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Abstracts

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Taxonomic status of *Rhinopoma muscatellum* Thomas, 1903 (Chiroptera: Rhinopomatidae) in Iran

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Rhinopoma muscatellum is one of the six mouse-tailed bats (Rhinopomatidae) and is known as an extremely frequent bat in the southern part of Iran with over 52 reported localities. The taxonomic status of *R. muscatellum* in Iran is not so clear, as different research groups have reported one or two subspecies. In the present study, using morphologic, morphometric and molecular markers, the taxonomy and geographic distribution of *R. muscatellum* from Iran are reviewed. Analyses of biometric data do not reveal any differences among populations. A multivariate analysis based on cranial and dental characteristics did not reveal any significant differences among populations. Moreover, we present a study of the genetic variability of this species using 584 bp of the mitochondrial D-loop from several localities in Iran. A total of 17 polymorphic sites were recorded including 15 transitions, and 2 transversions. Also, 567 characters were constant and 10 variable characters were parsimony informative. Mean nucleotide composition in the smaller mouse-tailed bat include A: 35.4%, C: 26.5%, T: 26.2% and G: 11.9%. Based on the D-loop sequences nucleotide diversity values (π) varied from 0.0342 to 0.0068, showing a close relationship among the haplotypes. The statistical parsimony network and phylogenetic analyses (ML and BI) also showed no clear differentiation between the haplotypes in the Iranian samples. Based on molecular and morphological results this study indicates all Iranian specimens of *R. muscatellum* belong to one subspecies. Therefore, it is recommended that *R. m. muscatellum* and *R. m. seianum* can be synonymized as *R. m. muscatellum.*

An artificial bat cave in Turkey: A follow up

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Bat population of an artificial cave in Turkey, which was created to replace the original cave that will be inundated due to a dam construction, was observed over four years. The artificial cave was constructed in 2007 and when the time was optimal bats were vacated. In November 2009, the original cave containing approximately 18,000 bats was evacuated and bats of the new cave have been under observation since 2010. In May 2010, 1900 individuals were counted belonging five species in artificial cave. A year later, in June, the number of bats in artificial cave was recorded as about 10,000. These bats have been determined to belong to *Rhinolophus ferrumequinum*, *R. hipposideros* and *R. blassii* from Rhinolophidae family, *Myotis myotis*, *M. blythii*, *M. mystacinus*, *M. capaccinii*, *M. emarginatus* and *Miniopterus schreibersii* from Vespertilionidae family. In later years, some fluctuations in numbers of species visiting the cave have been seen, and the number of individuals has decreased to 600 in winter months of 2012 and 2013. In July 2013 about 7000 individuals were counted in the cave and dozens of *Miniopterus schreibersii* were found dead as clinging to the walls of the cave, which was thought to be related to an epidemic. Every year from April, it has been observed that *Myotis myotis* and *M. blythii* form large colonies for breeding in the new cave. The last visit to the cave was in April 2014 and total of 2500 individuals belonging four species were found. As a result, after recording the size of artificial cave bat populations in winter and summer months, it was identified that artificial cave is used by more species in breeding period rather than overwintering period.

Phylogeny of the genus *Gazella*

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Limited knowledge of phylogenetic relationships within the genus *Gazella* often hampers conservation efforts for its endangered species. Furthermore, conflicting hypotheses regarding the origin of the genus (*i.e.*, Africa or Asia) were forwarded. To overcome these limitations, we designed and established six nuclear intron markers (derived from the cow and sheep genome) and investigated sequence variation of the new markers, the cytochrome *b* gene and the 18S gene. We could make use of 37 samples of all nine *Gazella* species covering almost the entire distribution range of the genus. Using *BEAST we could confirm the monophyly of *Gazella* with nine extant species and uncovered a clade of Asian origin comprising *G. subgutturosa*, *G. bennettii*, *G. marica*, *G. leptoceros* and *G. cuvieri*. Furthermore, we reconstructed the character state combination of gazelle's ancestors: they were

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most likely dessert dwelling mixed feeders, which only bore singletons and females wore horns. Adaptation to a more humid climate, thus, occurred independently at least three times within *Gazella* leading to two ecologically differentiated species types. Biogeographic analyses further indicate that the ancestral range of the genus *Gazella* was most likely located in the Middle East.

The amount of organic phosphates (like DPG) existing in blood is determining factor of mammal's bulk

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It is essential that oxygen is transported by the blood to all cells of a mammal at any moment. This ensures survival of all cells in a mammal's body. In case a mammal's bulk is large, the distance between cells in different tissues and the mammals' heart is larger. Therefore, red blood cells in bulky mammal's bodies should be capable of conveying oxygen to farther distances. To make it practical, oxygen should be glued red blood cells tenaciously. In other words, the cohesion of oxygen to red blood cells should be stronger in bulky than in small mammals. In mammalian bodies, the controlling factor of amount of cohesion of oxygen to red blood cells, are organic phosphates (like DPG). The less DPG in red blood cells of a mammal, the more cohesion of oxygen to red blood cell at the same rate. If oxygen is glued more tenaciously to red blood cells, oxygen could been carried to farther distance allowing mammals to have larger bulk at the same rate. The amount of organic phosphates (e.g. DOG) of red blood cells decreased with increasing size from mouse (45 mmHg), rat (42 mmHg), cat (38 mmHg), fox (35 mmHg), sheep (30 mmHg), horse (25 mmHg), to elephant (22.5 mmHg).

Polymorphism of major histocompatibility complex DQA and DQB class II genes in bottlenose dolphins (*Tursiops truncatus*) from the eastern Adriatic Sea

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The bottlenose dolphin (*Tursiops truncatus*) is the last resident marine mammal species in the Croatian (eastern) part of the Adriatic Sea, where it is considered endangered and is legally protected. A general concern for the conservation of endangered species is the maintenance of genetic variation within populations. Genetic diversity is particularly important in the major histocompatibility complex (MHC), a multigene family that is increasingly used for the study of adaptive variation in non-model vertebrates. The aim of this study was to examine allelic diversity at MHC class II DQA and DQB loci in the eastern Adriatic bottlenose dolphins. DNA was extracted from 48 bottlenose dolphins found dead along the Croatian coast of the Adriatic Sea during the last 15 years. Using the cloning-sequencing method, we investigated the genetic diversity of 246 bp and 171 bp fragments of exon 2 of the DQA and DQB genes, respectively. We found high diversity as seven DQA and nine DQB alleles were identified, with all alleles encoding unique amino acid sequences. Rates of non-synonymous substitutions were significantly higher than that of synonymous, indicating positive selection on both loci. Mean nucleotide distance estimated for DQB (0.103) was higher than for DQA (0.053). Furthermore, DQB nucleotide distance was higher than those found in most other cetacean species, while nucleotide distances for both loci were comparable to that of terrestrial mammals, suggesting a high extent of balancing selection. Our results should provide a basis for exploring the association between genetic constitution and parasitic pressure from natural environment in bottlenose dolphins.

Conservation priorities: A case study of Iranian mammals

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Approximately one fourth of the world's existing known mammal species are endangered and lack of proper conservation strategies can lead to inappropriate allocation of resources to larger species ignoring smaller taxa. Despite Iran's rich diversity of mammalian fauna, which is predominantly comprised of smaller species, most research has been conducted on various ecological aspects of large species. This investigation has been implemented with the aim of conservation prioritization of Iran's mammals, based on their evolutionary distinctiveness and globally endangered score. Moreover, species subject of graduate university dissertations as well as research projects funded by the Iranian Department of Environment have been assessed to give an overall comprehensive review of the state of the Iranian mammals for effective conservation. We recognized 50 species with the highest priority value headed by Asiatic cheetah, Asiatic black bear and dugong. Rodent and chiropteran species constituted the highest proportion of the high priority species of the country, respectively. In contrast, a total of 43 university theses have been done on the top species including 24 on ungulates and 12 on carnivores, indicating intensive attention from Iranian biologists to these larger species. The same conclusion was derived based on analysis of funds allocated to different research projects by the DoE. While supporting the present approach by the Iranian biologists to address top large species in order to fill existing gaps of knowledge, it is essential to meet conservation needs of smaller species, such as lesser carnivores, rodents and bats.

Neomys fodiens does not follow Bergmann's rule in the middle of its distribution range

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The body size of Palearctic *Sorex* shrews decreases at higher latitudes and does not follow Bergmann's rule. In the range between 40 and 42° N and 65–69° N, we confirmed that a number of body and cranial measurements of water shrew (*Neomys fodiens*) are negatively correlated to latitude, though with a weak dependency. A negative relationship between measurements of all cranial and dental characters (with exception of palatal length) and latitude is much stronger in the latitudes between 54 and 59° N. Such analysis for *N. fodiens* in the middle of distribution range had not been conducted before. Using ANOVA and PCA with prior log10 transformation of measurements for 158 water shrews from Estonia and Lithuania, we also found that these populations are separated morphologically. Although decreasing in size, the height of the coronoid process (one of the diagnostic characters between *N. fodiens* and *N. anomalus*) is still over 4 mm in the northern part of the investigated species range. Concluding, we found that over the short geographical scale, *N. fodiens* does not conform to Bergman's rule. In the full range of the species, non-conformance is less expressed than over the short geographic distance: Estonian shrews are significantly smaller than Lithuanian ones in body size and cranial measurements. Skulls of Estonian shrews are relatively shorter and, in the area of the brain case, wider. Estimated morphological differences may reflect differences in resource use, mainly relating to the efficiency of food gathering and processing along with diminishing food resources.