from literature, covering the last 23 million years. This time span is herein reduced to the most significant events which resulted in the configuration of the recent communities living in Spain. Early Miocene records of insectivores are rare. The beginning of the Middle Miocene shows a stepwise entrance of new elements, including gymnures of the tribe Galericiini; and within Heterosoricidae, *Heterosorex* is replaced by *Dinosorex*. The Late Miocene is characterized by a renewal of the Galericinae and the extinction of Dimylidae, Heterosoricidae and Crocidossoricinae. Noteworthy are the entrance of Desmaninae and Amblycoptini, and a first increase of shrew diversity. The Pliocene records the last occurrences of galericines (*Parasorex*) and uropsilines (*Desmanella*), but it also represents the 'Golden Age' of shrews and the spread of Desmaninae. The beginning of glacial dynamics at the Early Pleistocene derived in a dramatic decrease of the diversity in Soricidae. Middle and Late Pleistocene do indeed record a low diversity at the genus level, similar to the modern one, represented by the living genera *Erinaceus*, *Galemys*, *Talpa*, *Sorex*, *Neomys* and *Crociodura*. *Suncus* and *Atelerix* were probably introduced in Spain by humans during the Holocene. In the Balearic Islands, this period sees the extinction of *Nesiotites*.

Evolutionary and ecological constraints in Neotropical monkey assemblages

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Since Darwin, ecological similarity among closely related species has been recognized as a common pattern of niche evolution. Additionally, ecologically similar species tend to compete by resources. We can expect that similar species do not coexist, and if evolution is conserved, coexisting species may be phylogenetically distantly related. We evaluate these consequences at different spatial scales

on new world monkey's assemblages. This clade is a well studied system and it has been established that their habitat and main resources (i.e., fruits) influence the composition of local ensembles. We used climatic niche models for 63 species of Neotropical monkeys and calculated ancestral states of these, to evaluate if climatic conditions such as potential evapotranspiration (proxy of forest productivity) affect spatial distribution. We also evaluated whether or not diet composition evolved in a conserved fashion, using a common metric (Blomberg's K). We found that both components of primate niche are similar among closely related species. Therefore, competition may be an important driver of local species assemblages. To test this idea, we compiled information from 59 primate assemblages in Neotropical forests. Additionally, we obtain a list of potential species, based on climatic niche models for each locality and ignoring species interactions. This list was compared to lists with observed species assemblages, using a limiting similarity model (Sorensen index). We found that climatic communities showed many more species than observed ones, but when we included a filter to avoid that similar species coexist in one community, the probability to find communities similar in species richness than observed ones was high (mean = 0.82, SD = 0.15). These results support the idea that Neotropical monkey assemblages are affected by competition.

Phylogeny of the common shrew (*Sorex araneus* L., Mammalia) in Eastern Europe

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The common shrew is a small mammal with unique karyotypic diversity. At least 70 chromosomal races have been described in *S. araneus sensu stricto* and five cryptic species in *S. araneus sensu lato*. We investigate here the variation of the *cyt b* gene in the *Sorex araneus* group in Eastern Europe. A total of 82 samples of *S. araneus* and 7 samples of the Caucasian shrew (*Sorex satunini*) was studied (accession numbers JN984059–JN984127, 953 b.p.). Additional data were taken from the GenBank. Phylogenetic analysis was performed using BIOEDIT, MEGA, NETWORK. Phylogeographic trees and networks show separation between haplotypes of *S. araneus s. l.*, but they show lack of separation of *S. araneus s. s.* Median networks display "star-like" phylogeny testifying the "bottleneck" evidence. A distinct haplogroup in *S. araneus s. s.* is formed by a population distributed near the Sea of Azov. Perhaps an autochthonous population of the southern refugium of Neroosa race was preserved in the last glacial period. We have found two haplogroups (A and B) in a population of *S. satunini*. The first one, type A, is the most genetically distant (*p*-distance with *S. araneus* is 5.7%), and is regarded as parental. The second one, type B, is genetically closer to *S. araneus* than *S. antinorii* and *S. granarius* (*p*-distance with *S. araneus* is 2.2%). We suppose that the type B haplotypes were obtained from some species close to *S. araneus* in Southern or Western Europe.

Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage

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