Poster Session 2 – Taxonomy-Genetics

80 Geographic variation of the genus *Arvicanthis* (*Rodentia*: *Muridae*) from Sudan

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Arvicanthis niloticus (Demarest, 1842) populations are highly variable throughout the Nile valley (Egypt and Sudan) and also in western, central and eastern Africa but knowledge of their geographic variation is lacking, especially from Sudan. Therefore , the phenotypic variation in *Arvicanthis niloticus* populations of Sudan was assessed by geometric morphometric approach (GMA). Univariate and multivariate analyses of skeletal characters (shape and centroid size) differences for the dorsal and ventral views revealed little variation between and among localities for most characters. A significant skull shape difference (dorsal and ventral views) between the five populations of Sudan was evident (P-value <0.05) and that was mostly localized in the zygomatic area. Also, significant correlations (P-value <0.05) between skull geometry and some climatic variables were evident. The previous inter-population variability was largely explained by the masticatory muscles, degree of commensalism, local climatic-environmental variables, and/or the secondary consequence of the interaction between them, which may have induced some ecological, functional and behavioral adaptations. Clearly, the adaptive roles of the previous variables require further biological studies to predict the cranial evolutionary changes of *Arvicanthis niloticus* throughout its distributional range.

Poster Session 2 – Taxonomy Genetics

81 Maternal divergences within *Myospalax* and introgressive hybridization in the eastern Qinghai-Tibet Plateau

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The zokor (genus *Myospalax*) is a subterranean solitary species. It remains unknown what had caused the morphological complexity and difficulty in species circumscription within *Myospalax*. Hybridization and gene flow are proposed for explaining such a scenario, especially for ambiguous hybridization origin of *Myospalax smithii*. The morphological characters of this species suggested its relationship to both old and young species; however, hybridization usually occurs between young species or lineages with recent divergences. Our phylogenetic analyses of mitochondrial cytochrome b gene (Cyt b) and 12S rRNA gene obtained from 102 individuals representing all eight species of the genus *Myospalax* produced well discerning maternal phylogeny within the genus. Our results further rejected a hybridization origin hypothesis of *Myospalax smithii* between *Myospalax cansus* and *Myospalax myospalaxi*. However, we found that morphologically defined *Myospalax smithii* individuals interweaved with those belonging to *Myospalax baileyi*. These individuals from two species clustered into two well supported clades. We suggest that *Myospalax smithii* should be recognized as separate species, but the extensive hybridization and gene flow between it and *Myospalax baileyi* might have swamped out most pure *Myospalax smithii* individuals possibly due to heterosis of hybrids. Our results are consistent with the previous assumption regarding occurrence of hybridization between recently divergent lineages with close relationships. However, this conclusion was drawn based only on a combination of morphological and maternal evidence; further evidence with genetic signatures from both parents (e.g. nuclear genes) is needed. Overall, these results suggest that *Myospalax* provides a model system for studying speciation, reproduction isolation and gene flow of small mammals.

Poster Session 2 – Taxonomy Genetics

82 Systematics of an Andean akodontine, *Akodon mimus* (*Cricetidae*, *Sigmodontinae*): insights from molecular markers

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Akodon mimus (Thomas, 1901) is a medium-sized member of one of the most diverse genera of the second largest tribe of sigmodontine rodents, *Akodontini*. The scarce available data indicate that *Akodon mimus* is a monotypic form distributed in eastern Andean slopes between 2,000-3,700 m from southeastern Peru (Puno department) to central Bolivia (Cochabamba, La Paz and Santa Cruz departments), and inhabiting primarily elfin forests. Originally described in the genus *Oxymycterus*, it was later selected as the type species of *Microxus*, an entity coined by Thomas in 1909, in order to allocate several small-bodied long-nosed mostly Andean forms. After the influential treatise of Cabrera in 1961, *Microxus* was subsumed under *Akodon*, and never properly revisited its generic rank. With the advent of molecular markers in sigmodontine systematics, the placement of *Akodon mimus* nested in *Akodon* was cemented on the basis of one specimen from Puno, Peru. However, more recent studies retrieved an unstable position of *Akodon mimus* regarding the remainder species of *Akodon* or even to close genera such as *Castoria*, *Deltamys* and *Thaptomys*. We examined the phylogenetic position of *Akodon mimus* and also the relationship between Cochabamba and Puno populations referred to the species. Based on four loci and a dense taxonomic approach covering most of the *Akodontini*, we performed parsimony, maximum likelihood and Bayesian analyses. Our phylogenetic results point to the validity of the genus *Microxus* or, alternatively, to return to a polytipic *Akodon* composed by several subgenera (i.e., *Akodon* s. s., *Deltamys*, *Castoria* and *Microxus*). In addition, we detected high levels of genetic divergence between Cochabamba and Puno populations (ca. 10% p distance – cytochrome b locus), suggesting that they represent different species. In this context, *Akodon mimus* appears as another case of an Andean sigmodontine largely overlooked but with an unsuspected diversity.

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83 A phylogenetic study on Anatolian endemic *Dryomys laniger* (*Mammalia*: *Rodentia*) to determine an in-situ conservation area

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Dryomys laniger is an endemic rodent living in Turkey. It distributes along Taurus Mountain range and Anatolian diagonal mountain range between Antalya and Erzurum in Turkey. The main distribution range in these areas extends from about 1,500 meters up to 3,000 m a.s.l. in rocky habitats. In this study we aimed to offer suitable areas for potential in-situ conservation areas for the species by investigating cytb genetic diversity along with distribution areas. We collected 31 samples from 6 localities between 2015 and 2017. According to results, we expanded the distribution area of the species by determining some new distribution areas. We used the cytb gene region to find out genetic diversity and to draw a phylogenetic tree. According to the phylogenetic tree there are two main clades in Turkey. There are geographical barriers between clades which cut gene flow between the clades. On the other hand, we found that gene flow continues within clades. It might be pointed out that populations in Turkey would be divided into two different subspecies for the taxa. So, we offer two different areas to protect each of the subspecies.

Poster Session 2 – Taxonomy Genetics

84 The traits of contact zones between different chromosomal races of *Mus musculus domesticus* (*Rodentia*: *Muridae*) in two Robertsonian (Rb) systems of Greece

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The otherwise conservative acrocentric karyotype of the house mouse, *Mus musculus domesticus* (*Rodentia*, *Muridae*), demonstrates in various Euro-Mediterranean locations extreme chromosomal evolution, through the accumulation of Robertsonian (Rb) fusions: non-homologous uni-armed chromosomes fuse at their centromere, creating bi-armed chromosomes (2n=40-22). Homozygous populations for specific sets of Rb fusions, termed Rb races, that share a common origin form Rb systems. In Greece, three Rb systems have been described, namely, in Peloponnese, E Sterea Ellada and Ipiros. In most Rb systems, the characteristics of the contact (hybrid) zones between different chromosomal races have been the object of intensive research. We targeted specific contact zones at the Rb systems of E Sterea Ellada and Peloponnese, based on the karyological analysis of 50 house mice from 18 localities. Regarding the Rb system of E Sterea Ellada, we focused on areas of Attiki, where it was shown that the Rb population, ranging from 2n=39 to as low as 2n=27 (GRT2xGRT1 Rb races) is placed peripherally of Athens, in positions N and E of Mt Imittos. Overall, the whole study area behaved like a contact zone possibly between GRT2 with 2n=28 and the acrocentric population, the most interesting trait of which was the abrupt transition (ca. 6 km wide) from 2n37. On the other hand, in the Rb system of Peloponnese, we examined an area, where two well-known Rb races, GROL with 2n=24 and GRKA with 2n=28, characterized by monobrachial homology, were expected to come very close but form no hybrids. Indeed, our study revealed no hybrids between them; instead, the acrocentric population had entered between them, forming hybrids (2n=33-39) with either of them. Surprisingly, Rb(4.16) and Rb(8.17), were sporadically found in the study area, which have not been described before in Peloponnese and could have resulted from type 'b' whole arm reciprocal translocations.

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85 Karyology of *Meriones dahli* Shidlovsky, 1962 (*Rodentia*: *Mammalia*) in Turkey

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The material of five (2 male, 3 female) specimens of *Meriones dahli* was collected from east Anatolia. The specimens were investigated for aspects of their karyological characters. The data obtained from specimens was compared with the ones previously studied. The karyotypes of the specimens have 2n = 50, NFa = 78 and NF = 74. The karyotype consist of 13 pairs that are meta/submetacentric and 11 pairs that are acrocentric. The X chromosomes are medium-sized metacentric and the Y chromosome is small submetacentric.

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86 A new chromosomal race of the Evoron voles *Alexandromys evoronensis* of two isolated populations in the Russian Far East

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The Evoron vole *Alexandromys evoronensis* (Kowalskaia et Sokolov 1980) (2n = 38-40, NFa = 51-54) was described as an endemic of the Evoron-Chukchagir plain (ECh) of the lower Amur region in the Russian Far East. Morphologically, this species looks like Maximowicz's vole *Alexandromys maximowiczii* (Schrenck 1858) (2n = 36-44, NFa = 50-60). With their multiple chromosomal polymorphisms, both species have different chromosomal rearrangements (Meyer et al., 1996). As a result of hybridization of two species, sterile hybrids F1 were obtained (Kowalskaia et Sokolov 1980, Meyer et al., 1996). Biologically, the two species are reproductively isolated while in terms of the mtDNA control region they differ as subspecies of one species (Haring et al., 2010); and some researchers tend to consider them as one species *Alexandromys maximowiczii* (Lisovskyi et al., 2018). Recently, an Evoron vole was discovered in two isolated mountain valleys of the Zeya and Bureya rivers: Verkhnezeiskaya Plain (VZ) and Verkhnebureinskaya Depression (VB). This vole species' diagnostics was performed using karyological and mtDNA control region data. For the first time, a karyotype with 2n = 36 in VZ and 2n = 37 in VB population was described for the species (Sheremetyeva et al., 2017a, b). Comparing differential staining of chromosomes from the Evoron voles from three populations enabled us to suggest the existence of two chromosomal races: (i) in VZ and VB and (ii) in ECh. Hybridizing two geographically close populations of two species (36 chromosomal Evoron voles from VZ and 40 chromosomal Maximowicz's voles from Zeya City locality), made it possible to obtain the sterile 38 chromosomal F1. The results obtained testify the taxonomical species status both for *Alexandromys evoronensis* of VZ and *Alexandromys maximowiczii* (from Zeya).

Poster Session 2 – Taxonomy Genetics

87 Karyological study of the house mouse, *Mus musculus domesticus* (*Rodentia*, *Muridae*), at the Robertsonian (Rb) system of Ipiros, Greece

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The house mouse, *Mus musculus domesticus*, is a small rodent with an almost worldwide distribution that is typically characterized by an all-acrocentric karyotype. However, this karyotype often displays Robertsonian (Rb) fusions: the merging at the centromeric region of non-homologous, acrocentric chromosomes, in order to form bi-armed chromosomes. As a result, the diploid chromosome number in nature can range from 2n=22 to 2n=40. This karyotype trait concerns only several European and some circum-Mediterranean populations of the house mouse and in Greece three Rb systems are known so far. This work is part of a wider effort to study the least known Rb system, located in Ipiros, W Greece. For this Rb system, most data wre derived from around the city of Ioannina, NW Ipiros, where the lowest recorded 2n is 2n=28, characterized by Rb(15.17), Rb(3.10), Rb(5.12), Rb(14.16), Rb(8.9) and Rb(2.11). However, no data exists on the actual dimensions of the Rb system, its Rb races, etc. Therefore, the aim of the study was to seek the SE border of this Rb system by surveying an area ca. 65 S-SE of Ioannina. Thirty mice from 17 localities N-NE of Amvrakikos lagoon were karyologically studied. Among these, only one belonged to the acrocentric population (2n=40), whereas the remaining 29 were characterized by 2n=34-39. All six Rb chromosomes known from around Ioannina appeared with different frequencies in the studied sample, confirming that the surveyed area does belong to the studied Rb system, which apparently occupies a significant part of Ipiros. The high percentage of Rb heterozygotes in our sample suggests that the study area rather constitutes a relatively wide contact zone with the acrocentric population located at the east. In conclusion, the new data clarify important issues, regarding the Rb system of Ipiros, however, several questions remain to be pursued with our future studies.

Poster Session 2 – Taxonomy Genetics

88 Genetic structure of a peripheral population of the Northern mole vole: re-evaluation after eliminating nuclear pseudogene contaminants

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Mole voles (the genus *Ellobius*) are highly specialized subterranean rodents. Areal fragmentation, coupled with some features of reproductive system described for mole voles, is expected to result in low intra-population genetic diversity and strong inter-population differentiation. In the course of our previous study of the Northern mole vole, *Ellobius talpinus*, in the Novosibirsk region of Russia (Kuprina et al., 2016), an unexpected high haplotype diversity of the mitochondrial control region fragment had been revealed. In addition, there was a high sequence divergence (5.6%) between two predominating haplotypes. However, our subsequent molecular investigation (Kuprina et al., 2018, this volume) discovered that one of these haplotypes was actually a cryptic nuclear pseudogene. Using the new primers designed to amplify a target portion of the mitochondrion control region only, a 417-base pair fragment was sequenced. In total, 5 haplotypes defined by 6 polymorphic sites were identified among 56 individuals from 3 subpopulations. Thus, overall, a relatively high haplotype (H=31%) and low nucleotide (π =0.15%) diversities have been detected. The genetic variation within each of two most peripheral subpopulations was extremely low (H =0%, π=0.00%, n=11 and H=10%, π=0.03%, n=37). An analysis of molecular variance showed a very strong genetic differentiation among subpopulations on high geographic scale (~100 km; Fst=0.91) and the absence of differentiation on low scale (~10 km; Fst =-0.04). These reevaluated data consist with both theoretical predictions and information on population genetic structure of other studied social subterranean rodents. The research was funded by the RFBR (projects 16-04-00479 and 16-04-00888). Technical and financial support: Chromas and MCT RRCs of SPbSU.

Poster Session 2 – Taxonomy Genetics

89 Is there subspecies structure of the common hamster (*Cricetus cricetus* Linnaeus, 1758) in Russia? Craniometric analysis

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Genetic research on the common hamster has long been of interest and has generated a compelling picture of its evolutionary relationships and possible migration flows. However, despite the fact that most of the species range is located Russia, the works devoted to the subspecies structure are still solitary. Most of the researchers adhere to the traditional notions of 7-10 subspecies inhabiting the territory of Russia, but there has been no substantiated confirmation to this. Recently provided analysis of sequences of an mtDNA control region and cytb gene revealed at least three phylogenetic lineages. Most of the species range (approximately 3 million km^2), including central Russia, Crimea, the Ural region, and northern Kazakhstan), is inhabited by a single, well-supported phylogroup - E0. Phylogroup E1, previously reported from southeastern Poland and western Ukraine, was first found in Russia (Bryansk Province). Hamsters inhabiting Ciscaucasia represent distant phylogenetic lineage, named “Caucasus”. It is a sister to the phylogroup “North” from western Europe. However, the phylogeographical structure of the species may not coincide with the subspecies. The present study was carried out to perform a comparative analysis of the common hamster skulls belonging to the phylogeographical lineages «Caucasus» and E0. We studied 60 museum skulls from 3 Russian collections using 28 parameters. The analysis showed that the craniometric measurements of the Caucasian phylogroup significantly differ from E0 and coincides with the molecular-genetic data. Thus we confirmed that Caucasus inhabited by separate subspecies described by SI Ognev as *Cricetus cricetus stavropolicus*. The E0 phylogroup most likely corresponds to another subspecies of *Cricetus cricetus rufescens*. Here only the preliminary data are presented and the subspecies structure of this species in Russia requires further study. This study was supported by Russian Science Foundation №16-14- 10269 and Presidium of the Russian Academy of Sciences program "Biodiversity of Natural Systems and Biological Resources of Russia"

Poster Session 2 – Taxonomy Genetics

90 *Gerbillus dasyurus* (*Rodentia*: *Gerbillinae*) record from Hatay Province in Turkey

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Wagner's gerbil, *Gerbillus dasyurus*, is distributed in most parts of Sinai, the Arabian Peninsula, and in the Middle East. The species has been recorded from the Kilis Province in south eastern Turkey only. In the present study, 10 specimens from three localities in the Hatay Province were collected. *Gerbillus dasyurus* lives in rocky hills and slopes with poor soil and vegetation on blocky igneous rocks, and also in the rocky lava flow area in the north eastern part of the Hatay Province. The karyotype of the specimens was found to be 2n=60, NF=70, NFa =66. The population density was estimated to be 2.74. The mean of the baculum length is 2.37 mm, and the maximum median width is 0.52 mm (n=3). M1 has three roots, M2 has three, M1 and M2 have two, and M3 and M3 have one root. The tail is markedly longer than the head and body. All peculiarities verify that the samples investigated belong to *Gerbillus dasyurus*. However, the differences seen in the root number of M1, the proportion of the tail, and the shape of baculum etc. imply that a detailed study that covers all distribution area is necessary to show inter- and intrapopulational variations.

Poster Session 2 – Taxonomy Genetics

91 New records of Robertsonian (Rb) variability in Greek house mouse, *Mus musculus domesticus* (*Rodentia*: *Muridae*), populations from S Sterea Ellada

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Many mammalian species are characterized by chromosomal variability, which, occasionally, can even promote speciation events. Specifically, the karyotype of the house mouse, *Mus musculus domesticus*, is well-known for the appearance of Robertsonian (Rb) fusions, which cause non-homologous acrocentric chromosomes to fuse at the centromeric region and to form biarmed (Rb) chromosomes, leading to the reduction of the diploid chromosome number (2n=22-40). This phenomenon is prominent in Europe and in Greece, three distinct Rb systems have been described so far, i.e. in Peloponnese, Epirus and E Sterea Ellada. This work further investigated the recently discovered Rb variability in areas of SW Sterea Ellada and scanned new areas for additional Rb populations of the house mouse. Therefore, a total of 27 house mice were collected from western and eastern areas of S Sterea Ellada, and were karyologically studied, using the G-banding staining technique. Based on our results, even though the acrocentric population occupies most of S Sterea Ellada, surprisingly, a few individuals from SE Sterea Ellada were characterized by 2n=39, possibly heterozygous for Rb(11.14), a new Rb chromosome for Greece. Whether this population is phylogenetically linked to any of the known Rb populations of Greece, remains to be determined. On the other hand, near Messologhi, SW Sterea Ellada, a new Rb race with 2n=34 was found, which, interestingly, is related to the GRP1 Rb race (2n=30) from Patras, NW Peloponnese, i.e. on the opposite side of the Corinthian bay, because they both carry in common Rb(9.16), Rb(13.15) and Rb(11.17)! Incorporating data from previous surveys, the new Rb race forms a contact zone, ca. 15 km wide, with the acrocentric population at least at its eastern border. A hypothesis is presented on how the new Rb race is phylogenetically linked to the Rb system of Peloponnese, and the next research steps are proposed.

Poster Session 2 – Taxonomy Genetics

92 Taxonomic separation of the red-cheeked ground squirrel from South-East Kazakhstan

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At least three species of ground squirrels are known from south-east Kazakhstan. These species are often considered as one wide-range polymorphic species, the red-cheeked ground squirrel *Spermophilus erythrogenys* sensu lato. The distribution area and taxonomic borders of this combined species remain questionable. We used molecular and bioacoustic tools for taxonomic separation of ground squirrels inhabiting the Dzungarian Alatau region of south-east Kazakhstan and adjacent territories. We examined 30 live-trapped individuals from three different populations (10 individuals per population) for acoustic structure of their alarm calls and for nucleotide polymorphism of the mtDNA C-region (1005-1006 bp) and cytb (1140 bp). We also examined DNA of eight museum specimens of *Spermophilus brevicauda*, *Spermophilus intermedius*, *Spermophilus carruthersi* and *Spermophilus iliensis* originating from the species complex distribution area. Additionally, six cytb sequences from Genbank were used (*Spermophilus iliensis* AF157856, AF157857; *Spermophilus relictus* AF157876; *Spermophilus pallidicauda* AF157866, AF157869; *Spermophilus erythrogenys* AF157875). The alarm call variables were similar between the three study populations and distinctive by their maximum fundamental frequencies (8.46±0.75 kHz) from those of *Spermophilus erythrogenys* from the Kurgan region of Russia (5.62±0.06 kHz). The study animals were conservative in the structure of mtDNA (variation in C-region 3%, in cytb - 2.5%). On the phylogenetic tree based on the cytb polymorphism, the ground squirrels from south-east Kazakhstan and adjacent territories divided on three clades with high (98–100%) bootstrap support: 1) *Spermophilus iliensis* (west of species area); 2) *Spermophilus intermedius* (center); 3) *Spermophilus brevicauda* (=*Spermophilus carruthersi*) (south-east). Study populations of *Spermophilus intermedius* probably deserve the species-level taxonomic rank. These data suggest that *Spermophilus erythrogenys* represents a paraphyletic taxon on both genetic (mtDNA) and phenotypic (alarm call) traits. A new taxonomic revision is needed. Supported by the RFBR grant 18-04-00400.