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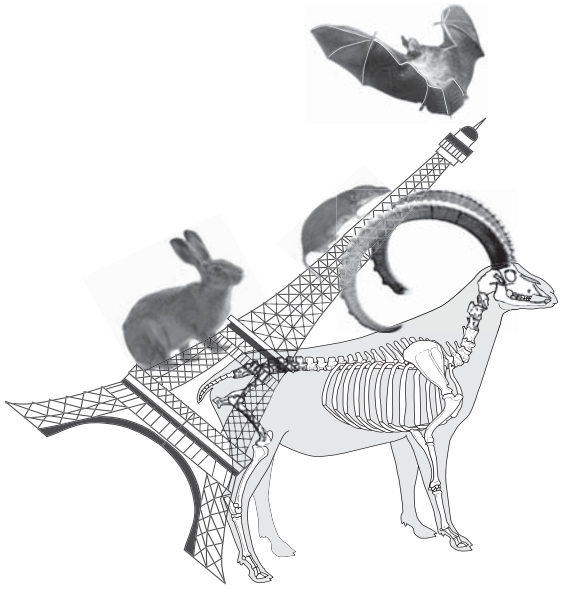

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Invited & Oral Communication

The mediterranean fruit bat (*Rousettus aegyptiacus*): position and dynamics of range margins.

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The Mediterranean population of *Rousettus aegyptiacus* represent the only ofshoot of the chiropteran family Pteropodidae beyond limits of tropes. We summarized all distributional data and revised its current status in most regions of its Mediterranean range with particular respect to the situation along the range margins in the region. Distribution of *R. aegyptiacus* in the Palaearctic shows three different patterns: (1) supposedly continuous distribution in the Nile valley and delta (mostly linear in the zone of date palm plantations in a narrow belt along Nile), (2) densely patched (or locally continuous) distribution in thermo-mediterranean arboreal zone, in S Turkey, Cyprus, N Levant to central Israel, i.e. 10 to ca. 50 km wide belt along the sea shore, locally with particularly high population densities; and (3) clearly discontinuous distribution in desert zones (Egypt, N Sudan, Arabian Peninsula, southern Iran and Pakistan), characterized by mutually isolated patches of distribution in desert oases and smaller areas of relative humid habitats (southern part of Nile valley, Estern desert oases, western slopes of the Hijaz and Sarawat ranges of SW Arabia, Hajjar Mts. of NE Oman, southern slopes of the Zagros Range in Iran). Detailed fine-scale data on an isolated marginal population in Dakhla Oasis, Egypt, suggests considerable potential of the species for survival in small isolated populations. The dramatic decline documented from 2005 to 2010 in Cyprus, synchronous with expansion of ranges margins in Turkey suggests, at the same time, considerble capacity for range dynamics.

Feeding habits of the golden jackal *Canis aureus*, the mongoose *Herpestes ichneumon* and the Genet *Genetta genetta* L. 1758 in the area of Djurdjura (North of Algeria).

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We studied the diets of three species of carnivores (*Canis aureus* golden jackal, genet *Genetta genetta* and the Mongoose *Herpestes ichneumon*) in the North Slope Djurdjura National Park (Kabylie, Algeria). For this, we analyzed during an annual cycle feces collected. The location and number of feces collected were carefully plotted on a map to indicate places of defecation, but also their characteristics. The diet analysis shows a high elasticity of the plan for the 3 species with a predominance of mammals followed by arthropods and plants. Some seasonal variations are highlighted. The comparison shows that the schemes jackal has tended to take prey mammalian middle while the other two species have a preference for small mammals. The results show and confirm the general nature of the three and opportunistic predators. The low waste reveals the quality of habitat that is its low human impact and / or its richness and prey availability. The jackal collects preferentially the boar in all seasons while the genet is more specialized on the field mouse. Various indices (Shannon-Weaver index, evenness index) were used to reflect the main features of the various species studied.

Low genetic diversity of Eurasian lynx (*Lynx lynx*) from Croatia

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Eurasian lynx (*Lynx lynx*) is one of the most endangered mammals in the Mediterranean region. At the end of the 19th century it has been eradicated from most of the South European habitats, including the Dinaric Mountains. Dinaric population has been established again in 1973 by reintroduction of six animals from Slovakia to Slovenia, followed by their expansion to Croatia and Bosnia and Herzegovina. By rough estimates today there are 40 – 60 animals present in Croatia and population is strictly protected. Besides poaching, habitat fragmentation and lack of prey, loss of genetic diversity due to inbreeding is thought to be one of the causes of population decline in the past 10 years. The goal of this research was to evaluate the consequences of founder effect and inbreeding on genetic diversity of Eurasian lynx from Croatia. In the period from 1980 to 2010 a total of 15 muscle, 30 bone and 15 tanned-skin samples have been collected. It has been confirmed that all analyzed samples from Croatia had the same mitochondrial DNA control region haplotype, identical to the one from the Baltic, Carpathian and reintroduced Swiss populations. Totally 60 Eurasian lynx samples from Croatia had 62 alleles on 20 microsatellites, or on average 3.1 alleles per locus. Allelic richness was 3,049 and the effective number of alleles was 2,113. Observed and expected heterozigosity were 0,435 and 0,490, respectively. Dinaric lynx population showed the lowest genetic diversity out of all researched Eurasian lynx populations.