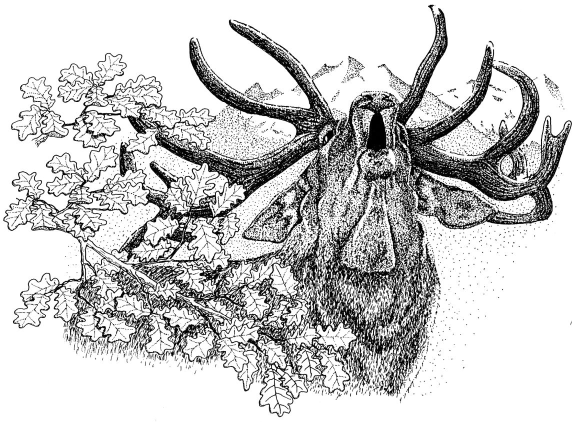
UNGULATES



MOLECULAR ANALYSIS USING MITOCHONDRIAL DNA AND MICROSATELLITES TO INFER THE GENETIC STRUCTURE OF KOREAN GORAL AND RELATED SPECIES

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Of the genus *Nemorhaedus, N. caudatus raddeanus* (Korean goral, long-tailed goral or Amur goral) occurs in Korea. Current population size in South Korea is estimated to be less than 800 individuals, and most of them are thought to be locally isolated into small populations, mainly due to road constructions. Thus, strategic conservation plan for this endangered species is urgently needed. To investigate the phylogenetic status of Koean goral and its relatives, complete mitochondrial cytochrome *b* and control region sequences were determined and analyzed. Korean goral showed a substantial cytochrome *b* sequence divergence (7.1%) from Chinese goral, that is higher than the difference (4.6%) between Korean goral and Himalayan goral. The result implies that current classification system for Korean and Russian goral as a subspecies of Chinese goral (*N. caudatus*) need to be re-examined. Eighteen microsatellite loci were utilized to estimate genetic diversity and population structure of Korean goral, Japanese serow and Korean native goats. Heterozygosity and the allele number per locus was used as index of genetic diversity. The result indicates that the level of genetic diversity of Korean goral is comparable to those of related species. The population structure analysis suggests that Korean goral populations are not differentiated by geographic pattern, whereas the Japanese population is differentiated into two distinct subpopulations in accordance with the geographical origins of samples from two different regions of Yamagata Prefecture and Nagano Prefecture.

ECO-EPIDEMIOLOGY OF ABOMASAL PARASITES IN FALLOW DEER (*DAMA DAMA* L.) IN A MEDITERRANEAN ECOSYSTEM: RELATIONSHIP TO HOST DEMOGRAPHY AND HABITAT FEATURES

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Monitoring macroparasites in wild animal populations is aimed to assess the potential role of parasites in regulating or destabilizing the dynamics of the host population, and to identify epidemiological parameters to be utilised as indicators of health population status.
During the period 2005-2006, 138 fallow deers (*Dama dama* L.), shot during a population-control program, in the Preserve of Castelporziano (Rome, Italy) were examined for abomasal Helminth parasites. The following species were identified: *Spiculopteragia asymmetrica*, *Apteragia quadrispiculata*, *Ostertagia leptospicularis* (with the minor morph *O. kolchida*), *Trichostrongylus axei* and *Skrjabinagia arctica*. For each nematode species, prevalence, abundance and mean intensity were calculated. The dominant species were *S. asymmetrica* (P=86.4%; A=73.4*), A quadrispiculata* (P=59.3%; A=25.9) and *O. leptospicularis* (P=55.9%; A=26.9). Dominance value was used to characterize the importance of each species in the parasite community, and diversity of species within the biocoenosis was measured using the Shannon-Weiner index of richness. For all the species but one *(O. leptospicularis*/*kolchida*) the parasite load significantly decreased with host age (Kruskal-Wallis test, $P<0.001$). All the species showed an aggregated distribution ($0.04<k<0.78$), fitting the negative binomial model (Kolmogorov-Smirnov one sample test, $P>0.05$). Aggregated distribution is typical of macroparasite infection, and it is considered an index of a naturally acquired ecological balance of the host-parasite system. In order to assess the association of selected variables with nematode counts and aggregation, a GLM analysis with negative binomial errors was performed. In the analysis, host age, gender, body mass, probability of sharing the pasture with domestic ruminants, season and habitat characteristics (in terms of quantity and quality of food resources) were included as explanatory variables. The results are discussed in relation to the interactions between host demographic parameters, parasites epidemiological patterns and habitat characteristics. Finally it is discussed the use of macroparasites as ecological index possibly describing the health status of the host population.

THE SAIGA ANTELOPE IN THE NORTH-WEST PRE-CASPIAN REGION: RESEARCH, CONSERVATION AND PERSPECTIVES OF RESTORATION

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During the 1950-60s in the North-West Pre-Caspian region there were up to 1,250,000 antelopes (*Saiga tatarica tatarica*). Currently in the region there is not more than 20,000 individuals. In 2004 the critical situation of the saiga in the whole range was reflected in resolutions adopted by CITES COP-13 and IUCN WCC. After tireless efforts of CMS/CITES in 2006 a Memorandum of Understanding (MoU) on conservation and restoration of the saiga has been signed by 4 range states and these countries started implementation of Action Plan (Elista, Kalmykia, 2002). Center for Wild Animals (CWA) of the Republic of Kalmykia was established in 2000 with the aim of protecting the genetic diversity of saiga and for restoring its population. The Center started experiments on captivity breeding of saigas for further release them into the nature and a program on improving public awareness. The CWA has 800 ha of land and after construction of large enclosures saigas kept here in almost near-natural conditions. CWA developed food rations suitable for all ages, including for suckling animals, made improvement in procedures for saiga immobilization and now is undertaking research on saiga genetics and non-invasive monitoring of hormonal status. Several international projects helped to conduct monitoring saiga population. "Chernye Zemli" Biosphere Reserve and "Stepnoi" Sanctuary provided good conditions for a significant part of the life cycle of saiga. Visual observations during rut season in last 4 years have shown quite low percent of adult males (1,7% - 9,1%), but data during lambing have shown an equal ratio of newborn females/males and about 8% of mortality in the first days of their life. Socio-economic survey for understanding main reasons of saiga decline was made within the Darwin Initiative project. With use of questionnaires living standards of the different strata of human population and their attitudes to the saiga were shown. In the 1990s there was a sharp decline in livestock numbers and rise poverty of rural people. Without State control the poaching became the leading factor of decline of saiga population. To improve this situation we carried out a project "Rotating cows as a tool for saiga conservation in Kalmykia", supported by the SEPS. Villagers supported this project and we hope it will show the link between saiga conservation and livelihoods. Supported by Darwin Initiative (12/028), INTAS (03-51-3579), SEPS (№ 383), Program "Biodiversity and Gene Pool Dynamics", RAS.

DOES HABITAT TYPE MODIFY GROUP SIZE IN ROE DEER AND RED DEER UNDER PREDATION RISK BY IBERIAN WOLF?

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We examined that the habitat type conditions the group size in red and roe deer under predation risk by Iberian wolves. Therefore, we predicted that: 1) the group size is higher in open habitats than in closed habitats as an antipredator response. 2) The group size variation according to habitat type is higher in the prey species that suffers higher predation rate by wolf. In the study area, wolf is the only predator of wild ungulates, constituting roe deer the most important prey. We made monthly surveys along paths to observe the group size of red and roe deer. In roe deer the group mean size in open habitats was significantly higher than in closed habitats. However, in red deer the group mean size was similar in both habitat types. In roe deer a significant seasonal variation in the group mean size was observed as antipredator response. The results indicate that under predation risk by wolf the habitat type conditions the grouping degree of roe deer. The forests offer higher protection to predators as the wolf than the heaths. In the heaths the species are more vulnerable and a higher group size can be more advantageous.

SPATIAL BEHAVIOUR OF ROE DEER IN MONTE RUFENO NATURAL RESERVE, CENTRAL ITALY

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The aim of our study is to contribute to the knowledge of the spatial behaviour of a roe deer population in central Italy. Preliminary information on the taxonomic position of the studied population highlights the sympatric occurrence of European and Italic aplotypes in Monte Rufeno. The study area was partially located within the Monte Rufeno Natural Reserve (2,892 ha), in northern Latium, bordering upon Province of Siena and Province of Terni. This area is characterized by a hilly territory; the mean altitude is around 500 m asl. The climate is temperate with less of 2 dry months in summer and a mean winter temperature about 0-10° C. The mean annual precipitation is about 1,000 mm. The roe deer population is regularly monitored; in 2005 the density was about 21.5 heads/km^2.

Seven adult roe deer (four females and three males) were captured and fitted with radio collars in February 2005. 10 locations every month were collected for each animal, with 1 fix in each 2-hr interval (from 4 a.m till 12 p.m.) and with at least a 14-hr interval between two consecutive fixes for the same animal, to avoid autocorrelation. Location was determined by triangulation with the software LOCATE. For the home range analysis we used data of two males and three females monitored from July 2005 to June 2006, excluding locations with confidences ellipses 10.5 ha. The overall home-range (12 months) and the periodic home-range sizes (July-September, October-March, April-June) were calculated using Minimum Convex Polygon and Kernel method. The mean annual home-range sizes of females was 200.2 ha ± 41.7 SD with MCP, 141.4 ha ± 54.5 SD with Kernel 95% and 14 ha ± 5.3 SD with Kernel-50%; the mean annual home-range sizes of males was 71 ha ± 17.7 SD with MCP, 21.8 ha ± 12 SD with Kernel 95% and 2.5 ha ± 0.8 SD with Kernel-50%. Males showed significantly lower kernel home-range size than females during the whole study period (Kernel-50%: Kruskal-Wallis test =12.09, d.f.=1, P=0.001; Kernel-95%: Kruskal-Wallis Test =12.60, d.f.=1, P=0.000). However we did not observe significant seasonal variation in home range size. In our study males showed home-range size similar to that described in other populations living in woodland areas, while home-range size of females was larger than that in the same populations.

INFLUENCE OF HUNTING WITH DOGS ON ROE DEER SPATIAL BEHAVIOUR: DIFFERENTIAL RESPONSES ACCORDING TO SEX AND AGE CLASSES

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Poor information is currently available on the biological effects of hunting on prey population and particularly on prey behaviour. Researchers used to focus on the hunting effects on the specific target prey, and only recently have they expanded their analyses to include the indirect effects of hunting. There is still a lack of information about the effects of hunting on non-target prey species. In our study area (Apennine Mountains, Italy), different hunting practices such as roe deer stalking, wild boar hunting, and small game hunting were allowed during different periods of the year. We analyzed how roe deer adapted their spatial behaviour during hunting season and we focused on their response to different hunting practices, in particular on the differences among individuals belonging to different age and sex classes. We captured roe deer (24 males, 33 females), marked them by means of VHF collars and collected spatial behaviour data in an intensive area of 16,000 ha. In the centre of the intensive area, a strictly protected 3000 ha-wide area (Oasi Alpe di Catenaia, OAC) is located where hunting is permanently banned. Surprisingly, roe deer stalking did not seem to affect the spatial behaviour of this species. In fact, the percentage of time the radio-collared animals spent outside of the protected area did not diminish when deer stalking was practiced. On the contrary, hunting with dogs (wild boar and small game hunting) seemed to affect roe deer spatial behaviour in view of the fact that roe deer increased the use of the habitat within OAC. Moreover, males and females showed a similar response to the harassment caused by hunting with dogs, even though with different magnitudes: females were more sensitive and showed a higher use of the protected area than males. Being this the case, hunting with dogs seemed to induce a sexual spatial segregation on a large time scale in roe deer, even though roe deer is thought to be slightly sexually dimorphic and is not known to exhibit sexual segregation. We found a significant behavioural difference among age classes too: at times when hunting with dogs was allowed, sub-adult (2-3 yr.) and adult (more than 3 yr.) roe deer had larger percentages of fixes outside OAC when compared to young roe deer (1 yr.). In conclusion, even though roe deer was not the target of hunting with dogs, this mode of hunting strongly modified their spatial behaviour, as it was able to evoke a differential response within the species.

WINTER HABITAT USE BY RED AND ROE DEER: IMPORTANCE OF SECURITY COVER

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Although pines (*Pinus* spp.) represent the main tree genus in Europe, most of the studies on habitat use by European deer (Cervidae) have been done in spruce-dominated forests. This neglects the fact that the two forest types are quite different in terms of ground vegetation being much more abundant in the pine stands, especially where they occur as mature stands. Red and roe deer pellet groups were counted in ca. 12,500 ha of pine forests during the early spring period over four years. Combination of food and cover decided of habitat attractiveness and the most intense use received these habitat types, which offered food and cover at the same time. However, the role of forage was important only where cover was already considered sufficient, suggesting that cover plays a primary role as a factor influencing the use made of winter habitat by deer. Habitat use by red and roe deer was similar both among habitats and within them, but as representatives of a smaller species roe deer seemed to be able satisfy their requirements for cover more easily than the larger red deer. No evidence of an interspecific influence of red on roe deer as suggested by Latham and Gorman (1997) was found in this study. In general, as predicted, mature pine stands were an attractive habitat for deer. It was concluded that, in hunted deer populations, the presence of security cover is important even in areas lacking large predators. In consequence, as and where necessary, the introducing of forest under stories into mature pine forests should be promoted as an element of big game management.

HABITAT USE AND SELECTION BY TWO SYMPATRIC POPULATIONS OF RED DEER AND ROE DEER IN A RECENTLY COLONISED AREA IN THE NORTHERN APENNINES, ITALY

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In the Apennines red deer populations, originated by releases in the second half of the past century, are increasing but still fragmented and isolated. In the study area of 2730 hectares, located between 200 and 1100 m a.s.l. in the province of Piacenza, red deer was first found in the eighties, originating by accidental release of few animals from a pen. Roe deer colonised the area in the Nineties by the natural expansion of populations reintroduced in neighbourhood provinces in the Eighties. The study last for a year starting in 2006. The study area was characterised by mixed deciduous woods (about 50%) and crops (37%), but also conifer woods (4%) and shrubs (3%) were present. Human settlements occupied 2% of the area and human density was moderately high (35 ind/km2). Wild boars were regularly present, while wolf was sporadic. Hunting was performed in the 89% of the area, but deer shooting was always forbidden. The habitat selection by the two species was investigated in order to appreciate seasonal differences, species relationship and human disturbance effects. 200 random points were chosen stratifying the area in altitudinal ranges. Each point was analysed, by direct surveys, to evaluate habitat characteristics in a 5 meters radius (micro analysis level) and by a GIS and a 1:25.000 land-use map (macro analysis level). Surveys were repeated seasonally to measure habitat changes and to classify the point in to one of two presence/absence categories by the collection of recent signs of each species. Data were analysed by comparing seasonal presence-absence patterns, obtaining seasonal habitat preference indexes and presence logistic regression models. Contingency tables showed significant seasonal changes in distribution and habitat selection for both species. Moreover a negatively related distribution of red and roe deer was evident in every season. Logistic regression models showed susceptibility of red deer to human disturbance, particularly during the hunting season (autumn) when the home range was the smallest recorded in the study period and presence was related to protected areas. Even the roe deer experienced human disturbance and in the hunting period its presence was associated with closed environments with a hard frutescent covering. Results are discussed with respect to the methodological pitfalls and to the known ecological information on the species.

REPRODUCTION AND FERTILITY OF A WILD BOAR (*SUS SCROFA* L.) POPULATION IN TUSCANY APENNINES, ITALY

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The aim of this study is to investigate reproduction and fertility of a wild boar (*Sus scrofa* L. 1758) population that lives in the area of Alpe di Catenaia (Arezzo, Italy). We collected 200 females shot during the hunting season 2006/2007. For each female we collected body weight, reproductive tracts, lower jaws, date and location of culling. Females were aged from tooth eruption and wear of lower jaw. Ovaries were sectioned and observed to evidence the presence of corpora lutea and follicles to determine females' age of puberty. Foetuses, found in the uterus, were counted, sexed (with morphological examination or genetic analysis) and aged to determine litter size, sex ratio and distribution of births. For the same reason we also aged and back-dated animals <6/7 months old (N=204) hunted in the same period.

Similarly to other studies conducted in France, Italy and Spain the mean litter size was 4.65. The foetuses were sexed with a morphological examination and showed a sex ratio of 1:1. They were also aged and therefore it was possible to verify that the mating period extended from October to December. Only females heavier than 35 kg and older than 10 months were pregnant. Taking into account pregnant females only we could not find any relation between the number of foetuses and age and body weight. However we found a difference between pregnant and not pregnant females both in body weight (Mann-Whitney test: Z=-5.129, P=0.000) and age (Mann-Whitney Test: Z=-5.175, P=0.000).

DIFFERENCES IN MINERAL REQUIREMENTS IN CAPTIVE IBERIAN RED DEER HINDS AND CALVES DURING LACTATION

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Iberian red deer (*Cervus elaphus hispanicus*) is the main big game species in the Iberian Peninsula. Supplementary feeding by mineral blocks is a common management practice in game estates to correct mineral deficiencies in natural diet. These supplements have been designed to satisfy animal requirements. However, current commercial blocks have been developed from nutritional plans based on livestock or on deer under intensive rising in New Zealand. Economic benefits by improving hunting trophies are the main reason for this practice, so real requirements for hinds and calves during lactation remain poorly known. We determined preferences for several minerals by multiple choice tests in captive Iberian red deer. Two hind groups and their calves were studied during the lactations period (18 weeks) of 2005 (N = 36 hinds + 36 calves) and 2006 (N = 23 + 23). Containers with 5kg of mineral were offered in a covered hut safe from rain and wind, and were weekly weighted. Se (1%), Cu (25%) and I (10%) were mixed with NaCl at concentrations of 7.5% and Zn (36%) was offered at 20%. Fe, Mg, K and Na were offered in pure compounds of iron carbonate, magnesium oxide, potassium chloride and sodium chloride. P was offered as calcium phosphate and Ca in the previous form and also as calcium carbonate. Consuming behaviour was recorded with video cameras from 7 a.m. to 7 p.m., so 490 minutes and 3618 intake events were assigned to the corresponding subject. Ratios of total mineral intake per animal between years showed that intake varied more than 100% for K (6.7), P (6.3), Ca (3.3), Se (3.0), Fe (2.7) and Zn (2.2), meanwhile Na, Mg, Cu and I showed similar intake levels. Video recording showed differences in time spent ingesting minerals between calves and hinds for every mineral. Calves/Hinds ratio of percentage of time ingesting for every mineral was compared between years and showed a variation over 100% in Cu (9.2), Ca (4.8), K (3.8), P (3.8) and Fe (2.6) meanwhile Mg, Se, Zn and I ratios remained stable. Observation data suggest that mineral requirements in hinds and calves are different and suggest both discriminate between mineral, probably ingesting those which they are in greater need. Moreover, a strong intake variation between years for several elements is showed. Therefore, results showed that mineral requirements change with stage of lactation, that some of them show variations between years even under similar housing conditions, depending on class age.

LEKKING IN FALLOW DEER (*DAMA DAMA*): A LONG WALK TO TERRITORIALITY

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From 1996 to 2002 spatial behaviour and mating success of 26 fallow deer bucks were studied in the lekking fallow deer population of the San Rossore Estate, Italy. Here we analyzed factors responsible to affect the ability of a buck to defend a lek territory and therefore to achieve the higher mating success. During each rut, radiocollared bucks were classified as follows: territorial lek males, i.e. bucks defending a lek territory and achieving a high mating success; short term territorial lek males, i.e. bucks defending temporarily a lek territory and achieving a lower mating success; and non territorial lek males, i.e. bucks not able to defend a lek territory. Bucks belonging to the last two categories tried to compensate their scarce mating success by adopting alternative but less profitable strategies (the following of females outside the lek or the temporary defence of single territories). These factors are involved in affecting the chance of a buck to defend a lek territory: age (the majority of bucks reached the status of territorial lek male when about 9 yrs old); foraging strategies adopted outside the rut, as territorial lek males showed a higher use of rich areas especially during the months before the rutting period; and antler size (larger antlers recorded in territorial males). From 2004 we monitored 25 subadult males (captured as prickets 1-2 yrs old, and monitored during rut as sores 2-4 yrs old) in order to understand the role played by behavioural experiences gained during early phases of the social maturation in affecting the future chance to defend a lek territory. Subadult males were split in two categories during the rut: lekking sores, i.e. males who combined prolonged visits to the lek with a high mobility outside the lek, as a result of continuous following of females, and no-lekking sores, i.e. males who visited only once the lek. Spatial behaviour recorded outside the rut showed us that lekking sores left earlier female groups to join male groups than other subadults, therefore reaching earlier male areas richer in resources. Lekking sores have to face a higher number of male-male interactions with other sores and bucks, and this may be a crucial step of the process leading to territoriality. Further step will be to determine if lekking sores will become adult lekking males, and no-lekking sores will be unable to use top success strategy being not able to defend a lek territory, being forced to adopt less profitable strategies.

THE ITALIAN DONKEY (*EQUUS ASINUS*): MOLECULAR VARIABILITY OF ENDANGERED AUTOCHTHONOUS BREEDS ASSESSED BY MITOCHONDRIAL AND MICROSATELLITE MARKERS

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In the last century, technology improvement and industrialization have dramatically changed the impact of human activities on natural and agricultural environments, strongly affecting wildlife and the management and use of livestock species. In modern agriculture a few cosmopolitan highly productive breeds are farmed worldwide, while the use of animals for work and transportation purposes has almost disappeared. As a consequence, diversity contributed by autochthonous livestock species and breeds is being quickly erased. Since domestication (~5000 y.b.p.) donkeys have been widely used by humans in agricultural activities and for transportation of people and goods. In the last century, Italian autochthonous donkeys suffered from a severe reduction in population size that led to the extinction of Cariovilli, Grigio Viterbese and Sant'Alberto donkeys. Eight autochthonous Italian breeds are still reared. These are all classified by FAO as critically endangered (Asinara, Pantesco, Grigio Siciliano and Romagnolo) or endangered (Amiatino, Sardo Grigio, Martina Franca and Ragusano) breeds. To evaluate the extant genetic variability of Italian donkey populations, two fragments of the mitochondrial DNA (mtDNA) control region (HVRI, 288 bp) and cytochrome b (274 bp) genes were sequenced and 16 microsatellite loci were typed in 292 individuals from these eight breeds. MtDNA data were then compared with databank sequences of donkeys from Europe, Africa and Asia, two wild subspecies Equus asinus africanus and E. a. somaliensis from Africa and other extant and extinct species of the genus *Equus*.

Among Italian donkey breeds 30 different mtDNA control region haplotypes were identified, some of which were never described before. Nucleotide diversity was relatively low, but not far from values detected in other European populations. Phylogenetic and network analyses disclosed a complex pattern of mtDNA variability and highlighted the presence also in Italy of the two divergent maternal lineages, Somalian and Nubian, which derive from two separated domestication events occurred in Africa from wild ancestors of different subspecies (*E. a. somaliensis* and *E. a. africanus*). Sequences were also grouped by geographic areas to shed light on possible underlying patterns due to past migration events. Analysis of microsatellite data revealed the presence of gene flow between breeds and of inbreeding at the intra-population level.

SPATIAL BEHAVIOUR OF ALPINE CHAMOIS (*RUPICAPRA RUPICAPRA*) TRANSLOCATED IN A PRE-ALPINE HABITAT

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We report here the results of a three-year monitoring of the spatial behaviour of a group (9 males and 14 females) of alpine chamois translocated in a low elevation (200-1600 m a.s.l.) pre-alpine area of North-eastern Italy. Post-release dispersal was more frequent in males (dispersers/total individuals: 5/9 males and 3/14 females), that also travelled greater distances from release sites than females (10.1 ± 8.7 and 4.5 ± 5.5 km). The dispersal phase started soon after release, in late April, and ended within 3-4 months. Subsequently, 11 females and 7 males became stationary, while 3 females and 2 males showed a roaming behaviour, with peaks of spatial instability in spring and during the mating season. This resulted in unusually large annual and seasonal home ranges. When excluding these individuals, annual home ranges (second and third year, kernel method, 95% isopleths) were similar for males and females (302 ± 177 and 380 ± 250 ha). In contrast with what often reported for high elevations alpine areas, we did not observe seasonal migrations between summer and winter home ranges, that remained largely overlapped. The mild winter conditions, with shallow snow cover for short periods, may explain this result.

POPULATION VIABILITY ANALYSIS OF EUROPEAN BISON HERD IN BIALOWIEZA FOREST, POLAND, WITH AND WITHOUT EXCHANGE OF GENES BETWEEN POLISH AND BELARUSIAN POPULATIONS

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European bison, the largest terrestrial mammals in Europe, became extinct in the wild at the beginning of the 20th century, and all bison living nowadays come from only 12 ancestors that survived in captivity. At present there are about 3000 bison all over the world, but the species is still endangered, among others because of low genetic variability and isolation of herds. The biggest population (about 700 individuals at the end of 2005) lives in the Bialowieza Forest situated on the border between Poland and Belarus. Free-living bison herds in the Polish and Belarusian parts of the Bialowieza Forest have been created since 1952 and 1953, respectively. Since 1980 a fence built along the border has divided the forest and precluded an exchange of bison between the two populations. The aim of the project is to simulate genetic and demographic processes in these herds and to compare their future development and viability when (1) the isolation of the Polish and Belarusian populations is maintained, and (2) the exchange of genes between them is possible. The project is based on the Population Viability Analysis (programme VORTEX). Hopefully the results of the project will help to persuade the Belarusian authorities to remove the fence and allow gene transfer between the two herds.

SEXUAL DIFFERENCES IN TOOTH WEAR PATTERN OF FALLOW DEER *DAMA DAMA* AND MANAGEMENT IMPLICATIONS

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Field estimation of ages of deer requires assessment of the degree of teeth wear. This technique is widely applied without regard to the sex of the animal being aged, while in evaluating harvest and management programs, age as well sex ratios have an important role. Sex based differences in life history traits such as diet, habitat use and foraging behaviour may affect tooth wear pattern differently in males and females. We examined how sex affects age determination based on tooth wear. Deer were aged counting cementum annuli in the root tips of I1 extracted from 172 jaws > 2.5 yrs old (70 females and 102 males). Incisors were demineralised, sectioned with the use of a cryostat and stained with Ehrlich's haematoxylin. Fallow deer were shot in the Preserve of Castelporziano near Rome (Italy) as part of the normal culling programme, between 2003 and 2005 (from November to May). Three experienced observers estimated age class of these jaws on the base of tooth wear. Ages of females have been under or overestimate (1-2 yrs) while ages of males were generally overestimated (1-5 yrs). The percentage of overestimation increased with age class, in relation to the higher tooth wear rates in males. A sex-specific photographic reference system for aging fallow deer *Dama dama* based on presence-absence of wear characters in jaws is presented. Aging based on tooth wear must be calibrated on sex with local specimens of both sexes and managers should use caution when comparing adult age ratios derived from tooth wear without regard to the sex.

ECOLOGICAL – ECONOMIC MODELLING IN FALLOW DEER (*DAMA DAMA*) MANAGEMENT: A NOVEL APPROACH

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The management of wildlife species as pests involves making choices that determine how much pests control will cost, and what kind of benefits it will deliver. In order to make these choices defensible, the effect courses of action have on how the costs and benefits of pests control accrue should ideally be understood. This study proposes a novel approach to estimate the choice of a wildlife management of an ungulate species in a conservation site (Migliarino-San Rossore-Massaciuccoli Regional Park, Tuscany region, Italy), combining biological and economical trends. In fact the management of wildlife resources provides contrasting benefits and costs, which ecological or economic approaches alone cannot analyze in their complexity and, at the same time, can only offer a limited insight.

The purpose of this work is to adopt an interdisciplinary integration of research expertise from natural sciences, economics and social sciences to manage a fallow deer (*Dama dama*) population in an ex-hunting Estate in Italy, now part of a Regional Park. The aim of this work is to develop a model to achieve a balance constrained by biological and economical variables.

The first step will be to develop a deterministic biological model that later would be implemented on a bio-economic one. At the end a sensitive analysis will be carried out to check which variable determines a “sensitive” change in the wild population structure and in the economic outputs for the protected natural area. This work provides techniques to people managing conservation and exploitation of environmental resources to realize the optimal balance between all the variables acting (ecological, economic, social...).

MINERAL DISTRIBUTION IN WINTER DIET CHOICES BY FREE-RANGING IBERIAN RED DEER (*CERVUS ELAPHUS HISPANICUS*) UNDER MEDITERRANEAN CLIMATE CONDITIONS

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Red deer are mixed feeders with a broad food spectrum, consisting of grasses, shrubs and trees, depending on the habitat and season. Their diet should contain a minimal amount of important minerals, essential for immunity, good antler growth and skeletal development. However, deer frequently can not get the required mineral doses from the daily diet, even in areas with a high natural nutrient supply. Our objective was to assess the distribution of several essential minerals in plants and potential daily mineral intake by Iberian red deer (*Cervus elaphus hispanicus*) in winter. During this season, the diet is mainly characterized by shrub-trees (60%) and grasses (40%). The experiment took place at the c. 1,000 ha Las Dehesas game state in Albacete (SE Spain), where around 200 Iberian red deer ranged with no supplementary food, anti-parasite or health treatment. Climate is typically Mediterranean with wet mild winters and hot, dry summers. Vegetation cover is typical for the Supramediterranean climatic stage. Forests are dominated by two canopy species, oaks and pines. Naturally occurring openings contain grasses, rosemary, lavender, thyme and juniper. Plant species were collected in the area in winter 2006. Leaves were then removed from branches by hand and oven-dried at 85ºC for 72 h. For mineral content determination, samples were wet digested (HNO3-(NH4)HF2) and diluted with Ultrapure deionized water. Concentrations of Ca, Na, Mg, K, Fe, Mn, Co, Cu, Se and Zn were quantified with optical emission spectroscopy. Deer showed preference for plants relatively enriched in Na, K, Mn, Cu, Se and Zn (evergreen oak, *Quercus ilex*; rosemary, *Rosmarinus officinalis*; and grasses of the genus *Brachypodium* sp.). Average daily intake per kg dry matter of Ca (5.64 g), Fe (0.34 g), Mn (38mg), Co (0.6mg) and Se (0.6mg) was adequate during winter. However, intake of Na (0.08g), Mg (1.00g), K (4.36g), Cu (5mg) and Zn (22mg) are rather below the optimal level (0.72g, 1.5g, 6.5g, 15mg and 35mg, respectively). Their deficiencies might result in metabolic problems, limiting the efficient absorption of other nutrients, and promoting reduced productivity. In conclusion, the natural habitat of Iberian red deer in central Spain might not supply an adequate amount of certain minerals, even if population density is adequate.

ESTIMATES OF ROE AND FALLOW DEER DENSITY: THE USE OF PELLET GROUP COUNT

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Accurate estimates of population density are required to plan correct wildlife management strategies. Any method currently used on wild ungulates has limits because basic assumptions may not be fulfilled or they may hardly be applicable in field conditions.

Pellet group counts (PGC) are widely used to assess deer density. Their precision and accuracy depend on dispersion pattern, sampling strategy and sampling effort. In a delineated area of the Maremma Regional Park (Southern Tuscany – Italy), PGC (clearance count) and direct counts (spotlight counts and strip transects) of roe and fallow deer have been compared to check the accuracy of PGC in Mediterranean open areas. This area, about 900 ha, was a mosaic of herbaceous crops and grassland, with some pastures and riparian vegetation. Local deer visibility was high, particularly in winter, because of low vegetation cover and group living habits. Since three homogeneous strata of high, medium and low deer densities were clearly defined on the basis of the results of a strip sampling survey performed in winter 2006, a stratified sampling scheme based on plot sampling was adopted both in summer 2006 and winter 2006/07. In both seasons, an overall number of 62 circular plots of 5 m radius was considered (effective sampled area = 0.05%).

In order to maintain an homogeneous sampling effort over the whole area, the number of plots assigned to each stratum was proportional to the stratum size. On the smaller stratum, plots were allocated according to unaligned systematic sampling, while in the two larger strata, a two-stage sampling strategy was adopted. In the first stage, some of the sub-area units partitioning the stratum were selected using a sequential sampling scheme with selection probabilities proportional to size and subsequently plots were allocated to the selected sub-areas according to unaligned systematic sampling. Spotlight counts (SC) were made during 3 nights, in both PGC sampling seasons. 73% and 67% of the total area were respectively spot-lighted in summer and winter, because of different road conditions. Each dawn strip transect (ST) was walked three times, in winter, in 3 successive days.

Density estimates (roe deer, ind/km^2) were: PGC = 6.5 (90% confidence interval based on the normality assumption: 4.4-8.6), SC= 6.79 in summer and PGC= 5.1 (90% confidence interval based on the normality assumption: 2.8-7.5), SC= 4.9, ST= 5.2 in winter. Density estimates (fallow deer) were: PGC= 4.4 (90% confidence interval based on the normality assumption: 2.9-5.9), SC= 5.4 in summer and PGC= 1.03 (90% confidence interval based on the normality assumption: 0.2-1.8), SC= 1.8, ST= 0.7 in winter. The use of PGC together with a suitable sampling scheme has shown good performance in obtaining reliable population estimates in our Mediterranean open area, which has been confirmed by the similar density estimates obtained by means of direct counts, for both species.

HAEMATOLOGICAL VALUES OF IBERIAN RED DEER NEONATES *(CERVUS ELAPHUS HISPANICUS*)

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Determination of the haematological parameters might be a useful tool for monitoring the health status of red deer. However, it is necessary to first assess their physiological values. Although several authors have addressed this topic in different subspecies of red deer, to the author's knowledge only one study has focussed on Iberian red deer. Blood haematological values were determined in 50 Iberian red deer calves during their three first days of life. These animals were born during the normal calving season (May to June) at the Experimental Farm of Castilla-La Mancha University in Albacete (SE Spain) and were the result of single calving. Weight of calves and mothers were 7.9±0.1 (5.0-10.4) kg and 92.6±1.6 (67.3-117.0) kg, respectively. Mothers were aged 4.2±0.4 (2-9) years. Samples were taken from the jugular vein without need of sedation. Calves were restrained by hand and none of them showed clinical signs of disease at the extraction moment. Blood samples were obtained about 9:00 a.m., using evacuated tubes with an anticoagulant (EDTAk3). Then, they were analysed by flow cytometry to determine red blood cells count (8.07±0.10; 6.7-9.67 106/mcL), haemoglobin concentration (11.62±0.16; 9.4-14.2 gr/dL), haematocrit (39.76±0.40; 33.8-46.3 %), mean red cell volume (49.50±0.52; 42.4-60.4 fL), red cell distribution width (20.24±0.36; 13.4-27.1 %), mean cell haemoglobin concentration (29.17±0.22; 26.1-35.8 g/dL), mean cell haemoglobin (14.60±0.23; 11.2-20.9), white blood cells count (WBC; 5.16±0.26; 2.10-13.04 103/mcL), lymphocytes percentage (31.51±1.77; 7.6-79.1 %), lymphocytes count (1.54±0.09; 0.28-3.58 103/mcL), WBC-lymphocytes percentage (68.49±1.77; 20.90-92.40 %), WBC-lymphocytes count (3.63±0.24; 0.93-11.12 103/mcL); platelets count (691.77±23.35;1119-153 103/mcL), mean platelet volume (6.08±0.053; 5.3-7.3 fL) and platelet distribution width (39.05±1.24; 25.1-49.9%). Comparing these results with the literature, calves had less red cell than adult deer. Erythrocytes were bigger, more heterogeneous in size and contained less haemoglobin (both in concentration and in total quantity) than adults. The white cells were also less numerous in calves, and differences also appear in the differentiate count. In contrast, calves had more platelets than adult animals.

TIME COURSE OF THE RELATIONSHIP BETWEEN ANTLER AND BODY MEASURES IN CAPTIVE IBERIAN RED DEER FROM 1 TO 6 YEARS OF AGE

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The relationship between antler and body weight of Iberian red deer (*Cervus elaphus hispanicus*) is widely known. However, fewer studies have assessed such relationships using historical data of the same individuals along their life, because such type of studies are much laborious. The present study monitored 16 Iberian red deer males from 1 to 6 years of age to assess the relationship between antler and body size variables along the growth of the animals. Antler variables examined included antler length, brow and central tine lengths, number of tines, diameter of main beam at burr, and the trophy score based on international standards. Body measures included body weight, particularly at start of antler growth, neck and thorax perimeter, and shoulder height. The results show a positive relationship between body and antler variables not only with increasing age, but also considering animals of the same age. Because the quality of animals has shown to be related to fluctuating asymmetry, the study also examined absolute asymmetry between left and right antlers. The results show inverse relationships between fluctuating asymmetry and body measures. In conclusion, antler size appears to show consistency in the honest advertising of body weight and male quality along the life of the animal.

SEASONAL CHANGES IN HABITAT PREFERENCES OF SELECTIVE AND BULK GRAZERS IN A COASTAL SAVANNA, TANZANIA

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For ungulates, two opposing factors, food quality and quantity, are decisive for their choice of habitat and forage species. We studied the seasonal patterns in habitat preferences and diet choice of three ruminant grazers in a coastal savanna in Saadani National Park, Tanzania. The species were chosen according to differences in food selectivity: reedbuck *Redunca redunca* as a small selective grazer, wildebeest *Connochaetes taurinus* as a large bulk grazer and waterbuck *Kobus ellipsiprymnus* as a large intermediate grazer. We expected that the selectively grazing reedbuck would pick out the nutrient richest plant species in the nutrient poor tall grass savanna, but predicted that the bulk grazing wildebeest, and probably the waterbuck, were limited to habitats offering a minimum average of nutritive quality. We related seasonal patterns in the habitat preferences of the three grazers according to their degrees of selectivity. We monitored their occurrence in different habitat types by direct observation (night and day transect counting with distance sampling) and indirect dung surveys. We analysed the plant species composition in their diet by means of microhistological dung analyses. We also analysed seasonal changes in habitat structure and vegetation composition (species composition, biomass and nutrient quality of the composing forage plant species) of the main habitat types. We observed a distinct shift in habitat use of all three study animals, which varied with the degree of selectivity. The more selective grazers, reedbuck and waterbuck, occurred more often in acacia forests with progressing dry season, whereas the bulk grazer wildebeest continued to use grazing lawns and black cotton plains. These results were reinforced by analyses of the nutrient content in the animal's dung. Reedbuck maintained a constant nutrient quality in its diet until the end of the dry season, whereas the nutrient content in the dung of bulk grazers declined significantly. The preference for acacia woodlands with low biomass quantities might be explained by the high proportion of remaining living leaves of *Panicum infestum* at the end of the dry season, a grass species highly preferred by all three study animals. Our results confirmed our initial expectations that selective grazers can persist in nutrient poor habitats in all seasons, whereas bulk feeding animals have to search for habitats with sufficiently high biomass and plant quality.

FERAL GOATS AS A LINKING SPECIES IN THE SPREAD OF DISEASE BETWEEN AGRICULTURAL AND FOREST SYSTEMS

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Feral goats may act as reservoir hosts of shared endoparasitic species communities with domestic stock. In areas of sympatry between feral goats and domestic stock there is the potential for goats to act as a linking species for parasites and disease between domestic stock and other wildlife. Faecal egg counts (FEC) and sward larval counts (SLC) can be employed to quantify the spread of gastro-intestinal parasites from pasture to the forest system and as transmission is by the faecal-oral route this quantification can be used as a proxy for the risk of the spread of Tuberculosis, Paratuberculosis, Foot and Mouth disease, Liver Fluke, Coccidiosis and other faecal-oral route infections. The current research focuses on sympatric populations of goats in Northern Ireland using a paired design to sample sward and dung on pasture and adjacent forest. This study will further our understanding of the spread of parasites and disease between wildlife and domestic stock, aid the control of disease and parasite transmission and contribute to the decision making process and policy for management of wild ungulates.

GENETIC RELATEDNESS AND SPATIAL BEHAVIOUR IN WILD BOAR

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The social organization of the wild boar (*Sus scrofa*) is centred around groups including adult females and their offspring. The association between young individuals can extend to the post-weaning period thus producing groups of subadults of both sexes. Adult males on the contrary remain solitary year-round.

However, the genetic relationships among members of social units have not been investigated so far, like their correlates with the space use.

We investigated the social organization of the wild boar using genetic and spatial data from a study population in Tuscany, Italy. In total 120 wild boar of different sex and age classes were captured by cage traps or nets, sampled, ear-tagged and monitored during the period 2002-2006. All of them were genetically analysed by using 10 polymorphic microsatellites ($He = 0.696$, $A = 6.6$) and a matrix of pairwise relatedness coefficient was calculated. Spatial data were gathered for 65 animals, suited with radiocollars or ear transmitters, which were followed on average for 8.7 months. Individuals were partitioned into groups according to capture data, confirmed by observations and telemetry. Accordingly, 21 social units were identified, joined by on average 4.4 (SD = 2.4) individuals. Mean relatedness within groups amounted to 0.285 (± 0.211), which was lower than the average value obtained for control groups of mother/offspring ($r = 0.492$; $t = 6.6$, $P<0.01$). The prediction that only first-degree-related individuals are present in a social unit was not confirmed, as both unrelated adult females and unrelated piglets were found in the same group. Overall, genetic relatedness was negatively correlated with geographic distance between home ranges, but this relationship was significant only in summer and autumn. This result can be put into relation with the progressive weakening of sow-piglets association and with the effects of hunting on the spatial behaviour of wild boars.

ABUNDANCE, HABITAT USE AND ASSOCIATION OF MUSK DEER WITH SYMPATRIC SPECIES IN UTTRANCHAL HIMALAYAS

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Out of the four species of musk deer the *Moschus chrysogaster* is found in India. The species is found in the high altitude of Himalayas. The Uttranchal Himalayas was surveyed between the altitudinal range of 2500-4500m a.s.l. Early morning trails were traversed for abundance estimation. The data on Indirect evidences I,e, pellet groups were collected to find out the current status and distribution of species in its distributional range in Uttranchal Himalayas. Along with the musk deer pellet groups the data on indirect evidences on other associated species such as Bharal, leopard, Indian pica, Himalayan black bear, languor, sambar, Himalayan thar, Serow, Yellow throated marten, wild bore were recorded to find out the association and the discrimination in the distribution of the species. Total 13 sites were surveyed and encounter rates as well as pellet group density were recorded. The encounter rate was found to be maximum at Saukherk area, while pellet group density (pellet groups/ha±S.E.) of musk deer were recorded from Saukherk (58.8±8.9) followed by Mulakherk (41.4±11.67) and Hitoli (30.78±7.07). The DFA was performed on transformed and standardised data and results show that musk deer prefers the areas with low herb density, while the associated species prefer the areas with high herb density. PCA and Logistic regression Analysis was performed to find out the habitat use of Musk deer. The first three component accounted for 23.7% of variation in data matrix Results shows that Musk prefer the habitat with high shrub cover, with low tree cover and also avoids the human disturbances.

RANGING OF EUROPEAN BISON (*BISON BONASUS*) MALES DURING RUT IN BIALOWIEZA PRIMEVAL FOREST, POLAND

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Breeding success of males in many species of ungulates depends not only on their social rank, body size, and condition, but also on the spatial strategy, movements during rut, and distribution of females. Number of males participating in mating and their breeding success may influence the genetic structure of populations and is especially important in species which experienced demographic bottle-neck in recent history. The European bison *Bison bonasus*, the largest terrestrial mammal of Europe, is an example of species which was reconstructed after extinction at the beginning of the 20th century, and brought back to the wild. The contemporary lowland line of European bison has only seven founders.

In 2005-2007, we studied spatial mating strategies of European bison males in one of the best preserved forests of Europe. Based on radio-tracking of 15 individuals, we identified three types of spatial strategies: strategy I - ranges used by a male before and during rut were similar in size and overlapping; strategy II - ranges used prior to and during rut were similar in size, but non-overlapping or slightly overlapping, strategy III - a male increased his range few-fold during rut compared to pre-rut period. Males employing strategies I and II did not increase their daily movement distances during rut. Usually for longer periods, they joined groups of cows passing through their rutting ranges and mated only with females from the same winter herd. In strategy II, spatial shift of male home-range was caused by distribution of cow activity areas; a male shifted his range to get access to cows. Strategy III was typical for the largest (probably high-rank) males. During the rut, they roamed among different groups of females, covered large ranges, and moved long distances (up to 15 km per day). Their rutting ranges covered the ranges of females originating from different winter aggregations. Those males joined groups of females for short periods and, thanks to their position in hierarchy, probably easily gained access to receptive females by driving other males away. Because of limited or no exchange of individuals between groups originating from different winter aggregations, those males probably have the largest influence on genetic structure of population. Paternity analysis will evaluate the influence of ranging strategy on male breeding success.

WILD BOARS IN THE NORTH-EAST OF EUROPE

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Archaeological excavations of wild boar remains (bones) revealed that this animal was common in the greater part of European Russia up to the XVIIIth century. Minimum area of distribution of this species in Russia was in the early XXth century.

In the 40s of the XXth century wild boar numbers in Russia began increasing. In the European part of the country the range expanded predominantly in east and north-east directions. Wild boars penetrated in the middle and north taiga too. In winter 1977-78 wild boars were found in Arkhangelsk Region at the latitude of the Arctic Circle. Thus, in the European part of Russia the restoration of this species' historical area and even its expansion took place.

Restoration of wild boars resources was carried out by the method of introduction (5935 individuals during 1937-1990). An important factor that favored wild boar relocation to the north-east of Europe was incomplete gathering of the crop and measures on animals' conservation.

In the north part of its area wild boar has a negative impact on the forest biocenosis. It was found that in Yaroslavl Region during spring period wild boar destroys about 50 % of hazel grouse clutches, 27 % of black grouse clutches and up to 20 % of capercailzie clutches. The reason is that in spring wild boar prefers to feed in forest borders, marsh edges, low forests. Here Tetraonidae build nests most often. Except upland fowl wild boar preys upon hare, gray partridge, waterfowl.

Now wild boar is the basic game species in many regions. After-harvesting wild boar numbers in Russia in 2006 make up about 225 ths heads including about 150 ths individuals in the European part of the country.

COPULATORY SUCCESS IN LEKKING FALLOW (*DAMA DAMA*) BUCKS: HYPOTHESES TESTING USING STRUCTURAL EQUATION MODELS

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We studied the possible causal factors explaining the copulatory success in lekking fallow bucks. We tested hypotheses using Structural Equation Models (SEM). Data were collected in the population of fallow deer in the Preserve of Castelporziano, Rome (Italy) during the rut of 1991 and 1992, in the traditional lekking area. Bucks were recorded by a videotape recorder and individually identified. Morphological measures were obtained by the trophy. We estimated the number of tines and spellers from drawings of the antlers, and we calibrated them by a blind test. These measures were used to calculate parameter describing animals' fluctuating asymmetry (FA). We performed also systematic behavioural observations at the lek, recording the position of each buck, the number of fights, its sexual activity and the number of females and fawns inside each display territory. A total of 13 behavioural parameters (including, among others, dominance, reproductive success, harem size) were used in the statistical analysis.

It is well known that "discrimination" hypothesis is made difficult by the presence of spurious correlations among behavioural and morphological parameters. We tried to circumvent this problem using the path analysis, with both latent and manifest variables, to model the impact of studied variables on copulatory success of fallow buck. We used information criteria such as AIC to select the model which better fits our data. According to literature, we developed four a priori models.

1) Random mating. In this model we assumed that copulatory success is only depending on lek attendance. This model is clearly not realistic but it may represent a sort of basic benchmark for our analysis
2) Male dominance.
3) Female choice.
4) The last model assumes that both female choice and male dominance interact to determine one male's copulatory success.

Model comparison and a careful analysis of models' fitting showed that the male dominance model is much more appropriate in explaining the observed covariance patterns.

ENVIRONMENTAL FACTORS AFFECTING WILD BOARS (*SUS SCROFA*) IN FREITA-ARADA NATURA 2000 SITE, PORTUGAL

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Mainly due to over hunting and habitat degradation, the wild boar in Portugal was considered almost threatened species at the end of the 1960's and its hunting was forbidden. Currently, the species is distributed all over the country apart from littoral big cities. This massive increase should be monitorized to prevent human and other species conflict and to avoid, like in the past, such a drastic population decline. In specific areas, in order to improve the wild boar population and habitat management measures it is crucial to know habitat preferences as well as other ecological aspects.
Geographic information systems (GIS) have a precious role in those procedures, attempting to incorporate and relate natural resources and species ecological parameters allowing the development of habitat suitability models. The aims of this study were: determine the variables which have influence on the dynamic of the wild boar population; develop a map representing the wild boar potential habitat; investigate the relationships between wild boar trends, habitat and game management in Freita-Arada Natura 2000 site (PTCON0047). Freita-Arada Natura 2000 site has approximately 29 000 ha and to determine the number of survey points, land cover and altimetry were analyzed in GIS-ArcMap. Data from wild boar activity, habitat characteristics (plant species, size and percentage of tree, shrubs and herbaceous cover), game management practices and intensity of these activities in a 100 mt radius around each point were collected. The dominant species belong to shrub stratum (47.2%) and conifers (27.8%). Cropland represents 13.7%, Eucalyptus sp 7.4% and deciduous forest and urban area represent 2.4% and 1.5%, respectively, Habitat suitability model was developed by combining ecological niche descriptors (food and shelter availability) into an arithmetic equation. Model's validation was achieved by using a binary logistic regression comparing the equation results with the population density in each survey point. In its first analysis results suggest food availability represents the best and biggest answer rate in the model ($P=0.146$; concordance = 55.3%). Tree cover (fruit) seemed to have more significance and it's more discriminating during reproductive period (concordance= 60%), meanwhile, herbaceous and shrub covers are important during all year.

PRELIMINARY STUDY ON MOUFLON (*OVIS ARIES*) POPULATION IN THE APUANE ALPS, ITALY

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Since 2003 we have been carrying out a research included in a plan of triennial study funded both by the Tuscany Regional Agency for the Development and the Innovation in the Agricultural-Forest Field and by the Regional Park of the Apuane Alps (Northern Tuscany) on mouflon (*Ovis aries*). The aim of this study was to find out the consistency, the distribution and the structure of the mouflon population. The mouflon, with the wild boar (*Sus scrofa*), is the most typical ungulate of the Regional Park, being still in expansion both the roe deer (*Capreolus capreolus*) and the red deer (*Cervus elaphus*); its presence is interesting for two points of view: both for the adaptation shown in a so unusual environment and for a probable presence of the wolf (*Canis lupus*) in the protected area. According to the data collected from February 2003 to December 2006, by means of censuses and direct observations, we obtained the first outcomes about the demographic and structural parameters of the studied population. The mean density for the four years resulted 35 individuals/100 ha, and the population was composed by 57% adults and 43% yearlings and juveniles. These results, mostly referred to a mountainous formation in the centre of the Apuane Alps called Panie Group where the most consisting nucleus of the studied ungulate is present, allowed us to suppose the possible expansion routes of the mouflon in the territory.

RESIDUAL GROUPS OF MOUFLON (*OVIS ARIES*) IN CASENTINESI FOREST (ITALY): HISTORY AND FUTURE OF AN ALLOCTONE PRESENCE

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The introduction of mouflon (*Ovis aries*) in the European continent was carried out during the second half of the 18th century. It is supposed that the Casentinesi Forest was one of the first area where the species was introduced; after the first introduction many successive releases of this ungulate were done through the years until the end of the seventies. At the end of eighties the species was declared vanished in the area of the National Park. At the beginning of 2003, the State Forest Administration and its wildlife biologists, provided an investigation about the history of this population through a critical analysis of the existing information in archives and through the numerous directed evidences and at the same time, undertook a field research based on sightings to collect data on residual presence and consistence of the mouflon in the Foreste Casentinesi, Monte Falterona and Campigna National Park (Tuscany, Romagna - Northern Apennines, Italy). At present a small population survives steadily in a very limited habitat. Two distinct herds were detected, with a total consistence fewer than 30-40 individuals, showing that the species never really disappeared from this area. This preliminary study allowed us to update the knowledge on the distribution and to estimate population parameters of this ungulate, supporting future management of the species.

INSULAR POPULATION OF MOUFLON (*OVIS ARIES*): AN EXPERIMENTAL CENSUS METHOD

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The island of Zannone (Archipelago of the Pontine Islands - Circeo National Park, Lazio region, central Italy) is characterized by typical Mediterranean environment with oak (*Quercus ilex*) forest formations. A small population of mouflon (*Ovis aries*) is present since the first years of the '900. During the last fifteen years the population was considered stable, but periodic censuses have never been conducted and the density was estimated only by personal and episodic valuations. Only during nineties the population was censuses with the "pellets count group" method. For this reason a deeper investigation on population structure, its density and habitat use was required. The difficulty in approaching an informative census technique of the mouflon population in Zannone Isle is due to the complex morphology of the landscape and to the absence of "open areas" observable from vantage points. From October 2006 to May 2007, two experimental sessions of census through block count were carried out (census by directed observations on divided areas), method often used in valleys of the Alps. The aim of the present study is to give a critical comment around this census technique and to assume a "valid protocol" to apply this instrument of ecological-biological analysis to other insular environments comparable to Zannone Isle.

THE MANAGEMENT OF MIGRANT AND RESIDENT FEMALE RED DEER IN A MOUNTAINOUS HABITAT

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As a large mammal, red deer has a long lifespan, a low reproductive rate, large home ranges and population dynamics strongly related to age and sex. Long term research, based on large numbers of individually recognisable animals, is necessary to assess the local population dynamics and parameters that are fundamental for a correct management. Conversely, managers of ungulate populations usually base their strategies on traditional knowledge or short-term studies, often with undesirable effects on population structure and viability.

From 2002 to 2006, 30 red deer hinds were radiotagged in the Travignolo Valley (Trentino, Eastern Italian Alps). Two different spatial strategies were assessed in the marked population: resident hinds (50%), occupying the same area throughout the year, and migrant hinds (50%), showing separated winter and summer areas, distant up to 30 km from each other. Radiotracking data have suggested that the current management approach should be improved in terms of i) size of management unit, ii) techniques for population estimates, iii) hunting plan.

Our study was funded and supported by the Paneveggio - Pale di San Martino Natural Park, the University of Siena, the Forest and Wildlife Service of Trento Province and the Hunters Association of Trento Province.

We are grateful to the many persons who helped us to carry out our work.

EFFECTS OF HIGH POPULATION PRESSURE AND HUMAN DISTURBANCE ON SOCIAL STRUCTURE, BEHAVIOUR AND HABITAT UTILISATION OF FALLOW DEER (*DAMA DAMA*) ON THE ISLAND OF LEMNOS, NORTH-EASTERN AEGEAN, GREECE

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In Greece, a wild fallow deer (*Dama dama*) population was established on the island of Lemnos, in a confined area in the late 60s. Nowadays a population of 65 animals survives under very intensive conditions (227 deer/km^2), with low water and food supply and high levels of human disturbance, especially during summer months. The aim of the present study was to describe the current population structure, and patterns of habitat use and behavioural adaptations of adult male and female fallow deer under such conditions. The study area was a small peninsula surrounded by the capital city of the island of Lemnos, in north-eastern Aegean, Greece. The area is characterized by steep rocky edges and cliffs that are separated by open fields of low vegetation, with scattered pine and deciduous forest patches and is entirely accessible to the animals. Data collection occurred between summer 2005 and summer 2006. Eighteen males and forty-seven females were observed using animal scan sampling procedures for 8h/d, for 15d per season. The sex ratio of the population was estimated to 1 male: 2.6 females, indicating a higher survival rate of the females. On the other hand, the ratio of fawns/females was relatively low (0.26), probably related with a reproductive strategy of reducing maternal effort in response to restricted food sources and high population density. Sexual segregation, typical of the species, was maintained especially during the summer period. Moreover, same-sexed groups tended to use diverse and distant parts within the study area, despite its small size. In terms of behavioural patterns, feeding was the dominant activity, with the exception of males >4 years, that exhibited hypophagia during the breeding period. Females showed the lowest levels of feeding and the highest mobility during summer, suggesting a positive relationship to high human disturbance during this season. Males appeared to be more accustomed to human presence, whereas protection of young was a high priority for females. In general, the population of fallow deer of the island of Lemnos appeared to be well habituated to the area, using mainly forest patches, with horizontal or medium inclination, away from human settlements. The relative stability of population size (~60 deer in 1986) possibly suggests that behavioural and physiological regulative processes occur towards this direction. However, this hypothesis needs to be tested by medium- and long-term monitoring of the population.

ROE DEER DIET IN A COASTAL MEDITERRANEAN AREA

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The European roe deer *Capreolus capreolus* (L., 1758) is the most abundant and widespread deer in Europe, living in a great variety of habitats. Aspects of its feeding behaviour have been studied in Central and northern Europe, but only little is known about the diet of roe deer living in the Mediterranean range, characterised by mild winters, but hot and dry summer months. We investigated the diet selection of roe deer in a coastal Mediterranean area (Maremma Regional Park, in Italy), to evaluate their adaptive strategies to the local forage availability. Here we present the results about the number of plant species used by roe deer.

Availability of food resources was estimated through plots in the herbaceous and woody layers, whereas the diet composition was studied through the detection of food residues in faecal samples. A total of 597 faecal samples were collected monthly along permanent transects (10km) between March 2003 and February 2005. Sub-samples were analysed under microscope (100-400x), comparing the anatomical features of the epidermal residues of the ingested plants with those of a reference collection.

A total of 332 plant species/genera were observed in the availability plots of the study sites, whereas 151 plant species/genera were identified in the faecal samples. In particular, nearly all tree and shrub species/genera were found in faecal samples, whereas the percentage of graminoid- and forb-species/genera built up 48% and 34%, respectively. Despite the low proportion of forb species found in the samples, this category built up 56% of all consumed species, whereas 33% were trees and shrubs and 11% graminoids. In contrast to many other European studies, the diet in our area was characterized by a relatively constant number of species used throughout the year: the number of species per faecal sample was relatively high (median: 9 species) and varied only little between seasons (Kruskal-Wallis $H = 8.07$, $P = 0.045$; median: spring = winter = 9, summer = autumn = 10). The total seasonal number of species ingested was similar from spring to autumn (112-119 species) and decreased only slightly in winter (101 species).

In conclusion, our study has shown that some aspects of the feeding behaviour of the European roe deer are also evident in the Mediterranean environment, *i.e.* wide range of species used, use of nearly all available tree- and shrub-species/genera, low proportional use of forb- and graminoid-species/genera.

CRANIOMETRIC CHARACTERS OF ROE DEER ITALIAN POPULATIONS ANALYSED IN A MULTIDIMENSIONAL SPACE

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The roe deer is a wide ranging cervid that show considerable morphological variability across its range (Palaearctic and continental Asia). More than 25 subspecies have been described based on phenotypic variation. Two subspecies are currently recognized in the Italian peninsula: *Capreolus capreolus capreolus* and *C. c. italicus*. The nominal form occurs in north-central Italy. The endemic subspecies has been formerly described by Festa (1925) on the base of body size and fur colour of 5 adults and 2 juveniles. Recent genetic studies based on mitochondrial DNA and microsatellite analyses clustered Italian samples into two different groups: the first one includes roe deer coming from north-central Italy, and the second one those coming from south-central Italy. Aim of this study is to analyse the craniometrical differences between these two forms in order to clarify the sistematics of roe deer in Italy, integrating genetic data with morphological ones and to compare the traditional and the geometric approach in morphometrics.

The craniometrical investigation was performed on 400 skulls from Eastern Alps, northern and central Apennines, Tuscany and Latium. Forty three measurements were taken on each specimens with a digital caliper and 93 (28 dorsal and 37 ventral) three-dimensional landmarks were digitized using a Microscribe 3DX. Using traditional morphometrics the stepwise discriminant analysis performed on the scores of the first and the second PC showed that more than 94% of the original grouped cases was correctly classified. The same results were obtained with log transformed data and with ratios.

In geometric morphometrics an average configuration per group was calculated to measure overall morphological similarity and an UPGMA clustering of the matrix of sum the Procrustes residuals was made. The analysis of morphological affinity among groups suggests differences among central and northern populations. The craniometric differentiation of groups seems to confirm the results obtained by genetical studies.

The validation of the endemic subspecies is not only a taxonomic problem, but plays an important role in the definition of adequate conservation strategies of the isolated populations and in the reintroduction policy.

LARGE-SCALE MITOCHONDRIAL DNA ANALYSIS OF THE DOMESTIC GOAT REVEALS SIX MATERNAL LINEAGES WITH HIGH HAPLOTYPE DIVERSITY

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The genetic diversity of domestic goats has been characterized with 2430 individuals from all over the old world, including 951 new individuals from regions poorly studied until now (mainly the Fertile Crescent). These individuals represented 1540 haplotypes for the HV1 segment of the mitochondrial DNA (mtDNA) control region. This large-scale study allowed the establishment of a clear nomenclature of the goat maternal lineages. Only five of the six previously defined lineages were divergent enough to be considered as different lineages. Moreover a new mitochondrial lineage has been localized around the Fertile Crescent. All lineages showed very high haplotype diversity. Most of this diversity was distributed among lineages and within geographic regions. The weak geographic structure may result from the worldwide distribution of the dominant A lineage (representing more than 90% of the individuals). The large-scale distribution of other lineages (except lineage F), may be due to the migration and trade activity of human. The recent fragmentation of local goat population into discrete breeds is not detectable with mitochondrial markers. About 77% of the mtDNA variation was distributed within breeds mainly because several breeds (about 25%) were constituted by at least two maternal lineages. The estimation of demographic parameters from mismatch analyses showed that all lineages had a recent demographic expansion corresponding roughly to the period when domestication took place. But even with a large data set it remains difficult to give relative dates of expansion for different lineages because of large confidence intervals. Finally, we propose standard criteria for the definition of the different maternal lineages based on the result of mismatch analysis and on the use of sequences of reference. Such a method could be also applied for clarifying the nomenclature of maternal lineages in other domestic species.

MITOCHONDRIAL DNA PHYLOGEOGRAPHY OF BEZOAR *CAPRA AEGAGRUS*

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Bezoar (*Capra aegagrus*) is a vulnerable species mainly distributed in Asia. To describe the evolutionary history and to assess the genetic diversity and population structure of this species, we sampled 487 individuals from 43 geographic localities representing the whole distribution area. We sequenced 590 bp of the HV1 segment of the mitochondrial DNA (mt DNA) control region. This fragment shows a high polymorphism with 436 variable sites over the 563 base pairs (bp) of the alignment. We observed 639 substitutions (393 transitions and 246 transversions) and 152 insertions/deletions (from 1 to 76 bp). A total 251 haplotypes were identified. The haplotype diversity (0.9894+/-0.0013) and nucleotide diversity (0.094491+/-0.045260) are both high. An analysis of molecular variance (AMOVA) revealed that about 46% of the mt DNA variation was distributed among populations. Moreover, the genetic structure and the evolutionary history of Bezoar were inferred from a phylogeographic analysis. The presence of geographic structure and significant differentiations between populations will be utilized for the definition of management units (MUs) in conservation genetic programs.

GENETIC STRUCTURE OF RED DEER *CERVUS ELAPHUS* POPULATIONS IN THE FORESTS OF NORTH-EASTERN POLAND

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We conducted genetic analyses of 300 samples of red deer *Cervus elaphus* tissues collected during the hunting seasons in 2004-2007 in 8 woodlands of north-eastern Poland (Augustów, Bialowieza - including also its Belarusian part, Borki, Knyszyn, Mielnik, Pisz, Rominty, and Napiwoda-Ramuki Forests). The entire studied region harbour populations of red deer originating from the 19th-20th century reintroductions. We analyzed 17 microsatellite loci. Moreover, for some of the samples, we sequenced 319-bp control region of mtDNA. Preliminary results of the analyses of microsatellite loci showed that the mean genetic diversity among populations of red deer in the studied forests was small. However, 2 or 3 groups were distinguished: (1) Bialowieza group (including individuals from Bialowieza, Knyszyn, and Mielnik Forests), (2) Mazurian group (animals from Augustów, Borki, Pisz, and Napiwoda-Ramuki Forests), and probably (3) Rominty group (including red deer from Rominty Forest, only). The existence of the third group needs further studies. To interpret the results of the genetic analyses, we also conducted studies on the history of reintroduction of the species in north-eastern Poland and made spatial analyses using Geographical Information System (GIS) software.

BODY SIZE CHANGES IN THE ENDEMIC PLEISTOCENE DEER OF MEDITERRANEAN ISLANDS

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Endemic mammals represent a special ground for the study of evolutionary mechanisms and speciation processes in isolated environments. Nevertheless, changes in size of vertebrates once segregated in isolated geographic areas such as islands, and notably the dwarfism of large mammals, is still a debated question. During the Pleistocene, endemic cervids were among the most common species in the unbalanced faunas of the Mediterranean islands. Even if several taxa were present, no species with an entirely comparable adaptation existed on different islands and it is difficult to identify a dominant factor in their evolution. Moreover, the largest endemic deer from Crete don't respect the "island rule", becoming even larger on islands. Many factors possibly lead to different body size evolution on each island, or on the same island at different time, depending on faunal structure, ecological interactions, resources, isolation and maybe island area and physiography. To assess size changes undergone by extinct endemic deer from Mediterranean islands (Corsica, Sardinia, Capri, Sicily, Crete, Karpathos, Kasos etc) we have compared average body mass of insular taxa with that of their mainland ancestors. We have preferred to used body mass because of changes in size of insular mammals is allometric whilst a size ratio computed by linear measurements, implies scaling is isometric. Body mass has been considered as the best proxy of body size, and different allometric equations, have been proposed, based on cranial teeth or long bone dimensions. Postcranial parameters are in general accepted as quite reliable body mass predictor. Nonetheless, since the wide variability in skeletal structure it is not easy to find equations that can be used for either "heavy" or "slender" artiodactyls. Accordingly, different morphotypes have been selected. This makes it possible to test the reliability of the estimated body mass using different equations. Results obtained provide evidence that evolutionary patterns and size changes of Pleistocene deer from the Mediterranean islands was mainly driven by intra-guild competition, vacant species and, to a lesser degree, by predation pressures. Nonetheless, differences in size rely on the interaction of different factors. For instance, besides the change in adaptive strategy for more efficient energy use, characteristics of islands and time of isolation would have played a role in the possible differential evolution of insular deer.

INTERNAL ORGANS MORPHOMETRY AND WEIGHTS OF THE WILD BOAR POPULATION *(SUS SCROFA*) IN TREVIGIAN PREALPS

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The first presence signs of wild boar (*Sus scrofa*) in Trevigian Prealps (northern Italy) go back to the end of the years ninety in north-east area of the Province. Currently the wild boars are uniformly distributed in all northern area of the territory. The effective wild boar origin has not clearly demonstrated even if there are proofs of the illegal introductions.

This study evaluated the morphometric and weights data of a wild boar sample shot during an eradication plan (between January 2004 and March 2007) started on from the Treviso Province. The data are compared with wild boar and swine literature.

The gastrointestinal tract mean length of thirty subjects, having mean body weight (BW) 81± 42 kg (mean ± SD), body length (BL) 133±19cm and chest circumference (CC) 103±20 cm, was: Curvatura ventriculi minor 17±4 cm; Curvatura ventriculi major 65±14 cm; whole intestine 1598±293 cm (small and large intestine, and caecum represent respectively the 76.2±2.1%, 22.4±2.1 and 1.3±0.2% of the intestine whole length).

The relative mean weight of internal organs (organ weight/BW) was: heart 0,52±0,09% (18 subjects; mean BW 65±36 kg and BL 122±20 cm); lungs 0,90±0,21% (17 subjects; mean BW: 65±37 kg and BL 123±21 cm); spleen 0,21±0,04% (21 subjects; mean BW 70±34 kg and BL 126±20 cm); liver 1,61±0,42 % (18 subjects; mean BW 61±26 kg and BL 123±19 cm); kidney 0,17±0,05% (25 subjects; mean BW 70±33 kg and BL 126±19 cm).

A strong correlation (Spearmans rank correlations, RLPlot version 1.3) between heart weight and BW (rho = 0.97; $P<0.001$) and spleen weight and BW (rho = 0.95; $P<0.001$) is observed.

The length ratio of the intestinal tracts, compared to the literature data, suggests potential genetic pollution of this wild boar population with domestic swine.

FLIGHT RESPONSE OF SARDINIAN MOUFLON TO THE HUMAN OBSERVER

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The analysis of flight response among mammals is a common approach aimed to test behavioural responses to predation risk. This behaviour may present intra-sexual and inter-sexual differences as well as seasonal variations linked to the annual cycle. From August 2005 to July 2006 flight distances of mouflon group types were recorded in a natural population of Sardinia. The analysis of flight distances of groups observed (n groups = 375, n mouflons = 1303) showed the key role played by lamb. Female groups with lambs fled (mean ± SE: 151.9 ± 10.7 m) at higher distances than males groups (116.3 ± 9.5 m) or female aggregations without lambs (122.2 ± 10.3 m). This was related to the female priority to secure the survival of offspring. Indeed, similar flight distances recorded for males and non-reproductive females were in contrast to general expectations among ungulate species, but it is probably due to the low sexual dimorphism of mouflon. Lower flight distances were recorded during the rut (103.3 ± 8.3 m) than during the lambing period (141.6 ± 10.9 m), as mating reduces the time and energy needed to look out for and escape from predators. However, females with lambs still persisted to flee at higher distances during the rut (125.2 ± 22.8 m), in contrast to what recorded for females without lambs (87.3 ± 16.7 m), as mothers aim first to protect their parental investment then to find a potential mate.

ASSESSING HABITAT QUALITY FOR THE WILD BOAR USING HUNTING DATA

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Habitat relationships are commonly used as a tool to assist in wildlife management. Such relationships could be difficult to estimate when adequate financial support is lacking to conduct extensive radio-telemetry research, as is often the case for the wild boar *Sus scrofa*. This species is also of great management concern with respect to its impact on agriculture, to its importance as game and to its role in human-wildlife conflicts, as well as invasive species in many countries and islands. We tested the effectiveness of data collected from hunting records as an indicator of wild boar habitat quality in Siena county, Italy. We selected 1595 driving hunts from 65 hunting units and calculated the standardized number of harvested animals in relation to catch effort. We used data from 40 units to build multiple linear regression models comparing habitat data with the number of harvested wild boars. Model predictions have been cross-validated according to data from the remaining 25 units. Variable used to estimate the number of harvested wild boars were not linearly correlated (*VIFs* ≈ 1.1; *CIs* << 15.0), suggesting that the dependent variable should represent an unbiased estimate of wild boar numbers. The model selected landcover heterogeneity, shrub cover, human disturbance, scrub-wood and oak-wood cover as the best descriptors and predictors of wild boar habitat quality.

THE VOCAL REPERTOIRE IN NORTHERN WHITE RHINO (*CERATOTHERIUM SIMUM COTTONI*)

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Ceratotherium simum cottoni is a nearly extinct northern subspecies of the white rhino. We studied the last still reproducing herd kept in Zoo Dvůr Králové nad Labem (Czech Republic) to describe vocal repertoire of these rare animals. Calls produced by eight individuals were recorded and further analysed as concerned both sound properties and behavioural contexts in which they are emitted. We distinguished 11 call types belonging to four categories: (1) tonal harmonic sounds (whining, squeak); (2) puffing sounds (puff, snort, threat); (3) growling sounds (grunt, snarl, grouch) including moaning call (groan); and (4) repetitive sounds (pant, hoarse). This repertoire is much larger than those reported in other rhino species. We tentatively interpret this finding as an adaptation to increased sociality which is typical for white rhinos. Although four of recognised call types reach the infrasound range, at least grouch call exhibiting the highest proportion of infrasound component is not used for a communication at distance. There are, however, other candidates for such a communication function - the repetitive sounds in particular pant which are not known from other rhino species. We hypothesise that repetitive character may enhance audibility of these signals in typical open habitats of white rhinos.

MHC-DRB3 VARIATION IN A FREE-LIVING POPULATION OF EUROPEAN BISON *BISON BONASUS*

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MHC genes play a crucial role in pathogen recognition and are the most polymorphic genes in vertebrates. Loss of variation in these genes in bottlenecked species is thought to put their survival at risk. We examined variation at the MHC II DRB3 locus in the European bison *Bison bonasus*, a species which has undergone an extreme bottleneck: the current population originated from only 12 founders. We also tested for the association of DRB3 genes with the incidence of posthitis, a disease affecting the reproductive organs of bulls and posing a new threat to the survival of the species. We found very limited MHC diversity, with only 4 alleles segregating in a sample of 172 individuals from a free-ranging Bialowieza population. The alleles were highly divergent and revealed the hallmark of positive selection acting on them in the past, that is, a significant excess of non-synonymous substitutions. This excess was concentrated in putative antigen-binding sites, suggesting that selection was driven by pathogens. However, we did not observe departures from Hardy-Weinberg equilibrium, an indicator of strong ongoing selection. Neither have we found a significant association between DRB3 alleles or genotypes and susceptibility to posthitis. Alleles conferring resistance to males may have been lost during the extreme bottleneck the species had undergone.

EVOLUTION AND TAXONOMY OF THE WILD OVIS SPECIES (ARTIODACTYLA, BOVIDAE) BASED ON CYTOCHROME B PHYLOGENY

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The genus *Ovis* is one of the more complex mammalian genera with regard to its evolution and systematic. The wild *Ovis* have a palearctic-nearctic distribution, and seven groups with different geographic distributions are distinguished. A molecular phylogeny of the wild *Ovis* species based on a large sample representative of most of the subspecies has been realized in order to clarify the taxonomy and evolutionary history of the wild sheep. Samples from 235 *Ovis* were collected from 37 regions in Europe, Asia, USA and Canada. The total mitochondrial cyt-b was amplified and data were analyzed using Bayesian, maximum likelihood, and neighbour joining methods. Several monophyletic groups supported by high bootstrap values are distinguished. A first group is composed of the Snow sheep (*O. nivicola*) and the two American sheep (*O. canadensis* and *O. dalli*). The other Eurasian sheep are divided in the Argali (*O. ammon*) and in the moufloniform group. This last group is subdivided in two monophyletic species, the Urial (*O. vignei*) and the mouflon (*O. gmelinii*). The European mouflon (*O. musimon*) is clearly included in *O. gmelinii*. The divergence between the American wild sheep (*O. dalli* and *O. canadensis*) from *O. nivicola* occurred about 4.21 ± 0.95 MYA. At about the same time (4.66 ± 0.83 MYA) the Argali (*O. ammon*) diverged from the other Eurasian groups. Then the *Mouflon (O. gmelinii*) and the Urial (*O. vignei*) diverged about 3.55 ± 0.89 MYA. From a taxonomic point of view, urial and mouflon are either classified as a single species (*Ovis orientalis*) or as separate two species (*O. gmelinii* and *O. vignei*). Differences in horn morphology and coat, as well as in chromosomes number (2n=58 in Urial and 2n=54 in mouflon) support the existence of two species. This is confirmed by the cyt-b phylogeny, which shows that the mouflon and Urial form two monophyletic groups strongly supported by high bootstrap values. However these two species are hybridizing in Iran. On a conservation point of view, the polyphyly of most of subspecies previously defined on morphological and geographical criteria question the use of these subspecies as conservation units.

SPATIAL MODELLING OF THE DISTRIBUTION OF THE WILD BOAR (*SUS SCROFA*) IN MAINLAND SPAIN

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In this work we performed a spatial model of the range of the wild boar (*Sus scrofa*) in mainland Spain. We used the data of the Atlas of Terrestrial Mammals of Spain and 41 environmental (climatic, topographic and lithologic), spatial and human variables. Climatic variables were digitized from paper climatic maps using Cartalinx 1.2. We used as operational unit the 5,167 UTM 10x10 km squares of mainland Spain. The mean values of the variables for each UTM square were obtained using the "GIS Analysis" module of the Geographical Information System IDRISI32. The data of presence/absence and the values of the variables were included in a data base (Access 2002). The statistical analyses were carried out with the statistical program SPSS 11.5. We characterised the UTM 10x10 km squares with presence of the species with respect to those with absence using stepwise logistic regression on the above mentioned variables. We used only the variables that remained significant after controlling for a false discovery rate (FDR) of $q<0.05$. Thus, we avoided an increase of type I error caused by the high number of variables used in the analysis. The probabilities of presence were corrected according to the prevalence of the species to show, for each UTM 10x10 km square, the favourability for the presence of the species. These results were shown in a map. The variables introduced in the final predictive model were grouped in orographical, spatial and human factors. Using a variation partitioning procedure we specified how much of the variation of the favourability model was explained by the pure effect of each factor and by their interaction. Only four variables explained 86.1 % of the total variation observed. The spatial factor was the most important factor explaining the favourability for the presence of the species.

SPATIAL STRUCTURE OF PHENOTYPIC CONDITIONS IN A MEDITERRANEAN POPULATION OF FALLOW DEER

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Biometrical measures have been extensively used as indexes of the phenotypic conditions of wild ungulates. In non territorial species, ideal free distribution predicts that animals should distribute on the available area (assuming costs are negligible and there are no obstacles to movements) in such a way that every individual maximises its own fitness, which turns out to predict that we should not observe any spatial structure of phenotypic traits. Here we studied the spatial distribution of body mass of fawns, females and subadult males in a population of fallow deer (*Dama dama* L.) where radiotelemetry studies showed that animals may easily move thorough an area of relatively small size (300 ha) in the Preserve of Castelporziano, Roma, Italy (6000 ha). Previous studies showed also that the five main habitats of the Preserve were characterised by different quality (protein and metabolizable energy content,) and quantity (standing biomass and productivity) of potential food items, so that we expected that deer should modify their spatial distribution (i.e. their local density) so that each one may obtain a similar amount of resources and, as a consequence, exhibit similar phenotypic traits.

From 2001 to 2006, outside the rutting season (November to May), we collected the body mass of 872 animals shot during a population-control program. Since body masses showed seasonal variations due to growth and/or phenology, all measures were appropriately standardized (SBM). We used a bivariate spline model to investigate the variations of SBM as a function of spatial position and we found the model to be highly significant ($\chi^2 = 35.1$, $P=0.0002$). North and south-east sectors of the Preserve were characterised by positive SBM values while the central part of the Preserve by negative values. Accordingly, the variogram showed an oscillatory pattern with two main scales of variation corresponding to 1500 and 5000 m.

We discuss the potential causes of the observed spatial variations in the light of predictions of ideal free distribution and we trace out a strategy for a further analysis of these data.

HAEMATIC PARAMETERS AND MEAT QUALITY OF DIFFERENTLY CAPTURED FALLOW DEER (*DAMA DAMA*)

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Stress is the response of an organism to any stressor and may cause a lower meat pH_u, with an ageing alteration and a meat defined Dry, Firm and Darks (DFD) that is not appreciated by the consumers. Therefore, we want to study the effects different capture-slaughtering system on fallow deer haematic parameters and meat quality. 28 fallow deer, bearing to the wild population living in San Rossore Natural Park were submitted to blood drawing: 12 deer in the enclosure after capture operations and 16 deer after being killed by a gamekeeper while they were standing free on a pasture. Blood was collected by vacuum-tainer, centrifuged and deep frozen; AST, ALT, CK, cholesterol, trygliceride, glucose, total protein, albumin, BUN and cortisol were determined. In the enclosure 4 deer were killed and a total of 8 carcasses were aged for 7 days. The loin, excised from the carcass, was analysed for: pH_u, meat colour, water holding capacity, tenderness, chemical composition. Data were analysed by non parametric methods to test the effect of the different treatment. As regard blood analyses a higher content of AST, ALT and CK was observed in the animals in the enclosure (510 *vs.* 191, 96 *vs.* 51, 5337 *vs.* 1346, for AST, ALT, CK, respectively). Cortisol and cholesterol content did not differ between the two groups. Triglycerides and glucose were fundamentally higher in the animals in the enclosure. Total protein, albumin and BUN were slightly higher in the animals in the enclosure (albumin statistically different: 3.5 *vs.* 3.1). pH_u showed a normal meat acidification: however, observing the data, pH_u of one fallow deer killed in the enclosure was higher than 6.0, threshold value for the onset of the DFD syndrome. Meat colour is rather dark; meat colour of the high pH_u-animal resulted very dark. Drip loss and cooking loss were quite low; water-holding capacity of the high pH_u-animal was very high, confirming a behaviour like DFD meat. Shear force was very low, thus meat was tender. Chemical composition showed a very low ether extract content. It is possible to conclude that capture operations can affect blood parameters, inducing stress in captured animals but without influencing meat quality that shows good characteristics. Nevertheless, the observation of one animal with a high meat pH_u and with a syndrome like-DFD, may suggest a further deepening, also with the aim to test the capture operations so to avoid any possible stress to the animals that must be slaughtered.

DAMAGE TO AGRICULTURE BY WILD BOAR *SUS SCROFA* IN LUXEMBOURG

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The wild boar *Sus scrofa* L. has long been known to be a cause of damage to agricultural crops. This is also the case in Luxembourg, where this problem has increased dramatically over the past 25 years. In this study we analysed more than 13000 cases of wild boar damage to agriculture over a 10-year period for type of crop and seasonality, and relate damage to the numbers of wild boar shot by hunters both over time and geographically. We found strong positive correlations for both data series. Assuming that the numbers shot reflect trends in population size, the results indicate that the amount of damage is strongly related to the numbers of wild boar present. In terms of wild boar management, we conclude that all short-term human-influenced factors contributing to the increase of wild boar populations should be critically examined. One notable example is year-round supplementary feeding with large quantities of food. In view of the results, such practice should be modified so that humans contribute as little as possible to the increase of wild boar populations.

DIVERSITY OF MOOSE (*ALCES ALCES*) DIET IN RUSSIA

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Moose is the largest browser that lives in Russia. During a year in the diet of this ungulate about 400 plant species are found. The greatest diversity of forage plants is observed during the period of plant vegetation. In a non-vegetation period moose has to eat plant species of low nutritive value or toxic ones. In winter moose diet on a certain site of its area consists of less than 20 species of plants. Maximum species diversity of moose diet in winter is noted in the north-west and south regions of Russia (Levins' measure (B) and Shannon-Wiener measure (H) for Leningrad Region – 5.47 and 2.59, respectively; for the Republic of Karelia – 5.49 and 2.58; for the Republic of Bashkortostan – 4.22 and 2.48). Low diversity of forage plants is observed in the north and east regions of Russia (for Murmansk Region: B= 3.19 and H=1.94; for Vologda Region: 3.36 and 2.00; for the Republic of Yakutia: 2.07 and 1.63, respectively). *Salix*, *Pinus*, *Betula*, *Abies*, *Juniperus communis* and *Populus tremula* (in certain regions) are the staple items in winter diet of moose in Russia. In regions with low species diversity of forage plants the basic diet of moose in winter consists of only 1-3 species of plants. Simpson's diversity index for the Republic of Yakutia concerning moose winter diet makes up 0.518, for Murmansk Region 0.687, for Leningrad Region 0.817. Moose prefers to feed on the species of the genera *Salix* (Ivlev's electivity measure (E) variability – from -0.021 to +0.737), species of the genera *Sorbus* (from +0.033 to +0.947), *Frangula alnus* (from -0.300 to +0.608), *Populus tremula* (from -0.004 to +0.972). Selectivity of moose feeding on species of *Pinus* (E variability – from -0.850 to +0.561), species of *Betula* (from -0.820 to +0.908), *Juniperus communis* (from -0.411 to +0.853) varies. This variability is caused by availability and diversity of forage plants within certain habitats. Negative feeding selectivity is typical for moose in relation to *Picea* (E - from -1.0 to -0.468), *Chosenia* (from -0.673 to -0.227) and species of the genus *Alnus* (from -1.0 to -0.125). Moose diet diversity in the territory of Russia depends on the availability of forage plants, their nutritive value and the level of toxicity of their vegetative organs.

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MORPHOMETRICS OF THE PREZEWALSKI HORSE *EQUUS PRZEWALSKII* (EQUIDAE)

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We studied comparatively cranial and dental variation of Przewalski horses born in the wild and in captivity. Eight "domesticated" lineages were represented in our sample. Only adult (no less than 5 years old) specimens were examined. Several multivariate statistical methods were employed to estimate effects of the following factors: lineage, posterity (remoteness from the wild), maintenance conditions, and sex.

According to dispersion analysis, the total level of sex differences is least expressed, the differences between captivity lineages are also slight, while overall domestication effect due to posterity and maintenance is most significant. Dental differences are generally more prominent as compared to the cranial ones.

Some features of the sex differences are quite surprising. The choanae are wider (with high significance) in females than in males. The tympanic bulla is generally wider and has shorter tube in females than in males. It is of interest to note that bullar differences are correlated with those of the pinna that is longer in males than in females.

Among the Przewalski horses, wildborns and their first offspring are most specific and similar to each other. Their more remote descendants belonging to the Post-War lineages are mutually quite similar. The latter grouping is not homogenous morphometrically, it could be subdivided in "New Askanian" and "Praha-Munich" lineages.

Such a similarity patterns is explained by predominance of domestication effect over differences between lineages. This effect is more expressed in proportions and less so in size of the skull and the dentition. In the captivity-born horses, as compared to the wildborns, the facial portion of the skull is generally shorter and higher while diastema is longer; the skull roof is somewhat narrower in postorbital region; choanae are conspicuously narrower. In the mandible, higher coronar process is characteristic feature of the captivity specimens. The latters also differ from the wildborns by shortening of posterior portions of both upper and lower toothrows. We also compared skulls of wildborn Przewalski horse with two known skulls of the steppe tarpan (*E.c.gmelini*). The latter differs significantly by shorter and narrower choanae, and by somewhat narrower occipital and lower facial skull regions.

WILD BOAR (*SUS SCROFA*) SPACE USE UNDER HUNTING PRESSURE: THE "RESERVE EFFECT"

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Natural reserve areas could become a management dilemma if pest or invasive species also benefit from this refuge. Harvested species could potentially use the protected areas to avoid being hunted during particular seasons, days or hours. Then, they could proliferate and supplant endangered species in such areas. Reserves often become "black spot" because any regulation can be easily practised inside. Although wild boar remains in Europe actively harvested, populations have known a strong increase during the last two decades leading to a simultaneous increase of crop damage, in particular near reserve areas. In the French part of the Geneva Basin, 47 wild boars were collared with VHF radio-transmitters, inside and outside a reserve. They were located daily and nightly along the year. We studied the distance between the individual centre of activity and the reserve edge in function of hunting activity (legal hunting season and hunting hours). We first predict that diurnal home ranges would be closer to the reserve "during" than "before" hunting period because animals are expected to avoid hunted areas at day. Then, as individuals are supposed to avoid negative effects of increased density, we expect at night that animals would restore their nocturnal distribution observed before hunting season. As predicted results show that diurnal home ranges are closer to the reserve edge "during" than "before" hunting season. In details we observe this behaviour on wild boars living exclusively "before" at less than 2 km of the reserve edge. We observe that animals leave the reserve at night. But compared to their initial nocturnal locations "before" hunting they remain closer to the reserve. These results show that wild boars may adjust their reserve occupation regarding to the hunting seasons and daily hours. But these behaviours are however limited to animals living in the close periphery. This suggests the importance of the knowledge that animals could have of their environment and the costs of home range displacement. As predicted by the increased density avoidance, animals spread out of the reserve during the night in hunting season. However, in order to avoid hunting activities at day, their night trips are forced to start and to finish in the reserve. Thus, even no hunting pressure persists at night, wild boars are more linked to the reserve place "during" than "before" hunting season.

INNOVATIVE CHANGE AND THE BIRTH OF A SUPPLEMENTARY CHEMOKINE RECEPTOR-LIKE GENE BY RECOMBINATION OF CCR2 AND CCR5 GENES IN THE EQUINE LINEAGE

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Chemokines play a crucial role in inter-cellular communication networks. They regulate processes such as leukocyte trafficking, apoptosis, and hematopoiesis by signal transduction via transmembrane receptors. The role of these so called chemokine receptors (CR) in innate immune defense can however be perverted by viral pathogens, that either mimic certain of the CR ligands, or utilize CRs as co-receptors for cell entry. Since it was found that HIV uses the second extracellular loop (ECL2) of the “CCR5” CR as a portal for entering into human T cells, and that changes at this loop can impair HIV susceptibility, this receptor gene became one of the prime targets of disease control studies. Our research on CRs in horse revealed the existence of a novel gene “CCR5X2” that clearly has emerged by a nonequal crossingover between the chromosomally proximal CCR2 and CCR5 CR genes. Upstream (5’) of ECL2, the novel CCR5X2 gene showed high sequence similarity with equine CCR5, while downstream ECL2, similarity to CCR2 was high. It appeared that this recombination went along with the insertion a 21 base pair (bp) fragment causing a seven amino acid insert at the ECL2. Whereas the equine CCR5 gene showed the expected sequence similarity to its mammalian orthologs, the ECL2 region of CCR2 has acquired the same 21bp insert as CCR5X2, probably by gene conversion. The three genes: the altered CCR2, the recombinant CCR5X2 and the “normal” CCR5, were found present in each of six horses, five donkeys and one zebra. Simultaneous heterozygosity within individuals confirmed that none of these forms is pseudo-allelic. The sequence comparison provided clear signs of positive selection at the CDS region of the recombinant gene. The very high sequence homology of the UTR and intron regions of CCR5X2 with those of the respective donor genes (>99%), together with intra- and inter-species comparisons, indicate that the events leading the emergence of this gene occurred shortly before the horse-donkey split. The Equid family evolved during some 50 million years in the neoarctic region, where it went precipitously extinct some 10,000 years ago. It is possible that the fixation of the “recombined haplotype” in the ancestor population of extant equine species has to do with the rapid population expansion of caballine horses in the Eurasian range after their crossing of the Bering Land Bridge. The 21 bp insert, and/or the novel gene, which both are unique among vertebrates, may provide a useful marker in studies of the evolutionary history of horses.

PARASITOLOGICAL, SEROLOGICAL AND ANATOMOPATHOLOGICAL SURVEY ON A MUFLON POPULATION (*OVIS ARIES)* LIVING IN THE CENTRAL ITALY

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The aim of this study is to investigate the main parasitic infection of muflons living in the Regional Park of Apuane Alps (Tuscany region, central Italy) in January 2003 - February 2007. One-hundred-seventy-seven faecal samples were monthly collected in different areas of the Park from free ranging animals. Entomological, mycological and serological investigations were carried out on twelve captured animals. Ectoparasites were collected and identified, and the presence of dermatophytes on the coat of captured animals was assessed through cultural examination by means of MacKenzie's brush technique. Faecal samples were processed by flotation technique in saturated sodium chloride solution and in high specific weight solution (potassium iodomercurate) for detection of gastrointestinal strongylides eggs, coccidia oocysts and trematode eggs, respectively. A prevalence of 65.5% (116/177) of gastrointestinal strongylides infection was found with an EPG varying from 100 to 650 in all the samples. The presence of bronchopulmonary strongylides was lower, with a prevalence of 23.7% (42/177). Larval morphology was suggestive of *Muellerius*, *Protostrongylus* and *Cystocaulus* genera, with the first one more represented when compared to the others. Coccidian species (*Eimeria crandallis*, *E. faurei* and *E.. granulosa*), like as gastro-intestinal strongylides, were found to have a prevalence of 58.2% (74/127) and an OPG value ranging from 100 to 800. Eggs of *Dicrocoelium dendriticum* were present in 12.9% of samples (23/177). Collected ticks were identified as *Dermacentor marginatus* and *Ixodes ricinus* and the amount of ticks found on captured animals was much lower (less than 20 ticks per animal) than that found on sheeps living in the same area (more than 40 ticks per animal) according with a study performed in the Arcipelago Toscano Park. The association between coccidia and gastrointestinal strongylides was present in 51.9% (92/177) of the samples, suggesting that parasitized animals could be more susceptible to develop a further enteric parasite infection. No correlation was found between intestinal parasites and the presence of *Dicrocoelium dendriticum* instead. Dermatophytes were not cultured from hair samples, suggesting that this animal species, as previously reported for sheep, does not seem to have a significant role as reservoir for these microorganisms. Anatomopathological and hystopathological exams confirmed parasitary hepatic and bronchopulmonary lesions: adults of *D. dendriticum* and lungworms were isolated from bile ducts and parasitic nodules on the lungs surface respectively. No serological positivity to *Toxoplasma gondii* was found in the examined samples.

EFFECTS OF WEANING ON FOAL PLAY BEHAVIOUR IN FREE-RANGING HORSES

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Weaning is a sensitive time in the life of horses. In the wild, this event causes temporary remarkable stress to the foal because of the conflict between mother and son, and it gradually starts when the foal is 7-8 months old. In captivity, two main methods of weaning are applied: the sudden separation of the foal from the mother, or a graduate separation (for a limited period of time, the foal can be in visual and physical contact with the mother).

The main scope of this research has been to estimate the effects that a premature artificial weaning (operated by the horse-keeper) has on foals of 3-6 months. Some free-ranging foals (N=13; 7 males, 6 females), were observed in the Maremma Regional Park for a year (May 2003-April 2004) for a total of 370 hours of monitoring, with the help of a video-camera.

In total, 9 patterns of play behaviour were observed, 7 of them belonging to social play and the others representing solitary (locomotory) play behaviour or interactions with objects. The moment of weaning has been used to split two sub-samples: the first one in which the mothers were present (4 months); the second with the observations carried out for 4 months after weaning.

The number of play bouts (N_{pres}=588; N_{ass}=798) was similar in the two sub-samples. However, the durations of play significantly differed between the samples (Wilcoxon test; Z= -1.648; $P < 0.05$), with a massive reduction of play behaviour after weaning. This suggests that a premature weaning may probably cause a deep stress to the foal.

CONSERVATION GENETICS OF CHAMOIS POPULATIONS IN SLOVAKIA

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In the Central Europe, the chamois (*Rupicapra rupicapra*) is represented by two currently recognized subspecies – Alpine chamois (*R. r. rupicapra*) and critically endangered Tatra chamois (*R. r. tatrica*). The only autochthonous population of Tatra chamois occurs in the High Tatra Mts. in northern Slovakia and southern Poland, and its present population size ranges between 430-490 individuals. During the first half of the 20th century, Tatra chamois underwent two significant population declines (bottlenecks), followed by low numbers over most of the second half of the last century. Ongoing population decline in the High Tatra stimulated creation of 'reserve population' in the other Slovak mountains - the Low Tatra. However, before recognizing the Tatra subspecies, and before its introduction to the Low Tatra, Alpine chamois were introduced to the Velka Fatra Mts. and the Slovensky Raj Mts. in the Low Tatra Mts. neighbourhood. As all three Slovak introduced populations were established from only a few individuals, their genetic variability might be reduced due to founder effect. Present population size in both, the Low Tatra and Slovensky Raj, fluctuate around 100 individuals. In the Velka Fatra, there might be present only 35-50 individuals. Because the Low Tatra, Velka Fatra and Slovensky Raj mountain ranges are geographically close, hybridisation between Tatra and Alpine chamois, resulting from occasional migrations, might have occurred.

In 2006, a project was started which aims to assess population genetic structure of chamois populations in Slovakia by using non-invasive DNA analyses from faeces. We will study genetic variability at neutral (mitochondrial DNA, microsatellites) and functional (MHC genes) markers. We will focus on potential introgression of Alpine chamois to the Tatra chamois genome, gene flow pattern, MHC variation and its relation to the level of parasitism, and effect of isolation on differentiation and kinship structure. We also plan to assess sexual structure of populations, relatedness of individuals, and effective population size of particular populations. Obtained data will be compared with published data on other chamois populations in Europe. The project will provide recommendations for conservation management of the populations.

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